

SUMMARY

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STUDY TITLE

Similarity Assessment of 2mEPSPS Protein to Known Toxins by Bioinformatics Analysis
(Update, March, 2011)

DATA REQUIREMENTS

Not Applicable

AUTHOR(S)

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STUDY COMPLETED ON

26 – May – 2011

PERFORMING LABORATORY

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LABORATORY STUDY ID

110329

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Similarity Assessment of 2mEPSPS Protein to Known Toxins by Bioinformatics Analysis
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SUMMARY

The *2mEPSPS* is a double mutated 5-enolpyruvylshikimate-3-phosphate synthase gene originally derived from maize (*Zea mays* L.). The EPSPS encoded by *2mEPSPS* gene provides tolerance to glyphosate-based herbicides. In this study, the amino acid sequence of the 2mEPSPS protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein sequences (nr) database (updated to March 29, 2011). The majority of the sequence alignments returned by the search were related to various EPSPS enzymes. The remaining alignments were related to unknown hypothetical proteins. The BLASTp search results indicated that the 2mEPSPS protein contains no meaningful sequence similarities with any known proteins that may present toxicity to humans or animals.

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Not Applicable

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Compound: 2mEPSPS

Title: Similarity Assessment of 2mEPSPS Protein to Known Toxins by Bioinformatics Analysis
(Update, March, 2011)

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Title: Regulatory Manager

Signature: _____

Date: 27 April 2011

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Title: Similarity Assessment of 2mEPSPS Protein to Known Toxins by Bioinformatics
Analysis
(Update, March, 2011)

Study Initiation Date: 03/16/2010

This report represents data generated after the effective date of the EPA FIFRA Good Laboratory Practice Standards.

United States Environmental Protection Agency
Title 40 Code of Federal Regulations Part 160
FEDERAL REGISTER, August 17, 1989

Organization for Economic Co-Operation and Development
ENV/MC/CHEM(98)17, Paris January 26, 1998

At the time this study was conducted, it was not subject to the Good Laboratory Practice Standards and was, therefore, not monitored by the quality assurance unit.



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QUALITY ASSURANCE STATEMENT

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NON-GLP STUDY

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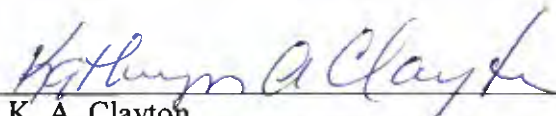
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Analysis
(Update, March, 2011)

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(Principle Investigator)

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Similarity Assessment of 2mEPSPS Protein to Known Toxins by Bioinformatics Analysis
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ABSTRACT

The *2mEPSPS* is a double mutated 5-enolpyruvylshikimate-3-phosphate synthase gene originally derived from maize (*Zea mays* L.). The EPSPS encoded by *2mEPSPS* gene provides tolerance to glyphosate-based herbicides. In this study, the amino acid sequence of the 2mEPSPS protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein sequences (nr) database (updated to March 29, 2011). The majority of the sequence alignments returned by the search were related to various EPSPS enzymes. The remaining alignments were related to unknown hypothetical proteins. The BLASTp search results indicated that the 2mEPSPS protein contains no meaningful sequence similarities with any known proteins that may present toxicity to humans or animals.

INTRODUCTION

The *2mEPSPS* is a double mutated 5-enolpyruvylshikimate-3-phosphate synthase gene originally derived from maize (*Zea mays* L.). The EPSPS encoded by *2mEPSPS* gene provides tolerance to glyphosate-based herbicides. The safety assessment of proteins expressed in transgenic plants may include an evaluation of whether or not the protein can function as a potential toxin when present in the human diet. It has been reported that assessing the potential toxicity of a protein may include comparison of the protein sequence to known protein toxin sequences (Codex Alimentarius, 2003) since there are no commonly recognized definition of a protein as a toxin based on their sequences, protein sequence comparison should be made against all available proteins as a conservative approach. Proteins identified with statistically significant similarity using a local alignment algorithm should then be evaluated for their relevance as potential toxins. For small-scale analyses, such as a single search of a query protein against a large database, a statistically significant similarity that ensures avoidance of false positives (labeling a sequence as related to something in the database when it is not) typically employs an expectation value (E-value) between 0.001 and 0.01. The E-value corresponds to the number of times one would expect to see a match of equal or greater quality by chance (false positive) in a search of the database. For E-values of 0.001 or 0.01, one would expect to find a false positive result once in 1000 or 100 searches, respectively (Pearson, 2000). For $E() = 1$, there is a statistically equal chance of a hit occurring due to homology or by random chance in a search of a given database. Although little can be done to avoid false negatives (labeling a sequence as unrelated to something in the database when in fact a homolog is present), visual inspection of the quality of less conservative alignments with $E() < 1$ may minimize false negative results (Pearson, 2000).

The objective of this study was to compare the amino acid sequence of the 2mEPSPS protein expressed in transgenic events with known protein toxins in the public GenBank non-redundant protein sequence (nr) database (Updated March 29, 2011).

METHODS

Query Sequence Preparation

The 2mEPSPS protein sequence was prepared in FASTA format for use with BLASTp search program (Appendix 1).

Toxicity Assessment

To assess potential toxicity of the 2mEPSPS protein, a search for similarity of protein sequences was conducted using the BLASTp program. Amino acid sequences of 2mEPSPS were queried using the BLASTp (Version 2.2.22+) against the GenBank non-redundant protein sequences (nr) database (updated to March 29, 2011), which incorporates non-redundant entries from all GenBank and RefSeq nucleotide translations (Genpept “nr”) along with protein sequences from SWISS-PROT (<http://www.expasy.org/sprot/>), PIR (<http://pir.georgetown.edu/>), PRF (<http://www.prf.or.jp/aboutdb-e.html>), and PDB (<http://www.wwpdb.org/>). The search was performed using an internal UNIX computer with default settings (Matrix = BLOSUM62, Gap Costs = Existence: 11, Extension: 1, Words =3) except that a cutoff expectation was set to 1, the low complexity filtering was turned off, and the sequence output was set to 5000 alignments. Although a statistically significant sequence similarity generally requires a match with an expectation value less than 0.01, a cutoff of $E() < 1.0$ ensures that proteins with even limited similarity will not be overlooked in the search (Pearson, 2000).

RESULTS AND DISCUSSION

The search of the 2mEPSPS protein sequence against GenBank non-redundant protein sequences returned a total of 3491 hits with 2565 hits with $E() < 0.01$ (Appendix 2). Among the 2565 alignments, 2364 hits were related to the shikimate pathway associated herbicide-tolerant proteins from various plant and bacterial species, and 164 were related to unknown proteins or

hypothetical proteins (Table 1). Among the 2364 shikimate pathway associated herbicide-tolerant proteins, 1864 proteins were related to 3-phosphoshikimate 1-carboxyvinyltransferase enzyme, 141 were related to 5-enolpyruvyl shikimate 3-phosphate synthase (EPSPS) enzyme, 348 proteins were related to UDP-N-acetylglucosamine 1-carboxyvinyltransferase enzyme, and 11 proteins were related to dehydroquinate synthase. The rest of the alignments were not significant, and none of them were associated with known toxins.

CONCLUSION

Bioinformatics analysis of the 2mEPSPS protein using BLASTp search against an up-to-date GenBank non-redundant protein (nr) database did not generate any significant sequence similarity with any known proteins that are harmful to humans or animals.

REFERENCES

Codex Alimentarius, C., 2003. GUIDELINE FOR THE CONDUCT OF FOOD SAFETY ASSESSMENT OF FOODS DERIVED FROM RECOMBINANT-DNA PLANTS Annex 1: Assessment of Possible Allergenicity, pp. 9-11.

Pearson, W.R., 2000. Flexible sequence similarity searching with the FASTA3 program package. *Methods Mol Biol* 132, 185-219.

Table 1 Summary of BLASTp Search Returned Alignments (E<0.01) of 2mEPSPS
Protein Sequence

Protein name	Number of Alignments	Alignment E-value range
3-Phosphoshikimate 1-carboxyvinyltransferase	1864	0 ~ 0.009
5-Enolpyruvyl shikimate 3-phosphate synthase (EPSPS)	141	0 ~ 0.009
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	348	$1.00 \times 10^{-09} \sim 0.009$
Dehydroquinase synthase	11	$1.00 \times 10^{-67} \sim 8.00 \times 10^{-41}$
Hypothetical protein or unnamed protein or unknown protein	164	0 ~ 0.008

APPENDIX

1. 2mEPSPS Amino Acid Sequence

```
1  MAGAEEIVLQ PIKEISGTVK LPGSKSLSNR ILLLAALSEG TTVVDNLLNS
51  EDVHYMLGAL RTLGLSVEAD KAAKRAVVVG CGGKFPVEDA KEEVQLFLGN
101 AGIAMRSLTA AVTAAGGNAT YVLDGVPRMR ERPIGDLVVG LKQLGADVDC
151 FLGTDCPPVR VNGIGGLPGG KVKLSGSISS QYLSALLMAA PLALGDVEIE
201 IIDKLISIPY VEMTLRLMER FGVKAEHSDS WDRFYIKGGQ KYKSPKNAYV
251 EGDASSASYF LAGAAITGGT VTVEGCGTTS LQGDVKFAEV LEMMGAKVTW
301 TETSVTVTGP PREPFGRKHL KAIDVNMNKM PDVAMTLAVV ALFADGPTAI
351 RDVASWRVKE TERMVAIRTE LTKLGASVEE GPDYCIITPP EKLNVT AIDT
401 YDDHRMAMAF SLAACAEVPV TIRDPGCTRK TFPDYFDVLS TFKVN*
```

2. 2mEPSPS Protein Sequence BLASTp Search Output Archive

The output file from BLASTp search of 2mEPSPS protein is 2145 pages. As such, this file is electronically stored in a secured computer in Dow AgroSciences and is available for view in PDF format.

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FASTA search outputs of 2mEPSPS

APPENDIX BLASTp Search Outputs of 2mEPSPS against GenBank Non-redundant Proteins Sequences “nr” (Update to March 29, 2011)

BLASTP 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query=

(445 letters)

Database: /usr/local/blast/db/blastlibs/nr

13,366,630 sequences; 4,577,707,244 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
emb CAA44974.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ze...	899	0.0
ref XP_002436424.1	hypothetical protein SORBIDRAFT_10g002230 [S...	895	0.0
emb CAD01096.1	5-enolpyruvylshikimate-3-phosphate synthase [Ele...	855	0.0
emb CAD01095.1	5-enolpyruvylshikimate-3-phosphate synthase [Ele...	854	0.0
gb AAR87844.1	5-enolpyruvylshikimate-3-phosphate synthase [Eleu...	852	0.0
gb AAR87845.1	5-enolpyruvylshikimate-3-phosphate synthase [Eleu...	848	0.0
gb AAL07437.1	AF413082_1 EPSP synthase [Oryza sativa] >gi 145491...	834	0.0
ref NP_001056712.1	Os06g0133900 [Oryza sativa Japonica Group] >...	834	0.0
gb ACH72672.1	5-enolpyruvylshikimate 3-phosphate synthase [Trit...	827	0.0
gb AAZ79230.2	plastid 5-enolpyruvylshikimate 3-phosphate syntha...	819	0.0
gb ABA54869.1	putative 5-enolpyruvylshikimate 3-phosphate synth...	783	0.0
gb AAT45244.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	782	0.0
gb ABQ00957.1	5-enol-pyruvylshikimate-phosphate synthase 2A [Co...	779	0.0
gb ABQ00961.1	5-enol-pyruvylshikimate-phosphate synthase 3A [Co...	779	0.0
gb EAZ35730.1	hypothetical protein OsJ_20021 [Oryza sativa Japo...	778	0.0
gb ACV53022.1	5-enolpyruvylshikimate-3-phosphate synthase [Amar...	776	0.0
gb AAY40474.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	776	0.0
gb ACV53021.1	5-enolpyruvylshikimate-3-phosphate synthase [Amar...	776	0.0
gb ABQ00962.1	5-enol-pyruvylshikimate-phosphate synthase 3B [Co...	775	0.0
gb ACV67277.1	5-enolpyruvylshikimate-3-phosphate synthase [Amar...	773	0.0
gb ACV67278.1	5-enolpyruvylshikimate-3-phosphate synthase [Amar...	771	0.0
gb AAV64030.1	5-enolpyruvylshikimate 3-phosphate synthase [Camp...	769	0.0
ref XP_002280922.1	PREDICTED: hypothetical protein [Vitis vinif...	766	0.0
gb AAL27697.1	5-enolpyruvylshikimate-3-phosphate synthase [Dicl...	765	0.0
gb AAL27698.1	AF371966_1 5-enolpyruvylshikimate-3-phosphate synt...	763	0.0
gb ABQ00959.1	5-enol-pyruvylshikimate-phosphate synthase 1B [Co...	763	0.0
gb ABQ00960.1	5-enol-pyruvylshikimate-phosphate synthase 1C [Co...	763	0.0
ref NP_182055.1	3-phosphoshikimate 1-carboxyvinyltransferase / ...	763	0.0
gb ABQ00958.1	5-enol-pyruvylshikimate-phosphate synthase 1A [Co...	760	0.0
gb AAT45243.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	759	0.0
emb CAA29828.1	EPSP [Arabidopsis thaliana]	758	0.0
gb AAT45245.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	757	0.0
gb AAY40475.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	755	0.0

gb ABV24481.1	5-enolpyruvylshikimate-3-phosphate synthase [Goss...	755	0.0
gb ABY61050.1	5-enolpyruvylshikimate-3-phosphate synthase [Goss...	754	0.0
gb AAY40473.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	754	0.0
sp P11043.1 AROA_PETHY RecName: Full=3-phosphoshikimate 1-carbox...		753	0.0
gb ADB85251.1	5-enolpyruvyl shikimate 3-phosphate synthase [Zoy...	748	0.0
gb ABE77393.4	EPSP synthase [Allium macrostemon]	746	0.0
gb AAY40472.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	746	0.0
gb ADB85252.1	5-enolpyruvyl shikimate 3-phosphate synthase [Zoy...	743	0.0
gb AAY40476.1	5-enol-pyruvylshikimate-phosphate synthase [Conyz...	743	0.0
ref XP_002511692.1	3-phosphoshikimate 1-carboxyvinyltransferase...	741	0.0
ref XP_002301279.1	3-phosphoshikimate 1-carboxyvinyltransferase...	741	0.0
gb ACB37380.1	5-enolpyruvylshikimate 3-phosphate synthase [Caly...	740	0.0
sp P17688.1 AROA_BRANA RecName: Full=3-phosphoshikimate 1-carbox...		739	0.0
ref XP_002880170.1	3-phosphoshikimate 1-carboxyvinyltransferase...	738	0.0
dbj BAA32276.1	3-phosphoshikimate 1-carboxyvinyltransferase [Or...	738	0.0
gb AAL65913.1	AF440389_1 5-enolpyruvylshikimate-3-phosphate synt...	737	0.0
gb ACD80082.1	5-enolpyruvylshikimate-3-phosphate synthase [Conv...	737	0.0
sp P23981.1 AROA1_TOBAC RecName: Full=3-phosphoshikimate 1-carbo...		736	0.0
ref XP_002894141.1	hypothetical protein ARALYDRAFT_474025 [Arab...	736	0.0
gb ABG88197.1	EPSP synthase [Phaseolus vulgaris]	735	0.0
gb AAS80163.1	5-enolpyruvylshikimate-3-phosphate synthase [Bras...	734	0.0
ref NP_175317.1	3-phosphoshikimate 1-carboxyvinyltransferase, p...	733	0.0
gb AAM63771.1	5-enolpyruvylshikimate-3-phosphate (EPSP) synthas...	731	0.0
sp P10748.1 AROA_SOLLC RecName: Full=3-phosphoshikimate 1-carbox...		730	0.0
ref NP_973996.1	3-phosphoshikimate 1-carboxyvinyltransferase, p...	717	0.0
ref XP_002993040.1	hypothetical protein SELMODRAFT_162776 [Sela...	665	0.0
ref XP_002972123.1	hypothetical protein SELMODRAFT_270937 [Sela...	662	0.0
emb CBI38901.3	unnamed protein product [Vitis vinifera]	659	0.0
gb AAK20397.1	AF349754_1 5-enolpyruvylshikimate 3-phosphate synt...	645	0.0
ref XP_001771376.1	predicted protein [Physcomitrella patens sub...	627	e-178
gb AAT45237.1	5-enol-pyruvylshikimate-phosphate synthase [Erige...	626	e-177
ref XP_001760785.1	predicted protein [Physcomitrella patens sub...	620	e-175
gb AAT45234.1	5-enol-pyruvylshikimate-phosphate synthase [Amara...	613	e-173
gb AAT45236.1	5-enol-pyruvylshikimate-phosphate synthase [Erige...	607	e-171
gb ACY30625.1	EPSP synthase [Ginkgo biloba]	598	e-169
sp P23281.1 AROA2_TOBAC RecName: Full=3-phosphoshikimate 1-carbo...		578	e-163
gb AAN77867.1	5-enolpyruvylshikimate-3-phosphate synthase [Viti...	574	e-162
ref XP_001422572.1	predicted protein [Ostreococcus lucimarinus ...	570	e-160
gb ABM68632.1	plastid EPSP synthase [Dunaliella salina]	555	e-156
ref XP_003059707.1	predicted protein [Micromonas pusilla CCMP15...	553	e-155
ref XP_001702942.1	5-enolpyruvylshikimate-3-phosphate synthase ...	550	e-154
ref XP_002946713.1	hypothetical protein VOLCADRAFT_79287 [Volvo...	548	e-154
gb AAQ75744.1	putative EPSP1 [Oryza sativa Japonica Group]	546	e-153
gb ACL00597.1	5-enolpyruvylshikimate-3-phosphate synthase [Goss...	537	e-150
emb CBN78624.1	3-Phosphoshikimate 1-Carboxyvinyltransferase [Ec...	525	e-147
gb ADI18434.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	523	e-146
gb ABR25383.1	5-enolpyruvylshikimate-3-phosphate synthase [Oryz...	514	e-144
gb ADI17605.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	499	e-139
ref XP_002288542.1	predicted protein [Thalassiosira pseudonana ...	488	e-136
ref XP_002178032.1	3-phosphoshikimate 1-carboxyvinyltransferase...	471	e-131
ref YP_001357866.1	3-phosphoshikimate 1-carboxyvinyltransferase...	454	e-125
ref ZP_04639362.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	454	e-125
ref YP_003041661.1	3-phosphoshikimate 1-carboxyvinyltransferase...	448	e-124
ref ZP_04628535.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	447	e-123
ref ZP_07744902.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	446	e-123
ref ZP_04611277.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	445	e-123
ref ZP_01814130.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	444	e-122
ref NP_902718.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	444	e-122
ref ZP_00991039.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	444	e-122
ref ZP_05888099.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	443	e-122
ref ZP_08104460.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	443	e-122
ref YP_002416694.1	3-phosphoshikimate 1-carboxyvinyltransferase...	443	e-122
ref ZP_04633106.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	442	e-122
ref ZP_01064779.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	441	e-122
ref ZP_04618801.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	441	e-121
ref ZP_05877099.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	441	e-121
ref ZP_02959853.1	hypothetical protein PROSTU_01752 [Providenci...	440	e-121
gb ADT86780.1	3-phosphoshikimate 1-carboxyvinyltransferase [Vib...	440	e-121
ref ZP_01215931.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	439	e-121
ref ZP_01899318.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	439	e-121
ref YP_003613235.1	3-phosphoshikimate 1-carboxyvinyltransferase...	439	e-121

ref YP_003913217.1	3-phosphoshikimate 1-carboxyvinyltransferase...	439	e-121
ref YP_001005833.1	3-phosphoshikimate 1-carboxyvinyltransferase...	439	e-121
gb ADZ43082.1	3-phosphoshikimate 1-carboxyvinyltransferase [Yer...	439	e-121
ref ZP_05945025.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	438	e-121
ref YP_002890011.1	3-phosphoshikimate 1-carboxyvinyltransferase...	438	e-121
ref YP_001176159.1	3-phosphoshikimate 1-carboxyvinyltransferase...	438	e-121
ref YP_003364600.1	3-phosphoshikimate 1-carboxyvinyltransferase...	438	e-121
emb CBY27762.1	5-enolpyruvylshikimate-3-phosphate synthase [Yer...	438	e-121
ref ZP_03699489.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	438	e-121
ref YP_001674263.1	3-phosphoshikimate 1-carboxyvinyltransferase...	437	e-120
ref NP_797399.1	3-phosphoshikimate 1-carboxyvinyltransferase [V...	437	e-120
ref YP_004188221.1	5-Enolpyruvylshikimate-3-phosphate synthase ...	437	e-120
ref YP_001501926.1	3-phosphoshikimate 1-carboxyvinyltransferase...	437	e-120
ref ZP_06038940.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	437	e-120
ref YP_001438518.1	3-phosphoshikimate 1-carboxyvinyltransferase...	436	e-120
ref ZP_05926140.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	435	e-120
ref YP_003209877.1	3-phosphoshikimate 1-carboxyvinyltransferase...	435	e-120
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ref NP_935111.1	3-phosphoshikimate 1-carboxyvinyltransferase [V...	435	e-120
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ref YP_004212257.1	3-phosphoshikimate 1-carboxyvinyltransferase...	435	e-120
ref YP_942554.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	435	e-120
ref ZP_01220232.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	434	e-120
ref YP_269053.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	434	e-119
ref YP_130637.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	434	e-119
ref ZP_06189463.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	434	e-119
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ref ZP_04404584.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	434	e-119
ref ZP_08099331.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	434	e-119
ref ZP_02903635.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	434	e-119
pdb 3NV5 A Chain A, 1.02 Angstrom Resolution Crystal Structure O...		434	e-119
ref YP_001334602.1	3-phosphoshikimate 1-carboxyvinyltransferase...	434	e-119
ref ZP_06033632.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	433	e-119
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ref ZP_04418631.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	433	e-119
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emb CBK85480.1	3-phosphoshikimate 1-carboxyvinyltransferase [En...	433	e-119
ref NP_928909.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	433	e-119
ref ZP_04960288.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	433	e-119
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ref ZP_04918492.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	433	e-119
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ref YP_539995.1	3-phosphoshikimate 1-carboxyvinyltransferase [E...	432	e-119
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ref ZP_06941240.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	432	e-119
gb EGB62579.1	EPSP synthase [Escherichia coli M863] >gi 3239767...	432	e-119
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ref NP_706826.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	431	e-118
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emb CBG33822.1	3-phosphoshikimate 1-carboxyvinyltransferase [Es...	422	e-116
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ref YP_003930386.1	5-enolpyruvylshikimate-3-phosphate synthetas...	410	e-112
ref YP_002910765.1	Prephenate dehydrogenase/3-phosphoshikimate ...	410	e-112
ref ZP_03317918.1	hypothetical protein PROVALCAL_00838 [Provide...	410	e-112
ref YP_772814.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	410	e-112
ref YP_442173.2	bifunctional prephenate dehydrogenase/3-phospho...	410	e-112
gb ABC39479.1	prephenate dehydrogenase/3-phosphoshikimate 1-car...	410	e-112
ref YP_003007701.1	3-phosphoshikimate 1-carboxyvinyltransferase...	409	e-112
ref NP_245776.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	409	e-112
ref YP_001807632.1	3-phosphoshikimate 1-carboxyvinyltransferase...	409	e-112
ref YP_003605803.1	3-phosphoshikimate 1-carboxyvinyltransferase...	409	e-112
ref ZP_01788712.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	409	e-112
ref ZP_02478328.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	409	e-112
ref YP_454671.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	409	e-112
ref ZP_07336590.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	408	e-112
ref ZP_02373925.1	bifunctional prephenate dehydrogenase/3-phosp...	408	e-112
ref YP_003048947.1	3-phosphoshikimate 1-carboxyvinyltransferase...	408	e-112

ref YP_545038.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	408	e-112
ref ZP_03825646.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	408	e-112
ref YP_001580441.1	3-phosphoshikimate 1-carboxyvinyltransferase...	408	e-112
ref ZP_03574299.1	prephenate dehydrogenase/3-phosphoshikimate 1...	408	e-112
ref ZP_02356546.1	bifunctional prephenate dehydrogenase/3-phosp...	408	e-112
gb ABY53228.1	3-phosphoshikimate 1-carboxyvinyltransferase [Hae...	408	e-111
ref ZP_07538500.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	407	e-111
ref ZP_00134045.2	COG0128: 5-enolpyruvylshikimate-3-phosphate s...	407	e-111
ref ZP_01791397.1	outer-membrane lipoprotein carrier protein pr...	407	e-111
ref YP_001651710.1	3-phosphoshikimate 1-carboxyvinyltransferase...	407	e-111
gb AAA24943.1	enolpyruvylshikimatephosphatesynthase [Haemophilu...	407	e-111
ref ZP_02363666.1	bifunctional prephenate dehydrogenase/3-phosp...	406	e-111
ref YP_004229109.1	3-phosphoshikimate 1-carboxyvinyltransferase...	406	e-111
ref ZP_01783517.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	406	e-111
ref ZP_04465725.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	406	e-111
ref ZP_07542841.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	406	e-111
sp A4G861.2	ARO_A_HERAR RecName: Full=3-phosphoshikimate 1-carbox...	405	e-111
ref ZP_01873490.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	405	e-111
ref YP_001896621.1	3-phosphoshikimate 1-carboxyvinyltransferase...	405	e-111
ref ZP_04978293.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	405	e-111
ref ZP_05991014.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	405	e-111
sp P52310.1	ARO_A_HAESO RecName: Full=3-phosphoshikimate 1-carbox...	405	e-111
gb ADZ27779.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nit...	405	e-111
ref ZP_02467913.1	bifunctional prephenate dehydrogenase/3-phosp...	405	e-111
emb CBA28839.1	3-phosphoshikimate 1-carboxyvinyltransferase [Cu...	405	e-111
ref YP_314712.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	405	e-111
ref YP_560019.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	404	e-110
ref ZP_001293174.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	404	e-110
ref ZP_05849995.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	404	e-110
ref NP_841981.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	404	e-110
ref YP_088767.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	404	e-110
ref ZP_08067507.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	404	e-110
ref YP_248938.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	404	e-110
ref YP_001354360.1	3-phosphoshikimate 1-carboxyvinyltransferase...	404	e-110
ref ZP_05989016.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	404	e-110
ref YP_001293174.1	3-phosphoshikimate 1-carboxyvinyltransferase...	403	e-110
ref YP_003907846.1	3-phosphoshikimate 1-carboxyvinyltransferase...	402	e-110
ref ZP_06842784.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	402	e-110
ref ZP_07889958.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	402	e-110
ref YP_003466751.1	5-enolpyruvylshikimate-5-phosphate synthetas...	401	e-110
ref ZP_04467199.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	401	e-109
ref YP_004138971.1	3-phosphoshikimate 1-carboxyvinyltransferase...	401	e-109
ref YP_001100819.1	3-phosphoshikimate 1-carboxyvinyltransferase...	400	e-109
ref NP_439734.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	400	e-109
dbj BAE20404.1	5-enolpyruvylshikimate-3-phosphate synthase [Lac...	400	e-109
ref ZP_08148670.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	400	e-109
ref YP_001344227.1	3-phosphoshikimate 1-carboxyvinyltransferase...	400	e-109
ref ZP_06573944.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	399	e-109
ref ZP_02412430.1	bifunctional prephenate dehydrogenase/3-phosp...	399	e-109
ref ZP_05920862.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	399	e-109
ref YP_003846937.1	3-phosphoshikimate 1-carboxyvinyltransferase...	399	e-109
ref YP_277892.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	398	e-109
ref YP_548624.1	bifunctional 3-phosphoshikimate 1-carboxyvinylt...	398	e-109
ref YP_004039563.1	3-phosphoshikimate 1-carboxyvinyltransferase...	397	e-108
gb AAX45943.1	5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	397	e-108
ref YP_003050881.1	3-phosphoshikimate 1-carboxyvinyltransferase...	397	e-108
emb CAA78480.1	aroA [Pasteurella multocida]	395	e-108
ref YP_002794869.1	AroA [Laribacter hongkongensis HLHK9] >gi 25...	394	e-107
emb CBW15902.1	5-enolpyruvylshikimate-3-phosphate synthetase [H...	393	e-107
ref YP_412757.2	3-phosphoshikimate 1-carboxyvinyltransferase [N...	393	e-107
ref YP_001565737.1	bifunctional 3-phosphoshikimate 1-carboxyvin...	393	e-107
ref ZP_06634730.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	393	e-107
ref ZP_02884875.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	393	e-107
ref YP_983018.1	bifunctional 3-phosphoshikimate 1-carboxyvinylt...	392	e-107
ref YP_001798044.1	3-phosphoshikimate 1-carboxyvinyltransferase...	392	e-107
gb AAX45945.1	5-enolpyruvylshikimate 3-phosphatesynthase [Biber...	392	e-107
ref YP_003256375.1	3-phosphoshikimate 1-carboxyvinyltransferase...	391	e-106
gb AAX45947.1	5-enolpyruvylshikimate 3-phosphatesynthase [Biber...	390	e-106
gb AAX45944.1	5-enolpyruvylshikimate 3-phosphatesynthase [Biber...	390	e-106
ref YP_986705.1	bifunctional 3-phosphoshikimate 1-carboxyvinylt...	389	e-106
ref YP_004126485.1	3-phosphoshikimate 1-carboxyvinyltransferase...	389	e-106

ref YP_003168109.1 bifunctional 3-phosphoshikimate 1-carboxyvin...	389	e-106
ref NP_777908.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	389	e-106
gb AAK45946.1 5-enolpyruvylshikimate 3-phosphatesynthase [Biber...	387	e-105
gb AAV31127.1 5-enolpyruvylshikimate-3-phosphate synthetase [Ye...	387	e-105
gb AAK45928.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	386	e-105
ref YP_746641.1 3-phosphoshikimate 1-carboxyvinyltransferase [N...	386	e-105
ref YP_003977767.1 3-phosphoshikimate 1-carboxyvinyltransferase...	386	e-105
gb AAK45938.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	386	e-105
ref YP_002552856.1 bifunctional 3-phosphoshikimate 1-carboxyvin...	386	e-105
gb ABB75365.1 3-phosphoshikimate 1-carboxyvinyltransferase [Nit...	385	e-105
gb ADX45885.1 3-phosphoshikimate 1-carboxyvinyltransferase [Aci...	385	e-105
ref YP_802756.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	385	e-105
gb AAK45933.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	385	e-105
ref ZP_04762539.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	385	e-105
gb AAK45930.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	385	e-105
gb AAK45941.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	385	e-105
gb AAK45929.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	385	e-104
gb AAK45936.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	384	e-104
gb AAT45241.1 5-enol-pyruvylshikimate-phosphate synthase [Nymph...	384	e-104
ref NP_660644.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	384	e-104
gb AAK45940.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	384	e-104
gb AAK45942.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	383	e-104
gb AAK45939.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	383	e-104
ref YP_971618.1 bifunctional 3-phosphoshikimate 1-carboxyvinylt...	383	e-104
gb AAK45931.1 5-enolpyruvylshikimate 3-phosphatesynthase [Mannh...	382	e-104
ref ZP_07045860.1 bifunctional 3-phosphoshikimate 1-carboxyvin...	382	e-104
ref YP_003277469.1 3-phosphoshikimate 1-carboxyvinyltransferase...	382	e-104
ref ZP_05909047.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	382	e-104
ref NP_760987.1 3-phosphoshikimate 1-carboxyvinyltransferase [V...	382	e-104
ref ZP_03719717.1 hypothetical protein NEIFLAOT_01566 [Neisseri...	382	e-104
ref ZP_03544339.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	382	e-104
gb EGB11856.1 hypothetical protein AURANDRAFT_19755 [Aureococcu...	381	e-103
ref ZP_04758091.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	381	e-103
ref NP_878673.1 3-phosphoshikimate 1-carboxyvinyltransferase [C...	380	e-103
ref NP_873807.1 3-phosphoshikimate 1-carboxyvinyltransferase [H...	380	e-103
gb EFV83522.1 3-phosphoshikimate 1-carboxyvinyltransferase [Ach...	379	e-103
gb AAA21529.1 5-enolpyruvylshikimate 3-phosphate synthase [Mann...	378	e-103
ref YP_001155282.1 3-phosphoshikimate 1-carboxyvinyltransferase...	376	e-102
ref YP_588703.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	376	e-102
gb AAF01290.1 AF182427_3 5-enolpyruvylshikimate-3-phosphate synt...	371	e-100
ref YP_003844455.1 3-phosphoshikimate 1-carboxyvinyltransferase...	371	e-100
ref ZP_07342849.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	371	e-100
ref NP_879749.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	371	e-100
ref NP_885305.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	371	e-100
ref YP_002923575.1 3-enolpyruvylshikimate-5-phosphate synthetas...	370	e-100
sp Q03321.4 AROA_AERSA RecName: Full=3-phosphoshikimate 1-carbox...	370	e-100
ref NP_890002.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	370	e-100
ref YP_785874.1 3-phosphoshikimate 1-carboxyvinyltransferase [B...	369	e-100
gb AAA22968.1 5-enolpyruvylshikimate-3-phosphate synthase (EC 2...	369	e-100
ref YP_522830.1 bifunctional 3-phosphoshikimate 1-carboxyvinylt...	369	e-100
emb CAX49833.1 3-phosphoshikimate 1-carboxyvinyltransferase (5-...	368	e-99
ref ZP_06980072.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	368	1e-99
gb ADO31856.1 3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	367	1e-99
ref YP_003083433.1 3-phosphoshikimate 1-carboxyvinyltransferase...	367	1e-99
ref ZP_03084951.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	367	2e-99
ref YP_004048828.1 5-enolpyruvylshikimate-3-phosphate synthase...	367	2e-99
gb ADZ03829.1 3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	367	2e-99
ref NP_274444.1 3-phosphoshikimate 1-carboxyvinyltransferase [N...	367	3e-99
ref ZP_06393938.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	366	3e-99
gb EGC67044.1 3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	366	4e-99
gb EGC51388.1 3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	366	5e-99
ref ZP_04727277.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	365	8e-99
ref YP_975365.1 3-phosphoshikimate 1-carboxyvinyltransferase [N...	365	8e-99
emb CBA05487.1 3-phosphoshikimate 1-carboxyvinyltransferase [Ne...	365	1e-98
emb CBX21677.1 unnamed protein product [Neisseria lactamica Y92...	364	1e-98
emb CBA07392.1 3-phosphoshikimate 1-carboxyvinyltransferase [Ne...	364	2e-98
ref YP_002943532.1 bifunctional 3-phosphoshikimate 1-carboxyvin...	363	2e-98
ref ZP_04718785.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	363	3e-98
ref ZP_06643322.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	363	3e-98
ref ZP_04738523.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	363	3e-98
ref ZP_04725392.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	363	4e-98

ref ZP_04729600.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	363	4e-98
ref ZP_08133171.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	363	4e-98
ref ZP_04740753.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	363	4e-98
ref YP_004154098.1	3-phosphoshikimate 1-carboxyvinyltransferase...	362	4e-98
ref YP_002001528.1	3-phosphoshikimate 1-carboxyvinyltransferase...	362	6e-98
gb ADY99871.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	361	1e-97
ref YP_208010.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	361	1e-97
ref ZP_07369427.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	361	1e-97
gb EGC53282.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	361	1e-97
ref YP_003249697.1	3-phosphoshikimate 1-carboxyvinyltransferase...	361	2e-97
ref YP_003643565.1	3-phosphoshikimate 1-carboxyvinyltransferase...	360	2e-97
emb CBY91058.1	3-phosphoshikimate 1-carboxyvinyltransferase (5-...	360	2e-97
gb EGC59129.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	360	3e-97
ref YP_002342947.1	3-phosphoshikimate 1-carboxyvinyltransferase...	360	3e-97
gb EGC65034.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	360	3e-97
ref YP_004124452.1	3-phosphoshikimate 1-carboxyvinyltransferase...	359	4e-97
gb EGC57232.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nei...	359	5e-97
ref ZP_06686582.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	358	1e-96
ref YP_002474989.1	3-phosphoshikimate 1-carboxyvinyltransferase...	358	1e-96
ref ZP_002753565.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	357	2e-96
ref ZP_01786780.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	357	2e-96
ref ZP_06735729.1	hypothetical protein NEIELOOT_02577 [Neisseri...	355	7e-96
ref YP_997872.1	bifunctional 3-phosphoshikimate 1-carboxyvinylt...	355	1e-95
ref YP_002521490.1	3-phosphoshikimate 1-carboxyvinyltransferase...	355	1e-95
ref ZP_01042651.1	5-enolpyruvylshikimate-3-phosphate synthase [...	354	2e-95
emb CAZ88944.1	3-phosphoshikimate 1-carboxyvinyltransferase:Cyt...	353	4e-95
ref YP_003319237.1	3-phosphoshikimate 1-carboxyvinyltransferase...	352	8e-95
ref ZP_04600796.1	hypothetical protein GCWU000324_00250 [Kingel...	350	3e-94
ref ZP_01552046.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	349	5e-94
ref YP_155746.1	5-enolpyruvylshikimate-3-phosphate synthase [Id...	347	2e-93
ref YP_004269980.1	3-phosphoshikimate 1-carboxyvinyltransferase...	347	3e-93
ref YP_001790000.1	bifunctional 3-phosphoshikimate 1-carboxyvin...	343	4e-92
ref YP_001021434.1	bifunctional 3-phosphoshikimate 1-carboxyvin...	342	6e-92
ref YP_001630496.1	3-phosphoshikimate 1-carboxyvinyltransferase...	339	4e-91
ref ZP_06390344.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	339	6e-91
emb CAJ75373.1	strongly similar to 3-phosphoshikimate 1-carboxy...	335	6e-90
ref ZP_03832181.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	330	2e-88
ref ZP_01852123.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	330	3e-88
ref YP_004177275.1	3-phosphoshikimate 1-carboxyvinyltransferase...	329	5e-88
ref YP_003629142.1	3-phosphoshikimate 1-carboxyvinyltransferase...	328	9e-88
ref YP_001599470.1	3-phosphoshikimate 1-carboxyvinyltransferase...	327	2e-87
ref ZP_06158732.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	326	5e-87
ref ZP_05317708.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	325	6e-87
ref YP_003603071.1	3-phosphoshikimate 1-carboxyvinyltransferase...	325	8e-87
ref YP_322772.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	325	1e-86
ref YP_003704460.1	3-phosphoshikimate 1-carboxyvinyltransferase...	322	5e-86
ref ZP_08079252.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	320	3e-85
ref NP_489059.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	317	2e-84
gb AAV52048.1	AroA [Actinobacillus ureae ATCC 25976]	317	2e-84
ref ZP_06157994.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	317	3e-84
ref ZP_01093993.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	317	3e-84
ref YP_001864974.1	3-phosphoshikimate 1-carboxyvinyltransferase...	315	7e-84
ref XP_002505432.1	predicted protein [Micromonas sp. RCC299] >g...	311	1e-82
ref YP_003370952.1	3-phosphoshikimate 1-carboxyvinyltransferase...	310	3e-82
ref ZP_05716512.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	309	7e-82
gb AAV52046.1	AroA [Haemophilus parasuis]	307	2e-81
emb CBY95002.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sa...	303	3e-80
emb CAA10164.1	5-enolpyruvylshikimate 3-phosphate synthase [Act...	300	3e-79
ref ZP_02737777.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	297	2e-78
ref XP_001746575.1	hypothetical protein [Monosiga brevicollis M...	295	8e-78
ref NP_630891.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	294	2e-77
ref ZP_07198687.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	294	2e-77
gb EFW98669.1	dehydroquinase class 1 [Grosmanella clavigera kw1407]	293	3e-77
gb AAL65914.1	AF440390_1 5-enolpyruvylshikimate-3-phosphate synt...	291	1e-76
ref YP_004193764.1	3-phosphoshikimate 1-carboxyvinyltransferase...	290	3e-76
ref XP_003007290.1	pentafunctional AROM polypeptide [Verticilli...	289	7e-76
gb ABA54838.1	3-phosphoshikimate 1-carboxyvinyltransferase [Nos...	288	2e-75
ref ZP_05082175.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	287	3e-75
ref XP_956000.1	pentafunctional AROM polypeptide [Neurospora cr...	286	4e-75
ref NP_864842.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	286	6e-75
ref XP_002896252.1	pentafunctional AROM polypeptide, putative [...	284	2e-74

ref ZP_05881560.1	5-Enolpyruvylshikimate-3-phosphate synthase [...]	281	1e-73
ref ZP_01287548.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	281	2e-73
emb CBI53120.1	unnamed protein product [Sordaria macrospora]	280	4e-73
ref YP_001529830.1	3-phosphoshikimate 1-carboxyvinyltransferase...	279	5e-73
ref YP_002430927.1	3-phosphoshikimate 1-carboxyvinyltransferase...	279	6e-73
emb CCA26166.1	unnamed protein product [Albugo laibachii Nc14]	279	7e-73
gb EFW44924.1	pentafunctional AROM polypeptide [Capsaspora owcz...	278	9e-73
ref NP_986731.2	AGR066Wp [Ashbya gossypii ATCC 10895] >gi 29978...	277	2e-72
ref XP_003048265.1	predicted protein [Nectria haematococca mpVI...	277	2e-72
ref XP_001910024.1	hypothetical protein [Podospira anserina S m...	277	2e-72
ref YP_001613674.1	3-phosphoshikimate 1-carboxyvinyltransferase...	277	3e-72
ref ZP_03493643.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	276	5e-72
gb EFQ95851.1	hypothetical protein PTT_04545 [Pyrenophora teres...	275	8e-72
gb AAV52047.1	AroA [Actinobacillus equuli]	275	9e-72
dbj BAH89270.1	putative 5-enolpyruvylshikimate 3-phosphite synth...	275	1e-71
gb AAA21937.1	3-phosphoshikimate-1-carboxyvinyltransferase [Aer...	275	1e-71
ref YP_003184077.1	3-phosphoshikimate 1-carboxyvinyltransferase...	275	1e-71
ref YP_002603512.1	3-phosphoshikimate 1-carboxyvinyltransferase...	275	1e-71
ref XP_002545280.1	pentafunctional polypeptide AROM [Candida tr...	274	2e-71
gb EDK39572.2	hypothetical protein PGUG_03670 [Pichia guillierm...	273	3e-71
ref XP_001484289.1	hypothetical protein PGUG_03670 [Meyerozyma ...]	273	4e-71
ref XP_002492733.1	Pentafunctional arom protein [Pichia pastori...	273	5e-71
gb AAW33954.1	AROM pentafunctional enzyme [Pichia pastoris]	273	6e-71
ref ZP_06935856.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	272	6e-71
ref ZP_05060087.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	272	6e-71
ref XP_002419765.1	pentafunctional AROM polypeptide, putative [...]	272	7e-71
ref XP_505337.1	YALIOF12639p [Yarrowia lipolytica] >gi 49651207...	272	9e-71
gb EFQ33466.1	3-phosphoshikimate 1-carboxyvinyltransferase [Glo...	271	1e-70
ref XP_002615931.1	hypothetical protein CLUG_04813 [Clavispora ...]	271	1e-70
ref XP_384463.1	hypothetical protein FG04287.1 [Gibberella zeae...	271	1e-70
ref XP_368116.2	hypothetical protein MGG_01128 [Magnaporthe ory...	271	2e-70
ref YP_066747.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	270	2e-70
ref XP_001528832.1	pentafunctional AROM polypeptide [Lodderomyc...	270	3e-70
ref YP_644215.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	270	3e-70
ref XP_001792082.1	hypothetical protein SNOG_01444 [Phaeosphaer...	270	3e-70
gb EFY99234.1	pentafunctional AROM polypeptide [Metarhizium ani...	270	3e-70
sp Q12659.1	ARO1_PNECA RecName: Full=Pentafunctional AROM polype...	270	4e-70
ref XP_001528849.1	pentafunctional AROM polypeptide [Lodderomyc...	270	4e-70
gb ABB04469.1	5-enolpyruvylshikimate 3-phosphate synthase [Yers...	270	5e-70
ref ZP_03367581.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	269	7e-70
ref XP_001384008.2	hypothetical protein PICST_89141 [Schefferso...	268	8e-70
ref YP_003689344.1	3-phosphoshikimate 1-carboxyvinyltransferase...	268	1e-69
ref XP_003169854.1	pentafunctional AROM polypeptide [Arthroderm...	268	1e-69
ref XP_001228231.1	hypothetical protein CHGG_10304 [Chaetomium ...]	268	1e-69
ref XP_002790866.1	pentafunctional AROM polypeptide [Paracoccid...	268	1e-69
ref YP_461861.1	3-phosphoshikimate-1-carboxyvinyltransferase [S...	268	2e-69
ref XP_002496718.1	ZYRO0D06578p [Zygosaccharomyces rouxii] >gi ...	266	3e-69
ref XP_002836591.1	hypothetical protein [Tuber melanosporum Mel...	266	3e-69
ref XP_003016933.1	repressor protein [Arthroderma benhamiae CBS...	266	5e-69
ref XP_449840.1	hypothetical protein [Candida glabrata CBS 138]...	266	5e-69
gb EFY84835.1	pentafunctional AROM polypeptide [Metarhizium acr...	266	5e-69
emb CBX30069.1	3-phosphoshikimate 1-carboxyvinyltransferase 1 [...]	266	6e-69
ref YP_174720.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	265	1e-68
ref XP_002153704.1	pentafunctional polypeptide (AroM), putative...	265	1e-68
ref XP_001243950.1	hypothetical protein CIMG_03391 [Coccidioides...	265	1e-68
ref XP_002847108.1	pentafunctional AROM polypeptide [Arthroderm...	264	2e-68
ref XP_003023519.1	repressor protein [Trichophyton verrucosum H...	264	2e-68
ref XP_001585666.1	hypothetical protein SS1G_13550 [Sclerotinia...	264	3e-68
ref XP_002478440.1	pentafunctional polypeptide (AroM), putative...	263	3e-68
ref ZP_06885153.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	263	5e-68
gb EFW96244.1	Pentafunctional arom protein [Pichia angusta DL-1]	262	7e-68
ref XP_001539094.1	3-dehydroquinate synthase [Ajellomyces capsu...	261	1e-67
ref ZP_03754397.1	hypothetical protein ROSEINA2194_02822 [Roseb...	261	1e-67
ref XP_003068793.1	3-dehydroquinate synthase, putative [Coccidi...	261	1e-67
gb EFW20721.1	3-dehydroquinate synthase [Coccidioides posadasii...	261	1e-67
emb CBY01360.1	similar to pentafunctional polypeptide AROM [Lep...	261	2e-67
ref XP_002555600.1	KLTH0G13090p [Lachancea thermotolerans] >gi ...	261	2e-67
ref XP_722769.1	hypothetical protein CaO19.4704 [Candida albica...	260	3e-67
ref XP_002146148.1	3-dehydroquinate synthase, putative [Penicil...	260	3e-67
ref XP_722916.1	hypothetical protein CaO19.12175 [Candida albic...	260	3e-67
ref NP_010412.1	AroIp [Saccharomyces cerevisiae S288c] >gi 1141...	259	4e-67

gb AAN70992.1 AF482690_1 arom polypeptide [Thanatephorus cucumeris]	259	4e-67
gb EGA63035.1 Aro1p [Saccharomyces cerevisiae FostersO]	259	5e-67
gb EGA59386.1 Aro1p [Saccharomyces cerevisiae FostersB]	259	6e-67
gb EDN60469.1 3-dehydroquinase dehydratase (3-dehydroquinase) [...]	259	6e-67
gb EGA83528.1 Aro1p [Saccharomyces cerevisiae Lalvin QA23]	259	6e-67
ref NP_594681.1 pentafunctional aromatic polypeptide Aro1 (pred...	259	6e-67
gb AAU95677.1 arom [Sclerotinia sclerotiorum]	259	7e-67
emb CAY78632.1 Aro1p [Saccharomyces cerevisiae EC1118]	259	7e-67
gb EDV08178.1 3-dehydroquinase dehydratase [Saccharomyces cerev...	259	8e-67
ref XP_002582444.1 pentafunctional AROM polypeptide [Uncinocarp...	259	8e-67
gb EGA75607.1 Aro1p [Saccharomyces cerevisiae AWRI796]	259	8e-67
gb EEH44586.1 pentafunctional AROM polypeptide [Paracoccidioides...]	258	9e-67
ref XP_002561515.1 Pcl6g12160 [Penicillium chrysogenum Wisconsi...]	258	1e-66
gb EEH20188.1 pentafunctional AROM polypeptide [Paracoccidioides...]	258	1e-66
gb EEU09331.1 Aro1p [Saccharomyces cerevisiae JAY291]	258	1e-66
ref YP_003709660.1 3-phosphoshikimate 1-carboxyvinyltransferase...	258	1e-66
ref YP_003878008.1 3-phosphoshikimate 1-carboxyvinyltransferase...	258	2e-66
ref YP_001818996.1 3-phosphoshikimate 1-carboxyvinyltransferase...	258	2e-66
sp P07547.3 ARO1_EMENI RecName: Full=Pentafunctional AROM polype...	257	3e-66
ref ZP_04452905.1 hypothetical protein GCWU000182_02215 [Abiotr...	257	3e-66
ref ZP_03714227.1 hypothetical protein EIKCOROL_01924 [Eikenell...	256	5e-66
gb AAV64002.1 AroA [Actinobacillus suis ATCC 33415]	256	5e-66
ref ZP_05791383.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	255	8e-66
ref YP_846833.1 3-phosphoshikimate 1-carboxyvinyltransferase [S...	255	9e-66
ref XP_001728822.1 hypothetical protein MGL_3989 [Malassezia gl...	255	9e-66
emb CBK80210.1 3-phosphoshikimate 1-carboxyvinyltransferase [Co...	255	1e-65
ref XP_003026716.1 hypothetical protein SCHCODRAFT_83545 [Schiz...	255	1e-65
ref XP_003192257.1 aromatic amino acid family biosynthesis-rela...	255	1e-65
ref XP_569127.1 aromatic amino acid family biosynthesis-related...	255	1e-65
gb EEH08604.1 pentafunctional AROM polypeptide [Ajellomyces cap...	254	2e-65
ref XP_002375788.1 pentafunctional polypeptide (AroM), putative...	253	3e-65
dbj BAE60669.1 unnamed protein product [Aspergillus oryzae]	253	3e-65
ref XP_001931677.1 pentafunctional AROM polypeptide [Pyrenophor...	253	3e-65
ref XP_455965.1 hypothetical protein [Kluyveromyces lactis NRRL...	253	4e-65
ref ZP_04624288.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	253	4e-65
ref ZP_06933986.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	253	4e-65
ref YP_003769882.1 3-phosphoshikimate 1-carboxyvinyltransferase...	252	7e-65
ref XP_001268882.1 pentafunctional polypeptide (AroM), putative...	252	8e-65
ref YP_001047210.1 3-phosphoshikimate 1-carboxyvinyltransferase...	252	9e-65
gb EER42257.1 pentafunctional AROM polypeptide [Ajellomyces cap...	251	2e-64
gb EEQ84223.1 3-dehydroquinase synthase [Ajellomyces dermatitid...	251	2e-64
ref XP_002626822.1 3-dehydroquinase synthase [Ajellomyces derma...	251	2e-64
gb EGC43649.1 3-dehydroquinase synthase [Ajellomyces capsulatus...	249	8e-64
ref YP_001122070.1 3-phosphoshikimate 1-carboxyvinyltransferase...	248	1e-63
emb CAD29607.2 pentafunctional arom polypeptide [includes: 3-de...	248	1e-63
ref XP_001879572.1 predicted protein [Laccaria bicolor S238N-H8...	248	1e-63
ref XP_752744.1 pentafunctional polypeptide (AroM) [Aspergillus...	248	1e-63
gb EDP56612.1 pentafunctional polypeptide (AroM), putative [Asp...	248	1e-63
ref XP_001264384.1 pentafunctional polypeptide (AroM), putative...	248	1e-63
ref YP_001538010.1 3-phosphoshikimate 1-carboxyvinyltransferase...	248	2e-63
ref ZP_04989980.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	247	3e-63
ref ZP_03727185.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	246	5e-63
ref YP_169611.1 3-phosphoshikimate 1-carboxyvinyltransferase [F...	246	7e-63
ref YP_002929840.1 3-phosphoshikimate 1-carboxyvinyltransferase...	245	1e-62
ref YP_898731.1 3-phosphoshikimate 1-carboxyvinyltransferase [F...	245	1e-62
ref ZP_06048035.1 5-Enolpyruvylshikimate-3-phosphate synthase [...]	245	1e-62
gb ABK26355.1 unknown [Picea sitchensis]	243	4e-62
ref ZP_03247089.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	243	4e-62
ref YP_502500.1 3-phosphoshikimate 1-carboxyvinyltransferase [M...	243	5e-62
ref YP_001891424.1 3-phosphoshikimate 1-carboxyvinyltransferase...	242	7e-62
ref ZP_04988536.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	242	1e-61
ref YP_001159802.1 3-phosphoshikimate 1-carboxyvinyltransferase...	242	1e-61
ref ZP_02026168.1 hypothetical protein EUBVEN_01424 [Eubacteriu...	241	1e-61
ref ZP_04985218.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	241	1e-61
ref YP_001678243.1 3-phosphoshikimate 1-carboxyvinyltransferase...	241	2e-61
emb CBQ73986.1 probable ARO1-Pentafunctional AROM polypeptide [...]	241	2e-61
ref XP_002171624.1 pentafunctional AROM polypeptide [Schizosacc...	240	2e-61
ref ZP_04755889.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	240	3e-61
ref YP_513574.1 3-phosphoshikimate 1-carboxyvinyltransferase [F...	239	4e-61
ref YP_389974.1 3-phosphoshikimate 1-carboxyvinyltransferase [D...	238	1e-60
emb CAA28836.1 arom polypeptide [Emericella nidulans]	238	1e-60

ref YP_002992653.1	3-phosphoshikimate 1-carboxyvinyltransferase...	238	1e-60
gb ADQ43380.1	putative EPSP synthase [Streptomyces cinamonensis]	238	2e-60
ref ZP_04696613.1	putative 5-enolpyruvylshikimate-3-phosphate s...	237	3e-60
ref XP_759754.1	hypothetical protein UM03607.1 [Ustilago maydis...	236	5e-60
ref ZP_01292020.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	236	7e-60
ref NP_243579.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	235	1e-59
ref YP_003895882.1	3-phosphoshikimate 1-carboxyvinyltransferase...	233	3e-59
gb ADI21744.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	233	5e-59
ref ZP_03462611.1	hypothetical protein BACPEC_01696 [Bacteroides...	233	5e-59
ref YP_002467599.1	3-phosphoshikimate 1-carboxyvinyltransferase...	230	3e-58
ref YP_002548675.1	3-phosphoshikimate 1-carboxyvinyltransferase...	229	5e-58
gb EFP87557.1	pentafunctional AROM polypeptide [Puccinia gramin...	229	5e-58
ref YP_001823336.1	putative 5-enolpyruvylshikimate-3-phosphate ...	225	1e-56
ref YP_002543594.1	3-phosphoshikimate 1-carboxyvinyltransferase...	225	1e-56
ref YP_003196997.1	3-phosphoshikimate 1-carboxyvinyltransferase...	224	1e-56
ref ZP_06279329.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	224	3e-56
ref ZP_06270491.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	224	3e-56
ref XP_001834882.2	arom polypeptide [Coprinopsis cinerea okayam...	223	3e-56
ref YP_001096916.1	3-phosphoshikimate 1-carboxyvinyltransferase...	223	3e-56
ref YP_001549512.1	3-phosphoshikimate 1-carboxyvinyltransferase...	223	4e-56
ref ZP_04998765.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	223	5e-56
ref ZP_07015206.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	223	5e-56
ref YP_003159302.1	3-phosphoshikimate 1-carboxyvinyltransferase...	223	5e-56
ref ZP_07330072.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	223	6e-56
ref YP_001323039.1	3-phosphoshikimate 1-carboxyvinyltransferase...	222	1e-55
gb EFN55352.1	hypothetical protein CHLNCRAFT_31300 [Chlorella ...	221	1e-55
gb ADW03091.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	221	2e-55
sp P39915.2	ARO2 BURPS RecName: Full=3-phosphoshikimate 1-carbo...	221	2e-55
emb CBK94981.1	3-phosphoshikimate 1-carboxyvinyltransferase [Eu...	221	2e-55
ref YP_003134364.1	3-phosphoshikimate 1-carboxyvinyltransferase...	221	2e-55
ref YP_001039475.1	3-phosphoshikimate 1-carboxyvinyltransferase...	220	3e-55
ref YP_003128029.1	3-phosphoshikimate 1-carboxyvinyltransferase...	220	4e-55
pir F64362	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5...	220	4e-55
ref YP_002951911.1	3-phosphoshikimate 1-carboxyvinyltransferase...	220	4e-55
ref NP_247478.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	220	4e-55
ref YP_001329672.1	3-phosphoshikimate 1-carboxyvinyltransferase...	219	5e-55
emb CBL11268.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ro...	219	5e-55
ref ZP_03524264.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	219	6e-55
ref ZP_04743620.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	219	7e-55
ref ZP_04588138.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	219	8e-55
ref YP_766557.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	218	1e-54
ref YP_002436161.1	3-phosphoshikimate 1-carboxyvinyltransferase...	218	1e-54
gb EFU19683.1	3-phosphoshikimate 1-carboxyvinyltransferase [Spi...	218	1e-54
emb CBL08458.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ro...	218	2e-54
emb CBK90704.1	3-phosphoshikimate 1-carboxyvinyltransferase [Eu...	218	2e-54
ref YP_001324353.1	3-phosphoshikimate 1-carboxyvinyltransferase...	217	3e-54
ref YP_468422.1	3-phosphoshikimate 1-carboxyvinyltransferase pr...	217	3e-54
ref YP_004058389.1	3-phosphoshikimate 1-carboxyvinyltransferase...	217	3e-54
ref YP_002937856.1	3-phosphoshikimate 1-carboxyvinyltransferase...	217	3e-54
ref XP_001210667.1	hypothetical protein ATEG_00581 [Aspergillus...	217	4e-54
ref YP_003549473.1	3-phosphoshikimate 1-carboxyvinyltransferase...	216	4e-54
ref ZP_06369933.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	216	5e-54
ref YP_001299190.1	3-phosphoshikimate 1-carboxyvinyltransferase...	216	6e-54
ref ZP_05976382.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	216	6e-54
ref YP_003873613.1	3-phosphoshikimate 1-carboxyvinyltransferase...	216	7e-54
ref YP_001977138.1	3-phosphoshikimate 1-carboxyvinyltransferase...	216	8e-54
ref NP_353664.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	216	8e-54
ref YP_003459196.1	3-phosphoshikimate 1-carboxyvinyltransferase...	215	9e-54
ref YP_002974419.1	3-phosphoshikimate 1-carboxyvinyltransferase...	215	1e-53
ref ZP_06419979.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	215	1e-53
ref YP_003963006.1	3-phosphoshikimate 1-carboxyvinyltransferase...	215	1e-53
ref ZP_03806228.1	hypothetical protein PROPEN_04630 [Proteus pe...	214	2e-53
ref ZP_07003703.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	214	2e-53
ref YP_002280056.1	3-phosphoshikimate 1-carboxyvinyltransferase...	214	2e-53
ref ZP_03395431.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	214	2e-53
ref ZP_07881352.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	214	2e-53
ref ZP_05255540.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	214	2e-53
ref XP_002943890.1	PREDICTED: hypothetical protein LOC100495501...	214	2e-53
ref ZP_06741032.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	214	3e-53
ref ZP_06835492.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	214	3e-53
ref ZP_03607002.1	hypothetical protein METSMIALI_00098 [Methano...	214	3e-53

ref YP_004277887.1	3-phosphoshikimate 1-carboxyvinyltransferase...	213	5e-53
ref YP_233984.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	213	5e-53
ref ZP_07263162.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	213	6e-53
ref YP_001272846.1	3-phosphoshikimate 1-carboxyvinyltransferase...	213	7e-53
ref NP_790877.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	213	7e-53
ref ZP_07034385.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	212	8e-53
ref YP_003247910.1	3-phosphoshikimate 1-carboxyvinyltransferase...	212	1e-52
ref YP_273200.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	212	1e-52
ref ZP_03301793.1	hypothetical protein BACDOR_03185 [Bacteroides...]	212	1e-52
gb EFW82034.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pse...	211	1e-52
ref ZP_06254597.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	211	1e-52
ref YP_447541.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	210	3e-52
ref ZP_07329272.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	210	4e-52
ref YP_003708293.1	3-phosphoshikimate 1-carboxyvinyltransferase...	209	5e-52
ref ZP_03206915.1	hypothetical protein BACPLE_00528 [Bacteroides...]	209	5e-52
ref YP_001239786.1	3-phosphoshikimate 1-carboxyvinyltransferase...	209	6e-52
ref NP_988325.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	209	6e-52
ref YP_003424319.1	3-phosphoshikimate 1-carboxyvinyltransferase...	209	7e-52
ref YP_003850067.1	3-phosphoshikimate 1-carboxyvinyltransferase...	208	1e-51
ref YP_002506738.1	3-phosphoshikimate 1-carboxyvinyltransferase...	208	1e-51
ref YP_004262686.1	3-phosphoshikimate 1-carboxyvinyltransferase...	208	1e-51
ref YP_004260363.1	3-phosphoshikimate 1-carboxyvinyltransferase...	208	1e-51
ref ZP_07978543.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	207	2e-51
gb EFP78589.1	pentafunctional AROM polypeptide [Puccinia gramin...]	207	2e-51
ref YP_003615995.1	3-phosphoshikimate 1-carboxyvinyltransferase...	207	3e-51
ref ZP_05392022.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	206	4e-51
ref ZP_05417355.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	206	5e-51
ref ZP_05279686.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	206	5e-51
ref ZP_03530535.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	206	6e-51
gb AAO33155.1	putative 3-phosphoshikimate 1-carboxyvinyltransfe...	206	6e-51
ref YP_004120716.1	3-phosphoshikimate 1-carboxyvinyltransferase...	206	6e-51
ref YP_004087750.1	3-phosphoshikimate 1-carboxyvinyltransferase...	206	7e-51
ref YP_001108530.1	3-phosphoshikimate 1-carboxyvinyltransferase...	205	1e-50
ref ZP_05494485.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	204	2e-50
ref YP_098022.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	204	2e-50
ref NP_811099.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	204	2e-50
ref YP_002872355.1	putative 3-phosphoshikimate 1-carboxyvinyltr...	204	2e-50
ref ZP_01053050.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	204	3e-50
ref ZP_08123678.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	203	3e-50
ref ZP_07945143.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	203	3e-50
ref ZP_06993276.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	203	3e-50
ref YP_004043905.1	3-phosphoshikimate 1-carboxyvinyltransferase...	203	5e-50
ref YP_001404722.1	3-phosphoshikimate 1-carboxyvinyltransferase...	203	5e-50
ref YP_288605.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	202	7e-50
ref ZP_03474784.1	hypothetical protein PRABACTJOHN_00439 [Parabact...	202	8e-50
gb ABV26712.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	202	1e-49
ref ZP_06093640.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	202	1e-49
ref ZP_02030211.1	hypothetical protein PARMER_00179 [Parabacter...	201	2e-49
ref YP_210369.1	putative 3-phosphoshikimate 1-carboxyvinyltrans...	201	2e-49
ref YP_001832750.1	3-phosphoshikimate 1-carboxyvinyltransferase...	201	3e-49
ref YP_003736795.1	3-phosphoshikimate 1-carboxyvinyltransferase...	201	3e-49
gb ABM21481.1	5'-enolpyruvylshikimate 3-phosphate synthase [Pse...	201	3e-49
emb CBW21292.1	putative 3-phosphoshikimate 1-carboxyvinyltransf...	200	3e-49
ref ZP_07334199.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	3e-49
gb ADX68016.1	3-phosphoshikimate 1-carboxyvinyltransferase [Wee...	200	3e-49
ref ZP_02329207.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	3e-49
ref NP_613913.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	200	3e-49
ref ZP_08075517.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	3e-49
ref ZP_01691566.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	3e-49
ref ZP_07721584.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	3e-49
ref ZP_08155395.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	4e-49
ref YP_003146820.1	3-phosphoshikimate 1-carboxyvinyltransferase...	200	4e-49
ref ZP_04841395.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	4e-49
ref ZP_07961875.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	200	4e-49
ref ZP_05618982.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	199	6e-49
ref ZP_07366540.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	199	6e-49
ref YP_003997622.1	3-phosphoshikimate 1-carboxyvinyltransferase...	199	6e-49
ref YP_004253987.1	3-phosphoshikimate 1-carboxyvinyltransferase...	199	6e-49
ref ZP_02066162.1	hypothetical protein BACOVA_03157 [Bacteroides...]	199	7e-49
ref YP_004007995.1	3-phosphoshikimate 1-carboxyvinyltransferase...	199	8e-49
ref ZP_06408448.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	1e-48

ref	YP_003313731.1	3-phosphoshikimate 1-carboxyvinyltransferase...	198	1e-48
ref	ZP_08112518.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	1e-48
dbj	BAJ27727.1	putative 3-phosphoshikimate 1-carboxyvinyltransf...	198	1e-48
ref	ZP_07213686.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	1e-48
ref	ZP_01961379.1	hypothetical protein BACCAC_03010 [Bacteroides...]	198	1e-48
ref	ZP_06275683.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	1e-48
ref	YP_001689222.1	3-phosphoshikimate 1-carboxyvinyltransferase...	198	1e-48
emb	CBL15191.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ru...]	198	2e-48
pir	S41329	5-enolpyruvylshikimate-3-phosphate synthase - Pseudo...	198	2e-48
ref	YP_004164981.1	3-phosphoshikimate 1-carboxyvinyltransferase...	198	2e-48
ref	ZP_05760597.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	2e-48
ref	NP_280114.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...]	198	2e-48
ref	ZP_07918691.1	conserved hypothetical protein [Bacteroides s...]	198	2e-48
ref	YP_003586028.1	3-phosphoshikimate 1-carboxyvinyltransferase...	198	2e-48
emb	CBK66251.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...]	198	2e-48
ref	ZP_06917240.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	198	2e-48
ref	ZP_07775185.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	2e-48
ref	ZP_04548784.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	2e-48
ref	ZP_06268360.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	197	2e-48
emb	CBI32963.3	unnamed protein product [Vitis vinifera]	197	2e-48
ref	ZP_06288831.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	197	2e-48
ref	YP_003813565.1	putative 3-phosphoshikimate 1-carboxyvinyltr...	197	2e-48
ref	YP_001304474.1	3-phosphoshikimate 1-carboxyvinyltransferase...	197	3e-48
ref	ZP_03968049.1	possible 3-phosphoshikimate 1-carboxyvinyltra...	197	3e-48
ref	ZP_07402495.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	3e-48
ref	ZP_07082504.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	3e-48
ref	ZP_05544099.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	3e-48
ref	ZP_06076094.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	197	4e-48
ref	YP_004266660.1	3-phosphoshikimate 1-carboxyvinyltransferase...	196	6e-48
ref	ZP_07627942.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	196	6e-48
ref	ZP_07040911.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	196	6e-48
ref	YP_001854793.1	3-phosphoshikimate 1-carboxyvinyltransferase...	196	6e-48
ref	ZP_07001809.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	196	7e-48
emb	CAA54317.1	5-enolpyruvylshikimate-3-phosphate synthase [Bur...]	196	7e-48
ref	YP_120804.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...]	196	7e-48
gb	ADZ09189.1	3-phosphoshikimate 1-carboxyvinyltransferase [Met...]	196	8e-48
ref	NP_275908.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...]	195	1e-47
ref	ZP_03312373.1	hypothetical protein DESPIG_02300 [Desulfovib...]	195	1e-47
ref	ZP_05916273.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	194	2e-47
ref	ZP_06287745.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	194	2e-47
ref	ZP_03644102.1	hypothetical protein BACCOPRO_02477 [Bacteroi...]	194	2e-47
ref	ZP_02160130.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	194	2e-47
ref	ZP_07322655.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	194	3e-47
ref	YP_698016.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...]	194	3e-47
ref	ZP_03016982.1	hypothetical protein BACINT_04593 [Bacteroides...]	194	3e-47
ref	ZP_07060276.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	194	3e-47
ref	NP_619403.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...]	193	4e-47
ref	ZP_06423357.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	193	4e-47
ref	YP_002565359.1	3-phosphoshikimate 1-carboxyvinyltransferase...	193	4e-47
ref	ZP_03630896.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	193	4e-47
ref	ZP_04999967.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	193	4e-47
ref	ZP_07306373.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	193	5e-47
ref	YP_001192862.1	3-phosphoshikimate 1-carboxyvinyltransferase...	193	5e-47
ref	ZP_06083401.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	193	5e-47
ref	ZP_04545361.1	3-phosphoshikimate 1-carboxy vinyl transferas...	193	5e-47
ref	ZP_07978939.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	6e-47
ref	ZP_06280883.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	6e-47
ref	YP_677344.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...]	192	6e-47
ref	ZP_08136605.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	7e-47
ref	ZP_05735072.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	7e-47
ref	ZP_03678570.1	hypothetical protein BACCELL_02920 [Bacteroid...]	192	9e-47
ref	ZP_02639510.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	1e-46
ref	YP_003387743.1	3-phosphoshikimate 1-carboxyvinyltransferase...	192	1e-46
ref	ZP_07934447.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	1e-46
ref	ZP_02642799.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	192	1e-46
ref	ZP_06005871.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	1e-46
ref	YP_003805618.1	3-phosphoshikimate 1-carboxyvinyltransferase...	191	1e-46
ref	YP_003399282.1	3-phosphoshikimate 1-carboxyvinyltransferase...	191	1e-46
ref	ZP_07310854.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	1e-46
ref	ZP_02951936.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	2e-46
ref	ZP_02630606.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	2e-46

ref ZP_02865398.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	2e-46
ref YP_695141.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	191	2e-46
ref ZP_06709873.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	191	3e-46
ref ZP_03458009.1	hypothetical protein BACEGG_00780 [Bacteroides...]	190	3e-46
ref YP_001295176.1	3-phosphoshikimate 1-carboxyvinyltransferase...	190	3e-46
ref YP_003383038.1	3-phosphoshikimate 1-carboxyvinyltransferase...	190	3e-46
ref YP_001823822.1	3-phosphoshikimate 1-carboxyvinyltransferase...	190	4e-46
ref YP_134905.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	190	4e-46
ref YP_003091787.1	3-phosphoshikimate 1-carboxyvinyltransferase...	190	4e-46
ref NP_629359.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	190	4e-46
ref YP_003575186.1	3-phosphoshikimate 1-carboxyvinyltransferase...	190	4e-46
ref ZP_08085077.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	189	5e-46
ref ZP_02180832.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	189	6e-46
ref YP_003129415.1	3-phosphoshikimate 1-carboxyvinyltransferase...	189	7e-46
ref ZP_04704720.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	189	8e-46
gb EGC87543.1	putative 3-phosphoshikimate 1-carboxyvinyltransfe...	189	8e-46
ref YP_003357655.1	putative 3-phosphoshikimate 1-carboxyvinyltr...	189	9e-46
ref YP_685260.1	3-phosphoshikimate 1-carboxyvinyltransferase [u...	189	9e-46
ref ZP_06587010.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	189	1e-45
ref YP_002478927.1	3-phosphoshikimate 1-carboxyvinyltransferase...	189	1e-45
ref ZP_04711269.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	188	1e-45
ref ZP_04696087.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	188	1e-45
ref XP_001449723.1	hypothetical protein [Paramecium tetraurelia...	188	1e-45
gb ADW03510.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	188	2e-45
ref ZP_04685981.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	188	2e-45
ref YP_860405.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	187	2e-45
gb ADY13184.1	3-phosphoshikimate 1-carboxyvinyltransferase [Spi...	187	2e-45
ref NP_561612.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	187	2e-45
ref ZP_06576756.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	187	2e-45
ref ZP_02635555.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	187	2e-45
ref YP_003488703.1	3-phosphoshikimate 1-carboxyvinyltransferase...	187	2e-45
ref YP_001512899.1	3-phosphoshikimate 1-carboxyvinyltransferase...	187	2e-45
ref NP_347531.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	187	3e-45
ref ZP_08160034.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	187	3e-45
ref YP_003196823.1	3-phosphoshikimate 1-carboxyvinyltransferase...	187	4e-45
ref ZP_01119134.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	187	4e-45
ref ZP_07289137.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	187	4e-45
ref ZP_05004205.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	4e-45
ref ZP_06823528.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	4e-45
ref ZP_07280355.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	5e-45
ref YP_003781065.1	3-phosphoshikimate 1-carboxyvinyltransferase...	186	5e-45
ref YP_003480512.1	3-phosphoshikimate 1-carboxyvinyltransferase...	186	5e-45
ref ZP_01733382.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	5e-45
gb AAS77246.1	putative 3-phosphoshikimate 1-carboxyvinyltransfe...	186	5e-45
ref YP_003327067.1	3-phosphoshikimate 1-carboxyvinyltransferase...	186	6e-45
ref YP_001394188.1	3-phosphoshikimate 1-carboxyvinyltransferase...	186	7e-45
ref ZP_07385752.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	8e-45
ref YP_004160822.1	3-phosphoshikimate 1-carboxyvinyltransferase...	186	8e-45
ref ZP_01252676.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	186	8e-45
ref YP_009687.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	186	9e-45
ref NP_824218.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	186	9e-45
ref YP_004003933.1	3-phosphoshikimate 1-carboxyvinyltransferase...	185	1e-44
ref YP_003402990.1	3-phosphoshikimate 1-carboxyvinyltransferase...	185	1e-44
ref ZP_06253467.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	185	1e-44
ref YP_003200775.1	3-phosphoshikimate 1-carboxyvinyltransferase...	185	1e-44
ref YP_003103946.1	3-phosphoshikimate 1-carboxyvinyltransferase...	185	1e-44
ref YP_004103569.1	3-phosphoshikimate 1-carboxyvinyltransferase...	185	1e-44
ref ZP_04853058.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	185	1e-44
ref YP_922900.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	185	2e-44
ref YP_003012523.1	3-phosphoshikimate 1-carboxyvinyltransferase...	184	2e-44
ref ZP_05858117.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	184	2e-44
ref YP_003118554.1	3-phosphoshikimate 1-carboxyvinyltransferase...	184	2e-44
ref YP_182676.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	184	2e-44
ref YP_304445.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	184	2e-44
ref YP_003646068.1	3-phosphoshikimate 1-carboxyvinyltransferase...	184	2e-44
ref YP_002309425.1	3-phosphoshikimate 1-carboxyvinyltransferase...	184	2e-44
ref ZP_05130027.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	184	2e-44
ref ZP_01059205.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	184	2e-44
ref YP_001620220.1	3-phosphoshikimate 1-carboxyvinyltransferase...	184	2e-44
ref ZP_08043247.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	184	3e-44
ref ZP_02076942.1	hypothetical protein EUBDOL_00735 [Eubacteriu...	183	4e-44

ref ZP_02437127.1	hypothetical protein BACSTE_03400 [Bacteroides...]	183	5e-44
ref ZP_04820906.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	183	5e-44
ref YP_967917.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...]	182	6e-44
ref YP_001922269.1	3-phosphoshikimate 1-carboxyvinyltransferase...	182	6e-44
ref ZP_07085696.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	182	7e-44
gb EFP93820.1	pentafunctional AROM polypeptide [Puccinia gramin...]	182	1e-43
ref ZP_01890962.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	182	1e-43
gb AAT74841.1	AROM polypeptide [Tetrahymena thermophila]	182	1e-43
ref YP_003871327.1	3-phosphoshikimate 1-carboxyvinyltransferase...	182	1e-43
ref ZP_06475046.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	182	1e-43
ref YP_003257006.1	3-phosphoshikimate 1-carboxyvinyltransferase...	182	1e-43
ref YP_003096551.1	5-Enolpyruvylshikimate-3-phosphate synthase ...	181	2e-43
ref ZP_03293534.1	hypothetical protein CLOHIR_01484 [Clostridiu...]	181	2e-43
ref YP_003301285.1	3-phosphoshikimate 1-carboxyvinyltransferase...	181	2e-43
ref YP_003178454.1	3-phosphoshikimate 1-carboxyvinyltransferase...	181	2e-43
ref YP_003636308.1	3-phosphoshikimate 1-carboxyvinyltransferase...	181	2e-43
ref ZP_06300243.1	hypothetical protein pah_c197o073 [Parachlamy...]	181	2e-43
ref YP_003935682.1	3-phosphoshikimate 1-carboxyvinyltransferase...	181	2e-43
ref ZP_06919663.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	181	2e-43
ref YP_003958651.1	3-phosphoshikimate 1-carboxyvinyltransferase...	181	3e-43
ref ZP_07356893.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	3e-43
ref ZP_07578367.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	3e-43
ref YP_003947542.1	3-phosphoshikimate 1-carboxyvinyltransferase...	180	3e-43
ref YP_004099765.1	3-phosphoshikimate 1-carboxyvinyltransferase...	180	4e-43
ref ZP_03700952.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	4e-43
ref YP_004273047.1	3-phosphoshikimate 1-carboxyvinyltransferase...	180	5e-43
ref ZP_06200730.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	5e-43
ref ZP_02861638.1	hypothetical protein ANASTE_00845 [Anaerofust...]	180	5e-43
ref ZP_00959872.1	hypothetical protein ISM_08555 [Roseovarius n...]	180	5e-43
ref ZP_07717729.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	5e-43
ref ZP_07607719.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	180	5e-43
ref YP_003958696.1	3-phosphoshikimate 1-carboxyvinyltransferase...	179	5e-43
ref ZP_02428786.1	hypothetical protein CLORAM_02197 [Clostridiu...]	179	6e-43
ref YP_565758.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...]	179	6e-43
ref YP_002959959.1	3-phosphoshikimate 1-carboxyvinyltransferase...	179	7e-43
ref YP_003241998.1	3-phosphoshikimate 1-carboxyvinyltransferase...	179	9e-43
ref ZP_04564427.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	179	1e-42
ref YP_003860848.1	putative 3-phosphoshikimate 1-carboxyvinyltr...	179	1e-42
gb EFS56521.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	178	1e-42
ref ZP_03702032.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	178	1e-42
ref YP_327187.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...]	178	1e-42
gb EFS39990.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	178	1e-42
gb EFT73592.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	178	1e-42
ref ZP_06426967.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	178	1e-42
ref NP_070326.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...]	178	1e-42
ref XP_001434983.1	hypothetical protein [Paramecium tetraurelia...]	178	2e-42
ref YP_004092883.1	3-phosphoshikimate 1-carboxyvinyltransferase...	178	2e-42
gb EFT10607.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	177	2e-42
ref YP_075248.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...]	177	2e-42
ref ZP_02950383.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	177	2e-42
ref YP_706273.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...]	177	2e-42
ref ZP_06406159.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	177	2e-42
ref YP_004255775.1	3-phosphoshikimate 1-carboxyvinyltransferase...	177	2e-42
ref ZP_04383385.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	177	2e-42
ref ZP_06263110.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	177	3e-42
ref YP_001031078.1	3-phosphoshikimate 1-carboxyvinyltransferase...	177	3e-42
ref ZP_02620468.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	177	3e-42
gb EFT64948.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	177	3e-42
ref YP_002783591.1	3-phosphoshikimate 1-carboxyvinyltransferase...	177	3e-42
ref ZP_02422012.1	hypothetical protein EUBSIR_00853 [Eubacteriu...]	177	3e-42
ref YP_003937400.1	3-phosphoshikimate 1-carboxyvinyltransferase...	177	3e-42
gb EFT77790.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	177	4e-42
ref ZP_03290752.1	hypothetical protein CLONEX_02970 [Clostridiu...]	176	4e-42
ref ZP_04057460.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	176	5e-42
ref YP_004045439.1	3-phosphoshikimate 1-carboxyvinyltransferase...	176	5e-42
ref YP_879090.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...]	176	5e-42
ref YP_055974.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...]	176	5e-42
ref ZP_01882742.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	176	6e-42
ref YP_003513920.1	3-phosphoshikimate 1-carboxyvinyltransferase...	176	6e-42
gb EFT31959.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...]	176	6e-42
gb ADZ12570.1	5-enolpyruvylshikimate-3-phosphate synthase [Riem...]	176	6e-42

ref ZP_06644106.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	176	7e-42
ref YP_001505320.1	3-phosphoshikimate 1-carboxyvinyltransferase...	176	7e-42
ref YP_002765629.1	3-phosphoshikimate 1-carboxyvinyltransferase...	176	7e-42
ref XP_001019959.1	3-dehydroquinase synthase [Tetrahymena therm...	176	7e-42
ref YP_003541749.1	3-phosphoshikimate 1-carboxyvinyltransferase...	176	8e-42
gb EGD35333.1	3-phosphoshikimate 1-carboxyvinyltransferase [Cap...	176	9e-42
ref YP_004036929.1	3-phosphoshikimate 1-carboxyvinyltransferase...	175	1e-41
ref YP_003581491.1	3-phosphoshikimate 1-carboxyvinyltransferase...	175	1e-41
ref YP_003309207.1	3-phosphoshikimate 1-carboxyvinyltransferase...	175	1e-41
ref ZP_07089459.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	175	1e-41
ref YP_004053366.1	3-phosphoshikimate 1-carboxyvinyltransferase...	175	1e-41
ref NP_633262.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	175	1e-41
ref YP_003155352.1	3-phosphoshikimate 1-carboxyvinyltransferase...	175	1e-41
ref ZP_02867959.1	hypothetical protein CLOSPI_01799 [Clostridiu...	175	2e-41
ref ZP_03929090.1	conserved hypothetical protein [Acidaminococc...	175	2e-41
emb CBL34654.1	3-phosphoshikimate 1-carboxyvinyltransferase [Eu...	174	2e-41
ref ZP_07920257.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	174	2e-41
ref YP_001887328.1	3-phosphoshikimate 1-carboxyvinyltransferase...	174	3e-41
ref ZP_05368127.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	174	3e-41
ref ZP_07800142.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	174	3e-41
ref NP_787695.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	174	4e-41
ref ZP_07899258.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	174	4e-41
ref ZP_07294998.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	173	4e-41
ref ZP_04861607.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	173	4e-41
pdb 1P88 A Chain A, Substrate-Induced Structural Changes To The ...		173	4e-41
ref ZP_06837390.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	173	4e-41
gb ABZ08445.1	putative EPSP synthase (3-phosphoshikimate 1-carb...	173	4e-41
ref YP_482851.1	3-phosphoshikimate 1-carboxyvinyltransferase [F...	173	5e-41
ref NP_789134.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	173	5e-41
emb CBK88194.1	3-phosphoshikimate 1-carboxyvinyltransferase [Eu...	173	6e-41
ref ZP_08026066.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	172	7e-41
gb AAD13108.1	5-enolpyruvylshikimate 3-phosphate synthase [Cory...	172	7e-41
ref XP_002773648.1	3-dehydroquinase synthase, putative [Perkins...	172	8e-41
ref YP_003400659.1	3-phosphoshikimate 1-carboxyvinyltransferase...	172	8e-41
ref YP_001137748.1	3-phosphoshikimate 1-carboxyvinyltransferase...	172	8e-41
ref YP_062746.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	172	1e-40
ref NP_599992.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	172	1e-40
ref YP_003716296.1	3-phosphoshikimate 1-carboxyvinyltransferase...	172	1e-40
ref YP_832132.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	171	1e-40
ref ZP_01201597.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	171	1e-40
emb CBK98719.1	3-phosphoshikimate 1-carboxyvinyltransferase [Fa...	171	2e-40
ref YP_001581882.1	3-phosphoshikimate 1-carboxyvinyltransferase...	171	2e-40
ref YP_003089374.1	3-phosphoshikimate 1-carboxyvinyltransferase...	171	2e-40
gb AAQ84158.1	PlmJK [Streptomyces sp. HK803]	171	2e-40
gb AAD51963.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	171	3e-40
ref YP_002488440.1	3-phosphoshikimate 1-carboxyvinyltransferase...	170	3e-40
ref ZP_07705928.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	170	3e-40
ref YP_003274671.1	3-phosphoshikimate 1-carboxyvinyltransferase...	170	4e-40
gb ADI07135.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	170	4e-40
ref YP_003141587.1	3-phosphoshikimate 1-carboxyvinyltransferase...	170	4e-40
ref ZP_07865192.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	170	5e-40
ref YP_004014739.1	3-phosphoshikimate 1-carboxyvinyltransferase...	170	5e-40
ref YP_003362359.1	5-enolpyruvylshikimate-3-phosphate synthase ...	169	6e-40
ref ZP_05401260.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	169	6e-40
ref YP_003535360.1	3-phosphoshikimate 1-carboxyvinyltransferase...	169	6e-40
ref YP_001710766.1	3-phosphoshikimate 1-carboxyvinyltransferase...	169	6e-40
emb CBK96585.1	3-phosphoshikimate 1-carboxyvinyltransferase [Eu...	169	7e-40
ref ZP_04448120.1	hypothetical protein BIFANG_03122 [Bifidobact...	169	7e-40
ref YP_872294.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	169	7e-40
ref YP_002906764.1	3-phosphoshikimate 1-carboxyvinyltransferase...	169	8e-40
ref YP_003681686.1	3-phosphoshikimate 1-carboxyvinyltransferase...	169	8e-40
ref ZP_00993693.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	169	8e-40
ref YP_003841879.1	3-phosphoshikimate 1-carboxyvinyltransferase...	169	9e-40
ref ZP_04445584.1	hypothetical protein COLINT_02294 [Collinsell...	169	1e-39
ref ZP_0274174.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	168	1e-39
ref NP_294820.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	168	2e-39
sp Q9RVD3.2 AROA_DEIRA RecName: Full=3-phosphoshikimate 1-carbox...		168	2e-39
ref YP_003653518.1	3-phosphoshikimate 1-carboxyvinyltransferase...	167	2e-39
ref ZP_02693258.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	2e-39
ref YP_003838341.1	3-phosphoshikimate 1-carboxyvinyltransferase...	167	2e-39
ref YP_004223355.1	5-enolpyruvylshikimate-3-phosphate synthase ...	167	2e-39

ref	ZP_03505661.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	2e-39
ref	YP_001311640.1	3-phosphoshikimate 1-carboxyvinyltransferase...	167	3e-39
ref	YP_843454.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	167	3e-39
ref	ZP_05271942.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	3e-39
ref	YP_659044.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	167	3e-39
ref	YP_001088340.1	3-phosphoshikimate 1-carboxyvinyltransferase...	167	4e-39
ref	ZP_05351032.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	4e-39
ref	ZP_07991977.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	4e-39
ref	ZP_02184530.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	4e-39
ref	ZP_04605604.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	167	4e-39
ref	ZP_02423949.1	hypothetical protein ALIPUT_00064 [Alistipes ...	166	5e-39
ref	YP_886256.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	166	5e-39
ref	ZP_03782667.1	hypothetical protein RUMHYD_02118 [Blautia hy...	166	5e-39
ref	ZP_07908824.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	166	6e-39
ref	YP_001222059.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	6e-39
ref	YP_002785524.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	6e-39
ref	ZP_05329984.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	166	7e-39
ref	ZP_02028886.1	hypothetical protein BIFADO_01332 [Bifidobact...	166	7e-39
ref	YP_003726593.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	8e-39
ref	YP_003982923.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	9e-39
ref	YP_003284025.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	9e-39
ref	ZP_03567874.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	166	9e-39
ref	YP_001360961.1	3-phosphoshikimate 1-carboxyvinyltransferase...	166	1e-38
ref	YP_952599.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	166	1e-38
gb	ADX73645.1	3-phosphoshikimate 1-carboxyvinyltransferase [Art...	166	1e-38
gb	AAD51957.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	165	1e-38
gb	AAD51960.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	165	1e-38
ref	YP_002834221.1	3-phosphoshikimate 1-carboxyvinyltransferase...	165	1e-38
ref	YP_003343719.1	3-phosphoshikimate 1-carboxyvinyltransferase...	165	1e-38
ref	YP_003161758.1	3-phosphoshikimate 1-carboxyvinyltransferase...	165	2e-38
ref	YP_004070625.1	5-enolpyruvylshikimate-3-phosphate synthase ...	164	2e-38
gb	AAD51961.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	164	2e-38
ref	YP_716153.1	3-phosphoshikimate 1-carboxyvinyltransferase [F...	164	2e-38
ref	ZP_03010719.1	hypothetical protein BACCOP_02601 [Bacteroides...	164	2e-38
gb	AAG47852.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	164	2e-38
ref	ZP_08023913.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	164	3e-38
ref	YP_003985678.1	3-phosphoshikimate 1-carboxyvinyltransferase...	164	3e-38
ref	ZP_07666535.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	164	3e-38
gb	EFR56629.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ali...	164	3e-38
ref	ZP_007756778.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	163	4e-38
gb	AAD51964.1	3-phosphoshikimate 1-carboxyvinyltransferase [Kle...	163	4e-38
dbj	BAJ47896.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ca...	163	5e-38
ref	ZP_06559559.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	163	5e-38
ref	ZP_01308785.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	163	5e-38
ref	YP_604470.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	163	5e-38
ref	ZP_07670058.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	163	6e-38
ref	YP_003687978.1	3-phosphoshikimate 1-carboxyvinyltransferase...	163	6e-38
ref	ZP_06425502.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	163	6e-38
ref	YP_001135951.1	3-phosphoshikimate 1-carboxyvinyltransferase...	163	6e-38
ref	ZP_07526056.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	162	7e-38
ref	ZP_01946380.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	162	7e-38
ref	YP_003543344.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	7e-38
ref	YP_004078450.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	8e-38
ref	YP_875152.1	5-enolpyruvylshikimate-3-phosphate synthase [Ce...	162	9e-38
ref	YP_001069689.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	9e-38
ref	YP_003938566.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	1e-37
ref	YP_002307523.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	1e-37
ref	YP_003373856.1	3-phosphoshikimate 1-carboxyvinyltransferase...	162	1e-37
ref	ZP_06927588.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	162	1e-37
ref	ZP_07456280.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	162	1e-37
dbj	BAJ30694.1	putative 3-phosphoshikimate 1-carboxyvinyltransf...	162	1e-37
ref	ZP_02918899.1	hypothetical protein BIFDEN_02218 [Bifidobact...	162	1e-37
ref	ZP_02456732.1	bifunctional prephenate dehydrogenase/3-phosp...	161	1e-37
ref	YP_001538880.1	3-phosphoshikimate 1-carboxyvinyltransferase...	161	2e-37
ref	ZP_05902570.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_05631302.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	YP_003970881.1	3-phosphoshikimate 1-carboxyvinyltransferase...	161	2e-37
ref	ZP_06417370.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_04664941.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_03646185.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_05616981.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37

ref	ZP_07802215.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_06265222.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	161	2e-37
ref	ZP_06982068.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	160	3e-37
ref	ZP_03324214.1	hypothetical protein BIFCAT_00999 [Bifidobact...	160	3e-37
ref	NP_819558.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	160	3e-37
ref	YP_001160527.1	3-phosphoshikimate 1-carboxyvinyltransferase...	160	3e-37
ref	ZP_07453845.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	160	3e-37
ref	ZP_03709874.1	hypothetical protein CORMATOL_00689 [Coryneba...	160	4e-37
ref	ZP_03742913.1	hypothetical protein BIFPSEUDO_03494 [Bifidob...	160	4e-37
ref	YP_002303912.1	3-phosphoshikimate 1-carboxyvinyltransferase...	160	4e-37
emb	CBK70704.1	3-phosphoshikimate 1-carboxyvinyltransferase [Bi...	160	5e-37
ref	YP_001112510.1	3-phosphoshikimate 1-carboxyvinyltransferase...	159	6e-37
ref	ZP_03391386.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	159	6e-37
ref	YP_003661054.1	3-phosphoshikimate 1-carboxyvinyltransferase...	159	7e-37
gb	ADL20421.1	3-phosphoshikimate 1-carboxyvinyltransferase [Cor...	159	7e-37
ref	NP_696144.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	159	8e-37
ref	ZP_03976086.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	159	8e-37
ref	YP_003782930.1	3-phosphoshikimate 1-carboxyvinyltransferase...	159	9e-37
ref	ZP_06977445.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	159	9e-37
ref	ZP_07940937.1	EPSP synthase [Bifidobacterium sp. 12_1_47BFA...	159	1e-36
ref	ZP_03806226.1	hypothetical protein PROPEN_04628 [Proteus pe...	159	1e-36
ref	YP_004220402.1	3-phosphoshikimate 1-carboxyvinyltransferase...	159	1e-36
ref	ZP_03930554.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	159	1e-36
ref	YP_181207.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	159	1e-36
ref	YP_004000333.1	aroA [Bifidobacterium longum subsp. longum B...	159	1e-36
ref	YP_002379387.1	3-phosphoshikimate 1-carboxyvinyltransferase...	159	1e-36
emb	CBL17641.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ru...	158	1e-36
ref	ZP_07879918.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	158	2e-36
ref	ZP_07148087.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	158	2e-36
ref	ZP_08010275.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	158	2e-36
ref	YP_638530.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	158	2e-36
ref	ZP_07747176.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	158	2e-36
emb	CAK45651.1	unnamed protein product [Aspergillus niger]	158	2e-36
ref	ZP_06141949.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	157	2e-36
ref	ZP_06757803.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	157	3e-36
ref	YP_003411129.1	3-phosphoshikimate 1-carboxyvinyltransferase...	157	3e-36
ref	ZP_04598887.1	hypothetical protein VEIDISOL_00288 [Veillone...	157	3e-36
ref	YP_002470344.1	3-phosphoshikimate 1-carboxyvinyltransferase...	157	3e-36
ref	ZP_02962867.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	157	3e-36
ref	YP_001424881.1	3-phosphoshikimate 1-carboxyvinyltransferase...	157	4e-36
ref	ZP_02444898.1	hypothetical protein ANACOL_04233 [Anaerotrunc...	157	4e-36
ref	ZP_06826700.1	short-chain-fatty-acid-CoA ligase [Streptomyc...	157	4e-36
ref	YP_377334.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	157	4e-36
ref	YP_463398.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	157	4e-36
ref	ZP_05613250.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	156	5e-36
ref	YP_003800841.1	3-phosphoshikimate 1-carboxyvinyltransferase...	156	5e-36
ref	ZP_03945961.1	possible 3-phosphoshikimate 1-carboxyvinyltra...	156	6e-36
ref	YP_002132567.1	3-phosphoshikimate 1-carboxyvinyltransferase...	156	6e-36
ref	YP_002490631.1	3-phosphoshikimate 1-carboxyvinyltransferase...	156	7e-36
ref	YP_004170224.1	3-phosphoshikimate 1-carboxyvinyltransferase...	156	7e-36
ref	ZP_01467675.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	156	7e-36
ref	ZP_04624289.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	156	7e-36
ref	ZP_08114716.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	156	7e-36
ref	ZP_07071831.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	155	9e-36
ref	YP_003164843.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	9e-36
ref	YP_001656551.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	9e-36
ref	YP_001227406.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	1e-35
ref	YP_003683578.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	1e-35
emb	CA090621.1	aroA [Microcystis aeruginosa PCC 7806]	155	1e-35
ref	YP_003428040.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	1e-35
ref	YP_003149664.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	1e-35
ref	YP_001596458.1	3-phosphoshikimate 1-carboxyvinyltransferase...	155	1e-35
gb	ADI58632.1	AsuB1 [Streptomyces nodosus subsp. asukaensis]	155	1e-35
gb	EGC77431.1	3-phosphoshikimate 1-carboxyvinyltransferase [Tre...	154	2e-35
ref	NP_126147.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	154	2e-35
ref	ZP_03682045.1	hypothetical protein CATMIT_00676 [Catenibact...	154	2e-35
ref	YP_003696703.1	3-phosphoshikimate 1-carboxyvinyltransferase...	154	2e-35
ref	ZP_06755918.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	154	2e-35
ref	YP_003852222.1	3-phosphoshikimate 1-carboxyvinyltransferase...	154	2e-35
ref	ZP_03297599.1	hypothetical protein COLSTE_01506 [Collinsell...	154	2e-35
ref	ZP_01131039.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	154	2e-35

ref	YP_001954667.1	3-phosphoshikimate 1-carboxyvinyltransferase...	154	3e-35
ref	ZP_08117640.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	154	3e-35
ref	YP_883328.2	3-phosphoshikimate 1-carboxyvinyltransferase [M...	154	3e-35
ref	NP_962268.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	154	4e-35
ref	YP_001624533.1	3-phosphoshikimate 1-carboxyvinyltransferase...	153	4e-35
ref	ZP_07834435.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	153	5e-35
ref	ZP_07270493.1	PlmJK [Streptomyces sp. SPB78] >gi 302427046 ...	153	5e-35
ref	ZP_07978743.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	153	5e-35
ref	NP_603830.1	3-phosphoshikimate 1-carboxyvinyltransferase [F...	153	6e-35
ref	ZP_05218136.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	153	6e-35
dbj	BAJ69373.1	3-phosphoshikimate 1-carboxyvinyltransferase [Bi...	153	6e-35
emb	CBL01390.1	3-phosphoshikimate 1-carboxyvinyltransferase [Fa...	153	6e-35
ref	YP_002323185.1	3-phosphoshikimate 1-carboxyvinyltransferase...	153	7e-35
ref	YP_948361.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	152	7e-35
ref	ZP_03980080.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	8e-35
ref	ZP_003990506.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	8e-35
ref	ZP_04859013.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	8e-35
ref	YP_003700189.1	3-phosphoshikimate 1-carboxyvinyltransferase...	152	8e-35
ref	ZP_07315528.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	9e-35
ref	YP_730742.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	152	9e-35
ref	ZP_03502269.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	9e-35
ref	ZP_06244016.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	9e-35
ref	YP_004281417.1	3-phosphoshikimate 1-carboxyvinyltransferase...	152	1e-34
ref	YP_003659482.1	3-phosphoshikimate 1-carboxyvinyltransferase...	152	1e-34
ref	ZP_07373029.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	1e-34
gb	ACY25322.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	152	1e-34
ref	ZP_07909038.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	152	1e-34
ref	YP_001568242.1	3-phosphoshikimate 1-carboxyvinyltransferase...	151	2e-34
ref	YP_004146791.1	3-phosphoshikimate 1-carboxyvinyltransferase...	151	2e-34
ref	YP_001213903.1	3-phosphoshikimate 1-carboxyvinyltransferase...	151	2e-34
ref	ZP_03488339.1	hypothetical protein EUBIFOR_00910 [Eubacteri...	151	2e-34
ref	ZP_007827894.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	151	2e-34
ref	YP_003757868.1	3-phosphoshikimate 1-carboxyvinyltransferase...	151	2e-34
ref	ZP_04888260.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	151	2e-34
ref	YP_307544.1	3-phosphoshikimate 1-carboxyvinyltransferase [D...	151	2e-34
ref	YP_003860717.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	3e-34
ref	ZP_04903345.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	150	3e-34
ref	ZP_05979475.2	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	3e-34
ref	ZP_03935572.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	3e-34
ref	YP_003916411.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	3e-34
ref	ZP_05634223.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	3e-34
ref	ZP_03055285.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	3e-34
ref	ZP_05845833.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	3e-34
ref	YP_001057853.1	5-enolpyruvylshikimate-3-phosphate synthase ...	150	3e-34
ref	YP_251417.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	150	4e-34
ref	ZP_07971108.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	4e-34
ref	ZP_06011838.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	4e-34
ref	ZP_07708388.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	4e-34
ref	YP_001559640.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	4e-34
ref	YP_003886854.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	4e-34
ref	YP_001014495.2	3-phosphoshikimate 1-carboxyvinyltransferase...	150	5e-34
ref	ZP_07468515.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	150	5e-34
ref	YP_001487221.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	5e-34
sp	Q8U0A0.2	ARO_A_PYRFU RecName: Full=Probable 3-phosphoshikimate...	150	5e-34
gb	ABK65737.1	3-phosphoshikimate 1-carboxyvinyltransferase [Myc...	150	5e-34
ref	YP_001803197.1	3-phosphoshikimate 1-carboxyvinyltransferase...	150	5e-34
ref	ZP_02235407.1	hypothetical protein DORFOR_02293 [Dorea form...	150	6e-34
ref	NP_939080.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	150	6e-34
ref	ZP_03226651.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	6e-34
ref	YP_001737477.1	3-phosphoshikimate 1-carboxyvinyltransferase...	149	6e-34
ref	ZP_00741040.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	6e-34
ref	ZP_06759571.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	7e-34
ref	ZP_03708034.1	hypothetical protein CLOSTMETH_02792 [Clostri...	149	7e-34
ref	ZP_08146095.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	7e-34
ref	ZP_07318142.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	7e-34
ref	ZP_05441142.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	7e-34
gb	ACF09788.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	149	7e-34
ref	YP_002881285.1	3-phosphoshikimate 1-carboxyvinyltransferase...	149	8e-34
gb	ACF09630.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	149	8e-34
ref	YP_003024563.1	3-phosphoshikimate 1-carboxyvinyltransferase...	149	8e-34
ref	ZP_06524660.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	8e-34

ref	ZP_08149589.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	8e-34
ref	NP_579428.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	149	8e-34
ref	YP_003973698.1	3-phosphoshikimate 1-carboxyvinyltransferase...	149	9e-34
ref	ZP_02072284.1	hypothetical protein BACUNI_03730 [Bacteroides...	149	9e-34
ref	YP_007881.1	putative 3-phosphoshikimate 1-carboxyvinyltrans...	149	9e-34
ref	YP_003462227.1	3-phosphoshikimate 1-carboxyvinyltransferase...	149	9e-34
ref	ZP_04575009.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	9e-34
ref	ZP_03799108.1	hypothetical protein COPCOM_01365 [Coproccu...	149	9e-34
ref	ZP_05863876.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	1e-33
ref	ZP_05649018.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	1e-33
dbj	BAI85758.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...	149	1e-33
ref	YP_291244.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	149	1e-33
gb	EFS75355.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...	149	1e-33
ref	ZP_06259151.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	1e-33
ref	ZP_00519130.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	149	1e-33
ref	ZP_02090016.1	hypothetical protein FAEPRAM212_00252 [Faecal...	148	1e-33
ref	YP_003312568.1	3-phosphoshikimate 1-carboxyvinyltransferase...	148	1e-33
ref	ZP_00206361.1	COG0128: 5-enolpyruvylshikimate-3-phosphate s...	148	1e-33
ref	ZP_08041384.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	148	2e-33
ref	ZP_01895125.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	148	2e-33
ref	ZP_03944986.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	148	2e-33
ref	NP_390141.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	148	2e-33
ref	YP_909548.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	148	2e-33
ref	YP_002446433.1	3-phosphoshikimate 1-carboxyvinyltransferase...	148	2e-33
ref	ZP_06384771.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	148	2e-33
ref	ZP_01728795.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	2e-33
gb	EGC23518.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	147	2e-33
ref	ZP_06875459.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	2e-33
ref	ZP_03624240.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	2e-33
ref	ZP_06871415.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	3e-33
ref	ZP_01773103.1	Hypothetical protein COLAER_02133 [Collinsell...	147	3e-33
ref	ZP_06595904.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	3e-33
ref	YP_475693.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	147	3e-33
ref	YP_001117356.1	3-phosphoshikimate 1-carboxyvinyltransferase...	147	4e-33
gb	AAR92125.1	5-enolpyruvylshikimate-3-phosphate synthase [Stre...	147	4e-33
ref	ZP_06808626.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	4e-33
gb	EFS91309.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pro...	147	4e-33
ref	ZP_05224153.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	4e-33
ref	ZP_07824432.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	4e-33
ref	YP_003994197.1	3-phosphoshikimate 1-carboxyvinyltransferase...	147	4e-33
ref	ZP_04234235.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	4e-33
ref	ZP_03932948.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	147	5e-33
ref	ZP_04568170.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	5e-33
ref	ZP_04279363.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	5e-33
ref	ZP_06900730.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	5e-33
ref	ZP_04970608.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	5e-33
ref	YP_001516633.1	3-phosphoshikimate 1-carboxyvinyltransferase...	146	6e-33
ref	YP_003329889.1	3-phosphoshikimate 1-carboxyvinyltransferase...	146	6e-33
ref	ZP_04289791.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	6e-33
ref	NP_972290.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	146	6e-33
ref	YP_002140051.1	3-phosphoshikimate 1-carboxyvinyltransferase...	146	7e-33
ref	YP_175399.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	146	7e-33
ref	ZP_04102639.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	7e-33
ref	ZP_07464879.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	8e-33
ref	ZP_04115329.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	8e-33
ref	YP_001843922.1	3-phosphoshikimate 1-carboxyvinyltransferase...	146	8e-33
ref	ZP_05645736.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	146	8e-33
ref	YP_003920757.1	3-phosphoshikimate 1-carboxyvinyltransferase...	146	8e-33
ref	ZP_04192296.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	145	9e-33
ref	YP_037018.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	145	9e-33
gb	ABZ07600.1	putative EPSP synthase (3-phosphoshikimate 1-carb...	145	9e-33
ref	YP_002123076.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	YP_003900684.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	ZP_06804840.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	145	1e-32
gb	EGC83183.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ana...	145	1e-32
ref	YP_002537816.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	YP_004204016.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	ZP_00052321.1	COG0128: 5-enolpyruvylshikimate-3-phosphate s...	145	1e-32
ref	ZP_04203661.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	145	1e-32
ref	ZP_05666868.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	145	1e-32
ref	ZP_02082253.1	hypothetical protein CLOLEP_03742 [Clostridiu...	145	1e-32

ref	YP_003436313.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	YP_002508788.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	1e-32
ref	ZP_04257264.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	145	2e-32
ref	YP_872950.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	145	2e-32
ref	YP_003430849.1	3-phosphoshikimate 1-carboxyvinyltransferase...	145	2e-32
ref	ZP_04212655.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
ref	NP_845288.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	144	2e-32
ref	ZP_04228425.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
emb	CBL28511.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sy...	144	2e-32
ref	ZP_02920877.1	hypothetical protein STRINF_01760 [Streptococ...	144	2e-32
ref	ZP_08047105.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
ref	ZP_00144747.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
ref	ZP_04223137.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
ref	YP_001421669.1	3-phosphoshikimate 1-carboxyvinyltransferase...	144	2e-32
ref	ZP_07727814.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	2e-32
ref	ZP_03981696.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
ref	ZP_04175135.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
gb	ABM75230.1	EPSP synthase (3-phosphoshikimate 1-carboxyvinylt...	144	3e-32
ref	ZP_02390652.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
ref	NP_856901.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	144	3e-32
ref	ZP_03109499.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
ref	ZP_04072541.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
ref	ZP_04217934.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	3e-32
ref	YP_003020815.1	3-phosphoshikimate 1-carboxyvinyltransferase...	144	4e-32
ref	ZP_04572355.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	4e-32
ref	YP_003563454.1	3-phosphoshikimate 1-carboxyvinyltransferase...	144	4e-32
ref	YP_001952384.1	3-phosphoshikimate 1-carboxyvinyltransferase...	144	4e-32
ref	ZP_01906772.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	144	4e-32
pdb	2BJB A Chain A, Mycobacterium Tuberculosis Epsp Synthase In ...		144	4e-32
ref	ZP_05655369.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	ZP_05915865.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	YP_003634887.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	4e-32
ref	YP_001799884.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	4e-32
ref	ZP_03099981.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	ZP_04079131.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	ZP_04197981.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	ZP_08058944.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	4e-32
ref	ZP_04120862.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	5e-32
ref	ZP_03417422.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	5e-32
ref	YP_003598217.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	5e-32
ref	NP_217744.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	143	5e-32
ref	ZP_05677975.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	5e-32
ref	NP_832685.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	143	5e-32
ref	YP_084260.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	143	5e-32
ref	ZP_05814046.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	5e-32
ref	ZP_07723502.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	5e-32
ref	YP_003136833.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	5e-32
ref	YP_002371268.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	5e-32
ref	ZP_07973206.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	6e-32
ref	YP_895431.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	143	7e-32
ref	ZP_06608175.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	143	7e-32
ref	YP_001035408.1	3-phosphoshikimate 1-carboxyvinyltransferase...	143	7e-32
gb	EGD29195.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	142	7e-32
ref	YP_002482018.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	8e-32
ref	ZP_07094728.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	8e-32
ref	ZP_06747931.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	8e-32
ref	YP_003827622.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	8e-32
ref	ZP_03234463.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	8e-32
ref	YP_002249558.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	8e-32
ref	ZP_03777933.1	hypothetical protein CLOHYLEM_04987 [Clostrid...	142	9e-32
ref	YP_001733439.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	9e-32
ref	YP_001645575.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	9e-32
ref	ZP_08062863.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref	ZP_03110090.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref	ZP_06291795.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref	ZP_07320814.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	142	1e-31
ref	ZP_05364937.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref	YP_901025.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	142	1e-31
ref	NP_378277.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	142	1e-31
sp	Q8FRI2.1 AROA_COREF RecName: Full=3-phosphoshikimate 1-carbox...		142	1e-31
ref	ZP_07726162.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31

ref ZP_07466969.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref YP_004203174.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	1e-31
ref YP_002750296.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	1e-31
emb CBW27913.1	putative 3-phosphoshikimate 1-carboxyvinyltransf...	142	1e-31
ref ZP_07713645.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
emb CBZ48633.1	3-phosphoshikimate 1-carboxyvinyltransferase [St...	142	1e-31
ref ZP_04570784.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
gb ADY22175.1	3-phosphoshikimate 1-carboxyvinyltransferase [Bac...	142	1e-31
ref ZP_04063025.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref NP_737389.2	3-phosphoshikimate 1-carboxyvinyltransferase [C...	142	1e-31
ref ZP_07051859.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	142	1e-31
ref NP_681133.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	142	1e-31
ref YP_003665177.1	3-phosphoshikimate 1-carboxyvinyltransferase...	142	1e-31
ref ZP_07268112.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	141	2e-31
ref YP_002997062.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref YP_002950111.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref YP_001277962.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
emb CAN73015.1	hypothetical protein VITISV_004387 [Vitis vinifera]	141	2e-31
gb ABX11283.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	141	2e-31
ref NP_897098.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	141	2e-31
ref YP_001550922.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref ZP_00604575.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	141	2e-31
ref YP_002744816.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref ZP_06808915.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	141	2e-31
ref YP_003108586.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
gb ADX24900.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	141	2e-31
ref ZP_04151690.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	141	2e-31
ref YP_001017896.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref ZP_04262650.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	141	2e-31
ref YP_001849633.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref YP_001692549.1	3-phosphoshikimate 1-carboxyvinyltransferase...	141	2e-31
ref ZP_04186657.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	141	3e-31
ref YP_001230236.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	3e-31
ref ZP_05347009.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	3e-31
ref ZP_03497830.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	3e-31
ref YP_003121639.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	3e-31
ref ZP_02410091.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	140	3e-31
ref ZP_05965183.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	3e-31
gb ABO69382.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	140	3e-31
ref NP_979297.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	140	3e-31
ref YP_003830415.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	3e-31
ref ZP_02207983.1	hypothetical protein COPEUT_02810 [Coproccocu...	140	3e-31
gb EFV82379.1	5-enolpyruvylshikimate-3-phosphate synthase [Achr...	140	3e-31
ref YP_003564759.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	3e-31
ref YP_004151127.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	4e-31
emb CBL06985.1	3-phosphoshikimate 1-carboxyvinyltransferase [Me...	140	4e-31
ref YP_003318133.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	4e-31
ref NP_906026.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	140	4e-31
ref ZP_04323863.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	4e-31
ref YP_003897787.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	4e-31
ref YP_002746075.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	5e-31
ref ZP_04301143.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	5e-31
ref YP_003718208.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	5e-31
gb EGD36849.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	140	5e-31
ref NP_301607.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	140	5e-31
ref NP_875440.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	140	5e-31
ref YP_383831.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	140	5e-31
ref YP_003988776.1	3-phosphoshikimate 1-carboxyvinyltransferase...	140	5e-31
ref ZP_02420864.1	hypothetical protein ANACAC_03511 [Anaerostip...	140	5e-31
ref ZP_04169387.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	6e-31
ref YP_357296.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	140	6e-31
ref ZP_04284624.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	6e-31
ref ZP_07445888.2	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	6e-31
ref ZP_01739541.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	140	6e-31
ref ZP_01628336.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	6e-31
ref NP_894231.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	139	6e-31
ref ZP_08070009.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	6e-31
ref ZP_05550675.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	6e-31
ref YP_003599482.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	7e-31
ref ZP_04295406.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	7e-31
ref YP_002338950.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	7e-31

ref	ZP_07109493.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	8e-31
ref	ZP_08086958.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	8e-31
ref	ZP_02433359.1	hypothetical protein CLOSCI_03637 [Clostridiu...	139	8e-31
gb	EFY02974.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	139	8e-31
ref	ZP_05403383.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	8e-31
gb	EGC25868.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	139	8e-31
ref	ZP_08060961.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	8e-31
ref	ZP_06680425.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	9e-31
ref	YP_574215.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	139	9e-31
ref	YP_003676763.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	9e-31
ref	NP_829586.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	139	9e-31
gb	ACN18643.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	139	9e-31
ref	ZP_07462927.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_06966618.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_05297675.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	YP_002771962.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	1e-30
gb	EGD37927.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	139	1e-30
ref	ZP_06697675.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_05658100.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	YP_001704276.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	1e-30
ref	ZP_06068698.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	YP_001654695.1	3-phosphoshikimate 1-carboxyvinyltransferase...	139	1e-30
ref	YP_139166.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	139	1e-30
ref	NP_622666.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	139	1e-30
ref	ZP_02425601.1	hypothetical protein ALIPUT_01748 [Alistipes ...	139	1e-30
ref	ZP_06198713.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_06598775.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_04156369.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_07319485.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_06727521.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	139	1e-30
ref	ZP_08049983.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	1e-30
ref	ZP_06674770.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	1e-30
ref	ZP_07547402.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	1e-30
ref	ZP_06341249.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	1e-30
ref	ZP_05380739.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
gb	ACN18424.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	138	2e-30
ref	ZP_01627121.1	response regulator receiver domain protein (C...	138	2e-30
ref	ZP_03729562.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
sp	Q2JLV2.2 AROA_SYNJB	RecName: Full=3-phosphoshikimate 1-carbox...	138	2e-30
ref	YP_328180.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	138	2e-30
ref	NP_219875.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	138	2e-30
ref	ZP_07638919.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
ref	YP_003723243.1	3-phosphoshikimate 1-carboxyvinyltransferase...	138	2e-30
ref	YP_754026.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	138	2e-30
gb	EGD32898.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	138	2e-30
ref	YP_003476808.1	3-phosphoshikimate 1-carboxyvinyltransferase...	138	2e-30
ref	YP_906373.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	138	2e-30
ref	ZP_05503074.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
ref	ZP_07929811.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
ref	ZP_06850660.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
ref	YP_002832573.1	3-phosphoshikimate 1-carboxyvinyltransferase...	138	2e-30
ref	ZP_06945970.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	138	2e-30
gb	ACN18367.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	137	2e-30
ref	YP_477562.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	137	2e-30
ref	YP_171991.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	137	2e-30
ref	ZP_07794480.1	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE ...	137	2e-30
ref	ZP_03824672.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	2e-30
emb	CBJ14884.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ch...	137	2e-30
ref	YP_002843827.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	2e-30
ref	ZP_03917251.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	2e-30
ref	ZP_05358720.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	2e-30
ref	ZP_06695533.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
ref	ZP_04150599.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
ref	YP_958304.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	137	3e-30
ref	YP_003417278.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	3e-30
ref	ZP_06163678.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
ref	YP_141056.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	137	3e-30
gb	ACN18616.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	137	3e-30
ref	YP_001010994.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	3e-30
ref	ZP_06194827.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
gb	ADY01630.1	3-phosphoshikimate 1-carboxyvinyltransferase [Vul...	137	3e-30

ref ZP_03971954.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
emb CBK63796.1	3-phosphoshikimate 1-carboxyvinyltransferase [Al...	137	3e-30
gb ACN18406.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	137	3e-30
ref YP_002829836.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	3e-30
ref YP_001680496.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	3e-30
ref ZP_05236131.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
ref NP_297019.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	137	3e-30
ref ZP_04162154.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
ref NP_465447.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	137	3e-30
ref YP_003433377.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	3e-30
ref ZP_05623317.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	3e-30
gb ACN18640.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	137	4e-30
ref YP_001664977.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	4e-30
ref ZP_05133085.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref ZP_01667017.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref ZP_04584797.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref ZP_05023338.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref YP_003786694.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	4e-30
ref ZP_02045125.1	hypothetical protein ACTODO_02015 [Actinomyce...	137	4e-30
ref YP_001200158.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	4e-30
ref ZP_07888310.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref ZP_04084926.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref YP_001930209.1	3-phosphoshikimate 1-carboxyvinyltransferase...	137	4e-30
ref ZP_01172026.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	4e-30
ref ZP_08065064.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	137	5e-30
gb ACN18610.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	136	5e-30
ref ZP_01822665.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	5e-30
ref YP_003506276.1	3-phosphoshikimate 1-carboxyvinyltransferase...	136	5e-30
ref ZP_07864434.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	5e-30
ref YP_001929990.1	putative 3-phosphoshikimate 1-carboxyvinyltr...	136	5e-30
ref ZP_07641931.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	5e-30
ref ZP_06062931.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	6e-30
ref ZP_02711877.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	6e-30
ref ZP_04849461.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	6e-30
ref ZP_01832802.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	6e-30
ref YP_003879090.1	3-phosphoshikimate 1-carboxyvinyltransferase...	136	6e-30
ref ZP_05563156.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	6e-30
ref YP_001055788.1	3-phosphoshikimate 1-carboxyvinyltransferase...	136	6e-30
ref ZP_07871245.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	7e-30
ref ZP_05627896.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	7e-30
ref ZP_07837595.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	7e-30
ref YP_820149.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	136	7e-30
ref ZP_06746991.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	136	7e-30
ref YP_001717324.1	3-phosphoshikimate 1-carboxyvinyltransferase...	136	7e-30
ref YP_001269252.1	bifunctional cyclohexadienyl dehydrogenase/ ...	136	7e-30
ref YP_001347346.1	prephenate dehydrogenase/3-phosphoshikimate ...	136	8e-30
gb ADX80168.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ent...	136	8e-30
ref YP_261402.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	135	8e-30
ref YP_724293.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	135	9e-30
ref ZP_08013228.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	9e-30
gb ACZ32941.1	3-phosphoshikimate 1-carboxyvinyltransferase [Chl...	135	9e-30
ref ZP_01366612.1	hypothetical protein PaerPA_01003760 [Pseudom...	135	9e-30
ref YP_515210.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	135	9e-30
ref YP_002439508.1	still frameshift 3-PHOSPHOSHIKIMATE 1-CARBOX...	135	1e-29
gb ACN18619.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	135	1e-29
ref YP_004200006.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	1e-29
ref YP_060391.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	135	1e-29
ref ZP_06060710.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
ref ZP_07643638.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
ref YP_002250779.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	1e-29
ref ZP_06877827.1	bifunctional cyclohexadienyl dehydrogenase/ 3...	135	1e-29
ref NP_225233.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	135	1e-29
ref YP_002319974.1	hypothetical protein AB57_2630 [Acinetobacte...	135	1e-29
ref YP_003840078.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	1e-29
ref YP_001713131.1	bifunctional protein [Includes: putative pre...	135	1e-29
gb EFU13047.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ent...	135	1e-29
ref YP_001085301.1	hypothetical protein AIS_2276 [Acinetobacter...	135	1e-29
ref ZP_00234980.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
ref ZP_00682490.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
ref YP_001706723.1	bifunctional protein [Includes: putative pre...	135	1e-29
ref YP_598767.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	135	1e-29

ref	ZP_01086437.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
ref	ZP_06750766.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	1e-29
gb	ABX52003.1	G6 [synthetic construct]	135	1e-29
ref	YP_790016.1	EPSP synthase/prephenate dehydrogenase [Pseudom...	135	1e-29
ref	YP_003474269.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	1e-29
ref	ZP_05825120.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	135	2e-29
gb	ADR61430.1	3-phosphoshikimate 1-carboxyvinyltransferase [Pse...	135	2e-29
ref	ZP_07737605.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	2e-29
ref	YP_001956607.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	2e-29
ref	ZP_01820852.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	2e-29
ref	ZP_02042497.1	hypothetical protein RUMGNA_03299 [Ruminococc...	135	2e-29
ref	ZP_06056213.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	2e-29
ref	ZP_01725453.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	135	2e-29
ref	YP_001374559.1	3-phosphoshikimate 1-carboxyvinyltransferase...	135	2e-29
ref	ZP_06788118.1	bifunctional cyclohexadienyl dehydrogenase/ 3...	134	2e-29
ref	YP_001667604.1	bifunctional cyclohexadienyl dehydrogenase/ ...	134	2e-29
ref	YP_003731401.1	bifunctional cyclohexadienyl dehydrogenase/ ...	134	2e-29
ref	YP_001847133.1	5-enolpyruvylshikimate-3-phosphate synthase ...	134	2e-29
ref	YP_518495.1	hypothetical protein DSY2262 [Desulfitobacteriu...	134	2e-29
ref	ZP_00584251.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	2e-29
ref	YP_002219472.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	2e-29
ref	YP_280561.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	134	2e-29
emb	CBW36848.1	3-phosphoshikimate 1-carboxyvinyltransferase [St...	134	2e-29
ref	YP_002728958.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	2e-29
ref	ZP_06027856.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	2e-29
ref	ZP_06612397.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	2e-29
gb	EFT94547.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ent...	134	2e-29
ref	ZP_05426434.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	2e-29
gb	ADY82353.1	bifunctional protein aroA [Acinetobacter calcoace...	134	2e-29
ref	YP_003528097.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	2e-29
gb	ACN18355.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	134	2e-29
ref	ZP_002729961.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	3e-29
ref	NP_358822.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	134	3e-29
ref	ZP_07107141.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	3e-29
ref	YP_004026961.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	ZP_07458332.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	3e-29
ref	ZP_01825180.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	3e-29
ref	YP_003759471.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	ZP_07957165.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	3e-29
ref	YP_002352953.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	YP_004002066.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	ZP_06691868.1	conserved hypothetical protein [Acinetobacter...	134	3e-29
ref	YP_003622471.1	5-enolpyruvylshikimate-3-phosphate synthase...	134	3e-29
ref	YP_816672.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	134	3e-29
ref	YP_003239117.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	NP_345829.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	134	3e-29
ref	YP_001694807.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	YP_001181460.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	3e-29
ref	YP_003414233.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	4e-29
ref	NP_743926.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	134	4e-29
ref	ZP_02437933.1	hypothetical protein CLOSS21_00371 [Clostridi...	134	4e-29
ref	YP_001681737.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	4e-29
ref	ZP_07645382.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	4e-29
ref	YP_002028921.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	4e-29
ref	YP_003876989.1	5-enolpyruvylshikimate-3-phosphate synthase ...	134	4e-29
ref	ZP_04438735.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	134	4e-29
ref	YP_001450649.1	3-phosphoshikimate 1-carboxyvinyltransferase...	134	4e-29
ref	YP_360747.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	134	4e-29
ref	YP_381441.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	133	4e-29
ref	ZP_06483994.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	4e-29
ref	NP_721197.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	133	5e-29
ref	YP_002513612.1	3-phosphoshikimate 1-carboxyvinyltransferase...	133	5e-29
gb	AAM16078.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	133	5e-29
ref	ZP_04935174.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	5e-29
ref	ZP_05593092.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	5e-29
gb	EDZ73120.1	YDR127Wp-like protein [Saccharomyces cerevisiae A...	133	5e-29
ref	ZP_02929027.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	5e-29
pdb	1RF4 A	Chain A, Structural Studies Of Streptococcus Pneumoni...	133	5e-29
ref	YP_527618.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	133	6e-29
emb	CBL19339.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ru...	133	6e-29
ref	YP_436095.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	133	6e-29

ref	ZP_05576906.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	6e-29
ref	YP_002720995.1	3-phosphoshikimate 1-carboxyvinyltransferase...	133	6e-29
ref	ZP_08050752.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	6e-29
ref	ZP_05475914.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	6e-29
ref	ZP_02210434.1	hypothetical protein CLOBAR_02842 [Clostridiu...	133	6e-29
ref	ZP_02709501.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	6e-29
ref	NP_607461.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	133	6e-29
sp	Q9ANY6.2	AROEA_ENTFA RecName: Full=3-phosphoshikimate 1-carbox...	133	7e-29
ref	YP_002562501.1	3-phosphoshikimate 1-carboxyvinyltransferase...	133	7e-29
ref	ZP_04261280.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	133	7e-29
ref	YP_693467.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	133	7e-29
ref	YP_014545.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	133	7e-29
ref	ZP_05790178.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	7e-29
ref	NP_815283.1	3-phosphoshikimate 1-carboxyvinyltransferase [E...	132	8e-29
ref	ZP_03393211.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	8e-29
ref	ZP_04434543.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	8e-29
ref	YP_001814262.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	9e-29
ref	ZP_05034721.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	9e-29
ref	ZP_04662200.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	9e-29
ref	ZP_04168122.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	9e-29
gb	EGD18578.1	3-phosphoshikimate 1-carboxyvinyltransferase [Xan...	132	9e-29
ref	YP_002742356.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_003179683.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_000371371.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	NP_147332.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	132	1e-28
ref	YP_003445878.1	3-enolpyruvylshikimate-5-phosphate synthetas...	132	1e-28
ref	YP_003485141.1	5-enolpyruvylshikimate-3-phosphate synthase ...	132	1e-28
emb	CBY17222.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ch...	132	1e-28
ref	ZP_01963432.1	hypothetical protein RUMOB_01148 [Ruminococc...	132	1e-28
ref	YP_602694.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	132	1e-28
ref	NP_664831.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	132	1e-28
ref	ZP_020371297.1	hypothetical protein BACCAP_02911 [Bacteroid...	132	1e-28
ref	YP_003226559.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_001972835.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_003190309.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_046840.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	132	1e-28
ref	ZP_05581100.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	1e-28
ref	ZP_08094921.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	1e-28
ref	ZP_03925314.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	1e-28
ref	YP_002315470.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	ZP_03167189.1	hypothetical protein RUM_LAC_00856 [Ruminococc...	132	1e-28
ref	YP_004024475.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	1e-28
ref	YP_342240.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	132	1e-28
ref	YP_444812.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	132	1e-28
ref	NP_779554.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	132	1e-28
ref	ZP_04173803.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	1e-28
ref	ZP_00366200.1	COG0128: 5-enolpyruvylshikimate-3-phosphate s...	132	1e-28
ref	ZP_01471841.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	1e-28
gb	ADI33303.1	5-enolpyruvylshikimate 3-phosphate synthase [Pseu...	132	2e-28
ref	ZP_06306238.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	132	2e-28
ref	YP_001830126.1	3-phosphoshikimate 1-carboxyvinyltransferase...	132	2e-28
ref	YP_163531.1	3-phosphoshikimate 1-carboxyvinyltransferase [Z...	132	2e-28
ref	ZP_06065709.1	conserved hypothetical protein [Acinetobacter...	131	2e-28
ref	ZP_07635012.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	2e-28
ref	YP_003072939.1	response regulator receiver domain protein [...	131	2e-28
ref	ZP_04669728.1	conserved hypothetical protein [Clostridiales...	131	2e-28
ref	YP_003992921.1	3-phosphoshikimate 1-carboxyvinyltransferase...	131	2e-28
ref	ZP_01861759.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	2e-28
ref	ZP_06307553.1	hypothetical protein CRC_01037 [Cylindrosperm...	131	2e-28
ref	ZP_01766625.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	2e-28
gb	AAM16074.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	131	2e-28
ref	ZP_00652443.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	2e-28
ref	NP_242533.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	131	2e-28
ref	YP_102068.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	131	2e-28
ref	NP_269459.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	131	2e-28
ref	YP_001727977.1	3-phosphoshikimate 1-carboxyvinyltransferase...	131	2e-28
ref	ZP_04856131.1	conserved hypothetical protein [Ruminococcus ...	131	2e-28
ref	ZP_06934711.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	2e-28
ref	YP_107312.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	131	2e-28
ref	YP_001009062.1	3-phosphoshikimate 1-carboxyvinyltransferase...	131	2e-28
ref	ZP_04760690.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	3e-28

ref ZP_06116562.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	3e-28
ref ZP_02401430.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	3e-28
ref ZP_07638225.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	131	3e-28
ref ZP_06499378.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	3e-28
ref ZP_05060593.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	131	3e-28
gb EGD13696.1	3-phosphoshikimate 1-carboxyvinyltransferase [Xan...	130	3e-28
ref YP_201025.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	130	3e-28
ref NP_892731.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	130	3e-28
gb ADP97128.1	3-phosphoshikimate 1-carboxyvinyltransferase [mar...	130	3e-28
ref ZP_04749034.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	3e-28
ref ZP_04957655.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	3e-28
ref YP_148049.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	130	3e-28
gb ABE11164.1	EPSP synthase [uncultured Prochlorococcus marinus...	130	3e-28
ref ZP_07556119.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	3e-28
ref ZP_07874350.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
ref YP_332315.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	130	4e-28
ref ZP_03147356.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
ref YP_001057772.1	3-phosphoshikimate 1-carboxyvinyltransferase...	130	4e-28
ref YP_363422.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	130	4e-28
ref ZP_04888327.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
ref YP_001904074.1	3-phosphoshikimate 1-carboxyvinyltransferase...	130	4e-28
ref YP_001126227.1	3-phosphoshikimate 1-carboxyvinyltransferase...	130	4e-28
gb EAY55824.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lep...	130	4e-28
ref ZP_05472815.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
ref ZP_05566093.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
gb AAM16060.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	130	4e-28
ref ZP_03127725.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	4e-28
gb AAT76791.1	5-enolpyruvylshikimate-3-phosphate synthase [Halo...	130	4e-28
ref ZP_01827678.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	5e-28
ref ZP_06184945.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	5e-28
ref ZP_04196642.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	5e-28
ref ZP_02410001.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	5e-28
ref ZP_04658748.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	5e-28
ref ZP_03761642.1	hypothetical protein CLOSTASPAR_05676 [Clostr...	130	5e-28
ref NP_341856.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	130	5e-28
ref YP_001836078.1	3-phosphoshikimate 1-carboxyvinyltransferase...	130	6e-28
ref YP_003251648.1	3-phosphoshikimate 1-carboxyvinyltransferase...	130	6e-28
ref ZP_05095037.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	6e-28
ref ZP_05138490.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	130	6e-28
ref ZP_03983417.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	6e-28
ref ZP_02084436.1	hypothetical protein CLOBOL_01962 [Clostridiu...	129	6e-28
ref ZP_07053534.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	7e-28
ref ZP_07340631.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	7e-28
ref ZP_06555080.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	129	7e-28
ref ZP_08014836.1	hypothetical protein HMPREF9464_00055 [Sutter...	129	7e-28
ref YP_002349603.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	7e-28
emb CAR84684.1	3-phosphoshikimate 1-carboxyvinyltransferase [Li...	129	8e-28
gb ADO78122.1	3-phosphoshikimate 1-carboxyvinyltransferase [Hal...	129	8e-28
ref NP_923984.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	129	8e-28
ref ZP_08005469.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	8e-28
ref ZP_03938367.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	9e-28
ref YP_003670909.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	9e-28
ref ZP_02713734.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	129	9e-28
ref YP_002572731.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
ref YP_001090863.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
ref YP_003595106.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
gb EGD10005.1	3-phosphoshikimate 1-carboxyvinyltransferase [Xan...	129	1e-27
ref YP_004101072.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
ref ZP_01968749.1	hypothetical protein RUMTOR_02328 [Ruminococc...	129	1e-27
ref NP_471371.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	129	1e-27
ref YP_001187348.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
ref YP_003796126.1	3-phosphoshikimate-1-carboxyvinyltransferase...	129	1e-27
ref YP_001172836.1	3-phosphoshikimate 1-carboxyvinyltransferase...	129	1e-27
ref NP_636962.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	129	1e-27
ref NP_641982.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	128	1e-27
gb AAM16059.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	128	2e-27
ref YP_003821881.1	3-phosphoshikimate 1-carboxyvinyltransferase...	128	2e-27
ref YP_002798775.1	bifunctional cyclohexadienyl dehydrogenase/ ...	128	2e-27
gb AAM16066.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	128	2e-27
ref YP_004094876.1	3-phosphoshikimate 1-carboxyvinyltransferase...	128	2e-27
gb EFR93399.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	128	2e-27

gb EFR90248.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	128	2e-27
sp Q1IKI5.2 AROA_ACIBL RecName: Full=3-phosphoshikimate 1-carbox...		128	2e-27
ref YP_592689.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	128	2e-27
ref ZP_05620446.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	128	2e-27
ref YP_002461505.1	3-phosphoshikimate 1-carboxyvinyltransferase...	128	2e-27
ref YP_607169.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	128	2e-27
emb CBL23833.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ru...	128	2e-27
ref ZP_06188741.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	128	2e-27
ref YP_001250157.1	3-phosphoshikimate 1-carboxyvinyltransferase...	128	2e-27
ref YP_811504.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	128	2e-27
ref ZP_06703798.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	128	2e-27
ref ZP_02177238.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	2e-27
ref YP_220088.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	127	2e-27
ref ZP_05898407.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	2e-27
ref ZP_07453238.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	3e-27
ref YP_002871287.1	bifunctional cyclohexadienyl dehydrogenase/ ...	127	3e-27
ref XP_002538414.1	3-phosphoshikimate 1-carboxyvinyltransferase...	127	3e-27
ref NP_422383.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	127	3e-27
ref ZP_03913621.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	3e-27
ref YP_004218168.1	3-phosphoshikimate 1-carboxyvinyltransferase...	127	3e-27
ref ZP_03994372.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	3e-27
ref YP_001541657.1	3-phosphoshikimate 1-carboxyvinyltransferase...	127	3e-27
sp Q608S5.2 AROA_METCA RecName: Full=3-phosphoshikimate 1-carbox...		127	3e-27
ref ZP_04294221.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	4e-27
ref NP_299603.1	3-phosphoshikimate 1-carboxyvinyltransferase [X...	127	4e-27
emb CBL25232.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ru...	127	4e-27
ref ZP_07829261.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	127	4e-27
ref YP_003924935.1	3-phosphoshikimate 1-carboxyvinyltransferase...	127	4e-27
ref YP_143723.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	127	5e-27
ref NP_785560.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	127	5e-27
emb CBK74531.1	3-phosphoshikimate 1-carboxyvinyltransferase [Bu...	127	5e-27
ref NP_441799.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	127	5e-27
ref NP_692701.1	3-phosphoshikimate 1-carboxyvinyltransferase [O...	127	5e-27
ref YP_003465144.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	5e-27
ref YP_091968.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	126	5e-27
ref ZP_06729331.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	126	5e-27
gb AAM16073.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	126	6e-27
ref YP_001224755.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	6e-27
ref ZP_07078084.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	126	6e-27
ref ZP_00787486.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	126	6e-27
gb EFR99623.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	126	6e-27
ref YP_001748251.1	bifunctional cyclohexadienyl dehydrogenase/ ...	126	6e-27
ref YP_001212170.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	6e-27
ref YP_004182677.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	6e-27
gb EFS02708.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	126	7e-27
ref NP_687654.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	126	7e-27
ref YP_001483896.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	7e-27
ref YP_001918207.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	7e-27
ref YP_113872.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	126	7e-27
ref ZP_08030107.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	126	7e-27
ref YP_004112024.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	7e-27
ref YP_818635.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	126	7e-27
ref YP_001033191.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	8e-27
ref YP_095448.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	126	8e-27
ref ZP_02462400.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	126	8e-27
ref YP_126720.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	126	9e-27
ref YP_001377406.1	3-phosphoshikimate 1-carboxyvinyltransferase...	126	9e-27
ref ZP_05041335.1	3-phosphoshikimate 1-carboxyvinyltransferase,...	125	9e-27
ref YP_850146.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	125	9e-27
ref ZP_01312238.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	9e-27
ref NP_228156.2	3-phosphoshikimate 1-carboxyvinyltransferase [T...	125	1e-26
ref ZP_05127216.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	1e-26
ref NP_953651.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	125	1e-26
ref ZP_05362235.1	3-phosphoshikimate 1-carboxyvinyltransferase/...	125	1e-26
ref ZP_02243759.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	1e-26
ref YP_002129031.1	3-phosphoshikimate 1-carboxyvinyltransferase...	125	1e-26
ref ZP_01904632.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	1e-26
ref YP_123698.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	125	1e-26
ref ZP_07895932.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	1e-26
ref YP_004063.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	125	2e-26
ref ZP_06604224.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	125	2e-26

ref YP_003063283.1	3-phosphoshikimate 1-carboxyvinyltransferase...	125	2e-26
gb AAM16087.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	125	2e-26
gb AAM16058.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	125	2e-26
ref NP_735069.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	124	2e-26
ref YP_191032.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	124	2e-26
ref YP_616539.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	124	2e-26
ref ZP_03953584.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	3e-26
ref YP_002731486.1	3-phosphoshikimate 1-carboxyvinyltransferase...	124	3e-26
ref YP_003376188.1	3-phosphoshikimate 1-carboxyvinyltransferase...	124	3e-26
ref ZP_03941378.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	3e-26
ref ZP_05636000.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	3e-26
ref YP_001262955.1	3-phosphoshikimate 1-carboxyvinyltransferase...	124	3e-26
ref ZP_06861446.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	3e-26
ref YP_003443611.1	3-phosphoshikimate 1-carboxyvinyltransferase...	124	3e-26
ref NP_267900.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	124	3e-26
ref YP_0349802.1	3-phosphoshikimate 1-carboxyvinyltransferase / ...	124	4e-26
ref ZP_04929449.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	4e-26
ref ZP_01123903.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	124	4e-26
ref YP_430188.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	124	4e-26
ref ZP_007740278.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	123	5e-26
ref ZP_05104162.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	123	5e-26
gb ABE11079.1	EPSP synthase 3-p [uncultured Prochlorococcus mar...	123	6e-26
ref NP_214059.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	123	6e-26
ref ZP_05293336.1	5-Enolpyruvylshikimate-3-phosphate synthase [...	123	7e-26
ref YP_003346483.1	3-phosphoshikimate 1-carboxyvinyltransferase...	123	7e-26
ref YP_002533868.1	3-phosphoshikimate 1-carboxyvinyltransferase...	122	8e-26
emb CBY95001.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sa...	122	8e-26
ref YP_003354315.1	3-phosphoshikimate 1-carboxyvinyltransferase...	122	8e-26
ref ZP_07396389.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	122	9e-26
ref ZP_08020996.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	122	1e-25
ref ZP_01103672.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	122	1e-25
ref YP_001244172.1	3-phosphoshikimate 1-carboxyvinyltransferase...	122	1e-25
ref YP_003703062.1	3-phosphoshikimate 1-carboxyvinyltransferase...	122	1e-25
ref ZP_01080057.1	EPSP synthase (3-phosphoshikimate 1-carboxyvi...	122	1e-25
ref YP_397110.1	EPSP synthase (3-phosphoshikimate 1-carboxyvi...	122	1e-25
ref ZP_05746273.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	121	2e-25
ref YP_003855771.1	3-phosphoshikimate 1-carboxyvinyltransferase...	121	2e-25
ref ZP_00239462.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	121	2e-25
ref ZP_01167045.1	still frameshift 3-phosphoshikimate 1-pcarbox...	121	2e-25
ref ZP_02354547.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	121	2e-25
ref ZP_08129288.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	121	2e-25
ref YP_003181690.1	3-phosphoshikimate 1-carboxyvinyltransferase...	121	2e-25
ref YP_003460455.1	3-phosphoshikimate 1-carboxyvinyltransferase...	121	2e-25
ref YP_002753305.1	3-phosphoshikimate 1-carboxyvinyltransferase...	121	2e-25
ref YP_002560520.1	3-phosphoshikimate 1-carboxyvinyltransferase...	121	2e-25
ref ZP_08017442.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	121	3e-25
ref YP_864107.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	120	3e-25
ref ZP_07655500.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	3e-25
ref YP_004167349.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	3e-25
ref ZP_07415893.2	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	3e-25
ref ZP_07577691.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	4e-25
gb EDZ39285.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lep...	120	4e-25
ref ZP_04157452.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	4e-25
ref YP_003640350.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	4e-25
ref YP_001839953.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	4e-25
ref YP_003809163.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	4e-25
ref ZP_01156384.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	5e-25
ref ZP_07836976.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	5e-25
ref YP_004011289.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	5e-25
ref YP_003151076.1	3-phosphoshikimate 1-carboxyvinyltransferase...	120	5e-25
gb EGC89612.1	3-phosphoshikimate 1-carboxyvinyltransferase [Egg...	120	5e-25
ref ZP_01622155.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	120	6e-25
ref YP_001233179.1	3-phosphoshikimate 1-carboxyvinyltransferase...	119	7e-25
ref ZP_03718009.1	hypothetical protein EUBHAL_03103 [Eubacteriu...	119	7e-25
ref ZP_02073823.1	hypothetical protein CL0L250_00573 [Clostridi...	119	7e-25
ref ZP_04433066.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	119	8e-25
ref ZP_06514727.1	LOW QUALITY PROTEIN: 5-enolpyruvylshikimate-3...	119	8e-25
ref ZP_07774219.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	119	9e-25
ref ZP_03430112.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	119	1e-24
ref YP_393384.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	119	1e-24
ref ZP_00055501.2	COG0128: 5-enolpyruvylshikimate-3-phosphate s...	119	1e-24

dbj BAJ79378.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ac...	119	1e-24
ref XP_001619008.1	hypothetical protein NEMVEDRAFT_vlg75553 [Ne...	118	1e-24
sp Q9WYI0.1 AROA_THEME RecName: Full=3-phosphoshikimate 1-carbox...		118	2e-24
ref ZP_05853789.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	118	2e-24
ref YP_002530500.1	3-phosphoshikimate 1-carboxyvinyltransferase...	118	2e-24
ref ZP_06392147.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	118	2e-24
ref ZP_02142005.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	118	2e-24
ref ZP_07946765.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	117	2e-24
ref ZP_04783741.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	117	3e-24
ref ZP_04583050.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	117	3e-24
emb CAN61775.1	hypothetical protein VITISV_024881 [Vitis vinifera]	117	3e-24
ref YP_003810268.1	3-phosphoshikimate 1-carboxyvinyltransferase...	117	3e-24
ref ZP_01870816.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	117	3e-24
ref ZP_01445538.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	117	3e-24
emb CAM75693.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ma...	117	3e-24
ref YP_001633700.1	3-phosphoshikimate 1-carboxyvinyltransferase...	117	3e-24
ref YP_741773.1	3-phosphoshikimate 1-carboxyvinyltransferase [A...	117	3e-24
ref YP_003060729.1	3-phosphoshikimate 1-carboxyvinyltransferase...	117	4e-24
ref YP_003149651.1	5-enolpyruvylshikimate-3-phosphate synthase ...	117	4e-24
gb ACS75029.1	AroA [Methylophilus methylotrophus]	117	5e-24
ref NP_930003.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	117	5e-24
ref YP_003291767.1	3-phosphoshikimate 1-carboxyvinyltransferase...	117	5e-24
ref YP_001431593.1	3-phosphoshikimate 1-carboxyvinyltransferase...	116	5e-24
ref ZP_07376339.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	116	6e-24
ref YP_798445.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	116	6e-24
emb CAH19218.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ps...	116	6e-24
ref YP_001002153.1	3-phosphoshikimate 1-carboxyvinyltransferase...	116	7e-24
ref YP_391465.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	116	7e-24
ref NP_767378.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	116	7e-24
ref YP_423626.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	116	7e-24
ref ZP_01305930.1	hypothetical protein RED65_00130 [Oceanobacte...	116	8e-24
ref NP_970228.1	EPSP synthase (3-phosphoshikimate 1-carboxyvinyl...	116	8e-24
ref YP_001435871.1	3-phosphoshikimate 1-carboxyvinyltransferase...	116	9e-24
ref YP_001878489.1	3-phosphoshikimate 1-carboxyvinyltransferase...	115	1e-23
ref YP_496604.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	115	1e-23
ref ZP_08081145.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	115	1e-23
ref ZP_02187665.1	5-enolpyruvylshikimate-3-phosphate synthase [...]	115	2e-23
ref YP_001939700.1	5-enolpyruvylshikimate-3-phosphate synthase ...	114	2e-23
ref YP_003756447.1	3-phosphoshikimate 1-carboxyvinyltransferase...	114	2e-23
ref ZP_07965739.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	114	2e-23
ref YP_001318531.1	3-phosphoshikimate 1-carboxyvinyltransferase...	114	3e-23
ref YP_916014.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	114	3e-23
ref YP_912693.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	114	3e-23
ref YP_001280145.1	bifunctional cyclohexadienyl dehydrogenase/ ...	114	3e-23
ref YP_002298688.1	3-phosphoshikimate 1-carboxyvinyltransferase...	114	4e-23
ref YP_828529.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	114	4e-23
ref YP_684057.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	114	4e-23
ref YP_253363.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	114	4e-23
ref YP_003627046.1	3-phosphoshikimate 1-carboxyvinyltransferase...	114	4e-23
gb AAM75972.1 AF481102.8	5-enolpyruvylshikimate-3-phosphate synt...	114	4e-23
ref YP_001154310.1	3-phosphoshikimate 1-carboxyvinyltransferase...	114	4e-23
ref ZP_01916521.1	prephenate dehydrogenase, putative/3-phosphos...	114	4e-23
ref YP_003186595.1	3-phosphoshikimate 1-carboxyvinyltransferase...	113	4e-23
ref ZP_05705366.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	113	5e-23
ref ZP_02154867.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	113	5e-23
ref YP_001356132.1	3-phosphoshikimate 1-carboxyvinyltransferase...	113	6e-23
ref ZP_07056514.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	113	6e-23
ref ZP_04677860.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	113	7e-23
ref YP_003321851.1	3-phosphoshikimate 1-carboxyvinyltransferase...	113	7e-23
ref ZP_01437294.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	113	7e-23
ref YP_755334.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	112	8e-23
ref YP_003263214.1	3-phosphoshikimate 1-carboxyvinyltransferase...	112	8e-23
emb CBK78945.1	3-phosphoshikimate 1-carboxyvinyltransferase [Cl...	112	9e-23
ref YP_003772576.1	3-phosphoshikimate 1-carboxyvinyltransferase...	112	9e-23
ref YP_002360949.1	3-phosphoshikimate 1-carboxyvinyltransferase...	112	1e-22
ref XP_001392796.2	shikimate dehydrogenase [Aspergillus niger C...	112	1e-22
gb AAQ75178.1	3-phosphoshikimate 1-carboxyvinyltransferase [Alv...	112	1e-22
ref YP_001543746.1	3-phosphoshikimate 1-carboxyvinyltransferase...	112	1e-22
ref ZP_06347541.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	112	1e-22
ref ZP_04455105.1	hypothetical protein GCWU000342_01121 [Shuttl...	112	1e-22
ref ZP_01551129.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	112	1e-22

ref	NP_559639.1	3-phosphoshikimate 1-carboxyvinyltransferase (a...	111	3e-22
ref	ZP_04389819.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	110	3e-22
ref	YP_004059748.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	3e-22
ref	YP_003516068.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	3e-22
ref	YP_003860414.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	3e-22
ref	ZP_01818831.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	110	3e-22
ref	ZP_01386111.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	110	3e-22
ref	YP_001996267.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	4e-22
ref	YP_003695752.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	4e-22
ref	YP_002019329.1	3-phosphoshikimate 1-carboxyvinyltransferase...	110	4e-22
ref	YP_903843.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	110	5e-22
ref	ZP_07572580.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	110	5e-22
ref	ZP_05046551.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	110	5e-22
ref	YP_003551577.1	5-enolpyruvylshikimate-3-phosphate synthase ...	110	6e-22
ref	ZP_06949694.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	109	7e-22
ref	YP_003817722.1	3-phosphoshikimate 1-carboxyvinyltransferase...	109	1e-21
ref	YP_254900.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	109	1e-21
ref	ZP_05038951.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	108	1e-21
ref	ZP_02468029.1	5-enolpyruvylshikimate-3-phosphate synthase [...	108	1e-21
ref	ZP_00958039.1	EPSP synthase, 3-phosphoshikimate 1-carboxyvi...	108	1e-21
ref	YP_003825018.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	1e-21
ref	YP_530294.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	108	1e-21
gb	ADQ77202.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sta...	108	2e-21
ref	ZP_04580452.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	108	2e-21
ref	ZP_07822573.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	108	2e-21
ref	YP_040877.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	108	2e-21
ref	YP_002542836.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	2e-21
ref	YP_508650.1	3-phosphoshikimate 1-carboxyvinyltransferase [J...	108	2e-21
ref	ZP_05842095.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	108	2e-21
ref	YP_631714.1	putative 3-phosphoshikimate 1-carboxyvinyltrans...	108	2e-21
ref	YP_003891978.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	2e-21
ref	ZP_01465782.1	probable 3-phosphoshikimate 1-carboxyvinyltra...	108	2e-21
ref	YP_004050170.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	2e-21
ref	YP_001603691.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	2e-21
ref	YP_003953653.1	3-phosphoshikimate 1-carboxyvinyltransferase...	108	2e-21
gb	ADX76594.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sta...	108	2e-21
ref	ZP_04060728.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	108	2e-21
ref	YP_001411431.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	3e-21
ref	ZP_05110808.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	3e-21
ref	YP_001219416.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	3e-21
ref	ZP_05780873.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	3e-21
ref	YP_002520696.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	3e-21
ref	YP_004149331.1	5-Enolpyruvylshikimate-3-phosphate synthase ...	107	3e-21
ref	ZP_07359438.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	3e-21
ref	YP_002378.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	107	3e-21
ref	YP_003395528.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	3e-21
ref	YP_745846.1	3-phosphoshikimate 1-carboxyvinyltransferase [G...	107	4e-21
gb	EGA97254.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sta...	107	4e-21
ref	YP_416804.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	107	4e-21
ref	YP_003545597.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	4e-21
ref	ZP_06896114.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	4e-21
ref	ZP_06318845.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	4e-21
ref	YP_001406072.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	4e-21
ref	ZP_01750762.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	4e-21
ref	YP_001045145.1	3-phosphoshikimate 1-carboxyvinyltransferase...	107	5e-21
ref	ZP_06324490.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	5e-21
ref	ZP_07658197.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	5e-21
ref	ZP_05124567.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	5e-21
ref	ZP_07327822.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	107	5e-21
emb	CAQ49888.1	3-phosphoshikimate 1-carboxyvinyltransferase [St...	107	5e-21
ref	ZP_01447705.1	EPSP synthase, 3-phosphoshikimate 1-carboxyvi...	106	6e-21
ref	YP_355096.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	106	6e-21
ref	YP_002887359.1	3-phosphoshikimate 1-carboxyvinyltransferase...	106	6e-21
ref	YP_612194.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	106	6e-21
ref	ZP_01037287.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	6e-21
ref	NP_105914.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	106	7e-21
ref	ZP_05084505.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	8e-21
ref	ZP_05076700.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	8e-21
ref	ZP_05051528.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	8e-21
ref	ZP_05275017.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	8e-21
ref	ZP_02146464.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	106	8e-21

ref YP_164847.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	106	9e-21
ref YP_001960561.1	3-phosphoshikimate 1-carboxyvinyltransferase...	106	9e-21
ref YP_003505660.1	3-phosphoshikimate 1-carboxyvinyltransferase...	106	9e-21
ref ZP_04866271.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	9e-21
ref ZP_01224478.1	prephenate [marine gamma proteobacterium HTCC...	105	1e-20
ref ZP_05739280.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	1e-20
ref YP_002121647.1	3-phosphoshikimate 1-carboxyvinyltransferase...	105	1e-20
ref YP_580471.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	105	1e-20
ref YP_002575765.1	3-phosphoshikimate 1-carboxyvinyltransferase...	105	1e-20
ref YP_892408.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	105	1e-20
ref YP_031813.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	105	1e-20
ref ZP_01039983.1	5-enolpyruvylshikimate-3-phosphate synthase [...	105	1e-20
ref YP_379927.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	105	1e-20
ref NP_782223.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	105	1e-20
ref ZP_06440909.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	1e-20
ref NP_711439.1	3-phosphoshikimate 1-carboxyvinyltransferase [L...	105	1e-20
ref ZP_06924309.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref ZP_05388284.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref ZP_07841013.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref YP_002761302.1	3-phosphoshikimate 1-carboxyvinyltransferase...	105	2e-20
ref ZP_01746715.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref YP_002908539.1	5-enolpyruvylshikimate-3-phosphate synthase ...	105	2e-20
ref ZP_05811043.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref ZP_01880117.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
ref ZP_05342087.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	105	2e-20
gb EEZ80251.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	104	2e-20
ref YP_001532365.1	3-phosphoshikimate 1-carboxyvinyltransferase...	104	3e-20
emb CBE68427.1	3-phosphoshikimate 1-carboxyvinyltransferase (5-...	104	3e-20
ref ZP_05071831.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	104	3e-20
gb AAM16064.1	3-phosphoshikimate 1-carboxyvinyltransferase [Zea...	104	3e-20
ref ZP_02149098.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	104	3e-20
ref ZP_00998531.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	104	3e-20
ref NP_907485.1	3-phosphoshikimate 1-carboxyvinyltransferase [W...	103	4e-20
ref YP_001794172.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	4e-20
ref ZP_07129404.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	4e-20
ref YP_003497302.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	4e-20
gb EFW32220.1	3-phosphoshikimate 1-carboxyvinyltransferase [Sta...	103	4e-20
ref YP_003267971.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	5e-20
ref YP_002956854.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	5e-20
ref ZP_01002590.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	5e-20
ref ZP_03613284.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	5e-20
ref ZP_01863096.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	5e-20
ref ZP_01015875.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	5e-20
ref ZP_05699157.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	103	6e-20
ref YP_809810.1	3-phosphoshikimate 1-carboxyvinyltransferase [O...	103	7e-20
ref YP_001202319.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	7e-20
ref YP_004158380.1	3-phosphoshikimate 1-carboxyvinyltransferase...	103	7e-20
gb AAA71897.1	3-phosphoshikimate-1-carboxyvinyltransferase [Sta...	103	7e-20
ref YP_264469.1	bifunctional cyclohexadienyl dehydrogenase/ 3-p...	103	8e-20
ref ZP_01544542.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	8e-20
ref NP_646171.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	102	8e-20
ref ZP_06502760.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	9e-20
ref YP_004139533.1	3-phosphoshikimate 1-carboxyvinyltransferase...	102	1e-19
ref YP_186348.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	102	1e-19
ref ZP_05101922.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	1e-19
ref YP_001170040.1	3-phosphoshikimate 1-carboxyvinyltransferase...	102	1e-19
ref ZP_00953711.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	1e-19
ref YP_765712.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	102	1e-19
ref ZP_07904321.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	1e-19
ref YP_001236311.1	3-phosphoshikimate 1-carboxyvinyltransferase...	102	1e-19
ref YP_931265.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	102	1e-19
ref ZP_04867454.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	102	1e-19
ref YP_004073619.1	3-phosphoshikimate 1-carboxyvinyltransferase...	102	2e-19
ref ZP_01125908.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	101	2e-19
ref YP_002978141.1	3-phosphoshikimate 1-carboxyvinyltransferase...	101	2e-19
ref YP_001526847.1	3-phosphoshikimate 1-carboxyvinyltransferase...	101	2e-19
ref ZP_03658338.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	101	2e-19
gb AAX21587.1	AroA [Francisella novicida] >gi 60477303 gb AAX21...	101	2e-19
gb ACJ54494.1	AroA [Francisella sp. FSC156] >gi 213950443 gb AC...	101	2e-19
ref ZP_04808519.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	101	3e-19
ref YP_003143352.1	3-phosphoshikimate 1-carboxyvinyltransferase...	100	4e-19

ref	ZP_08089003.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	100	4e-19
ref	ZP_06890569.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	100	4e-19
ref	YP_004172823.1	3-phosphoshikimate 1-carboxyvinyltransferase...	100	4e-19
ref	ZP_05089300.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	100	5e-19
ref	ZP_00948256.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	100	5e-19
ref	ZP_01304551.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	100	5e-19
ref	YP_002634191.1	3-phosphoshikimate 1-carboxyvinyltransferase...	100	6e-19
ref	YP_316829.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	100	6e-19
ref	ZP_07685443.1	hypothetical protein OSCT_1394 [Oscillochlori...	100	7e-19
ref	YP_003303682.1	3-phosphoshikimate 1-carboxyvinyltransferase...	100	7e-19
ref	ZP_01995870.1	hypothetical protein DORLON_01865 [Dorea long...	100	8e-19
ref	YP_002607312.1	3-phosphoshikimate 1-carboxyvinyltransferase...	100	8e-19
gb	ACJ54495.1	AroA [Francisella sp. FSC159]	100	9e-19
ref	YP_002287477.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	9e-19
ref	NP_371988.1	3-phosphoshikimate 1-carboxyvinyltransferase [S...	99	1e-18
ref	YP_003589561.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	1e-18
ref	ZP_01228876.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	99	1e-18
ref	ZP_04819347.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	99	1e-18
ref	YP_003447473.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	1e-18
ref	ZP_01452683.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	99	1e-18
ref	YP_001924782.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	1e-18
ref	ZP_01743483.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	99	1e-18
ref	YP_001038211.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	2e-18
ref	YP_003654661.1	3-phosphoshikimate 1-carboxyvinyltransferase...	99	2e-18
ref	YP_003577287.1	3-phosphoshikimate 1-carboxyvinyltransferase...	98	2e-18
ref	ZP_01054605.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	98	2e-18
ref	YP_484265.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	98	2e-18
gb	AAN87376.1	3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	98	2e-18
gb	AAX21584.1	AroA [Francisella tularensis subsp. holarctica] >...	98	2e-18
ref	NP_859670.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	98	2e-18
ref	ZP_05785141.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	98	3e-18
gb	AAX21593.1	AroA [Francisella tularensis subsp. holarctica] >...	98	3e-18
gb	AAX21592.1	AroA [Francisella tularensis subsp. holarctica]	98	3e-18
ref	YP_002016601.1	3-phosphoshikimate 1-carboxyvinyltransferase...	98	3e-18
ref	ZP_00370175.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	98	3e-18
ref	NP_945417.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	98	3e-18
ref	YP_002963190.1	3-enolpyruvylshikimate-5-phosphate synthetas...	98	3e-18
ref	ZP_05570493.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	98	3e-18
ref	ZP_07893857.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	97	4e-18
ref	YP_575526.1	3-phosphoshikimate 1-carboxyvinyltransferase [N...	97	4e-18
ref	YP_001989102.1	3-phosphoshikimate 1-carboxyvinyltransferase...	97	5e-18
gb	AAX21586.1	AroA [Francisella tularensis subsp. holarctica]	97	5e-18
ref	NP_662795.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	97	5e-18
ref	YP_001246893.1	3-phosphoshikimate 1-carboxyvinyltransferase...	97	5e-18
ref	YP_001786896.1	3-phosphoshikimate 1-carboxyvinyltransferase...	97	5e-18
ref	ZP_02996348.1	hypothetical protein CLOSP0_03471 [Clostridiu...	97	5e-18
ref	YP_989551.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	97	5e-18
ref	ZP_04056182.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	97	5e-18
ref	YP_032958.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	97	6e-18
ref	YP_758929.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	97	6e-18
ref	YP_676143.1	3-phosphoshikimate 1-carboxyvinyltransferase [M...	97	7e-18
ref	YP_002502152.1	3-phosphoshikimate 1-carboxyvinyltransferase...	97	7e-18
ref	ZP_01086603.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	8e-18
ref	YP_567330.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	96	8e-18
ref	ZP_01752691.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	8e-18
ref	ZP_05427835.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	96	9e-18
emb	CBI81616.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...	96	9e-18
ref	ZP_06488790.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17
ref	ZP_05079193.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17
ref	YP_001944126.1	3-phosphoshikimate 1-carboxyvinyltransferase...	96	1e-17
ref	ZP_07819631.1	putative 3-phosphoshikimate 1-carboxyvinyltra...	96	1e-17
ref	YP_001608574.1	3-phosphoshikimate 1-carboxyvinyltransferase...	96	1e-17
ref	YP_002971141.1	3-phosphoshikimate 1-carboxyvinyltransferase...	96	1e-17
ref	ZP_08106814.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17
dbj	BAJ56431.1	3-phosphoshikimate 1-carboxyvinyltransferase [He...	96	1e-17
ref	ZP_02617066.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17
ref	YP_001644318.1	3-phosphoshikimate 1-carboxyvinyltransferase...	96	1e-17
ref	YP_004106440.1	3-phosphoshikimate 1-carboxyvinyltransferase...	96	1e-17
ref	ZP_03368422.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17
gb	ADI35116.1	3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	96	1e-17
ref	ZP_01045034.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	96	1e-17

gb ADU41323.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	95	2e-17
ref ZP_07026530.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	95	2e-17
ref YP_001416018.1 3-phosphoshikimate 1-carboxyvinyltransferase...	95	2e-17
ref ZP_01617762.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	94	3e-17
ref YP_003471659.1 5-Enolpyruvylshikimate-3-phosphate synthase ...	94	3e-17
gb ADU81873.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	94	4e-17
ref YP_458387.1 3-phosphoshikimate 1-carboxyvinyltransferase [E...	94	4e-17
ref ZP_06622944.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	94	5e-17
dbj BAJ55592.1 3-phosphoshikimate 1-carboxyvinyltransferase [He...	94	5e-17
gb EES51981.1 3-phosphoshikimate 1-carboxyvinyltransferase [Lep...	94	5e-17
ref YP_779383.1 3-phosphoshikimate 1-carboxyvinyltransferase [R...	94	5e-17
ref ZP_08053835.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	94	6e-17
ref YP_001398032.1 3-phosphoshikimate 1-carboxyvinyltransferase...	94	6e-17
ref ZP_06054530.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	94	6e-17
dbj BAJ57933.1 3-phosphoshikimate 1-carboxyvinyltransferase [He...	93	7e-17
ref ZP_06159238.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	93	7e-17
sp A7H3F2.2 AROA_CAMJD RecName: Full=3-phosphoshikimate 1-carbox...	93	7e-17
ref YP_002266615.1 3-phosphoshikimate 1-carboxyvinyl transferas...	93	8e-17
ref YP_003928924.1 3-phosphoshikimate 1-carboxyvinyltransferase...	93	8e-17
ref ZP_04797190.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	93	1e-16
ref YP_003927283.1 3-phosphoshikimate 1-carboxyvinyltransferase...	93	1e-16
ref YP_003728473.1 3-phosphoshikimate 1-carboxyvinyltransferase...	93	1e-16
ref ZP_06371976.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	93	1e-16
gb ACB05442.1 chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	93	1e-16
dbj BAJ60090.1 3-phosphoshikimate 1-carboxyvinyltransferase [He...	92	1e-16
gb ACB05438.1 chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	92	1e-16
ref NP_207199.1 3-phosphoshikimate 1-carboxyvinyltransferase [H...	92	1e-16
ref ZP_05363634.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	92	1e-16
ref YP_001129873.1 3-phosphoshikimate 1-carboxyvinyltransferase...	92	2e-16
ref ZP_06373720.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	92	2e-16
ref ZP_05068167.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	92	2e-16
gb EFV89034.1 3-phosphoshikimate 1-carboxyvinyltransferase [Sta...	92	2e-16
ref YP_001997916.1 3-phosphoshikimate 1-carboxyvinyltransferase...	92	2e-16
gb EGC91177.1 3-phosphoshikimate 1-carboxyvinyltransferase [Tur...	92	2e-16
gb ACB05437.1 chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	92	2e-16
gb ACX99551.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	92	2e-16
gb ADO05722.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	91	2e-16
gb ADU83434.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	91	3e-16
ref YP_627732.1 3-phosphoshikimate 1-carboxyvinyltransferase [H...	91	3e-16
ref ZP_08054927.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	91	3e-16
ref NP_764708.1 3-phosphoshikimate 1-carboxyvinyltransferase [S...	91	4e-16
ref YP_001910521.1 3-phosphoshikimate 1-carboxyvinyltransferase...	91	4e-16
ref YP_188611.1 3-phosphoshikimate 1-carboxyvinyltransferase [S...	91	4e-16
ref ZP_07598734.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	91	4e-16
ref YP_001390821.1 3-phosphoshikimate 1-carboxyvinyltransferase...	91	5e-16
ref YP_001368591.1 3-phosphoshikimate 1-carboxyvinyltransferase...	91	5e-16
dbj BAJ41481.1 3-phosphoshikimate 1-carboxyvinyltransferase [La...	91	5e-16
ref ZP_04825363.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	91	5e-16
gb ADC28481.1 3-phosphoshikimate 1-carboxyvinyltransferase [Cam...	90	6e-16
ref ZP_03223145.1 3-phosphoshikimate-1-carboxyvinyltransferase ...	90	6e-16
ref YP_001000570.1 3-phosphoshikimate 1-carboxyvinyltransferase...	90	6e-16
ref NP_384359.1 3-phosphoshikimate 1-carboxyvinyltransferase [S...	90	6e-16
sp A1VZM9.2 AROA_CAMJU RecName: Full=3-phosphoshikimate 1-carbox...	90	6e-16
ref ZP_03609839.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	90	6e-16
ref YP_002301651.1 3-phosphoshikimate 1-carboxyvinyltransferase...	90	7e-16
gb ADU84995.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	90	7e-16
ref YP_301370.1 3-phosphoshikimate 1-carboxyvinyltransferase [S...	90	7e-16
gb ADN80165.1 5-Enol pyruvyl shikimate-3-phosphate synthase [He...	90	7e-16
gb ACX98152.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	90	7e-16
gb ADG03677.1 5-enolpyruvylshikimate 3-phosphate synthase [Ochr...	90	8e-16
sp A8FLU4.2 AROA_CAMJ8 RecName: Full=3-phosphoshikimate 1-carbox...	90	8e-16
ref XP_002163382.1 PREDICTED: hypothetical protein [Hydra magni...	90	8e-16
ref YP_001482408.1 3-phosphoshikimate 1-carboxyvinyltransferase...	90	8e-16
ref YP_001639594.1 3-phosphoshikimate 1-carboxyvinyltransferase...	90	9e-16
ref ZP_01068463.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	90	9e-16
gb EFV09124.1 3-phosphoshikimate 1-carboxyvinyltransferase [Cam...	90	9e-16
ref YP_001191935.1 3-phosphoshikimate 1-carboxyvinyltransferase...	89	1e-15
ref YP_002421176.1 3-phosphoshikimate 1-carboxyvinyltransferase...	89	1e-15
ref ZP_07399273.1 3-phosphoshikimate 1-carboxyvinyltransferase ...	89	1e-15
gb ADU80242.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	89	1e-15
gb ADO04216.1 3-phosphoshikimate 1-carboxyvinyltransferase [Hel...	89	1e-15

ref ZP_07476226.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	89	1e-15
ref YP_003057713.1	3-phosphoshikimate 1-carboxyvinyltransferase...	89	1e-15
ref NP_223697.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	89	1e-15
ref ZP_03305162.1	hypothetical protein ANHYDRO_01599 [Anaerococ...	89	1e-15
ref ZP_06499379.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	89	1e-15
ref ZP_05635999.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	89	1e-15
ref YP_003068413.1	3-enolpyruvylshikimate-5-phosphate synthetas...	89	1e-15
ref ZP_04679202.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	89	2e-15
sp P0A2Y4.1 AROA_PSES2	RecName: Full=3-phosphoshikimate 1-carbox...	89	2e-15
ref YP_425387.1	3-phosphoshikimate 1-carboxyvinyltransferase [R...	89	2e-15
ref YP_178972.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	89	2e-15
sp A8Z6D5.1 AROA_CAMC1	RecName: Full=3-phosphoshikimate 1-carbox...	88	2e-15
ref YP_023380.1	3-phosphoshikimate 1-carboxyvinyltransferase [P...	88	2e-15
ref NP_111838.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	88	2e-15
ref YP_001758244.1	3-phosphoshikimate 1-carboxyvinyltransferase...	88	3e-15
ref ZP_00367067.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	88	3e-15
ref YP_001253986.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	4e-15
ref YP_001490938.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	5e-15
ref YP_001773239.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	5e-15
ref ZP_01870782.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	87	6e-15
ref YP_220807.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	87	6e-15
ref YP_003105996.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	6e-15
ref YP_002803900.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	6e-15
ref YP_413526.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	87	7e-15
ref YP_001626705.1	3-phosphoshikimate 1-carboxyvinyltransferase...	87	7e-15
ref NP_697067.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	87	7e-15
ref ZP_06792105.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	8e-15
ref ZP_02614795.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	8e-15
ref ZP_08032456.1	EPSP synthase [Actinomyces sp. oral taxon 171...	86	9e-15
ref YP_001781111.1	3-phosphoshikimate 1-carboxyvinyltransferase...	86	9e-15
ref ZP_05822047.1	5-enolpyruvyl shikimate 3-phosphate synthase ...	86	9e-15
sp Q46550.1 AROA_DICNO	RecName: Full=3-phosphoshikimate 1-carbox...	86	1e-14
ref ZP_03784612.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	1e-14
ref ZP_05180057.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	1e-14
ref ZP_07891778.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	1e-14
ref ZP_04593499.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	1e-14
ref ZP_07475325.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	86	1e-14
ref YP_001258071.1	3-phosphoshikimate 1-carboxyvinyltransferase...	86	2e-14
ref ZP_05448692.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	85	2e-14
ref ZP_01070338.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	85	2e-14
ref ZP_05626392.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	85	2e-14
emb CBZ03356.1	5-Enolpyruvylshikimate-3-phosphate synthase [Clo...	85	2e-14
ref ZP_05922163.1	LOW QUALITY PROTEIN: 3-phosphoshikimate 1-car...	85	2e-14
ref NP_540834.1	3-phosphoshikimate 1-carboxyvinyltransferase [B...	85	2e-14
ref ZP_05156657.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	85	2e-14
gb AAK62987.2 AF387597_1	EPSP synthase [Nicotiana sylvestris] >g...	84	3e-14
gb AAK62989.2 AF387599_1	EPSP synthase [Nicotiana tomentosiformis]	84	3e-14
gb AAK27445.1 AF326475_1	5-enolpyruvyl shikimate 3-phosphate syn...	84	3e-14
gb AAK62986.2 AF387596_1	EPSP synthase 2 [Nicotiana tabacum]	84	3e-14
ref YP_001209041.1	3-phosphoshikimate 1-carboxyvinyltransferase...	84	5e-14
ref ZP_03636944.1	hypothetical protein HOLDEFILI_04270 [Holdema...	84	6e-14
ref ZP_06522794.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	83	9e-14
gb AAX21644.1 AroA	[Wolbachia persica]	83	1e-13
ref ZP_03655937.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	83	1e-13
emb CBL42035.1	5-enolpyruvylshikimate-3-phosphate synthase [but...	82	1e-13
pdb 2PQD A Chain A, Al00g	Cp4 Epsps Liganded With (R)-Difluorome...	82	1e-13
pdb 2GGD A Chain A, Cp4	Eps Synthase Ala100gly Liganded With S3...	82	2e-13
ref YP_001407856.1	3-phosphoshikimate 1-carboxyvinyltransferase...	81	3e-13
ref YP_374215.1	3-phosphoshikimate 1-carboxyvinyltransferase [C...	81	3e-13
ref YP_003109953.1	3-phosphoshikimate 1-carboxyvinyltransferase...	81	4e-13
gb ADI18937.1	5-enolpyruvylshikimate-3-phosphate synthase [uncu...	81	4e-13
pdb 2PQB A Chain A, Cp4	Epsps Liganded With (R)-Difluoromethyl T...	80	6e-13
ref YP_001697683.1	3-phosphoshikimate 1-carboxyvinyltransferase...	80	8e-13
sp Q9R4E4.2 AROA_AGRSC	RecName: Full=3-phosphoshikimate 1-carbox...	80	9e-13
gb AAL67577.1 AF464188_1	CP4EPSPS [Glycine max] >gi 27549260 gb ...	80	9e-13
ref YP_664289.1	3-phosphoshikimate 1-carboxyvinyltransferase [H...	79	1e-12
dbj BAD94823.1	5-enol-pyruvylshikimate-3-phosphate synthase clas...	79	1e-12
gb EDZ73130.1	YDR127Wp-like protein [Saccharomyces cerevisiae A...	79	1e-12
ref ZP_08072352.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	79	2e-12
ref ZP_08142635.1	bifunctional cyclohexadienyl dehydrogenase/ 3...	79	2e-12
gb ADU03259.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	78	3e-12

ref ZP_04126962.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	78	3e-12
ref YP_002828058.1	3-phosphoshikimate 1-carboxyvinyltransferase...	78	3e-12
ref ZP_03806227.1	hypothetical protein PROPEN_04629 [Proteus pe...	78	3e-12
ref ZP_03510971.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	77	6e-12
ref ZP_02862022.1	hypothetical protein ANASTE_01235 [Anaerofust...	75	1e-11
ref ZP_02164769.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	75	1e-11
gb ABC00780.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	75	2e-11
gb EFV96997.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	73	9e-11
gb ABZ09592.1	putative EPSP synthase (3-phosphoshikimate 1-carb...	73	9e-11
emb CBL42034.1	5-enolpyruvylshikimate-3-phosphate synthase [but...	72	1e-10
ref YP_261736.1	prephenate dehydrogenase /3-phosphoshikimate 1-...	72	1e-10
ref ZP_06221622.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	72	2e-10
ref ZP_06223002.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	72	2e-10
gb ACB05434.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	72	2e-10
ref NP_147921.2	3-phosphoshikimate 1-carboxyvinyltransferase [A...	72	2e-10
ref YP_001329109.1	3-phosphoshikimate 1-carboxyvinyltransferase...	72	3e-10
gb ACB05431.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	71	4e-10
ref ZP_03832182.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	70	6e-10
ref ZP_04126963.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	70	7e-10
ref YP_001815138.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	69	1e-09
ref ZP_01264335.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	69	1e-09
ref ZP_00051744.2	COG128: 5-enolpyruvylshikimate-3-phosphate s...	69	1e-09
ref ZP_03634371.1	hypothetical protein HOLDEFILI_01664 [Holdema...	69	2e-09
ref YP_088899.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	68	3e-09
gb ABZ10397.1	putative EPSP synthase (3-phosphoshikimate 1-carb...	68	3e-09
ref NP_872847.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	68	4e-09
gb ABZ06003.1	putative EPSP synthase (3-phosphoshikimate 1-carb...	67	5e-09
ref ZP_04978529.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	67	5e-09
ref ZP_07528285.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	67	6e-09
ref ZP_05990592.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	67	6e-09
gb AAA81514.1	5-enolpyruvylshikimate-3-phosphate-synthase [Esch...	67	7e-09
ref ZP_05922164.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	67	7e-09
emb CBI77162.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...	67	8e-09
emb CBI78616.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...	66	8e-09
ref YP_001053977.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	66	9e-09
ref YP_002475331.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	66	1e-08
ref ZP_02868920.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	66	1e-08
ref ZP_03366990.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	66	1e-08
emb CBI80133.1	3-phosphoshikimate 1-carboxyvinyltransferase [Ba...	66	1e-08
ref ZP_06552741.1	hypothetical protein AWRIB429_0131 [Oenococcu...	65	1e-08
ref ZP_03148433.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	65	2e-08
ref YP_001127373.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	65	2e-08
ref ZP_00135108.1	COG0766: UDP-N-acetylglucosamine enolpyruvyl ...	65	2e-08
ref ZP_07532482.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	65	2e-08
ref YP_001652299.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	65	3e-08
ref YP_265919.2	3-phosphoshikimate 1-carboxyvinyltransferase [C...	65	3e-08
gb ACB05432.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	64	4e-08
gb AAD47362.2	AF038578_5 cyclohexadienyl dehydrogenase/5-enolpyr...	64	4e-08
ref ZP_02477459.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	64	4e-08
ref ZP_03437775.1	hypothetical protein HPB128_142g26 [Helicobac...	64	4e-08
ref YP_001969131.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	64	5e-08
gb EFV96998.1	3-phosphoshikimate 1-carboxyvinyltransferase [Str...	64	5e-08
gb ABC00790.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	64	6e-08
ref YP_004066395.1	3-phosphoshikimate 1-carboxyvinyltransferase...	64	6e-08
ref YP_004168093.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	63	9e-08
ref ZP_08068303.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	62	1e-07
ref YP_004010930.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	62	1e-07
ref YP_003426316.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	62	2e-07
ref YP_660138.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	62	2e-07
emb CAN79289.1	hypothetical protein VITISV_044036 [Vitis vinifera]	62	2e-07
ref ZP_04858335.1	conserved hypothetical protein [Ruminococcus ...	62	2e-07
gb AAA97396.1	encodes EPSP synthase domain [Pneumocystis murina...	62	2e-07
ref YP_633066.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	62	3e-07
ref YP_980934.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	61	3e-07
gb AAK64441.1	AF377339_2 UDP-GlcNAc 1-carboxyvinyl transferase M...	61	3e-07
ref YP_003467663.1	3-phosphoshikimate 1-carboxyvinyltransferase...	61	3e-07
gb ACB05435.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	61	4e-07
gb ACB05433.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	61	4e-07
ref ZP_04752696.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	61	4e-07
ref ZP_05297041.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	61	4e-07
ref ZP_07896341.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	61	4e-07

ref YP_004062583.1	3-phosphoshikimate 1-carboxyvinyltransferase...	60	5e-07
ref YP_003495370.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	60	6e-07
ref YP_149194.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	60	7e-07
gb EFR84087.1	3-phosphoshikimate 1-carboxyvinyltransferase [Lis...	60	7e-07
ref ZP_07399236.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	60	8e-07
ref YP_003672818.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	60	9e-07
ref ZP_07956900.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	60	9e-07
gb ADU52755.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	60	1e-06
ref YP_003254430.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	60	1e-06
gb ACO70904.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	59	1e-06
gb ADU52729.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	1e-06
ref ZP_02439591.1	hypothetical protein CLOSS21_02057 [Clostridi...	59	1e-06
gb ADU52752.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	1e-06
ref YP_003701185.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	59	1e-06
ref YP_003565556.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	59	1e-06
ref YP_001354980.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	59	1e-06
gb ADU52795.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	1e-06
gb ADU52732.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
gb ADU52784.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
ref YP_003600279.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	59	2e-06
ref ZP_07921844.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	59	2e-06
gb ADU52763.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
gb ADU52785.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
gb ADU52728.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
ref ZP_05649870.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	59	2e-06
gb ADU52756.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
ref ZP_03612083.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	59	2e-06
gb ADU52776.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
gb ADU52783.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
gb ADU52727.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
ref YP_003151592.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	59	2e-06
gb ADU52757.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	59	2e-06
emb CBI20198.3	unnamed protein product [Vitis vinifera]	58	2e-06
gb EFR92855.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	58	2e-06
gb ADU52741.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	58	2e-06
gb ADU52779.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	58	2e-06
gb ADO96649.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	58	3e-06
ref YP_872128.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	58	3e-06
gb ADU52773.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	58	3e-06
ref ZP_05657191.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	58	3e-06
gb ADU52786.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	58	3e-06
gb ADU52745.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	58	4e-06
gb ADU52733.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	4e-06
ref YP_002317025.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	57	4e-06
gb ADU52765.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	4e-06
ref YP_001800982.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	57	5e-06
ref YP_004135636.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	57	5e-06
ref ZP_06062508.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	57	5e-06
ref YP_001617525.1	3-phosphoshikimate 1-carboxyvinyltransferase...	57	5e-06
gb AAA97397.1	encodes EPSP synthase domain [Pneumocystis orycto...	57	5e-06
gb ADU52791.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	5e-06
ref YP_003064871.1	3-phosphoshikimate 1-carboxyvinyltransferase...	57	6e-06
ref NP_393762.1	3-phosphoshikimate 1-carboxyvinyltransferase [T...	57	6e-06
gb ADU52731.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	6e-06
ref ZP_01796349.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	57	6e-06
gb ADU52774.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	6e-06
gb ADU52794.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	6e-06
ref ZP_01783755.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	57	6e-06
gb ADU52768.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	7e-06
gb ADU52747.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	7e-06
ref ZP_02004393.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	57	7e-06
ref YP_001291058.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	57	7e-06
ref YP_001942592.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	57	7e-06
ref YP_004139154.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	57	7e-06
gb ADU52744.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	57	8e-06
ref ZP_06810684.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	57	8e-06
gb AAV48979.1	hypothetical carboxyvinyltransferase [Weissella p...	57	8e-06
ref ZP_01792135.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	57	8e-06
ref YP_001095423.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	56	9e-06
emb CBW99666.1	3-phosphoshikimate 1-carboxyvinyltransferase [Le...	56	9e-06
gb EFT44670.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	56	9e-06

ref ZP_05593788.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	56	9e-06
ref ZP_07547874.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	56	1e-05
ref YP_001951063.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	56	1e-05
gb ADU52778.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	56	1e-05
ref ZP_01788180.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	56	1e-05
ref ZP_06444105.1	LOW QUALITY PROTEIN: UDP-N-acetylglucosamine ...	56	1e-05
ref ZP_08148960.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	56	1e-05
ref YP_248750.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	56	1e-05
ref NP_816244.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	56	1e-05
ref NP_215831.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	56	1e-05
ref NP_244616.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	56	1e-05
ref YP_015087.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	56	1e-05
gb ACB05436.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	56	1e-05
ref YP_004159437.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	55	1e-05
ref ZP_05670034.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref ZP_05647112.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
gb ADU52736.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	55	2e-05
emb CBL20721.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	55	2e-05
gb ADH42952.1	UDP-N-acetylglucosamine enolpyruvyl transferase [...	55	2e-05
ref ZP_07759297.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref ZP_05069059.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref ZP_00604477.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref YP_001341704.1	bifunctional cyclohexadienyl dehydrogenase/ ...	55	2e-05
ref ZP_05492794.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
emb CBW29426.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	55	2e-05
ref ZP_01911939.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref YP_001213408.1	UDP-N-acetylglucosamine enolpyruvyl transfer...	55	2e-05
ref YP_463577.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	55	2e-05
ref YP_561517.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	55	2e-05
gb ABC00783.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	55	2e-05
ref NP_466049.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	55	2e-05
ref YP_003181465.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	55	2e-05
ref NP_471999.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	55	2e-05
gb ADU52730.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	55	2e-05
ref ZP_03439747.1	hypothetical protein HP9810_49lg24 [Helicobac...	55	2e-05
ref ZP_05662363.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref YP_002349049.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	55	2e-05
ref ZP_06683403.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	2e-05
ref NP_439238.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	55	2e-05
ref YP_001292996.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	55	2e-05
gb ADU52739.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	55	2e-05
ref YP_001344097.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	55	3e-05
emb CBL40942.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	55	3e-05
ref ZP_01463041.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	3e-05
ref ZP_08145248.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	3e-05
ref YP_001675891.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	55	3e-05
ref ZP_08103692.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	3e-05
gb ADU52748.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	55	3e-05
ref ZP_05746581.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	55	3e-05
ref YP_001647859.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	3e-05
ref YP_002951194.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	3e-05
ref ZP_03982092.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	3e-05
ref ZP_06488789.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	54	4e-05
ref ZP_03128341.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	4e-05
ref YP_001503451.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	4e-05
emb CBW15237.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	54	4e-05
gb ADU52789.1	3-phosphoshikimate 1-carboxyvinyltransferase [unc...	54	4e-05
ref YP_001664112.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	4e-05
ref YP_003007876.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	4e-05
ref YP_727854.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	54	4e-05
gb ACB05440.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	54	4e-05
ref YP_795412.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	54	4e-05
ref YP_001197964.1	5-enolpyruvylshikimate-3-phosphate synthase ...	54	4e-05
ref YP_003555177.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	5e-05
ref YP_902699.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	54	5e-05
ref YP_003590968.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	54	5e-05
ref ZP_03936449.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	5e-05
ref YP_002774913.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	5e-05
ref YP_001797038.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	5e-05
ref ZP_05788793.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	5e-05
ref YP_002943080.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	5e-05

ref	ZP_03228143.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	5e-05
ref	YP_003338602.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	54	5e-05
ref	YP_003465659.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	54	6e-05
ref	YP_001939082.1	UDP-N-acetylglucosamine enolpyruvyl transfer...	54	6e-05
ref	ZP_06697214.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	6e-05
ref	ZP_08142636.1	bifunctional cyclohexadienyl dehydrogenase/ 3...	54	6e-05
ref	ZP_05359516.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	6e-05
ref	ZP_06347761.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	6e-05
ref	ZP_08080242.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	54	7e-05
ref	ZP_06008579.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	54	7e-05
ref	YP_381189.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	54	7e-05
ref	ZP_05215869.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	8e-05
ref	ZP_05085293.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	8e-05
ref	ZP_05077320.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	8e-05
ref	ZP_04153908.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	8e-05
ref	YP_002132763.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	8e-05
ref	ZP_05826488.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	53	8e-05
ref	YP_003800152.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	9e-05
ref	ZP_04165189.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	9e-05
ref	XP_002371877.1	AROM polypeptide/ shikimate-quininate 5-dehydr...	53	9e-05
gb	AAQ83833.1	AROM polypeptide [Toxoplasma gondii]	53	9e-05
gb	EEE19204.1	AROM polypeptide/ shikimate-quininate 5-dehydrogena...	53	9e-05
ref	YP_002490817.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	9e-05
ref	YP_547656.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	53	9e-05
ref	ZP_06066705.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	9e-05
ref	ZP_03753048.1	hypothetical protein ROSEINA2194_01459 [Roseb...	53	1e-04
ref	YP_850671.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	53	1e-04
ref	NP_961381.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	53	1e-04
ref	YP_001708014.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
emb	CBL22590.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	53	1e-04
ref	YP_001101301.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	ZP_07205703.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	ZP_01964667.1	hypothetical protein RUMOB_E02392 [Ruminococc...	53	1e-04
ref	YP_003193454.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	53	1e-04
ref	YP_003782309.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	ZP_05113520.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	YP_001663939.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	YP_001393545.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	ZP_06636240.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	XP_002283120.1	PREDICTED: hypothetical protein [Vitis vinif...	53	1e-04
ref	YP_001714915.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	YP_001376991.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	53	1e-04
ref	ZP_08004986.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	ZP_02927317.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	ZP_06752546.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	53	1e-04
ref	YP_004059547.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	1e-04
ref	YP_535495.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	1e-04
ref	YP_907486.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	1e-04
ref	YP_004153576.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	1e-04
ref	YP_001852345.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	52	1e-04
ref	YP_001197962.1	5-enolpyruvylshikimate-3-phosphate synthase ...	52	1e-04
ref	ZP_07931459.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	1e-04
ref	ZP_00742764.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	1e-04
ref	ZP_04188873.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	1e-04
ref	YP_177339.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	1e-04
gb	ABC00781.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	52	1e-04
ref	YP_001154891.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
ref	NP_739053.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref	ZP_05748914.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref	YP_001666059.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
ref	NP_847687.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref	ZP_05827805.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref	YP_002774968.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
ref	ZP_02420461.1	hypothetical protein ANACAC_03078 [Anaerostip...	52	2e-04
ref	NP_981704.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref	ZP_05092906.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref	YP_039278.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref	ZP_05367026.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref	YP_001762578.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
gb	AAA97398.1	encodes EPSP synthase domain [Pneumocystis jirove...	52	2e-04
ref	ZP_03928220.1	possible 3-phosphoshikimate 1-carboxyvinyltra...	52	2e-04

ref NP_834951.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref NP_624199.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref ZP_04946771.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	52	2e-04
ref YP_002006863.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
ref ZP_07991679.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref ZP_04748159.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref YP_002885677.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	52	2e-04
gb ABC00786.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	52	2e-04
ref ZP_07711396.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref ZP_03943118.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
ref YP_528639.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	52	2e-04
ref ZP_07053722.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	52	2e-04
emb CAN76209.1	hypothetical protein VITISV_041624 [Vitis vinifera]	52	3e-04
ref YP_001086592.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	51	3e-04
ref ZP_04466225.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	51	3e-04
ref NP_693894.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	51	3e-04
ref ZP_03784314.1	hypothetical protein RUMHYD_03797 [Blautia hy...	51	3e-04
gb ACB05443.1	chloroplast 5-enolpyruvylshikimate 3-phosphate sy...	51	3e-04
ref ZP_05270254.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	51	4e-04
ref ZP_04219897.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	51	4e-04
ref YP_003256074.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	51	4e-04
ref ZP_03940189.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	51	4e-04
ref ZP_03824066.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	51	4e-04
gb AAB32920.1	enolpyruvylshikimate-3-phosphate synthase type B ...	51	4e-04
emb CBL28304.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	51	5e-04
ref YP_001381377.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	51	5e-04
ref ZP_07729106.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	5e-04
ref NP_871332.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	50	6e-04
ref YP_003839890.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	6e-04
ref ZP_05345049.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	6e-04
ref YP_045400.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	50	6e-04
ref ZP_05116642.1	EPSP synthase (3-phosphoshikimate 1-carboxyvi...	50	6e-04
ref ZP_03237826.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	6e-04
ref ZP_03292078.1	hypothetical protein CLOHIR_00021 [Clostridiu...	50	6e-04
ref YP_002905746.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	6e-04
ref ZP_05226314.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	6e-04
ref ZP_05852759.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	7e-04
ref YP_002885719.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	7e-04
ref ZP_06804882.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	7e-04
ref YP_001997332.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	7e-04
ref ZP_05888320.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	8e-04
ref ZP_00990836.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	8e-04
ref ZP_01168542.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	50	9e-04
ref YP_001578518.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	9e-04
ref YP_002936386.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	9e-04
ref YP_003822651.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	9e-04
gb EFV87840.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	50	0.001
ref YP_002572527.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	0.001
ref YP_004024659.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	0.001
ref ZP_08088814.1	hypothetical protein HMPREF9474_00563 [Clostr...	50	0.001
ref YP_003675988.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	50	0.001
ref NP_661455.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	49	0.001
ref YP_003733525.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref ZP_06691517.1	conserved hypothetical protein [Acinetobacter...	49	0.001
ref ZP_06552740.1	hypothetical protein AWRIB429_0130 [Oenococcu...	49	0.001
ref ZP_06068840.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.001
ref ZP_04431559.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.001
ref YP_002753299.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref ZP_02871517.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	49	0.001
ref ZP_06851848.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.001
ref ZP_04795951.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.001
ref YP_001118249.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref ZP_01075177.1	prephenate [Marinomonas sp. MED121] >gi 86165...	49	0.001
gb ADP66777.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	49	0.001
ref YP_003478076.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref YP_003646229.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	49	0.001
ref YP_003476026.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref NP_227924.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	49	0.001
ref ZP_01814316.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.001
ref YP_003471188.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.001
ref YP_755129.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	49	0.001

ref	YP_003784095.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	49	0.001
ref	YP_001312124.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	NP_765253.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	49	0.002
ref	ZP_06059231.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	49	0.002
ref	YP_397892.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	49	0.002
ref	ZP_04446643.1	hypothetical protein COLINT_03386 [Collinsell...	49	0.002
ref	ZP_02536200.1	prephenate dehydrogenase/3-phosphoshikimate 1...	49	0.002
ref	ZP_01550531.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	ZP_07547188.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	YP_003638954.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	YP_002418285.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	YP_001906282.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	ZP_07818998.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	YP_002310095.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	ZP_03343953.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	49	0.002
emb	CAP05278.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	49	0.002
ref	YP_004151432.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	YP_002127468.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	ZP_04577736.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	ZP_01899239.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	YP_002017759.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	YP_003777449.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	NP_933254.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	49	0.002
ref	ZP_05855351.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	ZP_03394652.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	49	0.002
ref	YP_003993105.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	YP_001166802.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	49	0.002
ref	ZP_05112851.1	hypothetical protein SADFL1_736 [Labrenzia a...	49	0.002
ref	ZP_02862694.1	hypothetical protein ANASTE_01915 [Anaerofust...	49	0.002
ref	ZP_03729812.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.002
ref	ZP_04629099.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.002
ref	NP_759664.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.002
ref	ZP_04714868.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.002
gb	EGD01795.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	48	0.002
ref	YP_001490753.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	48	0.003
ref	NP_940224.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	NP_213879.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	ZP_02364356.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.003
ref	ZP_06895435.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.003
ref	YP_004189900.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	48	0.003
ref	YP_297317.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	YP_391256.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	NP_391557.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	ZP_04639705.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.003
ref	ZP_06873785.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.003
ref	YP_199929.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.003
ref	YP_002910234.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	48	0.003
ref	YP_002468681.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	48	0.004
gb	AAB32919.1	enolpyruvylshikimate-3-phosphate synthase type A ...	48	0.004
ref	YP_003922109.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	48	0.004
ref	ZP_05089357.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.004
ref	ZP_02886904.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	48	0.004
ref	NP_240203.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	48	0.004
ref	ZP_07965738.1	aroA protein [Segniliparus rugosus ATCC BAA-9...	48	0.004
ref	YP_459350.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.004
ref	ZP_06756496.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	YP_003677894.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.004
ref	ZP_07891665.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	ZP_05132794.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	YP_001439629.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.004
ref	ZP_06599658.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	YP_001763704.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.004
ref	ZP_06114897.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	NP_819777.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.004
ref	ZP_03992331.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.004
ref	ZP_06412234.1	5-enolpyruvylshikimate-3-phosphate synthase-1...	47	0.004
ref	YP_001011775.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.004
ref	ZP_07403093.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	ZP_07053752.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	ZP_07229751.1	prephenate dehydrogenase/3-phosphoshikimate 1...	47	0.005
ref	YP_003785769.1	UDP-N-acetylglucosamine 1 carboxyvinyltransf...	47	0.005

ref	YP_003208752.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.005
ref	ZP_03396860.1	prephenate dehydrogenase/3-phosphoshikimate 1...	47	0.005
ref	ZP_03708546.1	hypothetical protein CLOSTMETH_03307 [Clostri...	47	0.005
ref	NP_621855.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.005
ref	ZP_02464987.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	YP_001466853.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.005
ref	ZP_07256020.1	prephenate dehydrogenase/3-phosphoshikimate 1...	47	0.005
ref	ZP_06638530.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	ZP_02430755.1	hypothetical protein CLOSCI_00968 [Clostridiu...	47	0.005
ref	YP_443499.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.005
ref	NP_791573.1	prephenate dehydrogenase/3-phosphoshikimate 1-c...	47	0.005
ref	YP_002468128.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.005
ref	ZP_05092716.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	ZP_06285360.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	NP_563522.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.005
ref	ZP_05390962.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	ZP_05121187.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.005
ref	YP_002229476.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.005
ref	YP_772235.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.005
ref	YP_003589699.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	47	0.005
emb	CAC20647.1	UDP-N-acetylglucosamine enolpyruvyl transferase ...	47	0.005
ref	ZP_08116402.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
ref	ZP_01065877.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
ref	ZP_07147705.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
ref	ZP_07093610.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
emb	CBX27296.1	UDP-N-acetylglucosamine1-carboxyvinyltransferase...	47	0.006
ref	NP_638143.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.006
ref	YP_003319676.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	47	0.006
ref	ZP_05860438.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
ref	ZP_02905697.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.006
ref	YP_001807067.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.006
ref	ZP_08092037.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.007
ref	YP_001422952.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	YP_003180311.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	47	0.007
ref	ZP_01113773.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.007
ref	YP_004182161.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
emb	CBL05022.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	47	0.007
ref	YP_001020026.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	YP_003743403.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	YP_003650793.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	47	0.007
ref	YP_001356424.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	ZP_00958670.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.007
ref	YP_003346247.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	NP_350124.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.007
ref	YP_004001889.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	47	0.007
ref	YP_985078.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	47	0.008
ref	ZP_01453229.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.008
ref	ZP_03717239.1	hypothetical protein EUBHAL_02316 [Eubacteriu...	47	0.008
ref	YP_003975118.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.008
ref	ZP_02948415.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.008
ref	ZP_01861862.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.008
gb	ADP67872.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	47	0.008
emb	CBX30742.1	UDP-N-acetylglucosamine1-carboxyvinyltransferase...	47	0.008
ref	YP_003652039.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	47	0.008
emb	CBJ36651.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	47	0.008
ref	ZP_07843301.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.008
ref	ZP_06291770.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.008
ref	ZP_07204034.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	47	0.009
ref	YP_004229675.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.009
ref	YP_002526349.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.009
ref	YP_001998201.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	47	0.009
ref	YP_828618.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.009
ref	ZP_02357249.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.009
emb	CBK73555.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	46	0.009
ref	ZP_04587482.1	prephenate dehydrogenase/3-phosphoshikimate 1...	46	0.009
ref	ZP_04625219.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.009
ref	ZP_03932203.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.009
gb	ABC00785.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	46	0.009
ref	YP_149237.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.009
ref	YP_003633629.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	46	0.010
ref	ZP_01551380.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.010

ref YP_003529687.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.010
sp Q39K93.1 MURA_BURS3	RecName: Full=UDP-N-acetylglucosamine 1-c...	46	0.010
ref ZP_01011608.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.010
ref ZP_00945241.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.010
ref YP_002989223.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.010
ref ZP_02002319.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	46	0.010
ref ZP_05099909.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.011
ref ZP_02328243.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.011
ref YP_364841.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.011
ref YP_001044160.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.011
ref ZP_04059651.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.012
ref YP_002552204.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.012
ref YP_641033.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.012
ref ZP_06191504.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.012
ref ZP_04619481.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.012
ref ZP_07837024.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.012
ref YP_004218083.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.013
ref ZP_06393255.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfer...	46	0.013
ref YP_001027765.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.013
ref YP_003949133.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.013
ref ZP_02890556.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.013
ref YP_104237.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.013
ref ZP_02483554.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.013
ref ZP_02149399.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	46	0.013
ref YP_003751221.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.013
ref ZP_05920903.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.013
ref ZP_04612843.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.013
ref YP_001244411.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.014
ref YP_001179992.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.014
ref ZP_07821337.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.014
ref ZP_01742541.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	46	0.014
ref ZP_05942724.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.014
ref YP_001067956.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	46	0.014
ref NP_875765.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	46	0.015
ref ZP_02640560.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	46	0.015
ref YP_109734.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	46	0.015
emb CAM89150.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	45	0.015
ref YP_003382854.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.015
ref ZP_04809089.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.015
ref ZP_03456331.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.016
ref NP_301844.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.016
ref ZP_02404725.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.016
sp P33986.1 MURA_ACIGB	RecName: Full=UDP-N-acetylglucosamine 1-c...	45	0.016
ref YP_353708.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.016
ref ZP_02954248.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.016
ref NP_245117.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.016
ref YP_003872749.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.017
gb ABC00782.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	45	0.017
ref YP_002262034.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.017
emb CAM88970.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	45	0.017
ref YP_004114357.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.018
ref YP_988537.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.018
emb CAM89195.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	45	0.018
ref YP_003714284.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.018
ref ZP_04851607.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.018
ref YP_002287734.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.018
ref ZP_04637320.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.018
ref YP_003829891.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.019
emb CAM89447.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	45	0.019
ref ZP_08096916.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.019
ref ZP_07036313.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.019
ref ZP_07889067.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.020
ref YP_003606379.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.020
ref YP_622555.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.020
ref ZP_08151417.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.020
ref ZP_07635822.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.020
ref ZP_02183884.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.021
ref YP_001484727.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.021
ref YP_003940069.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.022
ref YP_487950.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.022
ref YP_003165888.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.022

ref YP_154801.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.022
gb EFE28162.2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	45	0.023
ref YP_001902771.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.023
ref YP_003853064.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.023
ref NP_829044.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.023
ref YP_003845758.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.023
ref YP_002647380.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.023
ref ZP_07739943.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.023
ref ZP_07469768.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.024
ref ZP_05138543.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.024
ref ZP_05295200.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.025
pdb 3KR6 A Chain A, Mura Dead-End Complex With Fosfomycin		45	0.025
ref YP_003111989.1	UDP-N-acetylglucosaminel-carboxyvinyltransfe...	45	0.026
ref NP_897726.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.026
ref YP_003908400.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.026
ref YP_003336158.1	UDP-N-acetylglucosaminel-carboxyvinyltransfe...	45	0.026
ref YP_004006518.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	45	0.027
ref ZP_06015902.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.027
ref YP_001480576.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.027
pdb 3ISS A Chain A, Crystal Structure Of Enolpyruvyl-Udp-GlcnaC ...		45	0.028
ref ZP_07389387.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.028
ref ZP_02330017.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.028
ref YP_393070.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.029
pdb 3KQJ A Chain A, Mura Binary Complex With Udp-N-Acetylglucosa...		45	0.029
ref YP_571399.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.029
ref YP_002575316.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.029
ref YP_002252270.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	45	0.029
ref ZP_01156460.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.029
gb EGD20404.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	45	0.030
pdb 2Z2C A Chain A, Mura Inhibited By Unag-Cnicin Adduct >gi 282...		45	0.030
ref NP_297114.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.030
gb ADH18157.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	45	0.030
ref NP_521074.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.030
ref ZP_08038603.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.031
ref YP_001337259.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.031
dbj BAA78108.1	UDP-N-acetylglucosamine enolpyruvoyl transferase...	45	0.031
ref YP_367767.2	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	45	0.032
ref ZP_01756491.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.032
ref YP_003042495.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	45	0.032
ref ZP_01264356.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	45	0.032
gb EGB61803.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	45	0.033
ref YP_595156.1	5-enolpyruvylshikimate-3-phosphate synthase [La...	45	0.033
ref YP_004028772.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.033
ref NP_949867.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.033
ref ZP_02144758.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.034
ref ZP_08056149.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.034
ref YP_002835673.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	44	0.034
ref NP_219968.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.035
gb ADX44916.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.035
ref YP_004025746.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.035
ref YP_909046.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.035
ref YP_002888077.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.036
ref NP_954143.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.036
ref YP_928947.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.036
ref YP_001858979.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.036
ref ZP_07398801.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.037
ref ZP_04633531.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.037
ref ZP_05815359.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.038
ref YP_969394.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.038
ref YP_585391.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.038
ref YP_003145844.1	UDP-N-acetylglucosaminel-carboxyvinyltransfe...	44	0.038
ref YP_003465691.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.040
ref NP_893417.1	UDP-N-glucosamine 1-carboxyvinyltransferase [Pr...	44	0.040
ref ZP_07661296.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	44	0.040
ref YP_001456079.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.041
emb CAM89159.1	3-phosphoshikimate-1-carboxyvinyltransferase [Br...	44	0.041
ref NP_995094.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	44	0.043
ref ZP_02441426.1	hypothetical protein ANACOL_00699 [Anaerotrunc...	44	0.043
gb EGD14948.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.046
ref YP_001007900.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.046
ref YP_003008906.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	44	0.046

ref NP_667483.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.046
ref YP_003672859.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.047
ref YP_001031867.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.047
ref YP_001488534.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.047
ref ZP_07388964.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.048
ref YP_003023579.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.048
ref ZP_02330012.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	44	0.048
gb ACY63808.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.049
ref ZP_01769920.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.049
ref YP_001057773.1	3-phosphoshikimate 1-carboxyvinyltransferase...	44	0.049
ref YP_252850.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.049
ref YP_002236399.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.050
ref ZP_02413233.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.050
ref ZP_07736075.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.051
ref YP_001060672.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.052
ref ZP_07519150.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.052
ref YP_003134756.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.053
ref YP_002721901.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.053
ref ZP_03711484.1	hypothetical protein CORMATOL_02331 [Corynebact...	44	0.053
ref ZP_02917249.1	hypothetical protein BIFDEN_00525 [Bifidobact...	44	0.053
ref YP_003254471.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.054
ref NP_875930.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	44	0.056
ref ZP_03613993.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.057
gb EGD09072.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.058
ref ZP_04171573.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.058
ref YP_004195902.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.059
ref YP_001514306.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.059
ref ZP_00502591.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.060
ref ZP_01223692.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.060
gb ABC00789.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	44	0.060
ref ZP_03756298.1	hypothetical protein CLOSTASPAR_00281 [Clostr...	44	0.061
ref ZP_05347124.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.062
ref YP_383350.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.063
ref YP_001717572.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.064
ref ZP_08069594.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.065
emb CB181343.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.065
ref ZP_07723059.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.065
ref ZP_02900958.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.066
ref ZP_06748712.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.066
ref ZP_05808171.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.066
ref YP_003368037.1	UDP-N-acetylglucosamine L-carboxyvinyltransferase...	44	0.067
ref ZP_03241130.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	44	0.067
ref ZP_07162908.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.068
sp Q39YP9.2 MURA_GEOMG RecName: Full=UDP-N-acetylglucosamine 1-c...		44	0.068
ref YP_001654787.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.068
gb EFW78574.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.069
ref YP_237203.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.069
ref ZP_05441356.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.073
ref ZP_03054973.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	44	0.073
ref NP_931225.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.075
ref ZP_05276290.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.076
ref ZP_05380835.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.078
ref ZP_06460536.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.080
ref YP_346601.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.080
pdb 1A2N A Chain A, Structure Of The Cl15a Mutant Of Mura Comple...		43	0.080
ref ZP_07029714.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.082
ref YP_911282.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.082
ref YP_002384263.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.082
ref YP_328277.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.082
ref ZP_08118552.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.085
ref YP_004111016.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.085
ref ZP_03166422.1	hypothetical protein RUMLAC_00068 [Ruminococc...	43	0.085
ref YP_872416.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.086
ref ZP_04574348.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.087
ref NP_643274.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.087
ref YP_004050374.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.088
pdb 3KQA A Chain A, Mura Dead-End Complex With Terreic Acid >gi ...		43	0.088
ref YP_003744447.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.090
ref NP_417656.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.090
ref ZP_03265448.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.093
pdb 1RYW A Chain A, Cl15s Mura Liganded With Reaction Products >...		43	0.093

ref	ZP_04587072.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.094
ref	ZP_06486109.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.096
ref	ZP_02825910.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.096
ref	NP_794195.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.096
ref	ZP_04209462.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.097
ref	YP_409520.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.097
ref	ZP_04148600.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.098
ref	YP_889184.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.098
emb	CAN72374.1	hypothetical protein VITISV_019596 [Vitis vinifera]	43	0.100
ref	ZP_04536540.1	UDP-N-glucosamine 1-carboxyvinyltransferase [...]	43	0.10
ref	ZP_03645634.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.10
ref	YP_107313.1	putative 3-phosphoshikimate 1-carboxyvinyltrans...	43	0.10
ref	ZP_04888326.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	43	0.10
ref	YP_003501381.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.10
ref	ZP_08131360.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.11
ref	YP_004200846.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	YP_002228009.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	NP_289763.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.11
ref	YP_001975520.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	YP_001530432.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	YP_560589.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.11
ref	ZP_04579893.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.11
ref	YP_002870557.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	YP_265898.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.11
ref	YP_001897176.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	ZP_07654793.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.11
ref	YP_004221522.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
ref	YP_003006081.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.11
gb	AAT48249.1	chloroplast CP4-EPSPS fusion protein precursor [G...	43	0.11
ref	XP_003190361.1	udp-n-acetylglucosamine enolpyruvyl transfer...	43	0.12
ref	YP_955107.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.12
ref	ZP_01995869.1	hypothetical protein DORLON_01864 [Dorea long...	43	0.12
gb	EFX33752.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	43	0.12
ref	ZP_07666170.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_06842366.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
pdb	1EJC	[A Chain A, Crystal Structure Of Unliganded Mura (Type2)...	43	0.12
ref	ZP_03298160.1	hypothetical protein COLSTE_02082 [Collinsell...	43	0.12
ref	ZP_01386237.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_01071728.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_05297647.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_07871794.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_06696044.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	43	0.12
ref	ZP_03289868.1	hypothetical protein CLONEX_02075 [Clostridiu...	43	0.12
ref	YP_081035.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.12
ref	YP_002921441.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	43	0.13
ref	YP_865138.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	43	0.13
ref	YP_002522434.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.13
ref	YP_219597.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.13
ref	ZP_04081432.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.13
ref	YP_003985434.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.13
ref	ZP_08096119.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.13
ref	YP_003245915.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.13
ref	ZP_00121228.1	COG0766: UDP-N-acetylglucosamine enolpyruvyl ...	42	0.13
ref	YP_003933214.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	42	0.13
ref	ZP_04067878.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.14
ref	YP_002361756.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.14
ref	YP_250171.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.14
gb	EGC09171.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	42	0.14
ref	ZP_05785274.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.14
ref	ZP_06488982.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.14
gb	ADZ43948.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	42	0.15
ref	ZP_03324899.1	hypothetical protein BIFCAT_01708 [Bifidobact...	42	0.15
gb	EFX83906.1	hypothetical protein DAPPUDRAFT_315300 [Daphnia p...	42	0.15
ref	ZP_03977045.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.15
ref	ZP_03305252.1	hypothetical protein ANHYDRO_01690 [Anaerococ...	42	0.15
ref	YP_001619798.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.15
ref	ZP_03927904.1	possible 3-phosphoshikimate 1-carboxyvinyltra...	42	0.16
ref	ZP_04326074.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.16
ref	ZP_04326505.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.16
ref	YP_004097013.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.16
ref	ZP_02027983.1	hypothetical protein BIFADO_00393 [Bifidobact...	42	0.17

ref	YP_001406481.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.17
ref	YP_002140495.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.17
ref	YP_002250527.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.17
ref	YP_404852.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.17
ref	ZP_01810241.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.17
ref	YP_003015882.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.17
ref	ZP_04087298.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.18
ref	ZP_05846245.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.18
ref	YP_001566541.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.18
ref	YP_515753.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.18
ref	ZP_03742236.1	hypothetical protein BIFPSEUDO_02803 [Bifidob...	42	0.19
ref	YP_001900785.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.19
ref	YP_002323757.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.19
ref	YP_591183.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.19
ref	ZP_02151795.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.19
ref	YP_004066396.1	3-phosphoshikimate 1-carboxyvinyltransferase...	42	0.20
ref	ZP_07829359.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.20
ref	ZP_01744961.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	42	0.20
ref	ZP_05970492.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.20
ref	ZP_07841530.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.21
ref	ZP_04969447.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.21
ref	YP_286592.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.21
ref	YP_003075109.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.21
ref	ZP_06439928.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.22
ref	YP_003257754.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.22
ref	ZP_03778898.1	hypothetical protein CLOHYLEM_05967 [Clostrid...	42	0.22
ref	YP_002153336.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.22
ref	YP_003844500.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.22
ref	YP_002603455.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.23
gb	AAN28945.1	UDP-N-acetylglucosamine enolpyruvyl transferase [...	42	0.23
ref	YP_081000.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.23
ref	ZP_02089276.1	hypothetical protein CLOBOL_06845 [Clostridiu...	42	0.24
ref	ZP_01070396.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.24
ref	YP_004149926.1	UDP-N-acetylglucosamine 1- carboxyvinyltrans...	42	0.24
ref	ZP_02242425.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.24
ref	ZP_01292174.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.24
ref	YP_003297836.1	UDP-N-acetylglucosaminel-carboxyvinyltransfe...	42	0.24
ref	ZP_06703939.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.24
ref	YP_783388.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.24
ref	ZP_07902948.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.25
ref	ZP_06873821.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.25
ref	ZP_04904861.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.25
ref	ZP_00144234.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.25
ref	YP_004067519.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.25
gb	EFZ74474.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	42	0.26
gb	EFW56382.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	42	0.26
ref	YP_752039.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	42	0.26
ref	ZP_06837441.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.27
ref	YP_001775384.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	42	0.27
ref	ZP_02184329.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.28
ref	ZP_06750145.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	42	0.28
ref	YP_315649.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.28
ref	NP_298704.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.28
ref	ZP_03830667.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.29
ref	ZP_00651089.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.29
ref	ZP_08035353.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.30
ref	ZP_07899155.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.30
ref	NP_457686.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.30
ref	YP_001970990.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.30
ref	YP_002431941.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.30
ref	ZP_02206262.1	hypothetical protein COPEUT_01025 [Coprococc...	41	0.30
ref	YP_226799.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.30
ref	YP_534260.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.30
ref	ZP_05551474.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.31
ref	YP_003241909.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.31
ref	YP_198570.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	41	0.32
ref	YP_001538788.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.32
ref	YP_001408257.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.32
ref	ZP_01969168.1	hypothetical protein RUMTOR_02753 [Ruminococc...	41	0.33
ref	NP_107611.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.33
ref	NP_623242.1	UDP-N-acetylglucosamine enolpyruvyl transferase...	41	0.33

ref	ZP_05060454.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.33
ref	YP_003826360.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.34
ref	NP_601757.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.34
ref	YP_003796667.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.35
ref	ZP_07378212.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.35
ref	ZP_04061074.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.35
ref	ZP_04667189.1	conserved hypothetical protein [Clostridiales...	41	0.36
ref	YP_003518733.1	MurA [Pantoea ananatis LMG 20103] >gi 291151...	41	0.37
ref	ZP_04678375.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.37
ref	YP_001564491.1	3-phosphoshikimate 1-carboxyvinyltransferase...	41	0.37
ref	ZP_06371949.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.37
ref	YP_003809885.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.38
ref	ZP_08062751.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.38
ref	ZP_02074519.1	hypothetical protein CLOL250_01289 [Clostridi...	41	0.38
ref	ZP_01314861.1	hypothetical protein Wendoof_01000308 [Wolbac...	41	0.39
ref	ZP_00373787.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.39
gb	ABC00788.1	5-enolpyruvylshikimate 3-phosphate synthase [Loli...	41	0.39
ref	YP_003615048.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.39
gb	EGC83932.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	41	0.40
ref	ZP_07958830.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.40
ref	YP_002217278.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.40
ref	ZP_02234216.1	hypothetical protein DORFOR_01076 [Dorea form...	41	0.40
ref	ZP_01994898.1	hypothetical protein DORLON_00887 [Dorea long...	41	0.40
ref	ZP_04570031.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.41
ref	YP_001139374.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.41
ref	YP_001411799.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.41
ref	YP_002352707.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.41
ref	YP_002767348.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.42
sp	Q9Z3Z6.1	MURA_PSEPU RecName: Full=UDP-N-acetylglucosamine 1-c...	41	0.42
ref	ZP_04383823.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.43
ref	ZP_01161681.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.43
ref	ZP_08117728.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.44
ref	ZP_06026389.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.44
ref	YP_258058.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.44
ref	ZP_02663066.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.45
ref	YP_692280.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.45
ref	YP_374487.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.45
ref	YP_003703632.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.46
ref	YP_003239506.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.46
ref	YP_001307565.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	41	0.46
ref	ZP_01308292.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.47
ref	ZP_00963330.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	41	0.47
ref	ZP_01786781.1	outer-membrane lipoprotein carrier protein pr...	41	0.47
ref	YP_808563.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	41	0.47
ref	ZP_06306534.1	UDP-N-acetylglucosamine 1- carboxyvinyltransf...	41	0.48
ref	ZP_05136197.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.48
ref	ZP_01751008.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.48
ref	YP_004129573.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.49
ref	YP_004111588.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.50
gb	EGC82619.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	40	0.51
ref	ZP_08139584.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.51
ref	YP_003201498.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.51
ref	ZP_06596455.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.51
dbj	BAE61979.1	unnamed protein product [Aspergillus oryzae]	40	0.51
ref	ZP_05736819.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.52
ref	YP_001697682.1	3-phosphoshikimate 1-carboxyvinyltransferase...	40	0.52
ref	NP_760986.1	EPSP synthase [Vibrio vulnificus CMCP6]	40	0.52
ref	ZP_04760892.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.53
ref	YP_001232776.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.53
ref	ZP_03244064.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	40	0.54
ref	ZP_05138598.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.55
ref	ZP_03461559.1	hypothetical protein BACPEC_00616 [Bacteroides...	40	0.55
ref	ZP_08016531.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.56
ref	ZP_04270550.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.57
ref	YP_001532320.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.58
ref	ZP_00440255.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	40	0.58
ref	YP_003553734.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.58
ref	YP_178947.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.59
ref	YP_002924690.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.60
ref	YP_002561158.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.60
ref	ZP_02042003.1	hypothetical protein RUMGNA_02779 [Ruminococc...	40	0.61

ref YP_002248837.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.62
ref ZP_06926955.1	UDP-N-acetylglucosamine enolpyruvyl transfera...	40	0.63
ref YP_003373468.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.63
ref YP_001482381.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.63
ref YP_001983255.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.64
ref ZP_04922705.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.64
ref ZP_06425412.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.65
ref ZP_06124956.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.65
pdb 1DLG A Chain A, Crystal Structure Of The C115s Enterobacter ...		40	0.66
ref YP_003697427.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	40	0.67
ref YP_524186.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.67
ref ZP_06871438.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.68
ref YP_932319.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.68
ref YP_003376608.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.69
ref YP_001341265.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.69
ref YP_820512.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.69
ref YP_002928087.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.70
ref ZP_02871516.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	40	0.71
ref ZP_02959441.1	hypothetical protein PROSTU_01297 [Providenci...	40	0.72
ref YP_001573242.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.72
gb ADY11861.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	40	0.73
emb CBZ54886.1	3-dehydroquinate synthase, related [Neospora can...	40	0.74
ref ZP_06374618.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.75
ref NP_602347.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.75
ref ZP_05658949.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.76
ref ZP_04742949.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.76
ref ZP_05922020.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.80
ref ZP_02963182.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.82
ref ZP_02188226.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.83
ref YP_141530.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.84
ref YP_453891.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.84
ref YP_001127413.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.87
ref YP_606819.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.87
emb CBK86766.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferas...	40	0.91
ref ZP_06117045.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.91
ref YP_001679476.1	udp-n-acetylglucosamine 1-carboxyvinyltransf...	40	0.91
ref YP_001279406.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.91
sp Q5LZ14.2 MURAI_STRT1 RecName: Full=UDP-N-acetylglucosamine 1-...		40	0.92
ref YP_003578698.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.93
ref YP_0033173072.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	40	0.93
ref ZP_08077826.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfe...	40	0.94
ref YP_001922680.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.95
ref NP_799037.1	UDP-N-acetylglucosamine 1-carboxyvinyltransfera...	40	0.96
ref YP_003273072.1	UDP-N-acetylglucosamine1-carboxyvinyltransfe...	40	0.97
ref YP_001483244.1	UDP-N-acetylglucosamine enolpyruvyl transfer...	40	0.97
gb EGD33360.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase...	40	0.98
ref ZP_05069943.1	3-phosphoshikimate 1-carboxyvinyltransferase ...	40	0.99
ref YP_001133588.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	0.99
ref YP_002929553.1	UDP-N-acetylglucosamine 1-carboxyvinyltransf...	40	1.00
gb ABC84481.1	putative 5-enolpyruvylshikimate-3-phosphate synth...	40	1.00

>emb|CAA44974.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 444

Score = 899 bits (2324), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 442/444 (99%), Positives = 442/444 (99%)

Query: 2 AGAEEIVLQPIKEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALR 61
AGAEEIVLQPIKEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALR
Sbjct: 1 AGAEEIVLQPIKEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALR 60

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAG AMR LTAAVTAAGGNATY
Sbjct: 61 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNATY 120

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ
Sbjct: 121 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 180

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK

Sbjct: 181 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 240

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT

Sbjct: 241 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 300

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET

Sbjct: 301 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 360

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT

Sbjct: 361 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 420

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 445
IRDPGCTRKTFPDYFDVLSTFVK

Sbjct: 421 IRDPGCTRKTFPDYFDVLSTFVK 444

>ref|XP_002436424.1| hypothetical protein SORBIDRAFT_10g002230 [Sorghum bicolor]
gb|EER87791.1| hypothetical protein SORBIDRAFT_10g002230 [Sorghum bicolor]
Length = 506

Score = 895 bits (2313), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 437/444 (98%), Positives = 440/444 (99%)

Query: 2 AGAEEIVLQPIKEISGTVKLP GSKSLNRILL AALSEGTTVVDNLLNSEDVHYMLGALR 61
AGAEEIVLQPIKEISGTVKLP GSKSLNRILL AALSEGTTVVDNLLNSEDVHYMLGAL

Sbjct: 63 AGAEEIVLQPIKEISGTVKLP GSKSLNRILL AALSEGTTVVDNLLNSEDVHYMLGALN 122

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
TLGLSVEADK AKRAVVVGCGGKFPVEDAKEEVQLFLGNAG AMR LTAAVTAAGGNATY

Sbjct: 123 TLGLSVEADKVAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNATY 182

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVR+NGIGGLPGGKVKLSGSISSQ

Sbjct: 183 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRINGIGGLPGGKVKLSGSISSQ 242

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK

Sbjct: 243 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 302

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT

Sbjct: 303 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 362

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
ETSVTVTGPPR+PFGRKHLKAIDVNMNKMMPDVAMTLAVVALF+GPTAIRDVASWRVKET

Sbjct: 363 ETSVTVTGPPRQPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFANGPTAIRDVASWRVKET 422

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT

Sbjct: 423 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 482

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 445
IRDPGCTRKTFPDYFDVLSTFVK

Sbjct: 483 IRDPGCTRKTFPDYFDVLSTFVK 506

>emb|CAD01096.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
gb|AAN63155.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
Length = 445

Score = 855 bits (2210), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/445 (97%), Positives = 439/445 (98%), Gaps = 1/445 (0%)

Query: 2 AGAEEIVLQPIKEISGTVKLP GSKSLNRILL AALSEGTTVVDNLLNSEDVHYMLGALR 61
AGAEE+VLQPIKEISG VKLP GSKSLNRILL+AL+EGTTVVDNLLNSEDVHYMLGAL+

Sbjct: 1 AGAEEVVLQPIKEISGVVVKLP GSKSLNRILL SALAEGTTVVDNLLNSEDVHYMLGALK 60

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120

TLGLSVEADKAAKRAVVVCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTAAGGNAT
Sbjct: 61 TLGLSVEADKAAKRAVVVCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNAT 120

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV GIGGLPGGKVKLSGSISS
Sbjct: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVKGIGGLPGGKVKLSGSISS 180

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ
Sbjct: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW
Sbjct: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
TETSVTVTGP REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE
Sbjct: 301 TETSVTVTGPQREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV
Sbjct: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 420

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 445
TIRDPGCTRKTFFPDYFDVLSTFVK
Sbjct: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 445

>emb|CAD01095.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
gb|AAN63156.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
Length = 445

Score = 854 bits (2207), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 434/445 (97%), Positives = 439/445 (98%), Gaps = 1/445 (0%)

Query: 2 AGAEEIVLQPIKEISGTVKLPKSKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALR 61
AGAEE+VLQPIKEISG VKLPKSKSLNRILL+AL+EGTTVVDNLLNSEDVHYMLGAL+
Sbjct: 1 AGAEEVVLQPIKEISGVVVKLPKSKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALK 60

Query: 62 TLGLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
TLGLSVEADKAAKRAVVVCGGKFPVE DAKEEVQLFLGNAG AMRSLTAAVTAAGGNAT
Sbjct: 61 TLGLSVEADKAAKRAVVVCGGKFPVEKDAKEEVQLFLGNAGTAMRSLTAAVTAAGGNAT 120

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV GIGGLPGGKVKLSGSISS
Sbjct: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVKGIGGLPGGKVKLSGSISS 180

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ
Sbjct: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW
Sbjct: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
TETSVTVTGP REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE
Sbjct: 301 TETSVTVTGPQREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
TERMVAIRTELTKLGASVEEGDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV
Sbjct: 361 TERMVAIRTELTKLGASVEEGDYCIITPPEKLNVTADITYDDHRMAMAFSLAACADVPV 420

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 445
TIRDPGCTRKTFFPDYFDVLSTFVK
Sbjct: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 445

>gb|AAR87844.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
Length = 445

Score = 852 bits (2202), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/445 (97%), Positives = 438/445 (98%), Gaps = 1/445 (0%)

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Query: 2   AGAEEIVLQPIKEISGTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
          AGAEE+VLQPIKEISG VKLPGSKSLNRILL+AL+EGTTVVDNLLNSEDVHYMLGAL+
Sbjct: 1   AGAEEVVLQPIKEISGVVKLPGSKSLNRILLLSALAEGTTVVDNLLNSEDVHYMLGALK 60

Query: 62  TLGLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
          TLGLSVEADKAAKRAVVVCGGKFPVE DAKEEVQLFLGNAG AMR+LTAAVTAAGGNAT
Sbjct: 61  TLGLSVEADKAAKRAVVVCGGKFPVEKDAKEEVQLFLGNAGTAMRALTAAVTAAGGNAT 120

Query: 121 YVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISS 180
          YVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRV GIGGLPGGKVKLSGSISS
Sbjct: 121 YVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVKGIGGLPGGKVKLSGSISS 180

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
          QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ
Sbjct: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
          KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLE MGAKVTW
Sbjct: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLETMGAKVTW 300

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE 360
          TETSVTVTGP REPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE
Sbjct: 301 TETSVTVTGPQREPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE 360

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
          TERMVAIRTELTKLGASVEEGPDYCI TPPEKLNVT AIDTYDDHRMAMAFSLAAC+VPV
Sbjct: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPV 420

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVKN 445
          TIRDPGCTRKTFPDYFDVLSTFVKN
Sbjct: 421 TIRDPGCTRKTFPDYFDVLSTFVKN 445

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>gb|AAR87845.1| 5-enolpyruvylshikimate-3-phosphate synthase [Eleusine indica]
Length = 445

Score = 848 bits (2190), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/445 (97%), Positives = 437/445 (98%), Gaps = 1/445 (0%)

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Query: 2   AGAEEIVLQPIKEISGTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
          AGAEE+VLQPIKEISG VKLPGSKSLNRILL+AL+EGTTVVDNLLNSEDVHYMLGAL+
Sbjct: 1   AGAEEVVLQPIKEISGVVKLPGSKSLNRILLLSALAEGTTVVDNLLNSEDVHYMLGALK 60

Query: 62  TLGLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
          TLGLSVEADKAAKRAVVVCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTAAGGNAT
Sbjct: 61  TLGLSVEADKAAKRAVVVCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNAT 120

Query: 121 YVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISS 180
          YVLDGVP RMR ERPIGDLVVGLKQLGADVDCFLGTD PPVRV GIGGLPGGKVKLSGSISS
Sbjct: 121 YVLDGVP RMLERPIGDLVVGLKQLGADVDCFLGTDYPPVRVKGIGGLPGGKVKLSGSISS 180

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
          QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ
Sbjct: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
          KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW
Sbjct: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE 360
          TETSVTVTGP REPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE
Sbjct: 301 TETSVTVTGPQREPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKE 360

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
          TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC+VPV
Sbjct: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPV 420

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVKN 445

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TIRDPGCTRKTFPDYFDVLSTFVKN
Sbjct: 421 TIRDPGCTRKTFPDYFDVLSTFVKN 445

>gb|AAL07437.1|AF413082_1 EPSP synthase [Oryza sativa]
dbj|BAB61062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oryza sativa
(japonica cultivar-group)]
gb|AAL06593.1| 5-enolpyruvylshikimate 3-phosphate synthase [Oryza sativa]
Length = 511

Score = 834 bits (2154), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 419/442 (94%), Positives = 433/442 (97%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVLQPI+EISG V+LPGSKSLSNRILL+ALSEGTTVVDNLLNSEDVHYML AL+ LG
Sbjct: 70 EEIVLQPIREISGAVQLPGSKSLSNRILLLSALSEGTTVVDNLLNSEDVHYMLEALKALG 129

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
LSVEADK AKRAVVVGCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTAAGGNATYVL
Sbjct: 130 LSVEADKVAKRAVVVGCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNATYVL 189

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRV GIGGLPGGKVKLSGSISSQYL
Sbjct: 190 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTCCPPVRVKGIGGLPGGKVKLSGSISSQYL 249

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALLMAAPLALGDVEIEIIDKLISIPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK
Sbjct: 250 SALLMAAPLALGDVEIEIIDKLISIPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 309

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTV+GCGTTSLQGDVKFAEVLEMMGAKVTWT+T
Sbjct: 310 SPGNAYVEGDASSASYFLAGAAITGGTVTVQCGTTSLQGDVKFAEVLEMMGAKVTWTD 369

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPPREP+G+KHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER
Sbjct: 370 SVTVTGPPREPYPGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 429

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
MVAIRTELTKLGASVEEGPDYCIITPPEKLN+TAIDITYDDHRMAMAFSLAAC+VPTIR
Sbjct: 430 MVAIRTELTKLGASVEEGPDYCIITPPEKLNITADITYDDHRMAMAFSLAACADVPVPTIR 489

Query: 424 DPGCTRKTFPDYFDVLSTFVKN 445
DPGCTRKTFP+YFDVLSTFV+N
Sbjct: 490 DPGCTRKTFPNYFDVLSTFVRN 511

>ref|NP_001056712.1| Os06g0133900 [Oryza sativa Japonica Group]
dbj|BAD67887.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Oryza sativa
Japonica Group]
dbj|BAD68865.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Oryza sativa
Japonica Group]
dbj|BAF18626.1| Os06g0133900 [Oryza sativa Japonica Group]
gb|EAY99539.1| hypothetical protein OsI_21508 [Oryza sativa Indica Group]
Length = 515

Score = 834 bits (2154), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 419/442 (94%), Positives = 433/442 (97%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVLQPI+EISG V+LPGSKSLSNRILL+ALSEGTTVVDNLLNSEDVHYML AL+ LG
Sbjct: 74 EEIVLQPIREISGAVQLPGSKSLSNRILLLSALSEGTTVVDNLLNSEDVHYMLEALKALG 133

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
LSVEADK AKRAVVVGCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTAAGGNATYVL
Sbjct: 134 LSVEADKVAKRAVVVGCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNATYVL 193

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRV GIGGLPGGKVKLSGSISSQYL
Sbjct: 194 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTCCPPVRVKGIGGLPGGKVKLSGSISSQYL 253

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK
Sbjct: 254 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 313

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTV+GCGTTSLQGDVKFAEVLEMMGAKVTWT+T
Sbjct: 314 SPGNAYVEGDASSASYFLAGAAITGGTVTVQCGTTSLQGDVKFAEVLEMMGAKVTWTD 373

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPPREP+G+KHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER
Sbjct: 374 SVTVTGPPREPYGKKHLKAVDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 433

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
MVAIRTELTKLGASVEEGPDYCIITPPEKLN+TAIDTYDDHRMAMAFSLAAC+VPVTIR
Sbjct: 434 MVAIRTELTKLGASVEEGPDYCIITPPEKLNITADITYDDHRMAMAFSLAACADVPVTIR 493

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFF+YFDVLSTFV+N
Sbjct: 494 DPGCTRKTFFPNYFDVLSTFVRN 515

>gb|ACH72672.1| 5-enolpyruvylshikimate 3-phosphate synthase [Triticum aestivum]
Length = 510

Score = 827 bits (2137), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 411/445 (92%), Positives = 431/445 (96%), Gaps = 1/445 (0%)

Query: 2 AGAEEIVLQPIKEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
+GAEE+VLQPI+EISG V+LPGSKSLNRILL+ALSEGTTVVDNLLNSEDVHYML AL
Sbjct: 66 SGAEEVVLQPIREISGAVQLPGSKSLNRILLLSALSEGTTVVDNLLNSEDVHYMLEALE 125

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LGLSVEADK AKRAVVVGCGG+FPVE DA+EEV+LFLGNAG AMR LTA AV AAGGNAT
Sbjct: 126 ALGLSVEADKAKRAVVVGCGGRFPVEKDAQEEVKLFLGNAGTAMRPLTAAVVAAGGNAT 185

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
YVLDGVPVRMRERPIGDLVVGL+QLGAD DCFLGT+CPPVR+NG GGLPGGKVKLSGSISS
Sbjct: 186 YVLDGVPVRMRERPIGDLVVGLQQLGADADCF LGTNCPPVRINGKGLPGGKVKLSGSISS 245

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYLS+LMAAPLAL DVEIEIIDKLIS+PYVEMTL+LMERFGV AEHSDSWDRFYIKGGQ
Sbjct: 246 QYLSLLMAAPLALEDVEIEIIDKLISVPYVEMTLKLMERFGVTAEHSDSWDRFYIKGGQ 305

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
KYKSP NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW
Sbjct: 306 KYKSPGNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 365

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
T+TSVTVTGPPR+PFGRKHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE
Sbjct: 366 TDTSVTVTGPPRQPPFGRKHLKAVDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 425

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
TERMVAIRTELTKLGA+VEEGPDYCIITPPEKLN+TAIDTYDDHRMAMAFSLAACAEVPV
Sbjct: 426 TERMVAIRTELTKLGATVEEGPDYCIITPPEKLNITADITYDDHRMAMAFSLAACAEVPV 485

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 445
TIRDPGCTRKTFF+YFDVLSTFVK
Sbjct: 486 TIRDPGCTRKTFFPNYFDVLSTFVK 510

>gb|AAZ79230.2| plastid 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
multiflorum]
Length = 437

Score = 819 bits (2116), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 409/437 (93%), Positives = 424/437 (97%), Gaps = 1/437 (0%)

Query: 10 QPIKEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QPIKEISG V+LPGSKSLNRILL+ALSEGTTVVDNLLNSEDVHYML AL LGLSVEA
Sbjct: 1 QPIKEISGAVQLPGSKSLNRILLLSALSEGTTVVDNLLNSEDVHYMLEALDALGLSVEA 60

Query: 70 DKA AKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 128

Sbjct: 61 DK AKRAVVVGCGG+FP+E DAKEEV+LFLGNAG AMR LTA AV AAGGNATYVLDGVPR 120
Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
MRERPI GDLVVGKQLGA+VDCFLGTDCPPVR+NGIGGLPGGKVKLSGSISSQYLS+LLM
Sbjct: 121 MRERPTGDLVVGKQLGANVDCFLGTDCPPVRINGIGGLPGGKVKLSGSISSQYLSLLM 180
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAPLALGDVEIEIIDKLIS+PYVEMTLRLMERFGV AEHSDSWDRFYIKGGQKYKSP NA
Sbjct: 181 AAPLALGDVEIEIIDKLISVPYVEMTLRLMERFGVTAHSDSWDRFYIKGGQKYKSPGNA 240
Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
YVEGDASSASYFLAGAAITGGTVT+V+GCGTTSLQGDVKFAEVLEMMGAKVTWT+TSVTVT
Sbjct: 241 YVEGDASSASYFLAGAAITGGTVTVQCGCTTSLQGDVKFAEVLEMMGAKVTWTDTSVTVT 300
Query: 309 GPPREPFGKRLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
GPPR+PFGRKHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI
Sbjct: 301 GPPRQPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIC 360
Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
TELTGKGA+VEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRDPGCT
Sbjct: 361 TELTKLGATVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 420
Query: 429 RKTFFPDYFDVLSTFVKN 445
RKTFF+YFDVLSTFVKN
Sbjct: 421 RKTFFNYFDVLSTFVKN 437

>gb|ABA54869.1| putative 5-enolpyruvylshikimate 3-phosphate synthase [Fagus
sylvatica]
Length = 520

Score = 783 bits (2021), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/441 (85%), Positives = 412/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIK+ISGT+KLPKSKSLNRILLALLAALSEGTTVVDNLLNS+D+HYMLGAL+TLGL
Sbjct: 80 EIVLQPIKDISGTIKLPKSKSLNRILLALLAALSEGTTVVDNLLNSDDIHYMLGALKTLGL 139
Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTA AVTAAGGNATYVLD 124
VE DKA KRA+V GCGG FPV ++++E+QLFLGNAG AMR LTA AVT AGGN++YVLD
Sbjct: 140 RVEEDKAIKRAIVEGCGGLFPVGKESRDEIQFLGNAGTAMRPLTA AVTVAGGNSSYVLD 199
Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GL+QLGA+VDCFLGT CPPVRV G GGLPGGKVKLSGSISSQYL+
Sbjct: 200 GVPRMRERPIGDLVDGLQQLGANVDCFLGTCKPPVRVFGKGGLPGGKVKLSGSISSQYLT 259
Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
AL+MAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFG+ EH+DSWDRF I+GGQKYKS
Sbjct: 260 ALVMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGISVEHNSWDRFLIRGGQKYKS 319
Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGAKVTW+ETS
Sbjct: 320 PGNAYVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEKMGAKVTWSETS 379
Query: 305 VTVTGPFPREPFGKRLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPFP++ +KHL+AIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM
Sbjct: 380 VTVTGPFPQDSSKKHLRAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 439
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
+A+ TEL KLG+VEEGPDYC+ITPPEKLNVT IDTYDDHRMAMAFSLAAC +VPVTI D
Sbjct: 440 IAVCTELRKLGAATVEEGPDYCVITPPEKLNVTIDTYDDHRMAMAFSLAACGDPVTIND 499
Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
PGCTRKTFFPDYF+VL F K+
Sbjct: 500 PGCTRKTFFPDYFEVLQRFTKH 520

>gb|AAT45244.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza canadensis]
Length = 523

Score = 782 bits (2020), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/442 (84%), Positives = 411/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVL+PI+EISGTV LKPGSKSLSNRILLALLAALSEGTTVVDNLLNS+DVHYMLGALR LG
Sbjct: 82 EEIVLQPIKEISGTVHLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRALG 141

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGNAG AMR LTAAVTAAGGN++Y+L
Sbjct: 142 LNVEENSAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNAGTAMRPLTAAVTAAGGNSSYIL 201

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL
Sbjct: 202 DGVPRMRERPIGDLVTGLKQLGANVDCSLGTNCPVRVVGSGGLPGGKVKLSGSISSQYL 261

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EHSD+WDRF+++GGQKYK
Sbjct: 262 TSLLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSEHSDTWDRFHVRRGGQKYK 321

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVL MGA+VTWTE
Sbjct: 322 SPGNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLGQMGAEVTWTEN 381

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL+ +DVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 382 SVTVKGPPRNSSGRGHLRPVDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 441

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI+
Sbjct: 442 MIAICTELRKLGATVEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIK 501

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFFPDYF+VL + K+
Sbjct: 502 DPGCTRKTFFPDYFEVLERYTKH 523

>gb|ABQ00957.1| 5-enol-pyruvylshikimate-phosphate synthase 2A [Conyza bonariensis]
Length = 446

Score = 779 bits (2012), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/442 (84%), Positives = 411/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVL+PI+EISGTV LKPGSKSLSNRILLALLAALSEGTTVVDNLLNS+DVHYMLGALR LG
Sbjct: 5 EEIVLQPIKEISGTVHLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRVLG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGNAG AMR LTAAVTAAGGN++Y+L
Sbjct: 65 LNVEENSAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNAGTAMRPLTAAVTAAGGNSSYIL 124

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL
Sbjct: 125 DGVPRMRERPIGDLVTGLKQLGANVDCSLGTNCPVRVVGSGGLPGGKVKLSGSISSQYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EHSD+WDRF+++GGQKYK
Sbjct: 185 TSLLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSEHSDTWDRFHVRRGGQKYK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVL MGA+VTWTE
Sbjct: 245 SPGNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLGQMGAEVTWTEN 304

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL+ +DVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 305 SVTVKGPPRNSSGRGHLRPVDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 364

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI+
Sbjct: 365 MIAICTELRKLGATVEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIK 424

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445

DPGCTRKTFPDYF+VL + K+
Sbjct: 425 DPGCTRKTFPDYFEVLERYTKH 446

>gb|ABQ00961.1| 5-enol-pyruvylshikimate-phosphate synthase 3A [Conyza bonariensis]
Length = 446

Score = 779 bits (2012), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 378/442 (85%), Positives = 410/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVL+PI+EISGTV LPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR LG
Sbjct: 5 EEIVLKPIQEISGTVHLPGKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRALG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGNAG AMR LTAAVTAAGGN++YVL
Sbjct: 65 LNVEENGAIKRAIVEGCGGVFPVGKEAKDEIQFLGNAGTAMRPLTAAVTAAGGNSSYVL 124

Query: 124 DGVPRMRERPIGDLVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL
Sbjct: 125 DGVPRMRERPIGDLVTGLKQLGANVDCSLGTNCPVVRVVGSGGLPGGKVKLSGSISSQYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EHS+WDIFY++GGQKYK
Sbjct: 185 TSLLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSVEHSDTWDRFYVRGGQKYK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSSLQGDVKFAEVLMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTVTEGCGT+SLQGDVKFAEVL MGA+VTWTE
Sbjct: 245 SPGNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSSLQGDVKFAEVLGMGAEVTWTEN 304

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL +DVMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 305 SVTVKGPPRNSSGRHLCPVDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 364

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI+
Sbjct: 365 MIAICTELRKLGA+VEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIK 424

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
DPGCTRKTFPDYF+VL + K+
Sbjct: 425 DPGCTRKTFPDYFEVLERYTKH 446

>gb|EAZ35730.1| hypothetical protein OsJ_20021 [Oryza sativa Japonica Group]
Length = 506

Score = 778 bits (2009), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 396/442 (89%), Positives = 414/442 (93%), Gaps = 10/442 (2%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVLQPI+EISG V+LPKSKSLSNRILL+ALSEGTTVVDNLLNSEDVHYML AL+ LG
Sbjct: 74 EEIVLQPIREISGAVQLPGKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLEALKALG 133

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
LSVEADK AKRAVVVGCGGKFPVE DAKKEEVQLFLGNAG AMR LTAAVTAAGGNATYVL
Sbjct: 134 LSVEADKAKRAVVVGCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNATYVL 193

Query: 124 DGVPRMRERPIGDLVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRE+PIGDLV GLKQLGADVDCFLGT+CP + ++SQYL
Sbjct: 194 DGVPRMREKPIGDLVFLGLKQLGADVDCFLGTCEPLFVSRELEDF-----LVASQYL 244

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK
Sbjct: 245 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 304

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSSLQGDVKFAEVLMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTV+GCGTSSLQGDVKFAEVLMMGAKVTWT+T
Sbjct: 305 SPGNAYVEGDASSASYFLAGAAITGGTVTVQCGTSSLQGDVKFAEVLMMGAKVTWTD 364

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPPREP+G+KHLKA+DVMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER

Sbjct: 365 SVTVTGPPREPYGKKHLKAVDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 424

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
MVAIRTELTKLGASVEEGPDYCIITPPEKLN+TAIDTYDDHRMAMAFSLAAC+VPVTIR

Sbjct: 425 MVAIRTELTKLGASVEEGPDYCIITPPEKLNITADITYDDHRMAMAFSLAACADVPTIR 484

Query: 424 DPGCTRKTFFPDYFDVLSTFVKN 445
DPGCTRKTFF+YFDVLSTFV+N

Sbjct: 485 DPGCTRKTFFPNYFDVLSTFVRN 506

>gb|ACV53022.1| 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]
Length = 518

Score = 776 bits (2004), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/441 (85%), Positives = 404/441 (91%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV+LPGSKSLNRIILLALSEGTTVVDNLL S+D+ YML ALRTLGL

Sbjct: 78 EIVLQPIKEISGTVQLPGSKSLNRIILLALSEGTTVVDNLLYSDDILYMLDALRTLGL 137

Query: 66 SVEADKAAKRAVVVGCGGKFPV+EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D AKRAVV GCGG FPV +D KEE+QLFLGNAG AMR LTAAGV AGGN++YVLD

Sbjct: 138 KVEDDSTAKRAVVEGCGGLFPVGKDGKEIQFLFLGNAGTAMRPLTAAVAVAGGNSSYVLD 197

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLG+DVDCFLGT+CPPVRVN GGLPGGKVKLSGSISSQYL+

Sbjct: 198 GVPRMRERPIGDLVAGLKQLGSDVDCFLGTNCPVRVNAKGLPGGKVKLSGSISSQYLT 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL LGDVEIEI+DKLIS+PYVEMT++LMERFGV EHSWSWDRFYI+GGQKYKS

Sbjct: 258 ALLMATPLGLGDVEIEIVDKLISVPYVEMTIKLMERFGVSVHSWSWDRFYIRGGQKYKS 317

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+VTVEGCGT+SLQGDVKFAEVLEMMGAKVWTWETS 304
P AYVEGDASSASYFLAGAA+TGGT+VT+GCGT+SLQGDVKFAEVLE MG KVTWTE S

Sbjct: 318 PGKAYVEGDASSASYFLAGAAVTGGT+VT+GCGT+SLQGDVKFAEVLEKMGCKVWTWENS 377

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPE+ G+KHL+AIDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM

Sbjct: 378 VTVTGPPEPSSGKKHLKAIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 437

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 424
+AI TEL KLGA+VEEG DYC+ITPPEKLN TAI+TYDDHRMAMAFSLAAC+VPVTI D

Sbjct: 438 IAICTELRKLGA+VEEGSDYCVITPPEKLNPTAITYDDHRMAMAFSLAACADVPTILD 497

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
PGCTRKTFFPDYFDVL F K+

Sbjct: 498 PGCTRKTFFPDYFDVLEKFAKH 518

>gb|AAY40474.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza sumatrensis]
Length = 446

Score = 776 bits (2003), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/442 (85%), Positives = 410/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
EEIVL+PI+EISGTV LPGSKSLNRIILLALSEGTTVVDNLLNS+DVHYMLGALR LG

Sbjct: 5 EEIVLQPIKEISGTVHLPKSKSLNRIILLALSEGTTVVDNLLNSDDVHYMLGALRALG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV+EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGNAG AMR LTAAGVTAAGGN++YVL

Sbjct: 65 LNVEENAAIKRAIVEGCGGVFPVGKEAKDEIQFLFLGNAGTAMRPLTAAVTAAGGNSSYVL 124

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL

Sbjct: 125 DGVPRMRERPIGDLVTGLKQLGANVDCSLGTNCPVRVVGSGGLPGGKVKLSGSISSQYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EHS+WD+R+FY++GGQKYK

Sbjct: 185 TSLLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSVHS+TWDRFYVRGGQKYK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP +AYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVL MGA+VTWTE
Sbjct: 245 SPGSAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLGQMGA EVTWTEN 304

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR L+ +DVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 305 SVTVKGPPRNSSGRGELRPVDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 364

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI+
Sbjct: 365 MIAICTELRKLGATVEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIK 424

Query: 424 DPGCTRKTFFPDYFDVLSFVKN 445
DPGCTRKTFFPDYF+VL + K+
Sbjct: 425 DPGCTRKTFFPDYFEVLEERYTKH 446

>gb|ACV53021.1| 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus palmeri]
Length = 518

Score = 776 bits (2003), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/441 (85%), Positives = 403/441 (91%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV+LPGSKSLNRIILLALASEGTTVVDNLL S+D+ YML ALRTLGL
Sbjct: 78 EIVLQPIKEISGTVQLPGSKSLNRIILLALASEGTTVVDNLLYSDDILYMLDALRTLGL 137

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D AKRAVV GCGG FVP +D KEE+QLFLGNAG AMR LTA AV AGGN++YVLD
Sbjct: 138 KVEDDSTAKRAVVEGCGGLFPVGKDGEIQLFLGNAGTAMRPLTAAVAVAGGNSSYVLD 197

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLG+D DCFLGT+CPPVRVN GGLPGGKVKLSGS+SSQYL+
Sbjct: 198 GVPRMRERPIGDLVAGLKQLGSDXDCFLGTNCPPVRVNAKGGLPGGKVKLSGSVSSQYLT 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL LGDVEIEI+DKLIS+PYVEMT++LMERFGV EHSWSWDRFYI+GGQKYKS
Sbjct: 258 ALLMATPLGLGDVEIEIVDKLISVPYVEMTIKLMERFGVSVHSWSWDRFYIRGGQKYKS 317

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P AYVEGDASSASYFLAGAA+TGGTVTV+GCGT+SLQGDVKFAEVL MG KVTWTE S
Sbjct: 318 PGKAYVEGDASSASYFLAGAAVTGGTVTVKGCGTSSLQGDVKFAEVLKMGCKVTWTENS 377

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPEP+ GRKHL+AIDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 378 VTVTGPPEPSSGRKHLRAIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 437

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
+AI TEL KLGA+VEEG DYC+ITPPEKLN TAI+TYDDHRMAMAFSLAAC+VPVTI D
Sbjct: 438 IAICTELRKLGATVEEGSDYCVITPPEKLNPTAIETYDDHRMAMAFSLAACADVPTILD 497

Query: 425 PGCTRKTFFPDYFDVLSFVKN 445
PGCTRKTFFPDYFDVL F K+
Sbjct: 498 PGCTRKTFFPDYFDVLEKFAKH 518

>gb|ABQ00962.1| 5-enol-pyruvylshikimate-phosphate synthase 3B [Conyza bonariensis]
Length = 446

Score = 775 bits (2002), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/442 (85%), Positives = 409/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 64
EEIVL+PI+EISGTV LPGSKSLNRIILLALASEGTTVVDNLLNS+DVHYMLGALR LG
Sbjct: 5 EEIVLKPIQEISGTVHLPGSKSLNRIILLALASEGTTVVDNLLNSDDVHYMLGALRALG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FVP ++AK+E+QLFLGNAG AMR LTA AVTAAGGN++YVL
Sbjct: 65 LNVEENGAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNAGTAMRPLTAAVTAAGGNSSYVL 124

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPR+RERPIGDLV GLKQLGA+VDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL
Sbjct: 125 DGVPRVRERPIGDLVTGLKQLGANVDCSLGTNCPPVRVVGSGGLPGGKVKLSGSISSQYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EHS+WDIFY++GGQKYK
Sbjct: 185 TSLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSVEHSDTWDRFYVRGGQKYK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTVVEGCGT+SLQGDVKFAEVL MGA+VTWTE
Sbjct: 245 SPGNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSSLQGDVKFAEVLGQMGAEVTWTEN 304

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL +DVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 305 SVTVKGPPRNSSGRGHLCPVDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 364

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M+AI TEL KLGA+VEEGPDYC ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTI+
Sbjct: 365 MIAICTELRKLGA+VEEGPDYCAITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIK 424

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
DPGCTRKTFPDYF+VL + K+
Sbjct: 425 DPGCTRKTFPDYFEVLERYTKH 446

>gb|ACV67277.1| 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus
tuberculatus]
Length = 518

Score = 773 bits (1995), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 373/441 (84%), Positives = 402/441 (91%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGT++LPGSKSLNRILLALLAALS+GTTVVDNLL S+D+ YML ALRTLGL
Sbjct: 78 EIVLQPIKEISGTIQLPGSKSLNRILLALLAALSQGTTVVDNLLYSDDILYMLDALRTLGL 137

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D KRAVV GCGG FV +D KEE+QLFLGNAG AMR LTA AV AGGN++YVLD
Sbjct: 138 KVEDDNTDKRAVVEGCGGLFPVGKDGKEEIQFLGNAGTAMRPLTAAVAVAGGNSSYVLD 197

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLG+DVDCFLGT+CPPVRVN GGLPGGKVKLSGS+SSQYL+
Sbjct: 198 GVPRMRERPIGDLVAGLKQLGSDVDVDCFLGTNCPPVRVNAKGLPGGKVKLSGSVSSQYLT 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL LGDVEIEI+DKLIS+PYVEMT+RLMERFGV EHS+WDIFY+I+GGQKYKS
Sbjct: 258 ALLMATPLGLGDVEIEIVDKLISVPYVEMTIRLMERFGVSVEHSDSWDRFFIRGGQKYKS 317

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P AYVEGDASSASYFLAGAA+TGGTVTV+GCGT+SLQGDVKFAEVL MG VTWTE S
Sbjct: 318 PGKAYVEGDASSASYFLAGAAVTGGTVTVKCGTSSLQGDVKFAEVLKMGCTVTWTENS 377

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPE GRKHL+AIDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 378 VTVTGPPESSGRKHLRAIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 437

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEG DY+ITPPEKLN TAI+TYDDHRMAMAFSLAAC+VPVTI D
Sbjct: 438 IAICTELRKLGA+VEEGSDYCVITPPEKLNPTAIETTYDDHRMAMAFSLAACADVPVTILD 497

Query: 425 PGCTRKTFPDYFDVLSTFVK 445
PGCTRKTFPDYFDVL F K+
Sbjct: 498 PGCTRKTFPDYFDVLEKFAKH 518

>gb|ACV67278.1| 5-enolpyruvylshikimate-3-phosphate synthase [Amaranthus
tuberculatus]
Length = 518

Score = 771 bits (1991), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 374/441 (84%), Positives = 402/441 (91%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGT++LPGSKSLNRIILLALLAALSEGTTVVDNLL S+D+ YML ALRTLGL
Sbjct: 78 EIVLQPIKEISGTIQLPGSKSLNRIILLALLAALSEGTTVVDNLLYSDDILYMLDALRTLGL 137

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D KRAVV GCGG FPV +D KEE+QLFLGNAG AMR LTAAV AGGN++YVLD
Sbjct: 138 KVEDDNTDKRAVVEGCGGLFPVGKDGKEEIQLFLGNAGTAMRPLTAAVAVAGGNSSYVLD 197

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLG+DVDCFLGT+CPPVRVN GGLPGGKVKLSGSISSQYL+
Sbjct: 198 GVPRMRERPIGDLVAGLKQLGSDVDCFLGTNCPVVRVNAKGGLPGGKVKLSGSISSQYLT 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL LGDVEIEI+DKLIS+PYVEMT+RLMERFGV EHSWSWDRF+I+GGQKYKS
Sbjct: 258 ALLMATPLGLGDVEIEIIVDKLISVPYVEMTIRLMERFGVSVHSDSWDRFFIRGGQKYKS 317

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P AYVEGDASSASYFLAGAA+TGGTVTV+GCGT+SLQGDVKFAEVLE MG KVTWTE S
Sbjct: 318 PGKAYVEGDASSASYFLAGAAVTGGTVTVKGCSTSSLQGDVKFAEVLEKMGCKVTWTENS 377

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPE GRKHL+AIDVNMNKMMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 378 VTVTGPPESSGRKHLRAIDVNMNKMMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 437

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEG DYC+ITPPEKL TAI+TYDDHRMAMAFSLAAC+VPVTI D
Sbjct: 438 IAICTELRKLGAATVEEGSDYCVITPPEKLIPTAIETIYDDHRMAMAFSLAACADVPTILD 497

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
PGCTRKTFFPDYFDVL F K+
Sbjct: 498 PGCTRKTFFPDYFDVLEKFAKH 518

>gb|AAV64030.1| 5-enolpyruvylshikimate 3-phosphate synthase [Camptotheca acuminata]
Length = 519

Score = 769 bits (1987), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 383/441 (86%), Positives = 412/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNS+DVHYMLGALRTLGL
Sbjct: 79 EIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSDDVHYMLGALRTLGL 138

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D A KRA+V GC G FPV +++ +EVQLFLGNAG AMR LTAAVTAAGGN++Y+LD
Sbjct: 139 RVEEDSAIKRAIVEGCSGLFPVGKESTDEVQLFLGNAGTAMRPLTAAVTAAGGNSSYILD 198

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDCFLGT+CPPVRV G GGLPGGKVKLSGSISSQYL+
Sbjct: 199 GVPRMRERPIGDLVTGLKQLGADVDCFLGTNCPVVRVIGKGLPGGKVKLSGSISSQYLT 258

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LM+RFGV EHS+WDWF I+GGQKYKS
Sbjct: 259 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMKRFVTVHSDNWDWFILQGGQKYKS 318

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P N+YVEGDASSASYFLAGAA+TGGT+TVEGCG++SLQGDVKFAEVLE MGAKVTWTE S
Sbjct: 319 PGNSYVEGDASSASYFLAGAAVTGGTITVEGCGSSSLQGDVKFAEVLEKMGAKVTWTENS 378

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPE GRKHL+A+DVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM
Sbjct: 379 VTVTGPPESSGRKHLRAVDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 438

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT+DTYDDHRMAMAFSLAAC VPVTI+D
Sbjct: 439 IAICTELRKLGAATVEEGPDYCVITPPEKLNVTAVDTYDDHRMAMAFSLAACANVPVTIKD 498

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
PGCTRKTFFPDYF+VL F K+
Sbjct: 499 PGCTRKTFFPDYFEVLQRFKAKH 519

>ref|XP_002280922.1| PREDICTED: hypothetical protein [Vitis vinifera]
emb|CBI38903.3| unnamed protein product [Vitis vinifera]
gb|ACY29662.2| 5-enolpyruvylshikimate-3-phosphate synthase [Vitis vinifera]
Length = 521

Score = 766 bits (1979), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 382/443 (86%), Positives = 409/443 (92%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPIKEISGT+ LPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL
Sbjct: 79 APEIVLQPIKEISGTTITLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 138

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL VE KR +V GCGG+FP + EVQLFLGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 139 GLHVEEQSENKRIVVQCGGQFPAGNGSVGEVQLFLGNAGTAMRPLTAAVTAAGGNASYV 198

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLV GLKQLGADV+CFLGT+CPPVRVNG GGLPGGKVKLSGSISSQY
Sbjct: 199 LDGVPRMRERPIGDLVTGLKQLGADVNCFLGTNCPVRVNGNGGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHS++WDRF I+GGQKY
Sbjct: 259 LTALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVEHSNTWDRFLIRGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 302
KSP NA+VEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGAKV+W E
Sbjct: 319 KSPGNFVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEQMGAKVSWME 378

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPPR+ GRKHL+AIDVNMNKMPPDVAMTLAVVAL+ADGPTAIRDVASWRVKETE
Sbjct: 379 NSVTVTGPPRDSGRKHLRAIDVNMNKMPPDVAMTLAVVALYADGPTAIRDVASWRVKETE 438

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLACA+VPVTI
Sbjct: 439 RMIAICTELRKLGATVEEGPDYCVITPPEKLNVTSIDTYDDHRMAMAFSLACADVPVTI 498

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 445
+DPGCTRKTFFDYF+VL F K+
Sbjct: 499 KDPGCTRKTFFDYFEVLQRFTKH 521

>gb|AAL27697.1| 5-enolpyruvylshikimate-3-phosphate synthase [Dicliptera chinensis]
Length = 516

Score = 765 bits (1976), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 379/438 (86%), Positives = 414/438 (94%), Gaps = 2/438 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIK+ISGTVKLPKSKSLNR+LLLAALSEGTTVV+NLL+SED+HYMLGALRTLGL
Sbjct: 77 EIVLQPIKDISGTVKLPKSKSLNRVLLAALSEGTTVVENLLSSEDIHYMLGALRTLGL 136

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE DKA ++AVV GC G+FP ++ K+EVQLFLGNAG AMR LTAAV AAGGNA YVLD
Sbjct: 137 AVEEDKANQKAVVEGCVGQFPASKEGKDEVQLFLGNAGTAMRPLTAAVVAAGGNARYVLD 196

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPR+RERPIGDLV GLKQLGADVDCFLGT+CPPVRV G GGLPGGKVKLSGS+SSQYL+
Sbjct: 197 GVPRLRERPIGDLVTGLKQLGADVDCFLGTNCPVRVVGKGLPGGKVKLSGSVSSQYLT 256

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM+APLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EH+D+WDRF I+GGQKYKS
Sbjct: 257 ALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVYVEHTDNWDRFLIRGGQKYKS 316

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P NA+VEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGAKV+WTE S
Sbjct: 317 PGNAFVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEKMGAKVSWTENS 376

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPR P G+KHL+AIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM

Sbjct: 377 VTVTGP RPVP-GKKHLRAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKETERM 435

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
+AI TEL KLGA+VEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI+D

Sbjct: 436 IAICTELRKLGATVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPVTIKD 495

Query: 425 PGCTRKTFFPDYFDVLSTF 442
PGCTRKTFF+YFDVLST+

Sbjct: 496 PGCTRKTFFPNYFDVLSTY 513

>gb|AAL27698.1|AF371966_1 5-enolpyruvylshikimate-3-phosphate synthase B [Dicliptera chinensis]
Length = 516

Score = 763 bits (1971), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 378/438 (86%), Positives = 412/438 (94%), Gaps = 2/438 (0%)

Query: 6 EIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

EIVLQPIK+ISGTVKLP GSKSLSNR+LL LLAALSEGTTVV+NLL+SED+HYMLGALRTLGL

Sbjct: 77 EIVLQPIKDISGTVKLP GSKSLSNRVLL LLAALSEGTTVENLLSSEDIHYMLGALRTLGL 136

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE DKA ++AVV GC G+FP ++ K+E+QLFLG AG AMR LTA AV AAGGNA YVLD

Sbjct: 137 HVEEDKANQKAVVEGCVGQFPASKEGKDEIQFLGKAGTAMRPLTAAVVAAGGNARYVLD 196

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDCFLGT+CPPVRV G GGLPGGKVKLSGSISSQYL+

Sbjct: 197 GVPRMRERPIGDLVTGLKQLGADVDCFLGTN CPPVRVVGKGLPGGKVKLSGSISSQYLT 256

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHSDSWDRFYIKGGQKYKS 244
ALLM+APLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EH+D+WDRF I+GGQKYKS

Sbjct: 257 ALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVYVEHTDNWDRFLIRGGQKYKS 316

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT VTVGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P NA+VEGDASSASYFLAGAA+TGGT VTVGCGT+SLQGDVKFAEVLE MGAKV+WTE S

Sbjct: 317 PGNAFVEGDASSASYFLAGAAV TGGT VTVGCGTSSLQGDVKFAEVLEKMGAKVSWTENS 376

Query: 305 VTVTGP RPFPGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGP RP P G+KHL+ AIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKETERM

Sbjct: 377 VTVTGP RPVP-GKKHLRAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKETERM 435

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
+AI TEL KLGA+VEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI+D

Sbjct: 436 IAICTELRKLGATVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPVTIKD 495

Query: 425 PGCTRKTFFPDYFDVLSTF 442
PGCTRKTFF+YFDVLST+

Sbjct: 496 PGCTRKTFFPNYFDVLSTY 513

>gb|ABQ00959.1| 5-enol-pyruvylshikimate-phosphate synthase 1B [Conyza bonariensis]
Length = 446

Score = 763 bits (1970), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/441 (85%), Positives = 411/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

EIVLQPIKEISGTV LPGSKSLSNRILL LLAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL

Sbjct: 6 EIVLQPIKEISGTVNLPGSKSLSNRILL LLAALAE GTTIVDNLLNSDDVHYMLGALRTLGL 65

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AMR LTA AVTAAGGN++YVLD

Sbjct: 66 NVEEDVAIKRAIVEGCGGVFPVGKEAKDDIQFLGNAGTAMRPLTAAVTAAGGNSSYVLD 125

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDL GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQYL+

Sbjct: 126 GVPRMRERPIGDLATGLKQLGADVDCSLGTN CPPVRIVGGGGLPGGKVKLSGSISSQYLT 185

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHSDSWD+F+I+G QKYKS

Sbjct: 186 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVSEHSDSWDQFFIRGDQKYKS 245

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VTWTE S

Sbjct: 246 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLGQMGAEVWTENS 305

Query: 305 VTVTGP+PREPFGRKHLKAIDVNMNKM+PDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNKM+PDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM

Sbjct: 306 VTVKGPPRDSSGRKHLRAVDVNMNKM+PDVAMTLAVVALYADGPTAIRDVASWRVKETERM 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT+IDTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLAACAEVPTI+D

Sbjct: 366 IAICTELRKL+GATVEEGPDYCVITPPEKLNVT+IDTYDDHRMAMAFSLAACADVPVTIKD 425

Query: 425 PGCTRKTFFPDYFDVLS+TFVKN 445
P CTRKTFFPDYF+VL F K+

Sbjct: 426 PSCTRKTFFPDYFEVLQRFAKH 446

>gb|ABQ00960.1| 5-enol-pyruvylshikimate-phosphate synthase 1C [Conyza bonariensis]
Length = 446

Score = 763 bits (1969), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/441 (85%), Positives = 411/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLP+SGSKSLSNRILL+LAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV L+PGSKSLSNRILL+LAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL

Sbjct: 6 EIVLQPIKEISGTVNLP+SGSKSLSNRILL+LAALAE+GTTIVDNLLNSDDVHYMLGALRTLGL 65

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KR +V GCGG FPV ++AK+++QLFLGNAG AMR LTA+VTAAGGN++YVLD

Sbjct: 66 NVEEDVAIKRVIVEGCGGVFPV+GKEAKDDIQLFLGNAGTAMRPLTAAVTAAGGNSSYVLD 125

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD+CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQYL+

Sbjct: 126 GVPRMRERPIGDLVTLGLKQLGADVDCSLGTNCP+PVRI+VGGGLPGGKVKLSGSISSQYLT 185

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHS+SDW+F+I+G QKYKS

Sbjct: 186 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVSEHSDSWDQFFIRGDQKYKS 245

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VTWTE S

Sbjct: 246 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLGQMGAEVWTENS 305

Query: 305 VTVTGP+PREPFGRKHLKAIDVNMNKM+PDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNKM+PDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM

Sbjct: 306 VTVKGPPRDSSGRKHLRAVDVNMNKM+PDVAMTLAVVALYADGPTAIRDVASWRVKETERM 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT+IDTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLAACAEVPTI+D

Sbjct: 366 IAICTELRKL+GATVEEGPDYCVITPPEKLNVT+IDTYDDHRMAMAFSLAACADVPVTIKD 425

Query: 425 PGCTRKTFFPDYFDVLS+TFVKN 445
P CTRKTFFPDYF+VL F K+

Sbjct: 426 PSCTRKTFFPDYFEVLQRFAKH 446

>ref|NP_182055.1| 3-phosphoshikimate 1-carboxyvinyltransferase /
5-enolpyruvylshikimate-3-phosphate / EPSP synthase
[Arabidopsis thaliana]
sp|P05466.3|AROARATH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase,
chloroplastic; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Flags: Precursor
gb|AAB82633.1| 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase [Arabidopsis
thaliana]
gb|AAY25438.1| At2g45300 [Arabidopsis thaliana]
dbj|BAE99170.1| 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase [Arabidopsis
thaliana]
Length = 520

Score = 763 bits (1969), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 366/443 (82%), Positives = 400/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI+EISG +KLPKSKSLSNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 78 ASEIVLQPIREISGLIKLPKSKSLSNRILLLAALSEGTTVVDNLLNSDDINYLMDALKRL 137

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE D RAVV GCGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 138 GLNVETDSENNRAVVEGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYV 197

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 198 LDGVPRMRERPIGDLVVGLKQLGADVCTLTNCPVRVNANGGLPGGKVKLSGSISSQY 257

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLM+APLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EHSWSWDRF++KGGQKY
Sbjct: 258 LTALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSVESHSWSWDRFVKGQKY 317

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TTVTEGCGTTSLQGDVKFAEVLE MG KV+WTE
Sbjct: 318 KSPGNAYVEGDASSASYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 377

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPPR+ FG +HL+AIDVNMNMKMPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 378 NSVTVTGPPRDAFGMRHLRAIDVNMNMKMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 437

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEG DYC+ITPP+K+ IDTYDDHRMAMAFSLAAC+VP+TI
Sbjct: 438 RMIAICTELRKLGATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADVPITI 497

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 445
DPGCTRKTFPDYF VL K+
Sbjct: 498 NDPGCTRKTFPDYFQVLERITKH 520

>gb|ABQ00958.1| 5-enol-pyruvylshikimate-phosphate synthase 1A [Conyza bonariensis]
Length = 446

Score = 760 bits (1962), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/441 (85%), Positives = 411/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV LPSKSLSNRILLLAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL
Sbjct: 6 EIVLQPIKEISGTVNLPKSKSLSNRILLLAALAEAGTTIVDNLLNSDDVHYMLGALRTLGL 65

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AMR LTAAVTAAGGN++YVLD
Sbjct: 66 NVEEDVAIKRAIVEGCGGVFPVGKEAKDDIQLFLGNAGTAMRPLTAAVTAAGGNSSYVLD 125

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQYL+
Sbjct: 126 GVPRMRERPIGDLVTGLKQLGADVDCSLGTNCPVRIVGGGLPGGKVKLSGSISSQYLT 185

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHSWSWDF+I+G QKYKS
Sbjct: 186 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVESHSWSWQFFIRGDQKYKS 245

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFA+V MGA+VTWTE S
Sbjct: 246 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAKVPQMGAEVTWTENS 305

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNMKMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 306 VTVKGPPRDSSGRKHLRAVDVNMNMKMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTIAIDTYDDHRMAMAFSLAAC+VPVTI+D
Sbjct: 366 IAICTELRKLGATVEEGPDYCVITPPEKLNVTIAIDTYDDHRMAMAFSLAACADVPVTIKD 425

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
P CTRKTFFPDYF+VL F K+
Sbjct: 426 PSCTRKTFFPDYFEVLQRFK 446

>gb|AAT45243.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza canadensis]
Length = 519

Score = 759 bits (1961), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 379/441 (85%), Positives = 413/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV LKPKSKSLNRILLALLAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL
Sbjct: 79 EIVLQPIKEISGTVNLPKSKSLNRILLALLAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL 138

Query: 66 SVEADKAAKRAVVVGGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AMR LTAAVTAAGGN++Y+LD
Sbjct: 139 NVEEDVAIKRAIVEGCGGVFPVGEKAKDDIQLFLGNAGTAMRPLTAAVTAAGGNSSYILD 198

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL+
Sbjct: 199 GVPRMRERPIGDLVTGLKQLGADVDCSLGTNCPVRVVGGLPGGKVKLSGSISSQYLT 258

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHSWSWDF+I+GGQKYKS
Sbjct: 259 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVHSWSWDFQFFIRGGQKYKS 318

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VTWTE S
Sbjct: 319 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGT+SLQGDVKFAEVLGMGA+VTWTENS 378

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNKMMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 379 VTVKGPPRDSSGRKHLRAVDVNMNKMMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 438

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLAACAEVPTIIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVAIDTYDDHRMAMAFSLAAC+VPVTI+D
Sbjct: 439 IAICTELRKLGATVEEGPDYCVITPPEKLNVAIDTYDDHRMAMAFSLAACADVPTIKD 498

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
P CTRKTFFPDYF+VL F K+
Sbjct: 499 PSCTRKTFFPDYFEVLQRFK 519

>emb|CAA29828.1| EPSP [Arabidopsis thaliana]
Length = 520

Score = 758 bits (1956), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 364/443 (82%), Positives = 398/443 (89%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI+EISG +KLPKSKSLNRILLALLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 78 ASEIVLQPIREISGLIKLPKSKSLNRILLALLAALSEGTTVVDNLLNSDDINYMALDKRL 137

Query: 64 GLSVEADKAAKRAVVVGGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE D RAVV GCGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 138 GLNVTDSENNRAVVEGCGGIFPASIDSKSDIELYLGAGTAMRPLTAAVTAAGGNASYV 197

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLVVGLKQLGADV+ C LGT+CPPVRV GGLPGGKVKLSGSISSQY
Sbjct: 198 LDGVPRMRERPIGDLVVGLKQLGADVCTLTNCPVRVNGGLPGGKVKLSGSISSQY 257

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLM+APLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EHSWSWDRF++KGGQKY
Sbjct: 258 LTALLMSAPLALGDVEIEIVDKLISIPYVEMTLKLMERFGVSVHSWSWDRFFVKGGQKY 317

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLMMGAKVTWTE 302
KSP NAYVEGDASSA YFLAGAAITG TTVTEGCGT+SLQGDVKFAEVL MG KV+WTE
Sbjct: 318 KSPGNAYVEGDASSASYFLAGAAITGTTVEGCGT+SLQGDVKFAEVLKMGCKVSWTE 377

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362

SVTVTGPPR+ FG +HL+AIDVNMNKMPPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 378 NSVTVTGPPRDAFGMRHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE 437

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEG DYC+ITPP+K+ IDTYDDHRMAMAFSLAAC+VP+TI

Sbjct: 438 RMIAICTELRKLGAATVEEGSDYCVITPPKVKTAETIDTYDDHRMAMAFSLAACADVPITI 497

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
D GCTRKTFPDYF VL K+

Sbjct: 498 NDSGCTRKTFPDYFQVLERITKH 520

>gb|AAT45245.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza canadensis]
Length = 454

Score = 757 bits (1955), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 365/442 (82%), Positives = 403/442 (91%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRTL 64
EEIVL+PI+EISGTV LPKSKSLSNRILLALLAALSEGTTVVDNLLNS+DVHYMLGALR LG

Sbjct: 13 EEIVLKPIQEISGTVHLPGSKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRALG 72

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L++E + A KRA+V GCGG FPV ++AK+E+QLFLGNAG AMR+LTAAVTAAGGN +YVL

Sbjct: 73 LNIENAAIKRAIVEGCGGLFPVGKEAKDEIQLFLGNAGTAMRTLTAAVTAAGGNLSYVL 132

Query: 124 DGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLG +VDC LGT+CPPV V G GGLPGGKVKLSGSISS YL

Sbjct: 133 DGVPRMRERPIGDLVTGLKQLGVNVDCLGTNCPPVHVVGSGGLPGGKVKLSGSISSVYL 192

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEIIDKLIS+PYV MTL+LM+RFGV EHSD+ DRF+++GGQKYK

Sbjct: 193 TSLLMAAPLALGDVEIEIIDKLISVPYVRMTLKLQRFVGSVEHSDTLDRFHVRRGGQKYK 252

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLMMGAKVTWTET 303
SP NAYVE DASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVL MGA+VTWTE

Sbjct: 253 SPGNAYVESDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLGQMGAEVTWTEN 312

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL+ +DVNMNKMPPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER

Sbjct: 313 SVTVKGPPRNSSGRHLRPVDVNMNKMPPDVAMTLAVVALYADGPTAIRDVASWRVKETER 372

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ TPPEKLNVTADITYDDHRMAM FSLAAC+VPVTI+

Sbjct: 373 MIAICTELRKLGAATVEEGPDYCVITPPEKLNVTADITYDDHRMAMTFSLAACADVPVTIK 432

Query: 424 DPGCTRKTFPDYFDVLSTFVKN 445
DPGCTRK+FPDYF+VL + K+

Sbjct: 433 DPGCTRSFPDYFEVLERYTKH 454

>gb|AAY40475.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza sumatrensis]
Length = 446

Score = 755 bits (1949), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/442 (81%), Positives = 407/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRTL 64
EEIVL+PI+EISGTV LPKSKSLSNRILLALLAALSEGTTVVDNLLNS+DVHYMLGALR +G

Sbjct: 5 EEIVLKPIQEISGTVHLPGSKSLSNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRAVG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGN+G AMR+LTAA+TAAGGN++YVL

Sbjct: 65 LNVEENAAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNSGTAMRTLTAAITAAGGNSSYVL 124

Query: 124 DGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLG +VDC LGT+CPPVRV G GGLPGGKV+LSGSISS YL

Sbjct: 125 DGVPRMRERPIGDLVTGLKQLGVNVDCLGTNCPPVRVVGSGGLPGGKVRLSGSISSVYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAP+ALGDVEIEIIDKLIS+PYV+MTL+LM++FGV EHSD+ DRF+++GGQKYK

Sbjct: 185 TSLMAAPVALGDVEIEIIDKLISVPYVQMTLKLKMQFGVSVESDITLDRFHVRRGGQKYK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVL MGA+VTWTE

Sbjct: 245 SPGNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLGQMGA EVTWTEN 304

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL+ +DVNMNMPDVAMTLAVVAL+ADG TAIRDVASWRVKETER

Sbjct: 305 SVTVKGPPRNSSGRGHLRPVDVNMNMPDVAMTLAVVALYADGRTAIRDVASWRVKETER 364

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAM FSLAACAEVPVTI+

Sbjct: 365 MIAICTELRKLGA+VEEGPDYCVITPPEKLNVTADITYDDHRMAMTFSLAACADVPVTIK 424

Query: 424 DPGCTRKTFFPDYFDVLSTFVKN 445
DPGCTRK+FPDYF+VL + K+

Sbjct: 425 DPGCTRKSFPDYFEVLERYTKH 446

>gb|ABV24481.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum]
Length = 521

Score = 755 bits (1949), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/443 (84%), Positives = 408/443 (92%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI EISGTVKLPKSGSKLSNRILLALLAALSEGTTVV+NLLNS+DVH+ML AL L

Sbjct: 79 ASEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVENLLNSDDVHHMLVALGKL 138

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL V+ D K+A+V GCGG+FPV + +E++LFLGNAG AMR LTAA+TAAGGN++YV

Sbjct: 139 GLYVKHDSEKKQAIIVEGCGGQFPVGKGEQIEFLFLGNAGTAMRPLTAAITAAGGNSSYV 198

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQY

Sbjct: 199 LDGVPRMRERPIGDLVTGLKQLGADVDCILGTNCPVRIEGKGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLISIPYVEMT++LMERFGV EH+DSWDRF+I+GGQKY

Sbjct: 259 LTALLMAAPLALGDVEIEIIDKLISIPYVEMTMKLMERFGVTVEHTDSWDRFFIRGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 302
SP NAYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLEMMGAKVTWTE

Sbjct: 319 MSPGNAYVEGDASSASYFLAGAAVTTGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 378

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPPR GRKHL+AIDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETE

Sbjct: 379 NSVTVTGPPRNSSGRKHLRAIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETE 438

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI

Sbjct: 439 RMIAICTELRKLGA+VEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 498

Query: 423 RDPGCTRKTFFPDYFDVLSTFVKN 445
+DPGCTRKTFFPDYF+VL K+

Sbjct: 499 KDPGCTRKTFFDYFEVLDRVTKH 521

>gb|ABY61050.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum]
gb|ACF16410.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum]
Length = 521

Score = 754 bits (1947), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 375/443 (84%), Positives = 410/443 (92%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI EISGTVKLPKSGSKLSNRILLALLAALSEGTTVV+NLLNS+DVH+ML AL L

Sbjct: 79 ASEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVENLLNSDDVHHMLVALGKL 138

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL V+ D K+A+V GCGG+FPV + +E++LFLGNAG AMR LTAA+TAAGGN++YV

Sbjct: 139 GLYVKHDSSEKKQAIVEGCGGQFPVKGEGQEIELFLGNAGTAMRPLTAAITAAGGNSSYV 198

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQY

Sbjct: 199 LDGVPRMRERPIGDLVTGLKQLGADVDCLTGTNCPVRIEGKGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLISIPYVEMT++LMEFVG EH+DSWDRF+I+GGQKY

Sbjct: 259 LTALLMAAPLALGDVEIEIIDKLISIPYVEMTIKLMERFGVTVEHTDSWDRFFIRGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 302
SP NAYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLEMMGAKVTWT+

Sbjct: 319 MSPGNAYVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTK 378

Query: 303 TSVTVTGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPPR P GRKHL+AIDVNMNKMPPDVAMTLAVVAL+ADGPTAIRDVASWRVKETE

Sbjct: 379 NSVTVTGPPRNPSSGRKHLRAIDVNMNKMPPDVAMTLAVVALYADGPTAIRDVASWRVKETE 438

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEGPD+C+ITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI

Sbjct: 439 RMIAICTELRKLGAATVEEGPDFCVITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI 498

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
+DPGCTRKTFPDYF+VL+ K+

Sbjct: 499 KDPGCTRKTFPDYFEVLARVTKH 521

>gb|AA40473.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza sumatrensis]
Length = 447

Score = 754 bits (1946), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 380/441 (86%), Positives = 412/441 (93%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTV LPSKSKSLNRIILLAAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL

Sbjct: 7 EIVLQPIKEISGTVNLPSKSKSLNRIILLAAALAEETTIVDNLLNSDDVHYMLGALRTLGL 66

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AMR LTAAVTAAGGN++YVLD

Sbjct: 67 NVEEDGAIKRAIVEGCGGMFPVGKEAKDDIQLFLGNAGTAMRPLTAAVTAAGGNSSYVLD 126

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVRV G GGLPGGKVKLSGSISSQYL+

Sbjct: 127 GVPRMRERPIGDLVTGLKQLGADVDCSLGTNCPVVRVVGGLPGGKVKLSGSISSQYLT 186

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LME FGV EHSDSWDRF+I+GGQKYKS

Sbjct: 187 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKMEWFGVSVHSDSWDRFFIRGGQKYKS 246

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VTWTE S

Sbjct: 247 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLGMGAEVTWTENS 306

Query: 305 VTVTGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNKMPPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM

Sbjct: 307 VTVKGPPRDSGRKHLRAVDVNMNKMPPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 366

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTIAIDTYDDHRMAMAFSLAAC+VPVTI+D

Sbjct: 367 IAICTELRKLGAATVEEGPDYCVITPPEKLNVTIAIDTYDDHRMAMAFSLAACADVPVTIKD 426

Query: 425 PGCTRKTFPDYFDVLSTFVKN 445
P CTRKTFPDYF+VL F K+

Sbjct: 427 PSCTRKTFPDYFEVLQRFK 447

>sp|P11043.1|AROA_PETHY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase,
chloroplastic; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Flags: Precursor

gb|AAA33699.1| 5-enolpyruvylshikimate-3-phosphate synthase precursor [Petunia x

hybridal
Length = 516

Score = 753 bits (1945), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 374/441 (84%), Positives = 405/441 (91%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLL+S+D+HYMLGAL+TLGL
Sbjct: 76 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLSSDDIHMYLGALKTLGL 135

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D A +RAVV GCGG FVPV +++KEE+QLFLGNAG AMR LTAAVT AGGN+ YVLD
Sbjct: 136 HVEEDSANQRAVVEGCGGLFPVGKESKEEIQFLGNAGTAMRPLTAAVTAGGNSRYVLD 195

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPI DLV GLKQLGA+VDCFLGT CPPVR+ GGLPGGKVKLSGSISSQYL+
Sbjct: 196 GVPRMRERPISDLVDGLKQLGAEVDCFLGTCPPVRIVSKGGLPGGKVKLSGSISSQYLT 255

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFG+ EHS SWDRF+++GGQKYKS
Sbjct: 256 ALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGISVEHSSSWDRFFVRGGQKYKS 315

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P A+VEGDASSASYFLAGAA+TGGT+TVEGCGT SLQGDVKFAEVLE MGA+VTWTE S
Sbjct: 316 PGKAFVEGDASSASYFLAGAAVTGGTITVEGCGTNSLQGDVKFAEVLEKMGAEVTTWENS 375

Query: 305 VTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPRR GRKHL+AIDVNMNKMMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 376 VTVKGPPRSSSRGRKHLRAIDVNMNKMMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 435

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEGPDYCIITPPEKLNVT IDTYDDHRMAMAFSLAAC+VPVTI D
Sbjct: 436 IAICTELRKLGATVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACADVPTIND 495

Query: 425 PGCTRKTFFPDYFDVLSFVKN 445
PGCTRKTFF+YFDVL + K+
Sbjct: 496 PGCTRKTFFPNYFDVLSQYSKH 516

>gb|ADB85251.1| 5-enolpyruvyl shikimate 3-phosphate synthase [Zoysia japonica]
Length = 391

Score = 748 bits (1930), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 380/391 (97%), Positives = 384/391 (98%), Gaps = 1/391 (0%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
ML AL+TLGL VEADKAAKRAVVVGCGGKFPVE D+KEEVQLFLGNAG AMR LTAAVTA
Sbjct: 1 MLEALKTLGLHVEADKAAKRAVVVGCGGKFPVEKDSKEEVQLFLGNAGTAMRPLTAAVTA 60

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKL 174
AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRV G GGLPGGKVKL
Sbjct: 61 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVKGSGGLPGGKVKL 120

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF
Sbjct: 121 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 180

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM
Sbjct: 181 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 240

Query: 295 GAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA
Sbjct: 241 GAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 300

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA 414
SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA
Sbjct: 301 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA 360

Query: 415 CAEVPTIRDPGCTRKTFFPDYFDVLSFVKN 445
CA+VPVTIRDPGCTRKTFFPDYFDVLS+FVKN

Sbjct: 361 CADVPVTIRDPGCTRKTFPDYFDVLSFVKN 391

>gb|ABE77393.4| EPSP synthase [Allium macrostemon]
Length = 522

Score = 746 bits (1926), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 373/441 (84%), Positives = 407/441 (92%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EI LQPIKEI+GTV LPSKSLNRIILLAAAL+EGTT+VDNLLNS+DV YML AL+TLGL
Sbjct: 82 EITLQPIKEITGTVNLPGSKSLNRIILLAAALAEAGTTIVDNLLNSDDVSYMLAALKTLGL 141

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
SVE D+ KRA VVG GG FPV ++++EVQLFLGNAG AMR LTA VTAAGGNA+Y+LD
Sbjct: 142 SVEDDRVNKRATVVVSGGLFPVGKESQKEVQLFLGNAGTAMRPLTAAVTAAGGNASYILD 201

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLVVGLKQLGADVDC LGTDCPPVRV+ GGLPGGKVKLS SISSQYL+
Sbjct: 202 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVDANGGLPGGKVKLSDSISSQYLT 261

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LMERFGV +HS +WDRF+IKGGQKYKS
Sbjct: 262 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVHVDHSSTWDRFFIKGGQKYKS 321

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAA+TGGTVTEGCGT+SLQGDVKFAEVLE MGAKVTWTE S
Sbjct: 322 PGNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLENMGAKVTWTENS 381

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPP++P +K LKA+DVNMNKMMPDVAMTLAVVAL+ADGPT IRDVASWRVKETERM
Sbjct: 382 VTVTGPPQDPQKKRLKAIDVNMNKMMPDVAMTLAVVALYADGPTTIRDVASWRVKETERM 441

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTVIRD 424
+AI TEL KLGA+V EGPDYCIITPPEKLNVT IDTYDDHRMAMAFSLAAC++VPVTI+D
Sbjct: 442 IAICTELRKLGAIVVEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACSDVPVTIKD 501

Query: 425 PGCTRKTFPDYFDVLSFVKN 445
PGCTRKTFPDYF+VL +K+
Sbjct: 502 PGCTRKTFPDYFEVLERYAKH 522

>gb|AAY40472.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza sumatrensis]
Length = 447

Score = 746 bits (1925), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/441 (85%), Positives = 410/441 (92%), Gaps = 1/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISG V LPSKSLNRIILLAAAL+EGTT+VDNLLNS+DVHYMLGALRTLGL
Sbjct: 7 EIVLQPIKEISGAVNLPGSKSLNRIILLAAALAEAGTTIVDNLLNSDDVHYMLGALRTLGL 66

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AMR LTA VTAAGGN++YVLD
Sbjct: 67 NVEEDGAIKRAIVEGCGMFPVGKEAKDDIQLFLGNAGTAMRPLTAGVTAAGGNSSYVLD 126

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVRV G GGLPGG+VKLSGSISSQYL+
Sbjct: 127 GVPRMRERPIGDLVTGLKQLGADVDCSLGTNCPVVRVVGGLPGGRVKLSGSISSQYLT 186

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LME FGV EHSWSWDRF+I+GGQKYKS
Sbjct: 187 ALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMWFVSVHSWSWDRFFIRGGQKYKS 246

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VTWTE S
Sbjct: 247 PGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLQMGAEVWTENS 306

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTV GPPR+ GRKHL+A+DVNMNKMMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETERM
Sbjct: 307 VTVKGPPRDSSGRKHLRAVDVNMNKMMPDVAMTLAVVALYADGPTAIRDVASWRVKETERM 366

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLG+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAAC+VPVTI+D
Sbjct: 367 IAICTELRKLGATVEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACADVPVTIKD 426

Query: 425 PGCTRKTFPDYFDVLTSTFVKN 445
P CTRKTFPDYF+VL F K+
Sbjct: 427 PSCTRKTFPDYFEVLQRFK 447

>gb|ADB85252.1| 5-enolpyruvyl shikimate 3-phosphate synthase [Zoisia japonica]
Length = 391

Score = 743 bits (1919), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 378/391 (96%), Positives = 383/391 (97%), Gaps = 1/391 (0%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
ML AL+TLGL VEADKAAKRAVVVG G KFPVE D+KEEVQLFLGNAG AMR LTA VTA
Sbjct: 1 MLEALKTLGLHVEADKAAKRAVVVGDCGKFPVEKDSKEEVQLFLGNAGTAMRPLTAAVTA 60

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV G GGLPGGKVKL
Sbjct: 61 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVKGSGGLPGGKVKL 120

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
SGSISSQYLSALLMAAPLALGDVEI+IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF
Sbjct: 121 SGSISSQYLSALLMAAPLALGDVEIKIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 180

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMM 294
YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMM
Sbjct: 181 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMM 240

Query: 295 GAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA
Sbjct: 241 GAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 300

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA
Sbjct: 301 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 360

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLTSTFVKN 445
CA+VPVTIRDPGCTRKTFPDYFDVLS+FVKN
Sbjct: 361 CADVPVTIRDPGCTRKTFPDYFDVLTSSFVKN 391

>gb|AA40476.1| 5-enol-pyruvylshikimate-phosphate synthase [Conyza sumatrensis]
Length = 444

Score = 743 bits (1917), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 359/442 (81%), Positives = 404/442 (91%), Gaps = 3/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRI LLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVL+PI++ISGTV LPGSKSLSNRI LLAALSEGTTVVDNLLNS+DVHYMLGALR +G
Sbjct: 5 EEIVLKPIQKISGTVHLPGSKSLSNRI LLAALSEGTTVVDNLLNSDDVHYMLGALRAVG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+VE + A KRA+V GCGG FPV ++AK+E+QLFLGN+G AMR+LTAA+TAAGGN++YVL
Sbjct: 65 LNVEENAAIKRAIVEGCGGVFPVGKEAKDEIQFLGNSGTAMRTLTAITAAGGNSSYVL 124

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGISISSQYL 183
DGVPRMRERPIGDLV GLKQLG +VDC LGT+CPPVRV G GGLPGG+V+LSGISISS YL
Sbjct: 125 DGVPRMRERPIGDLVTGLKQLGVNVDCLGNTCPPVRVVGSGGLPGGRVRLSGSISSVYL 184

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++LLMAAPLALGDVEIEIIDKLIS+PYV+MTL+LM++FGV EHSD+ DRF+++GGQK
Sbjct: 185 TSLLMAAPLALGDVEIEIIDKLISVPVQMTLKLKMQFGVSVEHSDTLDRFHVRRGGQK-- 242

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDAS+ASYFLAGAAITGGT VTVEGCGT+SL GDVKFAEVL MGA+VTW E
Sbjct: 243 SPGNAYVEGDASNASYFLAGAAITGGT VTVEGCGTSSLLGDVKFAEVLGQMGA EVTWAEN 302

Query: 304 SVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR GR HL+ +DVNMNMPDVAM LAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 303 SVTVKGPPRNSSGRGHLRPVDVNMNMPDVAMALAVVALYADGPTAIRDVASWRVKETER 362

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYC+ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI+
Sbjct: 363 MIAICTELRKLGA+VEEGPDYCVITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIK 422

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFFPDYF+VL + K+
Sbjct: 423 DPGCTRKTFFPDYFEVLERYTKH 444

>ref|XP_002511692.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Ricinus communis]
gb|EEF50361.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Ricinus communis]
Length = 518

Score = 741 bits (1913), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 373/443 (84%), Positives = 403/443 (90%), Gaps = 2/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPIKEISGTV LKPSKSLNRILLALLAALSEGTTVVDNLLNS+DV YMLGALRTL
Sbjct: 77 APEIVLQPIKEISGTVTLKPSKSLNRILLALLAALSEGTTVVDNLLNSDDVRYMLGALRTL 136

Query: 64 GLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
L VE + KRA++ GCGG FPV ++K +V+LFLGNAG AMR LTAAVTAAGGN++Y+
Sbjct: 137 RLRVEDNSELKRAIIEGCGGFPVVGRESKTDVELFLGNAGTAMRPLTAAVTAAGGNSSYI 196

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLV GL+QLGADV C T+CPPVRVNG GGLPGGKVKLSGSISSQY
Sbjct: 197 LDGVPRMRERPIGDLVAGLQQLGADVTC- STNCPVRVNGKGLPGGKVKLSGSISSQY 255

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LMER+GV EHS SWDRF+I+GGQKY
Sbjct: 256 LTALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMERYGVFVEHSSSWDRFFIRGGQKY 315

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLEMMGAKVTWTE 302
KSP N+YVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFAEVLE MGAKVTWTE
Sbjct: 316 KSPGNSYVEGDASSASYFLAGAAVTTGGTITVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 375

Query: 303 TSVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPPR +KHL+AIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE
Sbjct: 376 NSVTVTGPPRNSTQKHLRAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 435

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT IDTYDDHRMAMAFSLAAC +VPVTI
Sbjct: 436 RMIAICTELRKLGA+VEEGPDYCVITPPEKLNVTIDTYDDHRMAMAFSLAACGDPVTI 495

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 445
+DPGCTRKTFFPDYF+VL F K
Sbjct: 496 KDPGCTRKTFFPDYFEVLQRFQTK 518

>ref|XP_002301279.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Populus trichocarpa]
gb|EEE80552.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Populus trichocarpa]
Length = 518

Score = 741 bits (1912), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 367/441 (83%), Positives = 408/441 (92%), Gaps = 2/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIK+ISGTV LKPSKSLNRILLALLAALSEGTTVVDNLLNS+DVHYMLGALRTLGL
Sbjct: 79 EIVLQPIKDISGTVTLKPSKSLNRILLALLAALSEGTTVVDNLLNSDDVHYMLGALRTLGL 138

Query: 66 SVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE +K K+A+V GCGG+FPV ++A +V+LFLGNAG AMR LTAAVTAAGGN++Y+LD
Sbjct: 139 HVEDNKLKQAIVEGCGGQFPVGKEANVDVELFLGNAGTAMRPLTAAVTAAGGNSSYILD 198

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

GVPRMRERPIGDLV+GL+QLGADV C T+CPPVR+N GGLPGGKVKLSGSISSQYL+
Sbjct: 199 GVPRMRERPIGDLVIGLQQLGADVSCS-PTNCPVVRINANGGLPGGKVKLSGSISSQYL 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMER+GV EHSD+WDRF+++GGQKYKS
Sbjct: 258 ALLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERYGVFVEHSDNWDRFFVRGGQKYKS 317

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
PKN++VEGDASSASYFLAGAAITGGT+TVEGCG SLQGDVKFAEVLE MGAKVTT+ S
Sbjct: 318 PKNSFVEGDASSASYFLAGAAITGGTITVEGCGMDSLQGDVKFAEVLEKMGAKVTWTKNS 377

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGPPEP+ G+KHL+A+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM
Sbjct: 378 VTVTGPPEPSSQKHLRAVDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 437

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
+AI TEL KLGA+VEEGPDYC+ITPPEKLNVT IDTYDDHRMAMAFSLAAC EV VTI+D
Sbjct: 438 IAICTELRKLGA+VEEGPDYCVITPPEKLNVTIDTYDDHRMAMAFSLAACAEVQVTIKD 497

Query: 425 PGCTRKTFFPDYFDVLSFVKN 445
PGCTRKTFFPDYF+VL + K+
Sbjct: 498 PGCTRKTFFPDYFEVLERYTKH 518

>gb|ACB37380.1| 5-enolpyruvylshikimate 3-phosphate synthase [Calystegia hederacea]
Length = 520

Score = 740 bits (1911), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/442 (85%), Positives = 408/442 (92%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALS+GTTVVDNLL+S+D+HYMLGALRTL
Sbjct: 79 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSQGT+TVVDNLLSSDDIHYMLGALRTL 138

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L VE D A +RA V G GG FP ++ +E+QLFLGNAG AMR LTA+V AAGNA YVL
Sbjct: 139 LRVEEDSAIQRA+VEGSGGLFPASNESNDIQLFLGNAGTAMRPLTAAVVAAGGNARYVL 198

Query: 124 DGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGAD+DCFLGT+CPPVRV G GGLPGGKVKLSGS+SSQYL
Sbjct: 199 DGVPRMRERPIGDLVGLKQLGADIDCFLGTNCPVVRVIGKGLPGGKVKLSGSVSSQYL 258

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLALGDVEIEI+DKLIS+PYVEMT++LMERFGV EHSDSWDRF I+GGQKYK
Sbjct: 259 TALLMAAPLALGDVEIEIVDKLISVPYVEMTIKLMERFGVSEHSDSWDRFLIRGGQKYK 318

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFAEVLE MGA+V+WTE
Sbjct: 319 SPGNAYVEGDASSASYFLAGAAVTGGTITVEGCGTSSLQGDVKFAEVLEKMGAEVSWTEN 378

Query: 304 SVTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPEP P GRKHL+ IDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 379 SVTVKGPPRGPSGRKHLRGIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 438

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIR 423
M+AI TEL KLGA+VEEGPDYCIITPPEKLN+T IDTYDDHRMAMAFSLAAC+VPVTI+
Sbjct: 439 MIAICTELRKLGA+VEEGPDYCIITPPEKLNMTIDTYDDHRMAMAFSLAACADVPVTIK 498

Query: 424 DPGCTRKTFFPDYFDVLSFVKN 445
DPGCTRKTFFPDYFDVLS F K+
Sbjct: 499 DPGCTRKTFFPDYFDVLSKFSKH 520

>sp|P17688.1|AROA_BRANA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase,
chloroplastic; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Flags: Precursor
emb|CAA35839.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]
Length = 516

Score = 739 bits (1907), Expect = 0.0, Method: Compositional matrix adjust.

Identities = 368/443 (83%), Positives = 401/443 (90%), Gaps = 1/443 (0%)

```
Query: 4   AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
          A EIVLQPI+EISG +KLPGSKSLSNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 74  ASEIVLQPIREISGLIKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDDINYMALDALKKL 133

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
          GL+VE D   RAVV GCGG FP   D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 134 GLNVERDSVNNRAVVEGCGGIFPASLDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYV 193

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
          LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 194 LDGVPRMRERPIGDLVVGLKQLGADVECTLTNCPPVRVNANGGLPGGKVKLSGSISSQY 253

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
          L+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV AEHSDSWDRF++KGGQKY
Sbjct: 254 LTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSAEHSDSWDRFFVKGGQKY 313

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
          KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTTSLQGDVKFAEVLE MG KV+WTE
Sbjct: 314 KSPGNAYVEGDASSASYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 373

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          SVTVTGP R+ FG +HL+A+DVNMNKMPPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 374 NSVTVTGPSRDAFGMRHLRAVDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE 433

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
          RM+AI TEL KLG+VEEG DYC+ITPP K+   IDTYDDHRMAMAFSLAAC+VPVTI
Sbjct: 434 RMIAICTELRKLATVEEGSDYCVITPPAKVKPAEIDTYDDHRMAMAFSLAACADVPVTI 493

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
          +DPGCTRKTFPDYF VL + K+
Sbjct: 494 KDPGCTRKTFPDYFQVLESITKH 516
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>ref|XP_002880170.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arabidopsis lyrata
      subsp. lyrata]
gb|EFH56429.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arabidopsis lyrata
      subsp. lyrata]
      Length = 516
```

Score = 738 bits (1904), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 367/443 (82%), Positives = 400/443 (90%), Gaps = 1/443 (0%)

```
Query: 4   AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
          A EIVLQPI+EISG +KLPGSKSLSNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 74  ASEIVLQPIREISGLIKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDDINYMALDALKRL 133

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
          GL+VE D   RAVV GCGG FP   D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 134 GLNVTEDSENRAVVEGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYV 193

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
          LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 194 LDGVPRMRERPIGDLVVGLKQLGADVECTLTNCPPVRVNANGGLPGGKVKLSGSISSQY 253

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
          L+ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV EHSWSWDRF++KGGQKY
Sbjct: 254 LTALLMAAPLALGDVEIEIIVDKLISVPYVEMTLKLMERFGVSTEHSWSWDRFFVKGGQKY 313

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
          KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTTSLQGDVKFAEVLE MG KV+WTE
Sbjct: 314 KSPGNAYVEGDASSASYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 373

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          SVTVTGPPR+ FG +HL+ADVNMNKMPPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 374 NSVTVTGPPRDAFGMRHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE 433

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
          RM+AI TEL KLG+VEEG DYC+ITPP+K+   IDTYDDHRMAMAFSLAAC+VP+TI
Sbjct: 434 RMIAICTELRKLATVEEGSDYCVITPPKKVKPAEIDTYDDHRMAMAFSLAACADVPITI 493
```

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
DPGCTRKTFPDYF VL K+
Sbjct: 494 NDPGCTRKTFPDYFQVLERITKH 516

>dbj|BAA32276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oryza sativa Japonica
Group]
Length = 391

Score = 738 bits (1904), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 372/391 (95%), Positives = 383/391 (97%), Gaps = 1/391 (0%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
ML AL+ LGLSVEADK AKRAVVVGCGGKFPVE DAKEEVQLFLGNAG AMR LTA AVTA
Sbjct: 1 MLEALKALGLSVEADKVAKRAVVVGCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTA 60

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRV GIGGLPGGKVKL
Sbjct: 61 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRVKGIGGLPGGKVKL 120

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF
Sbjct: 121 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 180

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMM 294
YIKGGQKYKSP NAYVEGDASSASYFLAGAAITGGT VTV+GCGTTS LQGDVKFAEVLEMM
Sbjct: 181 YIKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGT VTVQCGTTS LQGDVKFAEVLEMM 240

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAKVTWT+TSVTVTGPPREP+G+KHLKA+DVNMNKMMPDVAMTLAVVALFADGPTAIRDVA
Sbjct: 241 GAKVTWTDTSVTVTGPPREPYGKKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 300

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA 414
SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN+TAIDTYDDHRMAMAFSLAA
Sbjct: 301 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNIT AIDTYDDHRMAMAFSLAA 360

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
CA+VPVTIRDPGCTRKTFP+YFDVLSTFV+N
Sbjct: 361 CADVPVTIRDPGCTRKTFPNYFDVLSTFVRN 391

>gb|AAL65913.1|AF440389_1 5-enolpyruvylshikimate-3-phosphate synthase [Orychopragmus
violaceus]
Length = 518

Score = 737 bits (1902), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 368/443 (83%), Positives = 401/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNS EDVHYMLGALRTL 63
A EIVLQPIKEISG +KLP GSKSLSNRILL LLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 76 ASEIVLQPIKEISGLIKLP GSKSLSNRILL LLAALSEGTTVVDNLLNS DDIN YMLDALKKL 135

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE D RAVV GCGG FP D+K +++L+LGNAG AMR LTA AVTAAGGNA+YV
Sbjct: 136 GLNVERDSENRAVVEGCGGIFPASVDSKSDIELYLG NAGTAMRPLTAAVTAAGGNASYV 195

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 196 LDGVPRMRERPIGDLVVGLKQLGADV ECTLTNCPPVRVNANGGLPGGKVKLSGSISSQY 255

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV AEHS+SWDRF++KGGQKY
Sbjct: 256 LTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSAEHS ESWDRFFVKGGQKY 315

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TTVTEGCGTTS LQGDVKFAEVLE MG KV+WTE
Sbjct: 316 KSPGNAYVEGDASSASYFLAGAAITGETVTVEGCGTTS LQGDVKFAEVLEKMGCKVSWTE 375

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTG P R+ FG +HL+A+DVNMNKMMPDVAMTLAVVALFADGPT IRDVASWRVKETE

Sbjct: 376 NSVTVTGPSRDAFGMRHLRAVDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 435

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEG DYC+ITPP K+ IDTYDDHRMAMAFSLAAC+VPVTI

Sbjct: 436 RMIAICTELRKLGA TVEEGSDYCVITPPAKVKPAEIDTYDDHRMAMAFSLAACADVPVTI 495

Query: 423 RDPGCTRKTFFPDYFDVLSTFVKN 445
+DPGCTRKTFFPDYF VL + K+

Sbjct: 496 KDPGCTRKTFFPDYFQVLESITKH 518

>gb|ACD80082.1| 5-enolpyruvylshikimate-3-phosphate synthase [Convolvulus arvensis]
Length = 520

Score = 737 bits (1902), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 377/442 (85%), Positives = 406/442 (91%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALS+GTTVVDNLL+S+D+HYMLGAL TLG
Sbjct: 79 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSQGT TVVDNLLSSDDIHYMLGALGTLG 138

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L VE D A +RA V G GG FP ++ +E+QL LGNAG AMR LTAAV AAGGNA YVL
Sbjct: 139 LRVEEDSAIQRATVEGSGGLFPASNEDEIQLSLGNAGTAMRPLTAAVVAAGGNARYVL 198

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGAD+DCFLGT+CPPVRV G GGLP GKVKLSGSISSQYL
Sbjct: 199 DGVPRMRERPIGDLVGLKQLGADIDCFLGTNCPVRVIGKGLPRGKVKLSGSISSQYL 258

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLALGDVEIEI+DKLIS+PYVEMT++LIMERFGV EHSWSWDRFYI+GGQKYK
Sbjct: 259 TALLMAAPLALGDVEIEIVDKLISVPYVEMTIKLMERFGVSEHSDSWDRFYIRGGQKYK 318

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTSSLQGDVKFAEVLEMMGAKVWTET 303
SP NAYVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFAEVLE MGA+V+WTE
Sbjct: 319 SPGNAYVEGDASSASYFLAGAAVTGGTITVEGCGTSSLQGDVKFAEVLEKMGAEVSWTEN 378

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR PFGRKHL+ IDVNMNMPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 379 SVTVKGPPRGPFGRKHLRGIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 438

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA VEEGPDYCIITPPEKLNVT IDTYDDHRMAMAFSLAAC+VPVTI+
Sbjct: 439 MIAICTELRKLGAIVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPVTIK 498

Query: 424 DPGCTRKTFFPDYFDVLSTFVKN 445
DPGCTRKTFFPDYFDVLS F K+
Sbjct: 499 DPGCTRKTFFPDYFDVLSKFSKH 520

>sp|P23981.1|AROAl_TOBAC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 1,
chloroplastic; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase 1;
Short=EPSP synthase 1; Flags: Precursor
gb|AAA34071.1| 5-enolpyruvylshikimate-3-phosphate synthase [Nicotiana tabacum]
Length = 518

Score = 736 bits (1901), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 366/442 (82%), Positives = 403/442 (91%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
EIVLQPIK+ISGTVKLP GSKSLSNRILL LLAALS+G TVVDNLL+S+D+HYMLGAL+TLG
Sbjct: 77 NEIVLQPIKD ISGTVKLP GSKSLSNRILL LLAALSKGRTTVVDNLLSSDDIHYMLGALKTLG 136

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L VE D +RA+V GCGG+FPV + ++EE+QLFLGNAG AMR LTAAVT AGG++ YVL
Sbjct: 137 LHVEDDNENQRAIVEGCGGQFPVGKKSEEEIQLFLGNAGTAMRPLTAAVTVAGGHSRYVL 196

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDCFLGT+CPPVR+ GGLPGGKVKLSGSISSQYL
Sbjct: 197 DGVPRMRERPIGDLVDGLKQLGAEVDVDCFLGTNCPVRIVSKGGLPGGKVKLSGSISSQYL 256

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLALGDVEIEIIDLKIS+PYVEMTL+LMERFGV EH+ SWD+F ++GGQKYK
Sbjct: 257 TALLMAAPLALGDVEIEIIDLKISVPYVEMTLKLMERFGVSEHTSSWDKFLVRGGQKYK 316

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP AYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGA+VTWTE
Sbjct: 317 SPGKAYVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEKMGAEVTWTEN 376

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR G KHL+A+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER
Sbjct: 377 SVTVKGPPRNSSGMKHLRAVDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 436

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+V EG DYCIIITPPEKLNVT IDTYDDHRMAMAFSLAAC+VPVTI+
Sbjct: 437 MIAICTELRKLKATVEEGSDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACADVPVTIK 496

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFF+YFDVL + K+
Sbjct: 497 DPGCTRKTFFPDYFDVLQQYSKH 518

>ref|XP_002894141.1| hypothetical protein ARALYDRAFT_474025 [Arabidopsis lyrata subsp.
lyrata]
gb|EFH70400.1| hypothetical protein ARALYDRAFT_474025 [Arabidopsis lyrata subsp.
lyrata]
Length = 523

Score = 736 bits (1900), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 365/443 (82%), Positives = 400/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+ EIVLQPI+EISG +KLPKSKSLSNRILLLAALSEGTT+VDNLLNS+D++YML AL+ L
Sbjct: 81 SSEIVLQPIREISGLIKLPKSKSLSNRILLLAALSEGTTLVVDNLLNSDDINMLDALKKL 140

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE D RAVV CGCG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 141 GLNVETDSENNRAVVEGCGGIFPASIDSKSDIELYLGAGTAMRPLTAAVTAAGGNASYV 200

Query: 123 LDGVPRMRERPIGLDVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIG LVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 201 LDGVPRMRERPIGLHVVLKQLGADVCTLTGNCPPVRVNANGGLPGGKVKLSGSISSQY 260

Query: 183 LSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV AEHSDSWDRF++KGGQKY
Sbjct: 261 LTALLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSAEHSDSWDRFFVKGQKY 320

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTSSLQGDVKFAEVLE MG KV+WTE
Sbjct: 321 KSPGNAYVEGDASSASYFLAGAAITGETVTVEGCGTSSLQGDVKFAEVLEKMGCKVSWTE 380

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGPP R+ FG +HL+AIDVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 381 NSVTVTGPSRDAFGMRHLRAIDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 440

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEG DYC+ITPP+K+ T IDTYDDHRMAMAFSLAAC+VP+TI
Sbjct: 441 RMIAICTELRKLKATVEEGSDYCVITPPKKVKPTEIDTYDDHRMAMAFSLAACADVPITI 500

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFFDYF VL K+
Sbjct: 501 NDPGCTRKTFFPDYFQVLERITKH 523

>gb|ABG88197.1| EPSP synthase [Phaseolus vulgaris]
Length = 522

Score = 735 bits (1897), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 360/441 (81%), Positives = 391/441 (88%), Gaps = 2/441 (0%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

EI ++PIK+ SG +KLPG+KSLSNRILLLAALSEGTTVVDNLLNS+D+HYMLGAL+ LGL
 Sbjct: 83 EIEVEPIKDFSGWIKLPGTKSLSNRILLLAALSEGTTVVDNLLNSDDIHYMLGALKWLGL 142
 Query: 66 SVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 VE DK AVV GCGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA YVLD
 Sbjct: 143 RVETDKIEINGAVVEGCGGIFPASIDSKSDIELYLGAGTAMRPLTAAVTAAGGNAWYVLD 202
 Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
 GVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRVN GGLPGGKVKL GSISSQYL+
 Sbjct: 203 GVPRMRERPIGDLVVGLKQLGADVDCFLGTNCPVRVNAGGGLPGGKVKLFGSISSQYLT 262
 Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
 ALLM+APLALGDVEIEIIDKLIS+PYVE+TL+LMERFGV EH DSWDRF + GGQKYKS
 Sbjct: 263 ALLMSAPLALGDVEIEIIDKLISVPYVEVTLKLMERFGVSVHEWDSWDRFLVHGGQKYKS 322
 Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
 P NAYVEGDASSASY LAGAAITGGTVTVEGCGT SLQGDVKFAEVLE MG KV WTE S
 Sbjct: 323 PGNAYVEGDASSASYLLAGAAITGGTVTVEGCGTKSLQGDVKFAEVLEKMGCKVWWTENS 382
 Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 VTVTGPPEP+ FGR+ L+AIDVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETE M
 Sbjct: 383 VTVTGPPEPDLFGRRLRAIDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETEEM 442
 Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIRD 424
 +AI TEL KLGA+VEEGPDYC+ITPP+KL V IDTYDDHR+ MAFSLAACAEVPVTI D
 Sbjct: 443 IAICTELRKLKATVEEGPDYCVITPPKLVKVAEIDTYDDHRIPMAFSLAACADVPVTIND 502
 Query: 425 PGCTRKTFFPDYFDVLSTFVK 445
 P CTRKTFFPDYF+VL K+
 Sbjct: 503 P-CTRKTFFPDYFEVLERLTKH 522

>gb|AAS80163.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brassica rapa subsp.
 campestris]
 Length = 514

Score = 734 bits (1894), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 366/443 (82%), Positives = 400/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDHYMLGALRTL 63
 A EIVLQPI++ISG +KLPGSKSLSNRILLLAALSEGTTVVDNLLNS+D++YML AL L
 Sbjct: 72 ASEIVLQPIRQISGLIKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDDINMLDALNKL 131
 Query: 64 GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
 GL+VE D RAVV GCGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
 Sbjct: 132 GLNVERDSENNRAVVEGCGGIFPASLDSKGDIELYLGAGTAMRPLTAAVTAAGGNASYV 191
 Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
 LDGVPRMRERPIG+LVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
 Sbjct: 192 LDGVPRMRERPIGELVVGLKQLGADVDCFLGTNCPVRVNANGGGLPGGKVKLSGSISSQY 251
 Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
 L+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV AEHSDSWDRF++KGGQKY
 Sbjct: 252 LTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSAEHSDSWDRFFVKGGQKY 311
 Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
 KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTTSLQGDVKFAEVLE MG KV+WTE
 Sbjct: 312 KSPGNAYVEGDASSASYFLAGAAITGETTVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 371
 Query: 303 TSVTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
 SVTVTGP R+ FG +HL+A+DVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETE
 Sbjct: 372 NSVTVTGPSRDAFGMRHLRAVDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 431
 Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
 RM+AI TEL KLGA+VEEG DYC+ITPP K+ IDTYDDHRMAMAFSLAACAEVPVTI
 Sbjct: 432 RMIAICTELRKLKATVEEGSDYCVITPPAKVKPAEIDTYDDHRMAMAFSLAACADVPVTI 491
 Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 445
 +DPGCTRKTFFPDYF VL + K+
 Sbjct: 492 KDPGCTRKTFFPDYFQVLESITKH 514

>ref|NP_175317.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative /
5-enolpyruvylshikimate-3-phosphate, putative / EPSP
synthase, putative [Arabidopsis thaliana]
gb|AAG29739.1|AC084414_7 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative
[Arabidopsis thaliana]
gb|AAG50661.1|AC084242_5 5-enolpyruvylshikimate-3-phosphate, putative [Arabidopsis thaliana]
gb|AAK25934.1|AF360224_1 putative 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase
[Arabidopsis thaliana]
gb|AAK64123.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Arabidopsis
thaliana]
Length = 521

Score = 733 bits (1892), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 365/443 (82%), Positives = 399/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI+EISG +KLPKSKSLNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 79 ASEIVLQPIREISGLIKLPKSKSLNRILLLAALSEGTTVVDNLLNSDDINYMALDALKIL 138

Query: 64 GLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE RAVV CGGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 139 GLNVETHSENNRAVVEGCGGVFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYV 198

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 199 LDGVPRMRERPIGDLVVGLKQLGADVCTLTNCPPVRVNANGGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV AEHS+SWDRF++KGGQKY
Sbjct: 259 LTALLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSAEHSSESWDRFFVKGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTTSLQGDVKFAEVLE MG KV+WTE
Sbjct: 319 KSPGNAYVEGDASSASYFLAGAAITGETTVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 378

Query: 303 TSVTVTGPPREPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTG P R+ FG +HL+AIDVNMNMKMPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 379 NSVTVTGPSRDAFGMRHLRAIDVNMNMKMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 438

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLG+VEEG DYC+ITPP+K+ IDTYDDHRMAMAFSLAAC+VP+TI
Sbjct: 439 RMIAICTELRKLGATVEEGSDYCVITPPKKVPAEIDTYDDHRMAMAFSLAACADVPITI 498

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 445
DPGCTRKTFFDYF VL K+
Sbjct: 499 NDPGCTRKTFFPDYFQVLERITKH 521

>gb|AAM63771.1| 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative
[Arabidopsis thaliana]
Length = 521

Score = 731 bits (1888), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 364/443 (82%), Positives = 399/443 (90%), Gaps = 1/443 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A EIVLQPI+EISG +KLPKSKSLNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
Sbjct: 79 ASEIVLQPIREISGLIKLPKSKSLNRILLLAALSEGTTVVDNLLNSDDINYMALDALKIL 138

Query: 64 GLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE RAVV CGGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 139 GLNVETHSENNRAVVEGCGGVFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYV 198

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVP+MRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 199 LDGVPQMRERPIGDLVVGLKQLGADVCTLTNCPPVRVNANGGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV AEHS+SWDRF++KGGQKY
Sbjct: 259 LTALLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSAEHSSESWDRFFVKGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT VTTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TTTVEGCGTTS LQGDVKFAEVLE MG KV+WTE
Sbjct: 319 KSPGNAYVEGDASSASYFLAGAAITGET VTTVEGCGTTS LQGDVKFAEVLEKMGKVSWE 378

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTG P R+ FG +HL+AIDVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 379 NSVTVTGPSRDAFGMRHLRAIDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 438

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI 422
RM+AI TEL KLGA+VEEG DYC+ITPP+K+ IDTYDDHRMAMAFSLAAC+VP+TI
Sbjct: 439 RMIAICTELRKLGAATVEEGSDYCVITPPKKVPAEIDTYDDHRMAMAFSLAACADVPITI 498

Query: 423 RDPGCTRKTFFPDYFDVLSTFVKN 445
DPGCTRKTFFPDYF VL K+
Sbjct: 499 NDPGCTRKTFFPDYFQVLERITKH 521

>sp|P10748.1|AROA_SOLLC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase,
chloroplastic; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Flags: Precursor
gb|AAA34136.1| 5-enolpyruvylshikimate-3-phosphate synthase precursor (EC 2.5.1.19)
[Solanum lycopersicum]
Length = 520

Score = 730 bits (1884), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 365/442 (82%), Positives = 399/442 (90%), Gaps = 1/442 (0%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
EIVL PIK+ISGTVKLP GSKSLSNRILL LLAALSEG TVVDNLL+S+D+HYMLGAL+TLG
Sbjct: 79 HEIVLXPIKDISGTVKLP GSKSLSNRILL LLAALSEGRTTVVDNLLSSDDIHYMLGALKTLG 138

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L VE D +RA+V GCGG+FPV + ++EE+QLFLGNAG AMR LTAAVT AGG++ YVL
Sbjct: 139 LHVEDDNENQRAIVEGCGGQFPVGKKSEEEIQLFLGNAGTAMRPLTAAVTVAGGHSRYVL 198

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVR+ GGLPGGKVKLSGSISSQYL
Sbjct: 199 DGVPRMRERPIGDLVDGLKQLGAEDVDCSLGTNCPVRIVSKGGLPGGKVKLSGSISSQYL 258

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EHS WDRF +KGGQKYK
Sbjct: 259 TALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVFVEHSSGWDRLVKGGQKYK 318

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT VTTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTE 303
SP A+VEGDASSASYFLAGAA+TGGT VTTVEGCGT+SLQGDVKFAEVLE MGA+VTWTE
Sbjct: 319 SPGKAFVEGDASSASYFLAGAAVTGGT VTTVEGCGTSSLQGDVKFAEVLEKMGAEVTWTE 378

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTV GPPR G KHL+AIDVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETER
Sbjct: 379 SVTVKGPPRNSSGMKHLRAIDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETER 438

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+V EG DYCIIITPPEKLNVT IDTYDDHRMAMAFSLAAC+VPVTI+
Sbjct: 439 MIAICTELRKLGAATVEEGSDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACADVPVTIK 498

Query: 424 DPGCTRKTFFPDYFDVLSTFVKN 445
+PGCTRKTFFPDYF+VL + K+
Sbjct: 499 NPGCTRKTFFPDYFEVLQKYSKH 520

>ref|NP_973996.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative /
5-enolpyruvylshikimate-3-phosphate, putative / EPSP
synthase, putative [Arabidopsis thaliana]
Length = 489

Score = 717 bits (1850), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 365/468 (77%), Positives = 399/468 (85%), Gaps = 26/468 (5%)

Query: 4 AEEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63

Sbjct: 22 A EIVLQPI+EISG +KLPGSKSLSNRILLLAALSEGTTVVDNLLNS+D++YML AL+ L
ASEIVLQPIREISGLIKLPGSKSLSNRILLLAALSEGTTVVDNLLNSDDINMLDALKIL 81

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL+VE RAVV GCGG FP D+K +++L+LGNAG AMR LTAAVTAAGGNA+YV
Sbjct: 82 GLNVETHSENNRAVVEGCGGVFPASIDSKSDIELYLNAGTAMRPLTAAVTAAGGNASYV 141

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLVVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQY
Sbjct: 142 LDGVPRMRERPIGDLVVGLKQLGADV ECTLTGNCPPVRVNANGGLPGGKVKLSGSISSQY 201

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEI+DKLIS+PYVEMTL+LMERFGV AEHS+SWDRF++KGGQKY
Sbjct: 202 LTALLMAAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSAEHSWDRFFVKGGQKY 261

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
KSP NAYVEGDASSASYFLAGAAITG TVTVEGCGTTSLQGDVKFAEVLE MG KV+WTE
Sbjct: 262 KSPGNAYVEGDASSASYFLAGAAITGETTVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTE 321

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVTVTGTP R+ FG +HL+AIDVNMNMPDVAMTLAVVALFADGPT IRDVASWRVKETE
Sbjct: 322 NSVTVTGPSRDAFGMRHLRAIDVNMNMPDVAMTLAVVALFADGPTTIRDVASWRVKETE 381

Query: 363 RMVAIRTELTK-----LGASVEEGPDYCIITPPEKLNVT 397
RM+AI TEL K LGA+VEEG DYC+ITPP+K+
Sbjct: 382 RMIAICTELRKVKFFFSLSLSVSAHKKFCGICVQLGATVEEGSDYCVITPPKKVKPAE 441

Query: 398 IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
IDTYDDHRMAMAFSLAAC+VP+TI DPGCTRKTFPDYF VL K+
Sbjct: 442 IDTYDDHRMAMAFSLAACADVPITINDPGCTRKTFPDYFQVLERITKH 489

>ref|XP_002993040.1| hypothetical protein SELMODRAFT_162776 [Selaginella moellendorffii]
gb|EFJ05879.1| hypothetical protein SELMODRAFT_162776 [Selaginella moellendorffii]
Length = 453

Score = 665 bits (1715), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 327/442 (73%), Positives = 367/442 (83%), Gaps = 1/442 (0%)

Query: 2 AGAEEIVLQPIKEISGTVKLPKSGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
A E++ L+P+ ISGTVKLPKSGSKSLSNR LLLAAL+EGTT V+NLL+S+DV YM+ AL+
Sbjct: 9 AHLEKLELKPVTTISGTVKLPKSGSKSLSNRTLLLAALAEGTTFVENLLSDDVRYMVAAK 68

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEE-VQLFLGNAGIAMRSLTAAVTAAGGNAT 120
TLGL V D+A A VVGCGGKFPV++ E ++LFLGNAG AMR LTAAGV AG NA
Sbjct: 69 TLGLDVSIEDRANNTATVVGCGGKFPVKEQNGEGIELFLGNAGTAMRPLTAAVAVAGRNR 128

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y+LDGVPRMRERPIGDLV GLKQLGADV+C T CPPV VN GGLPGG +KLSGSISS
Sbjct: 129 YILDGVPRMRERPIGDLVDGLKQLGADVECNPSTRCPPVTVNAKGGLPGGNIKLSGSISS 188

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYL+ALL++APLA GDVEIEI+DKLIS+PYV+MTL+LMERFGV + +W++F I G Q
Sbjct: 189 QYLTALLLSAPLATGDVEIEIVDKLISVPYVDMTLKLMERFGVSVQRYGAWEKFTIAGNQ 248

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y+SP AYVEGDASSASYFLAGAAITGGTV VEGCGTTSLQGDVKFA+VLE MGA V W
Sbjct: 249 TYRSPGKAYVEGDASSASYFLAGAAITGGTVKVEGCGTTSLQGDVKFAKVEKMGATVEW 308

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
TE+SVTVTGPP + LK IDVNMN MPDVAMTLAVVAL+ADGPTAIRDVASWRVKE
Sbjct: 309 TESSVTVTGPPVSTKTGRRLKGIDVNMNAMPDVAMTLAVVALYADGPTAIRDVASWRVKE 368

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
TERM+AI TEL KLGA+VEEGPDYCIITPP+ + AIDTYDDHRMAMAFSLAAC P+
Sbjct: 369 TERMIAICTELRKLGATVEEGPDYCIITPPKTIKPA AIDTYDDHRMAMAFSLAACGGTPI 428

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
TI DP C RKTFF YFDV S+
Sbjct: 429 TINDPSCVRKTFPTYFDVVFSSM 450

>ref|XP_002972123.1| hypothetical protein SELMODRAFT_270937 [Selaginella moellendorffii]
gb|EFJ27040.1| hypothetical protein SELMODRAFT_270937 [Selaginella moellendorffii]
Length = 453

Score = 662 bits (1709), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 324/439 (73%), Positives = 365/439 (83%), Gaps = 1/439 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E++ L+P+ ISGTVKLPKSGKSLSNR LLLAAL+EGTT V+NLL+S+DV YM+ AL+TLG
Sbjct: 12 EKLELKPVTTIISGTVKLPKSGKSLSNRITLLAALAEGTTFVENLLSDDDVRYMVAALKTLG 71

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEE-VQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L V D+ A VVGCGGKFPV++ E ++LFLGNAG AMR LTAAV AG NA Y+L
Sbjct: 72 LDVSEDRPNNTATVVVGCGGKFPVKEQNGEGIELFLGNAGTAMRPLTAAVAVAGRNARYIL 131

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLV GLKQLGADV+C T CPPV VN GGLPGG +KLSGS+SSQYL
Sbjct: 132 DGVPRMRERPIGDLVGLKQLGADVDCNPNSTRCPPVTVNAKGLPGGNIKLSGSVSSQYL 191

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALL++APLA GDVEIEI+DKLIS+PYV+MTL+LMERFGV + W++F I G Q Y+
Sbjct: 192 TALLLSAPLATGDVEIEIVDKLISVPYVDMTLKLMERFGVSVQRYGGWEKFTIAGNQTYR 251

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP AYVEGDASSASYFLAGAAITGGTV VEGCGTTSLQGDVKFA+VLE MGA V WTE+
Sbjct: 252 SPGKAYVEGDASSASYFLAGAAITGGTVKVEGCGTTSLQGDVKFAKVLKMGATVIEWTES 311

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPP + LK IDVNMN MPDVAMTLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 312 SVTVTGPPVSAKTGRRLKGIDVNMNMPDVAMTLAVVALYADGPTAIRDVASWRVKETER 371

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M+AI TEL KLGA+VEEGPDYCIITPP+ + AIDTYDDHRMAMAFSLAAC + P+TI
Sbjct: 372 MIAICTELRKLGA+VEEGPDYCIITPPKTIKPAIDTYDDHRMAMAFSLAACGDTPTITIN 431

Query: 424 DPGCTRKTFPDYFDVLSTF 442
DP C RKTFF YFDV S+
Sbjct: 432 DPSCVRKTFPTYFDVFSSM 450

>emb|CBI38901.3| unnamed protein product [Vitis vinifera]
Length = 463

Score = 659 bits (1700), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 346/430 (80%), Positives = 381/430 (88%), Gaps = 15/430 (3%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EIVLQPIKEISGT+ LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL
Sbjct: 47 EIVLQPIKEISGTITLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 106

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE KR +V GCGG+FPV + ++VQLFLGN A R+LTAAVTAAGGNA+YVLD
Sbjct: 107 QVEEQSENKRIVVQCGGQFPVGNQSVQVQLFLGNACATRALTAAVTAAGGNASYVLD 166

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RMRERPIGDLV GLKQLGADV+CFLGT+CPPV VNG GGLPGGKVKLSGSISSQYL+
Sbjct: 167 GVLRMERERPIGDLVTGLKQLGADVNCFLGTNCPVYVNGNGGLPGGKVKLSGSISSQYLT 226

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYK 243
ALLMAAPLALGDVEIEIID+LISIPYVEMTL++MERFGV EH ++WDR F I+GG+KY
Sbjct: 227 ALLMAAPLALGDVEIEIIDRLISIPYVEMTLKVMERFGVSVHEGNTWDRRFLIRGGKKY- 285

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE GAKV+WTE
Sbjct: 286 -----NASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEQTGAKVSWTEN 333

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPPR+ GRKHL+AIDVNMN+MPDVA+TLAVVAL+ADGPTAIRDVASWRVKETER
Sbjct: 334 SVTVTGPPRDSSGRKHLRAIDVNMNMPDVAITLAVVALYADGPTAIRDVASWRVKETER 393

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M+AI TEL KLGA+V EGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLAAC+VPVTI+
Sbjct: 394 MIAICTELRKLGA+VVEGPDYCVITPPEKLNVTSIDTYDDHRMAMAFSLAACADVPTIK 453

Query: 424 DPGCTRKTFP 433
DPGCT++ P
Sbjct: 454 DPGCTKEKLP 463

>gb|AAK20397.1|AF349754_1 5-enolpyruvylshikimate 3-phosphate synthase [*Lolium rigidum*]
Length = 347

Score = 645 bits (1663), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/346 (93%), Positives = 336/346 (97%), Gaps = 1/346 (0%)

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
LSVEADK AKRAVVVGCGG+FP E DAKEEV+LFLGNAG AMR LTA AV AAGGNATYVL
Sbjct: 2 LSVEADKVAKRAVVVGCGGRFPXEKDAKEEVKLFLGNAGTAMRPLTAAVVAAGGNATYVL 61

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGVPRMRERPIGDLVVGLKQLGA+VDCFLGTDCPPVR+NGIGGLPGGKVKLSGSISSQYL
Sbjct: 62 DGVPRMRERPIGDLVVGLKQLGANVDCFLGTDCPPVRINGIGGLPGGKVKLSGSISSQYL 121

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S+LLMAAPLALGDVEIEIIDKLIS+PYVEMTLRLMERFGV AEHSDSWDRFYIKGGQK K
Sbjct: 122 SSLLMAAPLALGDVEIEIIDKLISVPYVEMTLRLMERFGVTAHSDSWDRFYIKGGQKXK 181

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP NAYVEGDASSASYFLAGAAITGGTVTV+GCGTTSLQGDVKFAEVLEMMGAKVTWT+T
Sbjct: 182 SPGNAYVEGDASSASYFLAGAAITGGTVTVQCGGTTSLQGDVKFAEVLEMMGAKVTWTD 241

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
SVTVTGPPR+PFGGRKHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER
Sbjct: 242 SVTVTGPPRQPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 301

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
MVAI TELTKLGA+VEEGPDYCIITPPEKLNVTADITYDDHRMAMA
Sbjct: 302 MVAICTELTKLGATVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 347

>ref|XP_001771376.1| predicted protein [*Physcomitrella patens* subsp. *patens*]
gb|EDQ63766.1| predicted protein [*Physcomitrella patens* subsp. *patens*]
Length = 473

Score = 627 bits (1618), Expect = e-178, Method: Compositional matrix adjust.
Identities = 325/449 (72%), Positives = 367/449 (81%), Gaps = 5/449 (1%)

Query: 2 AGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
A EEI LQPIK ISG +KLPGSKSLSNR LLLAALSEG TVV+NLL+SEDV YM+GAL+
Sbjct: 25 ASVEEITLQPIKTISGKIKLPGSKSLSNRTLLAALSEGTVVENLLDSEDVRYMIGALK 84

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEE---VQLFLGNAGIAMRSLTAAVTAAGG 117
TLG + D+A R V+ G GG FPV DA+E V+LFLGNAG AMR LTA AVTAAGG
Sbjct: 85 TLGYDIHEDRAENRCVIKSGGVFPVARDAEERGQVVKLFLGNAGTAMRPLTAAVTAAGG 144

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGT-DCPPVRVNGIGGLPGGKVKLSG 176
NA+Y LDGVPRMRERPI DLV+GL+QLGADV C +CPPV +N GGLPGG V+LSG
Sbjct: 145 NASYELDGVPRMRERPIVDLVMLQLQLGADVCTCTEDYPNCPVILINAKGGLPGGTVRLSG 204

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+SSQYLSALLMAAPLALGDVEI ++DKL+S+PYV+MTLRLMERFGVK + D W+RF I
Sbjct: 205 KVSSQYLSALLMAAPLALGDVEIIMVDKLVSPYVDMTLRLMERFGVKVDRHDGWERFSI 264

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
KGGQ YKSP +AYVEGDASSASYFLAGAA+TGGT+TVEGCGTTSLQGDVKFAEVLE MGA
Sbjct: 265 KGGQTYKSPGSAYVEGDASSASYFLAGAAVTGGTITVEGCGTTSLQGDVKFAEVLEKMG 324

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASW 356
V W + +VTVTG P + K LKAIDV+MN MPDVAMTLAV+ LFADGP AIRDV +W
Sbjct: 325 TVQWGDHVTVTGAPADFTTGKRLKAIDVDMNAMPDVAMTLAVLGLFADGPVAIRDVENW 384

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
RVKETERM AI ELTKLGA VEEG DYCI+TPP+++ +DTYDDHRMAMAFSLAAC
Sbjct: 385 RVKETERMRAIVDELTKLGAEEVEEGQDYCIVTPPKRITPAKVDTYDDHRMAMAFSLAACG 444

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
+ +TIRDPGCTRKTFP YF L ++
Sbjct: 445 DTAITIRDPGCTRKTFPTYFTELEKLCQH 473

>gb|AAT45237.1| 5-enol-pyruvylshikimate-phosphate synthase [Erigeron annuus]
Length = 360

Score = 626 bits (1614), Expect = e-177, Method: Compositional matrix adjust.
Identities = 302/360 (83%), Positives = 332/360 (92%), Gaps = 1/360 (0%)

Query: 45 DNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGI 103
DNLLNS+DVHYMLGALR LGL+VE + A KRA+V GCGG FPV ++AK+E+QLFLGNAG
Sbjct: 1 DNLLNSDDVHYMLGALRALGLNVEENGAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNAGT 60

Query: 104 AMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNG 163
AMR LTAAVTAAGGN++YVLDGVPRMRERPIGDLV GLKQLGA+VDC LGT+CPPVRV G
Sbjct: 61 AMRPLTAAVTAAGGNSSYVLDGVPRMRERPIGDLVTGLKQLGANVDCSLGTNCCPPVRVVG 120

Query: 164 IGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV 223
GGLPGGKVKLSGSISSQYL++LLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV
Sbjct: 121 SGGLPGGKVKLSGSISSQYLTSLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGV 180

Query: 224 KAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQG 283
EH+D+WDRF+++GGQKYKSP NAYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQG
Sbjct: 181 SVEHNDTWDRFHVRRGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQG 240

Query: 284 DVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRGRHLKAIDVNMNMPDVAMTLAVVALF 343
DVKFAEVL MGA+VTWTE SVTV GPPR GR HL+ +DVNMNMPDVAMTLAVVAL+
Sbjct: 241 DVKFAEVLGQMGAEVTVTENSVTVKGPPRNSGRGHLRPVDVNMNMPDVAMTLAVVALY 300

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDD 403
ABGPTAIRDVASWRVKETERM+AI TEL KLGA+VEEG DYCI+TPPEKLNVTADITYDD
Sbjct: 301 ABGPTAIRDVASWRVKETERMIAICTELRKLATVEEGTDYCVITPPEKLNVTADITYDD 360

>ref|XP_001760785.1| predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ74524.1| predicted protein [Physcomitrella patens subsp. patens]
Length = 454

Score = 620 bits (1599), Expect = e-175, Method: Compositional matrix adjust.
Identities = 326/453 (71%), Positives = 364/453 (80%), Gaps = 12/453 (2%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEI LQPIK ISGT+KLPGSKSLSNR LLLALLALSEGTTVV+NLL+SEDV YM+ AL+TLG
Sbjct: 2 EEITLQPIKTISGTIKLPGSKSLSNRTLLALLALSEGTTVVENLLDSEDVRYMVAALQTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPV----EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
+E D+AA R V+ G GG FP+ E + E V LFLGNAG AMR LTAAV AAGGN +
Sbjct: 62 FKIEEDRAANRLVIEGEGGVFPIARDAEKSGETVNLFLGNAGTAMRPLTAAVVAAGGNVS 121

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGG-----LPGGKV 172
YVLDGVPRMRERPI DLV GL+QLGADV C +CPPV +N LPGG V
Sbjct: 122 YVLDGVPRMRERPIIDLVLGLQQLGADVCKTEEYPNCPPIINDKSSGSKSKGGLPGGT 181

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
LSG +SSQYLSALLMAAPLALGDVEI +IDKL+S+PYV+MTLRLMERFGVK E W+
Sbjct: 182 HLSGVSSQYLSALLMAAPLALGDVEIVMIDKLVSVPYVDMTLRLMERFGVKVERHGGWE 241

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLE 292
RF IKGGQ YKSP NAYVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFA VLE
Sbjct: 242 RFSIKGGQTYKSPGNAYVEGDASSASYFLAGAAVTGGTITVEGCGTSSLQGDVKFAAVLE 301

Query: 293 MMGAKVTWTETSVTVTGPPREPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD 352
MGAKV WTE SVTVTG P +P K LK+IDV+MN MPDVAMTLAV+ LF+DGP AIRD
Sbjct: 302 KMGAKVEWTEHSVTVTGAPVDPRTGKRLKSIDVDMNAMPDVAMTLAVLGLFSDGPVAIRD 361

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
V +WRVKETERM AI ELTKLGA VEEG DYCI+TPP+++ I+TYDDHRMAMAFSL
Sbjct: 362 VENWRVKETERMRAIVDELTKLGAEEVVEEGDYCIVTPPKRITPAKIETYDDHRMAMAFSL 421

Query: 413 AACAEVPTTIRDPGCTRKTFPDYFDVLSTFVKN 445
AAC +VP+TI DPGCTRKTFP YF L ++
Sbjct: 422 AACGDVPITILDPGCTRKTFPTYFTELEKLCQH 454

>gb|AAT45234.1| 5-enol-pyruvylshikimate-phosphate synthase [Amaranthus
tuberculatus]
Length = 357

Score = 613 bits (1582), Expect = e-173, Method: Compositional matrix adjust.
Identities = 298/357 (83%), Positives = 323/357 (90%), Gaps = 1/357 (0%)

Query: 47 LLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPV-EDAKEEVQLFLGNAGIAM 105
LL S+D+ YML ALRTLGL VE D KRAVV GCGG FPV +D KEE+QLFLGNAG AM
Sbjct: 1 LLYSDDILYMLDALRTLGLKVEDDNTDKRAVEGCGGLFPVGKDGKEEIQFLGNAGTAM 60

Query: 106 RSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG 165
R LTAAV AGGN++YVLDGVPRMRERPIGDLV GLKQLG+DVDCFLGT+CPPVRVN G
Sbjct: 61 RPLTAAVAVAGGNSSVLDGVPRMRERPIGDLVAGLKQLGSDVDCFLGTNCPVRVNAKG 120

Query: 166 GLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 225
GLPGGKVKLSGSISSQYL+ALLMA PL LGDVEIEI+DKLIS+PYVEMT+RLMERFGV
Sbjct: 121 GLPGGKVKLSGSISSQYLTALLMATPLGLGDVEIEIVDKLISVPYVEMTIRLMERFGVSV 180

Query: 226 EHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTSSLQGDV 285
EHSDSWDRF+I+GGQKYKSP AYVEGDASSASYFLAGAA+TGGTVTV+GCGT+SLQGDV
Sbjct: 181 EHSDSWDRFFIRGGQKYKSPGKAYVEGDASSASYFLAGAAVTGGTVTVKCGTSSLQGDV 240

Query: 286 KFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFAD 345
KFAEVL MG KVTWT+ SVTVTGPPRE GRKHL+AIDVNMNKMMPDVAMTLAVVAL+AD
Sbjct: 241 KFAEVLKMGCKVTWTDNSVTVTGPPRESSGRKHLRAIDVNMNKMMPDVAMTLAVVALYAD 300

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
GPTAIRDVASWRVKETERM+AI TEL KLGA+VEEG DYCI+ITPPEKLN TAI+TYD
Sbjct: 301 GPTAIRDVASWRVKETERMIAICTELRKLGAATVEEGDYCIVITPPEKLNPTAIETYD 357

>gb|AAT45236.1| 5-enol-pyruvylshikimate-phosphate synthase [Erigeron annuus]
Length = 358

Score = 607 bits (1564), Expect = e-171, Method: Compositional matrix adjust.
Identities = 309/358 (86%), Positives = 336/358 (93%), Gaps = 1/358 (0%)

Query: 47 LLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPV-EDAKEEVQLFLGNAGIAM 105
LLNS+DVHYMLGALRTLGL+VE D A KRA+V GCGG FPV ++AK+++QLFLGNAG AM
Sbjct: 1 LLNSDDVHYMLGALRTLGLNVEEDGAIKRAIVEGCGGVFPVGKEAKDDIQFLGNAGTAM 60

Query: 106 RSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG 165
R LTAAVTAAGGN++YVLDGVPRMRERPIGDLV+GLKQLGADVDC LGT+CPPVRV G G
Sbjct: 61 RPLTAAVTAAGGNSSVLDGVPRMRERPIGDLVMGLKQLGADVDCSLGTNCPVRVVG 120

Query: 166 GLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 225
GLPGGKVKLSGSISSQYL+ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV
Sbjct: 121 GLPGGKVKLSGSISSQYLTALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSV 180

Query: 226 EHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTSSLQGDV 285
EHSDSWDRF+I+GGQKYKSP NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDV
Sbjct: 181 EHSDSWDRFFIRGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDV 240

Query: 286 KFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFAD 345
KFAEVL MGA+VTWTE SVTV GPPR+ GRKHL+A+DVNMNKMMPDVAMTLAVVAL+AD
Sbjct: 241 KFAEVLQMGAEVTVTENSVTVGPPRDSSGRKHLRAVDVNMNKMMPDVAMTLAVVALYAD 300

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 403
GPTAIRDVASWRVKETERM+AI TEL KLGA+VEEGPDYCI+ITPPEKLNVTATIDTYD
Sbjct: 301 GPTAIRDVASWRVKETERMIAICTELRKLGAATVEEGPDYCVITPPEKLNVTATIDTYD 358

>gb|ACY30625.1| EPSP synthase [Ginkgo biloba]
Length = 353

Score = 598 bits (1543), Expect = e-169, Method: Compositional matrix adjust.
Identities = 290/350 (82%), Positives = 311/350 (88%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTD 155
LFLGNAG AMR LTAAVTAAGG A Y+LDGVPRMRERPIGDLVVGLKQLGADV C L TD
Sbjct: 1 LFLGNAGTAMRPLTAAVTAAGGKARYILDGVPRMRERPIGDLVVGLKQLGADVGCVLNTD 60

Query: 156 CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL 215
CPPV +N GGLPGG VKLSGSISSQYL+ALLM APLALGDV+IEIIDKL+SIPYVEMTL
Sbjct: 61 CPPVYINANGGLPGGTVKLSGSISSQYLTALMTAPLALGDVQIEIIDKLVSIPYVEMTL 120

Query: 216 RLMERFVGKAEHSDSWDRFYIKGGQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
+LMERFGV + D W+ F IKGGQ YKSP A+VEGDASSASYFLAGAAITGGTVTVEG
Sbjct: 121 KLMERFGVTVDHRDGEHFSIKGGQYKSPGKAFVEGDASSASYFLAGAAITGGTVTVEG 180

Query: 276 CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAM 335
CGT+SLQGDVKFAEVLE MGAKVTW++ SVTVTGPP + RKHL IDVNMNKMMPDVAM
Sbjct: 181 CGTSSLQGDVKFAEVLEKMGAKVTWSDNSVTVTGPPVKASRRKHLHGIDVNMNKMMPDVAM 240

Query: 336 TLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 395
TLAVVALFADGPTAIRDVA+WRVKETERM+AI TEL KLGA+VEEGPDYCIITPPE+LNV
Sbjct: 241 TLAVVALFADGPTAIRDVANWRVKETERMLAICTELRKLGAATVEEGPDYCIITPPERLNV 300

Query: 396 TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
T+IDTYDDHRMAMAFSLAAC +VPVTI DPGCTRKTFPDYFDV ++
Sbjct: 301 TSIDTYDDHRMAMAFSLAACGDVPVTINDPGCTRKTFPDYFDVFGVRAQH 350

>sp|P23281.1|AROA2_TOBAC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 2;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase 2; Short=EPSP synthase 2
gb|AAA34072.1| 5-enolpyruvylshikimate-3-phosphate synthase [Nicotiana tabacum]
Length = 338

Score = 578 bits (1489), Expect = e-163, Method: Compositional matrix adjust.
Identities = 289/338 (85%), Positives = 308/338 (91%)

Query: 108 LTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGL 167
LTAAV AGGN+ YVLDGVPRMRERPIGDLV GLKQLGA+VDCFLGT CPPVR+ GGL
Sbjct: 1 LTAAVAVAGGNSRYVLDGVPRMRERPIGDLVDGLKQLGAEVDCFLGTGCCPPVRIVSKGGL 60

Query: 168 PGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEH 227
PGGKVKLSGSISSQYL+ALLMAAPLALGDVEIEIIDKLIS+ YVEMTL+LMERFG+ EH
Sbjct: 61 PGGKVKLSGSISSQYLTALLMAAPLALGDVEIEIIDKLISVLYVEMTLKLMERFGISVEH 120

Query: 228 SDSWDRFYIKGGQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKF 287
S SWDRF ++GGQYKSP AYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKF
Sbjct: 121 SSSWDRFVVRGGQYKSPGKAYVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKF 180

Query: 288 AEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGP 347
AEVLE MGA+VTWTE SVTV GPPR KHL+AIDVNMNKMMPDVAMTLAVVALFADGP
Sbjct: 181 AEVLEQMGAEVWTENSVTVKGPPRNSSAMKHLRAIDVNMNKMMPDVAMTLAVVALFADGP 240

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMA 407
TAIRDVASWRVKETERM+AI TEL KLGA+VEEGPDYCIITPPEKLNVT IDTYDDHRMA
Sbjct: 241 TAIRDVASWRVKETERMIAICTELRKLGAATVEEGPDYCIITPPEKLNVT AIDTYDDHRMA 300

Query: 408 MAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
MAFSLAAC+VPVTI DPGCTRKTFP+YFDVL + K+
Sbjct: 301 MAFSLAACADVPVTINDPGCTRKTFPNYFDVLQQYSKH 338

>gb|AAN77867.1| 5-enolpyruvylshikimate-3-phosphate synthase [Vitis vinifera]
Length = 330

Score = 574 bits (1480), Expect = e-162, Method: Compositional matrix adjust.
Identities = 285/331 (86%), Positives = 311/331 (93%), Gaps = 1/331 (0%)

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKL 174
AGGNA+YVLDGVPRMRERPIGDLV GLKQLGADV+CFLGT+CPPVRV+G GGLPGGKVKL
Sbjct: 1 AGGNASYVLDGVPRMRERPIGDLVTGLKQLGADVNCFLGTNCCPPVRVSGNGGLPGGKVKL 60

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
SGSISSQYL+ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EHS++WDRF
Sbjct: 61 SGSISSQYLTALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVEHSNTWDRF 120

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMM 294
I+GGQKYKSP NA+VEGDASSASYFLAGAA+TGGTVTEGCGT+SLQGDVKF E L M
Sbjct: 121 LIRGGQKYKSPGNAFVEGDASSASYFLAGAAVTGGTVTEGCGTSSLQGDVKFVEFLS-M 179

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAKV+WTE SVTVTGPP++ GRKHL+AIDVNMNKMMPDVAMTLAVVAL+A+GPTAIRDVA
Sbjct: 180 GAKVSWTETSVTVTGPPQDSSGRKHLRAIDVNMNKMMPDVAMTLAVVALYAEGPTAIRDVA 239

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA 414
SWRVKETERM+AI TEL KLG+VEEGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLAA
Sbjct: 240 SWRVKETERMIAICTELRKLGAATVEEGPDYCVITPPEKLNVTIDTYDDHRMAMAFSLAA 299

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
CA+VPVTI+DPGC RKT PDYF+VL F K+
Sbjct: 300 CADVPVTIKDPGCIKRTSPDYFEVLQRFTKH 330

>ref|XP_001422572.1| predicted protein [Ostreococcus lucimarinus CCE9901]
gb|ABP00889.1| predicted protein [Ostreococcus lucimarinus CCE9901]
Length = 436

Score = 570 bits (1470), Expect = e-160, Method: Compositional matrix adjust.
Identities = 294/447 (65%), Positives = 339/447 (75%), Gaps = 19/447 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L+P+K+I GTV+LPGSKSLSNRILLALLAAL+EGTT V+NLL+S+D+ YM+ AL+ LG
Sbjct: 2 EQLTLKPMKKIEGTVRLPGSKSLSNRILLALLAALAEGTKVENLLDSDDIRYMDALKVLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
LS D+ + GCGGK PVE A +LFLGNAG AMR LTA AV AA G T++LD
Sbjct: 62 LSFTEDRENNILEITGCGGKLPVEGA---ELFLGNAGTAMRPLTAAV-AAAGKGT FILD 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RMRERPI DLV GL QLG +C +GT CPPV+V GLPGG+V+LSGS+SSQYL+
Sbjct: 117 GVERMRERPIQDLVDGLVQLGVKAECTMTGCPPVKVEA-NGLPGGRVELSGSVSSQYLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL G +EI I+D+LIS PYVEMT+ LMERFGVK E +D F I+GGQKY S
Sbjct: 176 ALLMAAPLCEGSIEIVDELISKPYVEMTITLMERFGVKVEKADDLQSFQIGGQKYIS 235

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P +A+VEGDASSASYFLAGA ITGGTVTV GCG+ S+QGD FA +E MGA + W S
Sbjct: 236 PGS AFVEGDASSASYFLAGATITGGTVTVIGCGSESIQGD TNFAYTMEQMGATLEWGPNS 295

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VT TGP + LKAIDVNMN MPD AMTLAV ALFADG T IRDVASWRVKETERM
Sbjct: 296 VTCTGP-----KGPLKAIDVNMNAMPDAAMTLAVAALFADGITTIRDVASWRVKETERM 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAE 417
+AI TEL KLG V EG DYC+ITPP KL+ A IDTYDDHRMAMAF+LAAC +
Sbjct: 350 IAICTELRKLGCDFEGADYCVITPPHKLDPKMKANVDIDTYDDHRMAMAFALAACGD 409

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVK 444
V V I DP CT+KTFP YFDVL + K
Sbjct: 410 VDVVINDPKCTKKTFTFYFDVLKSVAK 436

>gb|ABM68632.1| plastid EPSP synthase [Dunaliella salina]
Length = 514

Score = 555 bits (1429), Expect = e-156, Method: Compositional matrix adjust.
Identities = 284/443 (64%), Positives = 337/443 (76%), Gaps = 11/443 (2%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++VLQPIK+ISGTV+LPGSKS+SNR+LLLAAL+EGTTVV NLL+S+D+ YM+GAL+ LG
Sbjct: 81 DQLVLQPIKQISGTVRLPGSKSISNRVLLLAALAEGTTVVKNLDSDDIRYMGALKGLG 140

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E VV GCGG+F E +LFLGNAG AMR LTAAV AA G +VLD
Sbjct: 141 IELEERWDKGMVVKGCGGQFSAEGG---ELFLGNAGTAMRPLTAAV-AAAGRGKFVLD 195

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RMRERPI DLV GL QLG D C LGT CPPV VN GLP GKV+L GS+SSQYL+
Sbjct: 196 GTARMRERPIQDLVDGLVQLGVDACPLGTGCPPVEVNA-QGLPSGKVQLKGSVSSQYLT 254

Query: 185 ALLMAAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
ALLMAAPL+ G +EI I D+L+S PYV+MT+++MERFGV E + I Q Y
Sbjct: 255 ALLMAAPLSKGTEGIEIVITDELVSQPYVDMTVQIMERFGVTVERLNLQHMRIPPNQTY 314

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
K+ A+VEGDASSASYFLAGA ITGGTV VEGCG+ S+QGDV+FAEV+ +MGAKV W+
Sbjct: 315 KTSGEAFVEGDASSASYFLAGATITGGTVVVEGCGSASVQGDVRF AEVVMGLMGAKVWESL 374

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETE 362
S+ +TGP FG K L+ ID + N +PD AMTLAV ALFAD PT IR+V +WRVKETE
Sbjct: 375 YSIKITGP--SAFG-KPLQGIDHDCNDIPDAAMTLAVAALFADKPTTIRNVYNWRVKETE 431

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
RMVAI E KLGA+VEEG DYCI+ITPP+++ AIDTYDDHRMAMAFSLAAC VPVTI
Sbjct: 432 RMVAIVNETRKLGAATVEEGRDYCVITPPKQIQSAAIDTYDDHRMAMAFSLAACGPPVPVTI 491

Query: 423 RDPGCTRKTFPDYFDVLSFVKN 445
DPGCTRKTFPDYF VL + ++
Sbjct: 492 NDPGCTRKTFPDYFRVLESVTQH 514

>ref|XP_003059707.1| predicted protein [Micromonas pusilla CCMP1545]
gb|EEH55659.1| predicted protein [Micromonas pusilla CCMP1545]
Length = 459

Score = 553 bits (1426), Expect = e-155, Method: Compositional matrix adjust.
Identities = 286/439 (65%), Positives = 336/439 (76%), Gaps = 15/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L+PIK+I GTV LKSGK+SNRILL+AL+EG T V NLL+S+D+ YM+ AL+ LG
Sbjct: 29 EKLYLEPIKIEGTVTLPKSGKSMNRILLLSALAEGKTKVLNLLDSDDIRYMGALKQLG 88

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
L + D+A + GC GK PV+ A +LFLGNAG AMR LTAAV AAG + T++LD
Sbjct: 89 LEITEDRANNILEIEGCAKIPVKGA---ELFLGNAGTAMRPLTAAVAAAG-DGTFILD 143

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RMRERPI DLV GLKQLG D +C +GT CPPV+V GLPGG+V+L GS+SSQYL+
Sbjct: 144 GVERMRERPIEDLVDGLKQLGVDAECTMGTCPPVKVVA-NGLPGGRVELKGSVSSQYLT 202

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM+APL+ GD+EI I D L+S PY++MT++L+MERFGV+ D RF +KGGQ YKS
Sbjct: 203 ALLMSAPLSTGDIEIVITDILVSKPYIDMTVKLMERFGVEVGVFDDMQRFVVKGGQTYKS 262

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETS 304
P A+VEGDASSASYFLAGA ITGG V V GCGT SLQGD KFA+ + +MGAKV W +
Sbjct: 263 PGEAFVEGDASSASYFLAGATITGGKVKVIGCGTDSLQGDTKFADTMGLMGAKVEWGKND 322

Query: 305 VTVTGTGPPREPFGGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERM 364
VTVTGP G K LKAIDVNMN MPD AMTLAV AL+ADG T IRDVASWRVKETERM
Sbjct: 323 VTVTGP-----GGK-LKAIDVNMNAMPDAAMTLAVAALYADGVTTIRDVASWRVKETERM 376

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVT 421
+AI TEL KLG V EG DYCI+ITPP + +DTYDDHRMAMAFSLAAC V VT
Sbjct: 377 IAICTELRKLKCDVFEGEDYCVITPPASGKINEGIDVDTYDDHRMAMAFSLAACGGVGVT 436

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I DP CT+KTFP+YFD L+

Sbjct: 437 INDPTCTKKTFFPNYFDALA 455

>ref|XP_001702942.1| 5-enolpyruvylshikimate-3-phosphate synthase [Chlamydomonas reinhardtii]
gb|EDO96795.1| 5-enolpyruvylshikimate-3-phosphate synthase [Chlamydomonas reinhardtii]
Length = 512

Score = 550 bits (1416), Expect = e-154, Method: Compositional matrix adjust.
Identities = 294/453 (64%), Positives = 340/453 (75%), Gaps = 22/453 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EE+ +QP+K+I+GTVKLPKSGSKSLNRIILLALLAALSEGTT+V NLL+S+D+ YM+GAL+ L
Sbjct: 70 EELTIQPVKKIAGTVKLPKSGSKSLNRIILLALLAALSEGTTLVKNLLDSDDIRYMGALKALN 129

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + A VV GCGG+F A +LFLGNAG AMR LTAAG AAG +VLD
Sbjct: 130 VKLEENWEAGEMVVHGCGRFDSAGA---ELFLGNAGTAMRPLTAAVVAAG-RGKFVLD 184

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RMRERPI DLV GL QLG D C +GT CPPV VN GLP GKV LSG +SSQYL+
Sbjct: 185 GVARMRERPIEDLVGDLVQLGVDACKTMTGCPPVEVNS-KGLPTGKVYLSGKVSSQYLT 243

Query: 185 ALLMAAPLAL-----GD-VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
ALLMAAPLA+ GD +EI I D+L+S PYV+MT++LMERFGV E + I
Sbjct: 244 ALLMAAPLAVPGGAGDAIEIIKDELVSQPYVDMTVKLMERFGVVVERLNLQHLRIPA 303

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKV 298
GQ YK+P AYVEGDASSASYFLAGA ITGGTVTVEGCG+ SLQGDV+FAEV+ ++GAKV
Sbjct: 304 GQTYKTPGEAYVEGDASSASYFLAGATITGGTVTVEGCGSDSLQGDVRFVFAEVMGLLGAKV 363

Query: 299 TWTETSVTVTGPPEPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
W+ S+T+TGP FG K + ID + N +PD AMTLAV ALFAD PTAIR+V +WRV
Sbjct: 364 EWSPYSITITGP--SAFG-KPITGIDHDCNDIPDAAMTLAVAALFADRPTAIRNVYNWRV 420

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPE-----KLNVTATIDYDDHRMAMAFSL 412
KETERMVAI TEL KLGA VEEG DYCI+TPP K NV IDTYDDHRMAMAFSL
Sbjct: 421 KETERMVAIVTELKLGAEVEEGRDYCIVTPPPGGVKGVKANV-GIDTYDDHRMAMAFSL 479

Query: 413 AACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
A A VPV IRDPGCTRKTFP YF V + ++
Sbjct: 480 VAAAGVPVIRDPGCTRKTFPTYFKVFESVAQH 512

>ref|XP_002946713.1| hypothetical protein VOLCADRAFT_79287 [Volvox carteri f. nagariensis]
gb|EFJ51939.1| hypothetical protein VOLCADRAFT_79287 [Volvox carteri f. nagariensis]
Length = 509

Score = 548 bits (1411), Expect = e-154, Method: Compositional matrix adjust.
Identities = 292/453 (64%), Positives = 337/453 (74%), Gaps = 22/453 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EE+ LQP+K+I G VKLPKSGSKSLNRIILLALLAAL+EGTT V NLL+S+D+ YM+GAL+ L
Sbjct: 67 EELTLQPVKKIEGHVVKLPKSGSKSLNRIILLALLAALAEGETTSVKNLLDSDDIRYMGALKALN 126

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + VV GCGG+F A +LFLGNAG AMR LTAAG AAG +VLD
Sbjct: 127 VQLEENWETGEMVVHGCGRFNSSGA---ELFLGNAGTAMRPLTAAVVAAG-RGKFVLD 181

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RMRERPI DLV GL QLG D C LGT CPPV VN GLP GKV LSG +SSQYL+
Sbjct: 182 GVARMRERPIQDLVDGLVQLGVDACKTLGTGCPPVEVNS-NGLPTGKVYLSGKVSSQYLT 240

Query: 185 ALLMAAPLAL-----GD-VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
ALLMAAPLA+ GD +EI I D+L+S PYV+MT++LMERFGV+ E D I
Sbjct: 241 ALLMAAPLAVPGGPGGDAIEIIKDELVSQPYVDMTVKLMERFGVRVERLDGLQHLRIPA 300

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKV 298

GQ+Y SP AYVEGDASSASYFLAGA ITGGT+TVEGCG+ SLQGDV+FAEV+ ++GAKV
Sbjct: 301 GQRYVSPGEAYVEGDASSASYFLAGATITGGTITVEGCGSDSLQGDVRF AEVVMGLLGA 360

Query: 299 TWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
W+ S+T+TGP + + ID + N +PD AMTLAV ALFAD PTAIR+V +WRV
Sbjct: 361 EWSPYSITITGPSAS---GQPITGIDHDCNDIPDAAMTLAVAALFADRPTAIRNVYNWRV 417

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPE-----KLNVT AIDTYDDHRMAMAFSL 412
KETERMVAI TEL KLGA+VEEG DYCI+TPP K NV AIDTYDDHRMAMAFSL
Sbjct: 418 KETERMVAIVTELRLKLGATVEEGRDYCIVTPPPGGVAGVKPNV-AIDTYDDHRMAMAFSL 476

Query: 413 AACAEVPTTIRDPGCTRKTFPDYFDVLSTFVKN 445
A A VPV IRDPGCTRKTFP YF V + K+
Sbjct: 477 VAAAGVPVIIRDPGCTRKTFPTYFKVFESVAKH 509

>gb|AAQ75744.1| putative EPSF1 [Oryza sativa Japonica Group]
Length = 331

Score = 546 bits (1408), Expect = e-153, Method: Compositional matrix adjust.
Identities = 283/298 (94%), Positives = 290/298 (97%), Gaps = 1/298 (0%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
ML AL+ LGLSVEADK AKRAVVVCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTA
Sbjct: 1 MLEALKALGLSVEADKAKRAVVVCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTA 60

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKL 174
AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGT+CPPVRV GIGLPGGKVKL
Sbjct: 61 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVKGIGLPGGKVKL 120

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF
Sbjct: 121 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 180

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTTSLQGDVKFAEVLEMM 294
YIKGGQKYKSP NAYVEGDASSASYFLAGAAITGGT+TVEGCGTTSLQGDVKFAEVLEMM
Sbjct: 181 YIKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGT+TVEGCGTTSLQGDVKFAEVLEMM 240

Query: 295 GAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD 352
GAKVTWT+TSVTVTGPPREP+G+KHLKA+DVNMNMPDVAMTLAVVALFADGPTAIRD
Sbjct: 241 GAKVTWTDTSVTVTGPPREPYGKKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD 298

>gb|ACL00597.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum]
Length = 410

Score = 537 bits (1383), Expect = e-150, Method: Compositional matrix adjust.
Identities = 273/327 (83%), Positives = 298/327 (91%), Gaps = 1/327 (0%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSD VHYMLGALRTL 63
A EIVLQPI EISGTVKLPKSKLSNRILLLAALSEGTTVV+NLLNS+DVH+ML AL L
Sbjct: 79 ASEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSD VHYMLGALRTL 138

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
GL V+ D K+A+V GCGG+FPV + +E++LFLGNAG AMR LTAA+TAAGGN++YV
Sbjct: 139 GLYVKHDSKKQAIVEGCGGQFPVKGEGQEIELFLGNAGTAMRPLTAAITAAGGNSSYV 198

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQY 182
LDGVPRMRERPIGDLV GLKQLGADVDC LGT+CPPVR+ G GGLPGGKVKLSGSISSQY
Sbjct: 199 LDGVPRMRERPIGDLVTGLKQLGADVDCILGTNCPVRIEGKGLPGGKVKLSGSISSQY 258

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPLALGDVEIEIIDKLISIPYVEMT++LMERFGV EH+DSWDRF+I+GGQKY
Sbjct: 259 LTALLMAAPLALGDVEIEIIDKLISIPYVEMTMKLMERFGVTVEHTDSWDRFFIRGGQKY 318

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
SP NAYVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFAEVLEMMGAKVTWTE
Sbjct: 319 MSPGNAYVEGDASSASYFLAGAAVTTGGT+TVEGCGTSSLQGDVKFAEVLEMMGAKVTWTE 378

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMN 329
SVTVTGPPR GRKHL+AIDVNMN

Sbjct: 379 NSVTVTGPPRNSSGRKHLRAIDVNMNK 405

>emb|CBN78624.1| 3-Phosphoshikimate 1-Carboxyvinyltransferase [Ectocarpus
siliculosus]
Length = 515

Score = 525 bits (1351), Expect = e-147, Method: Compositional matrix adjust.
Identities = 280/442 (63%), Positives = 326/442 (73%), Gaps = 14/442 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + PI ISG V+LPGSKSLSNR+LLL+AL+EGTT V+NLL+SED+ YMLGAL+TL
Sbjct: 85 ESLTVSPISLISGEVELPGSKSLSNRVLLLSALAEGTTKVENLLDSEDIQYMLGALKTLK 144

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+SV++D AK VVG G F V D E LFLGNAG AMR LTA V A G +V+D
Sbjct: 145 VSVDSLEAKTVEVVGAGPFEVSDPTE---LFLGNAGTAMRPLTAVVCA--GKGEFVMD 199

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRMRERPI DLV GLKQLG DV C T CPPV + GL GG ++SG ISSQYLS
Sbjct: 200 GTPRMRERPIVDLVDGLKQLGVDVSCS-DTGCPPVNIKA-AGLNGGTRVSGKISSQYLS 257

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL+ G+V IEI D+L+S PYV MT++LM++FGVK ++ RF IK GQKY S
Sbjct: 258 ALLMAAPLSSGEVVIEITDELVSAPYVHMTIKLMDKFGVKVKNEGDM-RFTIKDGQKYVS 316

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFL GAAITGG VTV GCG S+QGDV+FAEVLE MGA +TW +
Sbjct: 317 PGTIAVEGDASSASYFLGGAITGGPVTVRGCGRDSVQGDVRFKAEVLEKMGATLTWEANA 376

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TV+ P L+ +DV+ ++PD AMTLAV+ALFA+GPTAIR+V +WRVKETERM
Sbjct: 377 MTVSRDLETP-----LRGVDVDCGEIPDAAMTLAVIALFAEGPTAIRNVYNWRVKETERM 431

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAACAEVPTIR 423
AI TEL KLGA VEEG DYCI+TPP+ + AIDTYDDHRMAM FSLAACAE VPTI
Sbjct: 432 KAIVTELKGLGAEVEEGRDYCIVTPPKAVKPRVAIDTYDDHRMAMCFSLAACAGVPVTIN 491

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
DP CT KTFP YF VL N
Sbjct: 492 DPECTAKTFPTYFKVLGDLTTN 513

>gb|ADI18434.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured delta
proteobacterium HF4000_08N17]
Length = 427

Score = 523 bits (1346), Expect = e-146, Method: Compositional matrix adjust.
Identities = 270/444 (60%), Positives = 329/444 (74%), Gaps = 17/444 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ +++ L PI++ISG+V LPGSKSLSNRILL+ L+EG T + NLL+S+DV M+ AL
Sbjct: 1 MSLPDKLTLSPIQKISGSVVLPGSKSLSNRILLLSMLAEGKTEIQNLLDSDVRRMVEAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
TLG+ +E ++A V G G PV++A L LGNAG A+R LTAA+T G+
Sbjct: 61 ETLGIQLEENRAENLITVSGTSGIIPKEAT---LMLGNAGTAIRPLTAALTL--GHGR 114

Query: 121 YVLDGVP RMRERPI DLV GL QLGA++ C GTDCPPV V GLPGG +LSG+ISS 180
+VLDGV RMRERPI DLV GL QLGA++ C GTDCPPV V GLPGG +LSG+ISS
Sbjct: 115 FVLDGVP RMRERPI DLV NGLSQLGANLRCINGTDCPPVEVIA-DGLPGGITRLSGAISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYL+A+L+AAP A +V+IEI DKL+S+PYVEMTLRLM FGV H +++ F+I Q
Sbjct: 174 QYLTAILLAAPYADKEVQIEITDKLVSVPYVEMTLRLMRSFGVSVNH-ENFRLFHPR-Q 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTW 300
Y+SP + +VEGDASSASYFLAGAAIT GTVTV+GCGT SLQGD +FAEVLE MGAKV W
Sbjct: 232 TYRSPGSI FVEGDASSASYFLAGAAITKGTVTVKGCGTDSLQGDARFAEVLEKMGAKVEW 291

Query: 301 TETSVTVTGPPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360

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      V +TG          L IDV+MN+MPD AMTLAV ALFA GPTAIR++ +WRVKE
Sbjct: 292 EPQQVKLTG-----NSLNGIDVDMQMPDAAMTLAVAALFASGPTAIRNIYNWRVKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
      TER+ A+ TEL KLGA VEEG DY +I PPE++ IDTYDDHRMAMAFSLAAC E P+
Sbjct: 344 TERLQAVSTELRKLGAEEVEEGDYDLVIQPPPEQIRKAEIDTYDDHRMAMAFSLAACGESPI 403

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
      TI +PGC KTFPDYF+VL+ +
Sbjct: 404 TINNPGCVSKTFPDYFEVLNGLCR 427

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>gb|ABR25383.1| 5-enolpyruvylshikimate-3-phosphate synthase [Oryza sativa Indica Group]
Length = 273

Score = 514 bits (1324), Expect = e-144, Method: Compositional matrix adjust.
Identities = 263/273 (96%), Positives = 269/273 (98%)

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Query: 96  LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTD 155
      LFLGNAG AMR LTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGT+
Sbjct: 1  LFLGNAGTAMRPLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTE 60

Query: 156 CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL 215
      CPPVRV GIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL
Sbjct: 61 CPPVRVKGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL 120

Query: 216 RLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
      RLMERFGVKAHSDSWDRFYIKGGQKYKSP NAYVEGDASSASYFLAGAAITGGTVTV+G
Sbjct: 121 RLMERFGVKAHSDSWDRFYIKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTVTVQG 180

Query: 276 CGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAM 335
      CGTTSLSQGDVKFAEVLEMMGAKVTWT+TSVTVTGPPREP+G+KHLKA+DVNMNKMMPDVAM
Sbjct: 181 CGTTSLSQGDVKFAEVLEMMGAKVTWTDTSVTVTGPPREPYGKKHLKAIDVNMNKMMPDVAM 240

Query: 336 TLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      TLAVVALFADGPTAIRDVASWRVKETERMVAIR
Sbjct: 241 TLAVVALFADGPTAIRDVASWRVKETERMVAIR 273

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>gb|ADI17605.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured delta proteobacterium HF0130_19C20]
Length = 427

Score = 499 bits (1284), Expect = e-139, Method: Compositional matrix adjust.
Identities = 263/440 (59%), Positives = 315/440 (71%), Gaps = 17/440 (3%)

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Query: 1  MAGAEIEVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      M +++ L PIK ISGTV LPGSKS+SNRILL+ L+EG T + NLL+S+D M+ AL
Sbjct: 1  MNFPDKLALSPIKNISGTVNLPKSGKSLSNRILLLSMLAEGHTEIHNLLSDDDRMRMVEAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
      +TL + + ++ + V G GK PV +A L LGNAG +R LTAA+T G
Sbjct: 61 KTLRVDLLEERNQNKISVFGTSGKIPVTEA---TLMLGNAGTVIRPLTAALTI--GKGR 114

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISS 180
      +VLDGV RMREPI DLV GLKQLGA+V+C GTD PPV V GLPGG LSG+ISS
Sbjct: 115 FVLDGVQRMREPIIDLVEGLKQLGAEVNCTDSDPPVEVIA-NGLPGGTTSLSGTISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      QYLSA+LMA+P A +V+IEI DKL+S+PYVEMTL+LM RFGV E+ + + F I
Sbjct: 174 QYLSAILMASPYAKTEVKIEIKDKLVSLPYVEMTLQLMLRFGVSVEN-NKYKHFRIPR-I 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTW 300
      YKSP +VEGDASSASYFLAGAAITGG VTV+GCGT SLQGD +FAEVLE MGA V W
Sbjct: 232 PYKSPGVKFVEGDASSASYFLAGAAITGGPVTVKCGCTESLQGDSRFAEVLEKMGANVIEW 291

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
      E ++V+ R L IDV+MN MPD AMTLAV ALFA G TAI ++ +WRVKE
Sbjct: 292 GEREISVS-----RSSLNGIDVDMNMMPDAAMTLAVTALFASGKTAIHNIHNRVKE 343

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Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
TER+ A+ TEL KLG+ VEEG DY +I PP+K+ I+TY+DHRMAMAFSLAAC + V
Sbjct: 344 TERLKAVSTELRKLGSVEEGEDYLVIIIPPKKIQNAEITYEDHRMAMAFSLAACGDASV 403

Query: 421 TIRDPGCTRKTFFPDYFDVLS 440
TI DPGC KTFP YFDV S
Sbjct: 404 TINDPGCVSKTFPRYFDVFS 423

>ref|XP_002288542.1| predicted protein [Thalassiosira pseudonana CCMP1335]
gb|EED93978.1| predicted protein [Thalassiosira pseudonana CCMP1335]
Length = 486

Score = 488 bits (1256), Expect = e-136, Method: Compositional matrix adjust.
Identities = 264/448 (58%), Positives = 311/448 (69%), Gaps = 15/448 (3%)

Query: 2 AGAEIEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
A ++ + PI + GTV LPGSKSLSNR LLLAALS G T V+NLL S+D+ YML AL
Sbjct: 45 AEKNQLTVTPATLEGTVTLPGSKSLSNRCLLLAALSSGNTRVENLLESDDIRYMLEALD 104

Query: 62 TLGLSVEADKAAKRAVVV-GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
TL + VE D K +V V G G +E V+LFLGNAG AMR L AA+ G
Sbjct: 105 TLKVPVERDAIDKTSVTVTGQAGPINSPTPEEVVELFLGNAGTAMRPLAALCM--GEGK 162

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+VLDGVPVRMRERPI DL+ GLKQLGADV C T CPPV +N GL GGK +SG +SS
Sbjct: 163 FVLDGVPVRMRERPISDLIDGLKQLGADVSCVEETGCPPVTINA-SGLKGGKASISGMSS 221

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIK 237
Q+LS+LLMA+P GDV I I D+LIS PYV +T+ LM++FGV + D F I
Sbjct: 222 QFLSSLLMASPAVDGDVTISIKDELISAPYVSLTIGLMKKFGVNVKIEGDMDGTPSFIIG 281

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAK 297
+KY SP++ VEGDASSASYFLAGAAITGGTVTV GCG+ S+QGDV FA V+E MGA
Sbjct: 282 ADEKYTSPESILVEGDASSASYFLAGAAITGGTVTVRGCSDSVQGDVAFANVMEQMGA 341

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
VTW S+T+T R+P LK +DV+ K+PD AMTLAV ALFA+GPT IR+V SWR
Sbjct: 342 VTWAPESITIT---RDP--NTKLKGVVDVDCGKIPDAAMTLAVAALFAEGPTTIRNVYSWR 396

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAA 414
+KETERM AI E TKLGA+VEE DYCII PP+ V I+TYDDHRMAM FSLAA
Sbjct: 397 LKETERMKAIVAECTKLGAATVEEFEDYCIHPPKDNKVNENVVIETYDDHRMAMTFSLAA 456

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFDVLS 442
C V V I DPGCT KTFP YF++L +
Sbjct: 457 CGGVNVIIHDPGCTGKTFPTYFEMLGSI 484

>ref|XP_002178032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeodactylum
tricornutum CCAP 1055/1]
gb|EEC50846.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeodactylum
tricornutum CCAP 1055/1]
Length = 483

Score = 471 bits (1212), Expect = e-131, Method: Compositional matrix adjust.
Identities = 257/441 (58%), Positives = 305/441 (69%), Gaps = 17/441 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++PIK + GTV LPGSKSLSNR LLLAALSEG T V+NLL+S+D+ YML AL L + VE
Sbjct: 50 VKPIKSLDGTVTLPKSKSLSNRCLLLAALSEGKTRVNNLLDSDDICYMLQALEQLAVPVE 109

Query: 69 ADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V G G ++ +LFLGNAG AMR L AA+ G ++LDGV R
Sbjct: 110 R-HSDDSVTVTGKAGPINSPTPEKVCFLFLGNAGTAMRPLAALCM--GKGKFLLDGVSR 166

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
MRERPI DLV GLKQLGADV C + CPPV +N GL GG +SG +SSQ+LS+LLM
Sbjct: 167 MRERPIADLVGLKQLGADVSCVEESGCPPVTINA-NGLQGGCASISGMSSQFLSSLLM 225

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKSP 245

AAPL GD+ I I D+LIS PYV +T+ LM++FGV + D F I +KY SP
Sbjct: 226 AAPLVGDGINISIKDELISAPYVALTIGLMKKFGVNV DIEGDMGAPSFKIASSEKYISP 285

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSV 305
K+ VEGDASSASYF+AGAAITGGTVTV GCG+ S+QGDV FA V+E MGA +TW S+
Sbjct: 286 KSILVEGDASSASYFVAGAAITGGTVTVRGCSESQGDVAFANVMEQMGATITWAPESI 345

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TVT R+P LK +DV+ K+PD AMTLAV ALFA+GPT IR+V SWR+KETERM
Sbjct: 346 TVT---RDP--SVKLGVDVDCGKIPDAAMTLAVAALFAEGPTTIRNVYSWRLKETERMK 400

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFSLAACAEVPVT 421
AI E TKLGA VEE DYCII PP K N+ I+TYDDHRMAM FSL AC V V
Sbjct: 401 AIVAECTKLGAIVEEFEDYCIHPP-KDNIINDNVLIETYDDHRMAMTFSLVACGGVSVI 459

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I DPGCT KTFP YF++L +
Sbjct: 460 INDPGCTGKTFPTYFEMLESI 480

>ref|YP_001357866.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurovum sp.
NBC37-1]
sp|A6Q7Q0.1|AROA_SULNB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAF71509.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurovum sp.
NBC37-1]
Length = 427

Score = 454 bits (1168), Expect = e-125, Method: Compositional matrix adjust.
Identities = 236/435 (54%), Positives = 308/435 (70%), Gaps = 15/435 (3%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L+PI+ I G V LPGSKSLSNR LL+AAL+EGTT + NLL S+D +ML AL+ LG+
Sbjct: 4 ITLKPIRYIEGEVNLPGSKSLSNRALLIAALAEGETTRITNLESDDTRHMLNALKLLGVE 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ VVG GG F KE ++LFLGNAG AMR L AA+T G+ TYVL G
Sbjct: 64 YTLSEDRTECTVVGNGGPF---HTKEPLELFLGNAGTAMRPLCAALTL--GSGTYVLTGE 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM+ERPIG LV L++ GA + PP+++ GL GG+V++ GSISSQ+L+AL
Sbjct: 119 PRMKERPIGHLVDALREAGAKITYLENEGYPPLKIEA-DGLKGGEVRIDGSISSQFLTAL 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAP+A GD++I+I+ +L+S PY+++TL +M++FGV+ +++++RF+IKGGQ Y++ +
Sbjct: 178 LMAAPMARGDMQIDIVGELVSKPYIDITLHIMKQFGVEV-RNENYERFFIKGGQIYQALE 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVT 306
VEGDASSASYFLA AAI GGTV V G G TS+QGDV FA+VLE MGA V W + V+
Sbjct: 237 TFMVEGDASSASYFLAAAAIKGGTVKVTGIGKTSVQGDVAFADVLEKMGAKVEWGDDYVS 296

Query: 307 VTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V+ R L A++++ N +PD AMT+A ALFA G T +R++ +WRVKET+R+ A
Sbjct: 297 VS-----RGELNAVNMDFNHIPDAAMTIATTALFAKGTTLRNIYNWRVKETDRLHA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ EL K+GA VEEG DY ITPP +L AIDTYDDHRMAM FSL A V VTI +P
Sbjct: 349 MAMELRKVGAKVEEGEDYLTITPPVQLKHA AIDTYDDHRMAMCFSLALALDPVSVTINEPE 408

Query: 427 CTRKTFPDYFDVLST 441
CT KTFP YF+VL +
Sbjct: 409 CTAKTFPTYFEVLES 423

>ref|ZP_04639362.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia mollaretii
ATCC 43969]
gb|EEQ12115.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia mollaretii
ATCC 43969]
Length = 428

Score = 454 bits (1167), Expect = e-125, Method: Compositional matrix adjust.
Identities = 241/441 (54%), Positives = 310/441 (70%), Gaps = 16/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESITLQPIALINGTVNLPGSKSVSNRALLLAALAEAGTQLNNLLDSDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++V R V G G G K A + ++LFLGNAG AMR L AA+ GN+ VL
Sbjct: 63 VNVRLSADRTRCEVDGVGKLA---AAQPLELFLGNAGTAMRPLAALCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEQENYPPRLRLG--GFRGGKLTVDGVSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I+I +L+S PY+++TL LM+ FGV EH +++ F+IKGGQ Y++
Sbjct: 176 ALLMAAPLAEQDTDIQIQGELVSKPYIDITLHLMKAFGV DVEH-ENYQIFHIKGGQTYRT 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V V G G S+QGD KFA+VLE MGAKVTW +
Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKKSQGD TKFADVLEKMGAKVTWGDDY 294

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFADGPTIIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A + +P+TI D
Sbjct: 347 SAMATELRKVGQAQVEEGEDYIRVPPAQLITAEIGTYNDHRMAMCFSLVALSNIPITILD 406

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
P CT KTFPDYF+ L+ +N
Sbjct: 407 PKCTAKTFFPDYFEQLARLSQN 427

>ref|YP_003041661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Photorhabdus
asymbiotica subsp. asymbiotica ATCC 43949]
emb|CAQ84918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Photorhabdus
asymbiotica]
Length = 431

Score = 448 bits (1152), Expect = e-124, Method: Compositional matrix adjust.
Identities = 237/435 (54%), Positives = 295/435 (67%), Gaps = 16/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI I+GTV LPGSKS+SNR LLLAA +EGTT + NLL+S+D+ +ML AL LG
Sbjct: 5 QSLTLQPISSINGTVNLPGSKSVSNRALLLAFAEGTTCLTNLLDSDIRHMLNALTEL 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R V G G G K V+LFLGNAG AMR L AA+ N +L
Sbjct: 65 VSYRLSDDRTRCEVDGMGGLIT---GKGPVELFLGNAGTAMRPLAALCLGKNN--IILT 119

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G G G +V + G +SSQ+L+
Sbjct: 120 GEPRMKERPIGHLVDALRQGGAEIDYLEQENYPPRLRIK--GFIGGRVTVDGRVSSQFLT 177

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI I +L+S PY+++TL LM+ FG+ EH D + F+IKG QKY S
Sbjct: 178 ALLMTAPLAENDCEIHIQGELVSKPYIDITLALMKSFGITVEH-DQYQVFIKGGQKYHS 236

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V V G G SLQGD KFA VLE MGAK+ W +
Sbjct: 237 PGHYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKNSLQGD TKFANVLEKMGAKIRWGDDF 296

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L ID++MN++PD AMT+A ALFA+G T IR++ +WRVKET+R+
Sbjct: 297 VECE-----RGTLTGIDMDMNEIPDAAMTIATTALFAEGKTIVIRNIYNWRVKETDRL 348

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP+++ I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 349 YAMATELRKVGAEVEEGRDYIRITPPQRILPAEIGTYNDHRMAMCFSLVALSDTPVTILD 408

Query: 425 PGCTRKTFFPDYFDVL 439

PGCT KTFPDYF+ L

Sbjct: 409 PGCTAKTFFPDYFNQL 423

>ref|ZP_04628535.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia bercovieri
ATCC 43970]

gb|EEQ06594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia bercovieri
ATCC 43970]
Length = 428

Score = 447 bits (1149), Expect = e-123, Method: Compositional matrix adjust.
Identities = 237/440 (53%), Positives = 307/440 (69%), Gaps = 16/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + LQPI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG

Sbjct: 3 ESLTLQPIALINGTVNLPGSKSVSNRALLLAALAEGTTQLNNLLSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

++V R V G G G E ++LFLGNAG AMR L AA+ G++ VL

Sbjct: 63 VNVRLSADTRCEVDGVGGLAAESP---LELFLGNAGTAMRPLAALCL--GDSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG + + GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLRG--GFRGGNLTVDGVSQSFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

ALLMAAPLA D EI+I +L+S PY+++TL LM FGV +H +++ F+IKGGQ Y++

Sbjct: 176 ALLMAAPLAEQDTEIQIGELVSKPYIDITLHLMNAFGVDVKH-ENYQIFHIKGGQSYRT 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGAKVTW +

Sbjct: 235 PGAYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKSVQGDIFADVLEKMGAKVTWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELRGIDMDMNHIPDAAMTIATTALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424

A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A + +P+TI D

Sbjct: 347 SAMATELRKVGQAQVEEGEDYIRVVPPAQLITAEIGTYNDHRMAMCFSLVALSAIPITILD 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444

P CT KTFPDYF+ L+ +

Sbjct: 407 PKCTAKTFFPDYFQLARLSQ 426

>ref|ZP_07744902.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio caribbenthicus
ATCC BAA-2122]

gb|EFP94657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio caribbenthicus
ATCC BAA-2122]
Length = 426

Score = 446 bits (1147), Expect = e-123, Method: Compositional matrix adjust.
Identities = 235/438 (53%), Positives = 300/438 (68%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + L PI +++G V LPGSKS+SNR LLLAA++ G T + NLL+S+D+ +ML AL +LG

Sbjct: 2 ESLTLHPISKVNGVVNLPGSKSVSNRALLLAAMARGKTRLTNLLSDDIRHMLNALSSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

++ + V G G F DA E+++FLGNAG AMR L AA+ G YVL

Sbjct: 62 VNYTSLSEDKTVCDVEGLGRPF---DAPEELEIFLGNAGTAMRPLAALCL--GTGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV L+Q GA V PP+++ G G L GG V++ GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVSSLRQAGAKVTYLEEEGYPLKIIGTG-LSGGTVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

A LMAAP+A DV I+II +L+S PY+++TL +M +FGVK E+++ + F I+ GQ Y+S
Sbjct: 176 AFLMAAPMAGDDVTIKIIGELVSKPYIDITLHIMAQFGVKVENNN-YAEFVIRKGGQNYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG + V G G S+QGD++FAE L MGA + W +
Sbjct: 235 PGFEFLVEGDASSASYFLAAAAIKGGEIKVTGIGRNSIQGDIQFAEALAKMGADIEWGDDF 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V G+ LKA+D++ N +PD AMT+A ALFADG TAIR+V +WRVKET+R+
Sbjct: 295 VI-----SRVGK--LKAVDLDFNHIPDAAMTIATTALFADGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRD 424
A+ TEL K+GA VEEG DY +ITPPE L AIDTYDDHRMAM FSL A + PVTI D
Sbjct: 347 HAMATELRKVGAEVEEGHDYIVITPPESLKHAAIDTYDDHRMAMCFSLVALSNTPTVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYFD L +
Sbjct: 407 PKCTSKTFFPDYFDKLESL 424

>ref|ZP_04611277.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia rohdei ATCC 43380]
gb|EEQ04640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia rohdei ATCC 43380]
Length = 428

Score = 445 bits (1144), Expect = e-123, Method: Compositional matrix adjust.
Identities = 238/436 (54%), Positives = 303/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL LG
Sbjct: 3 ESLTLQPIALINGTVNLPGSKSVSNRALLAALAEGTTQLNNLLDSDDIRHMLNALEALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G G G A + ++LFLGNAG AMR L AA+ GN+ VL
Sbjct: 63 VKFRLSADRTRCEVDGLGGKLV---ASQPLELFLGNAGTAMRPLAAALCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEQENYPPLRLRG--GFSGGKLTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D EI+I +L+S PY+++TL +M+ FG+ H D++ F IKGGQ Y++
Sbjct: 176 ALLMAAPLAEQDTEIQIGELVSKPYIDITLHMMKAFGIDVVH-DNYHVFQIKGGQTYRT 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAKVTW +
Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKKSQGDTKFADVLEKMGAKVTWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELHGIDMDNMNIPDAAMTIATAALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRD 424
A+ TEL K+GA VEEG D+ + PP +L I+TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGQDFIRVVPPAQLIAAEIETYNDRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFFPDYFEQLA 422

>ref|ZP_01814130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrionales bacterium SWAT-3]
gb|EDK28469.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrionales bacterium SWAT-3]
Length = 426

Score = 444 bits (1143), Expect = e-122, Method: Compositional matrix adjust.
Identities = 233/435 (53%), Positives = 297/435 (68%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+++SG V LKPGSKS+SNR LLLAALS GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLLTLQPIQKVSQEVNLPKSGKSVSNRALLAALSTGTRTLNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G GG F + A ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VDYQLSADKTVCVETGVGGAFSNDK---LELFLGNAGTAMRPLAALCL--GRGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GADV+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVNALREAGADVEYLENENYPLKITGTG-LKSGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V I+I +L+S PY+++TL +M++FGV ++D + F I GQ YK+
Sbjct: 176 AFLMAAPLAEGEVSIIKIEGELVSKPYIDITLHIMKQFGVDVNNND-YQEFVIPTGQSYKA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISRC-----GELKGIDMDYNHIDPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTVIR 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIIVNPVLAELKHAIDTYDDHRMAMCFSLVALSDPTPTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
PGCT KTFPDYFD L
Sbjct: 407 PGCTSKTFFPDYFDKL 421

>ref|NP_902718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chromobacterium
violaceum ATCC 12472]
gb|AAQ60717.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chromobacterium
violaceum ATCC 12472]
Length = 456

Score = 444 bits (1143), Expect = e-122, Method: Compositional matrix adjust.
Identities = 235/439 (53%), Positives = 295/439 (67%), Gaps = 15/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L P ++G++KLPKSGKSLSNR LLLAALS G+T+V +LL+S+D+ +ML AL+ LG
Sbjct: 29 EQLHLNPCTRLAGSIKLPKSGKSLSNRLLALLAALSGGSTLVRLDSDDIRHMLSALKLLG 88

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E ++ V GCGG FPV++A +LFLGNAG A R LTAA+ GG +Y L
Sbjct: 89 VKIEQQGDSRDFRVQCGGVFPVKNA---ELFLGNAGTAFRPLTAALALMGG--SYQLS 142

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L GA ++ PP+ V+ +++ G++SSQ+L+
Sbjct: 143 GVPRMHERPIGDLVDALNAAGARIEYLQPGFPPLAVSPADVRCAAPIQVKGNVSSQFLT 202

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL G EIE++ +LIS PY+E+TL LM RFGV+ E D W RF I GGQ Y S
Sbjct: 203 ALLMALPLTGGQAEIEVVGELISKPYIEITLNLMARFGVRVER-DGWQRFVIPGGQHYIS 261

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P YVEGDASSASYFLA A+ GG V VEG G S+QGDV+FAE LE MGA V +
Sbjct: 262 PGEVYVEGDASSASYFLAAGLAGGVPVRVEGVGEASIQGDVRFAEALERMGASVRLGDNW 321

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ E LKAID++ N +PD AMTLAV AL ADG T +R++ASWRVKET+R+
Sbjct: 322 I-----EARAEGRLKAIDLDCNHIPDAAMTLAVALAADGTTTLRNIAASWRVKETDRL 374

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTVIR 423
A+ EL K+GA+VEEGPDY +TPP L A IDTYDDHRMAM FSL + PV I
Sbjct: 375 SAMAAELRKVGATVEEGPDYIRVTPPAALTPNAEIDTYDDHRMAMCFSLVSLGAPVVIN 434

Query: 424 DPGCTRKTFFPDYFDVLSTF 442

DPGC KTFP YF L+
Sbjct: 435 DPGCVAKTFPGYFQALAAAL 453

>ref|ZP_00991039.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio splendidus
12B01]
gb|EAP93912.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio splendidus
12B01]
Length = 426

Score = 444 bits (1141), Expect = e-122, Method: Compositional matrix adjust.
Identities = 232/435 (53%), Positives = 297/435 (68%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI+++SG V LPKSKS+SNR LLLAALS GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIQKVSSEVNLPGSKSVSNRALLLAALSTGTRLTNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F + A ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VDYQLSADKTVCSEVTGVGGAFFSSDKA---LELFLGNAGTAMRPLAALCL--GRGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GADV+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALQEAGADVEYLENENYPPLKITGTG-LKSGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V I+I +L+S PY+++TL +M++FGV ++D + F I GQ Y +
Sbjct: 176 AFLMAAPLAEGEVTIKIEGELVSKPYIDITLHIMKQFGVDVINND-YQEFVIPTGQSYSA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVWTWETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
V LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISRC-----GELKGIDMDYNHIDPAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L+ AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIIVNPVAQLSHAAIDTYDDHRMAMCFSLVALSDPTVTIND 406

Query: 425 PGCTRKTFPDYFDVL 439
PGCT KTFPDYFD L
Sbjct: 407 PGCTSKTFPDYFDKL 421

>ref|ZP_05888099.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio coralliilyticus
ATCC BAA-450]
gb|EEX31666.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio coralliilyticus
ATCC BAA-450]
Length = 426

Score = 443 bits (1140), Expect = e-122, Method: Compositional matrix adjust.
Identities = 233/438 (53%), Positives = 305/438 (69%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI +++G V LPKSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIKVNVEVNLPGSKSVSNRALLLAALAKGTRLTNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G F DA E ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYTSLQDKTVCVEEGLGKAF---DAPEALELFLGNAGTAMRPLAALCL--GSGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV+ D PP+++ G G L GG V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVEALRQAGADVEYLENEDFPPLKIKGTG-LKGGTVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA DV I I+ +L+S PY+++TL +M +FGV+ E++D + F I+ GQ Y +
Sbjct: 176 AFLMSAPLAQDDVTIRIVGELVSKPYIDITLHIMSQFGVEVENND-YQEFVIRKQSYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKKSIGDIIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGELNAVDMDFNHIDPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ++TPP++L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIIVTPPQQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYFD L++
Sbjct: 407 PKCTSKTFPDYFDKLASL 424

>ref|ZP_08104460.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sinaloensis
DSM 21326]
gb|EGA68516.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sinaloensis
DSM 21326]
Length = 426

Score = 443 bits (1140), Expect = e-122, Method: Compositional matrix adjust.
Identities = 238/436 (54%), Positives = 305/436 (69%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI ++SG V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIKVSQVNLPGSKSVSNRALLAALAKGTTRLTNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G F V +A+E LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYQLSDDKTVCVEGLGRPFNVAAEQE--LFLGNAGTAMRPLAALCL--GSGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA+V+ D PP+++ G G L GG V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVNLRLQAGAEVEYLEAQDYPLKITGTG-LKGGTVEIDGSISSQFLT 175

Query: 185 ALLMAAPLAGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA DV I+II +L+S PY+++TL +M +FGV E+ D + F I+ GQ Y +
Sbjct: 176 AFLMSAPLAQDDVTIKIIGELVSKPYIDITLHIMAQFGVTVENRD-YQEFVIRSGQSYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKKSIGDIIQFADALEKMGAEIEWGDDY 294

Query: 305 V-TVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V + G LKAID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R
Sbjct: 295 VISRVGT-----LKAIDMDFNHIDPDAAMTIATTALFAEGTTAIRNVYNWRVKETDR 345

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY I+TPP +L AIDTYDDHRMAM FSL A ++ PVTI
Sbjct: 346 LAAMATELRKVGAEVEEGEDYIIVTPPAQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIN 405

Query: 424 DPGCTRKTFPDYFDVL 439
DP CT KTFPDYFD L
Sbjct: 406 DPKCTSKTFPDYFDKL 421

>ref|YP_002416694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio splendidus
LGP32]
sp|B7VM38.1|ARO_A_VIBSL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAV18185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio splendidus
LGP32]
Length = 426

Score = 443 bits (1139), Expect = e-122, Method: Compositional matrix adjust.
Identities = 232/435 (53%), Positives = 296/435 (68%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+++SG V LKSGKSLSNR LLLAALS GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLLTLQPIQKVSQEVNLPKSGKSVSNRALLAALSTGTRTLNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G GG F + A ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VDYQLSADKTVCVETGVGGAFSSDKA---LELFLGNAGTAMRPLAALCL--GRGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GADV+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALREAGADVEYLENENYPLKITGTG-LKSGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V I+I +L+S PY+++TL +M++FGV ++D + F I GQ Y +
Sbjct: 176 AFLMAAPLAEGEVTIKIEGELVSKPYIDITLHIMKQFQVDVINND-YQEFVIPTGQSYTA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISRC-----GELKGIDMDYNHIDPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIIVNPVLAELTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
PGCT KTFPDYFD L
Sbjct: 407 PGCTSKTFFPDYFDKL 421

>ref|ZP_04633106.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
frederiksenii ATCC 33641]
gb|EEQ14304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
frederiksenii ATCC 33641]
Length = 426

Score = 442 bits (1138), Expect = e-122, Method: Compositional matrix adjust.
Identities = 236/436 (54%), Positives = 303/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LKSGKSLSNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLLTLQPIALINGTVNLPKSGKSVSNRALLAALAEAGTQLNLLSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GK E + ++LFLGNAG AMR L AA+ GN+ VL
Sbjct: 63 VKFRLSADRTRCEVDGLGKGLVAE---QPLELFLGNAGTAMRPLAALCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GK+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPLRLRG--GFHGGKLTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I+I +L+S PY+++TL LM+ FG+ H +++ F+IKGGQ Y++
Sbjct: 176 ALLMTAPLAEQDTDIQIQGELVSKPYIDITLHLMKAFGIDVVH-ENYQIFHIKGGQTYRT 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAKV+W +
Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKSVQGDTKFADVLEKMGAKVSWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELHGIDMDMNHIPDAAMTIATTALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGQDYIRVPPPTQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440

P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFPDYFEQLA 422

>ref|ZP_01064779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sp. MED222]
gb|EAQ53854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sp. MED222]
Length = 426

Score = 441 bits (1135), Expect = e-122, Method: Compositional matrix adjust.
Identities = 232/435 (53%), Positives = 296/435 (68%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+++SG V LPGSKS+SNR LLLAALS GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIQKVSGEVNLPGSKSVSNRALLLAALSTGTTRLTNLLDSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G GG F + A ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VDYQLSADKTVCEVTGVGGAFSSDKA---LELFLGNAGTAMRPLAALCL--GRGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA+V+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALQEAGANVEYLENENYPPLKITGTG-LKSGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V I+I +L+S PY+++TL +M++FGV +SD + F I GQ Y +
Sbjct: 176 AFLMAAPLAEGEVTIKIEGELVSKPYIDITLHIMKQFGVDVINS-DYQEFVPTGQSYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAIAKGGEIKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISRC-----GELKGIDMDYNHIDPAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIIVNPVAELTHAAIDTYDDHRMAMCFSLVALSDPTVTIND 406

Query: 425 PGCTRKTFPDYFDVL 439
PGCT KTFPDYFD L
Sbjct: 407 PGCTSKTFPDYFDKL 421

>ref|ZP_04618801.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia aldovae ATCC
35236]
gb|EEP96655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia aldovae ATCC
35236]
Length = 428

Score = 441 bits (1134), Expect = e-121, Method: Compositional matrix adjust.
Identities = 237/441 (53%), Positives = 303/441 (68%), Gaps = 16/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLTLHPIALINGTVNLPKSGKSVSNRALLLAALAEGTTQLNLLDSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G G G E + ++LFLGNAG AMR L AA+ GN VL
Sbjct: 63 VKYRLSADRTRCDVDGLGGKLI AE---QPLELFLGNAGTAMRPLAALCL--GNNDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLRG--GFRGGKLTVDGSSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y+S
Sbjct: 176 ALLMTAPLAEQDTEIQIGELVSKPYIDITLHLMKAFGVDVVH-ENYQVFIKGGQIYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAK++W +

Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKKSQGDTKFADVLEKMGAKISWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA+GPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFANGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 SAMATELRKVGAEVEEGNDYIRVVPQAQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 445
P CT KTFPDYF+ L+ N

Sbjct: 407 PKCTAKTFPDYFEQLARLSHN 427

>ref|ZP_05877099.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio furnissii CIP 102972]
gb|EEX41380.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio furnissii CIP 102972]
Length = 426

Score = 441 bits (1133), Expect = e-121, Method: Compositional matrix adjust.
Identities = 236/433 (54%), Positives = 296/433 (68%), Gaps = 15/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LKSGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG

Sbjct: 2 ESLLTLPISKIDGEVNLPGSKSVSNRALLAALAKGTTRLNLLDSDIRHMLNALSCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F V + +E LFLGNAG AMR L AA+ G ++L

Sbjct: 62 VVYRLSEDKTECEVEGLGKPFVSELQE---LFLGNAGTAMRPLAALCL--GEGEFILT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLENENYPLRITGTG-LESGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I +L+S PY+++TL +ME+FGV+ ++D + F I GQ Y S

Sbjct: 176 AFLMSAPLAKGVITIQIDGELVSKPYIDITLHIMEQFGVQVINND-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FAE LE MGA + W E

Sbjct: 235 PGNFLVEGDASSASYFLAAAAIKGGQVKVTGIGKNSIQGDIQFAEALKMGAHIEWGEDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+

Sbjct: 295 VIAR-----RGELNAVLDLDFNHIPDAAMTIATAALFANGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG DY IITPP+KL AIDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVEEGEDYIIITPPQKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFD 437
P CT KTFPDYFD

Sbjct: 407 PKCTSKTFPDYFD 419

>ref|ZP_02959853.1| hypothetical protein PROSTU_01752 [Providencia stuartii ATCC 25827]
gb|EDU58576.1| hypothetical protein PROSTU_01752 [Providencia stuartii ATCC 25827]
Length = 424

Score = 440 bits (1131), Expect = e-121, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI I+GT+ LKSGSKS+SNR LLLAA++ GTT++ NLL+S+D+ +ML AL LG

Sbjct: 2 QSLTLQPISSINGTINLPGSKSVSNRALLAAMANGTTLTNLLDSDIRHMLNALSCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + R V G GG+ D E+++FLGNAG AMR LTAA++ A N VL

Sbjct: 62 VNYQLSEDKTRCRVQGVGRLCHTD---ELEIFLGNAGTAMRPLTAALSLANNN--IVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA +D + PP+R+ G G GG++ + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALREGGATIDYLEQENYPPLRLRG--GFSGGEISVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA + I I +L+S PY+++TL LM FGV+ ++ + RF IKG Q+Y+S
Sbjct: 175 ALLMAAPLAEKETIITISGELVSKPYIDITLALMATFGVEVDNH-QYQRFVIKGGQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G SLQGD KFA VLE MGA + W +
Sbjct: 234 PGEYLVVEGDASSASYFLAAAAIKGGTVRVVTGIGRNSLQGDTKFANVLEKMGATIRWGDDF 293

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ R L ID++MN +PD AMT+ VALFA G T IR++ +WRVKET+R+
Sbjct: 294 IECQ-----RGTNGIDMDMNAIPDAAMTIGTVALFAQGETVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG D+ I PP +L I+TY+DHR+AM FSL A ++ PVTI D
Sbjct: 346 YAMATELRKVGAEVEEGHDFIRIVPPAQLQHAEIETYNDRHAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
PGCT KTFPDYF L+
Sbjct: 406 PGCTAKTFFPDYFQQLA 421

>gb|ADT86780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio furnissii NCTC
11218]
Length = 426

Score = 440 bits (1131), Expect = e-121, Method: Compositional matrix adjust.
Identities = 236/433 (54%), Positives = 295/433 (68%), Gaps = 15/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIISKIDGEVNLPGSKSVSNRALLAALAKGTRTLTNLLDSDDIRHMLNALSKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F V + +E LFLGNAG AMR L AA+ G ++L
Sbjct: 62 VVYRLSEDKTECEVEGLGKPFVTVSELQE--LFLGNAGTAMRPLAALCL--GEGEFILT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLENENYPPLRITGTG-LESGVTIDGSISQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I +L+S PY+++TL +ME+FGV+ ++D + F I GQ Y S
Sbjct: 176 AFLMSAPLAKGVITIQIDGELVSKPYIDITLHIMEQFGVQVINND-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FAE LE MGA + W E
Sbjct: 235 PGNFLVEGDASSASYFLAAAAIKGGQVKVTGIGKNSIQGDIQFAEALKMGAHIEWGEDY 294

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVLDLDFNHIPDAAMTIATAALFANGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA+VEEG DY IITPP+KL AIDTYDDHRMAM FSL A + PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDYIIITPPKLIHAAIDTYDDHRMAMCFSLVALRDTPTVIND 406

Query: 425 PGCTRKTFFPDYFD 437
P CT KTFPDYFD
Sbjct: 407 PKCTSKTFFPDYFD 419

>ref|ZP_01215931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychromonas sp.
CNPT3]
gb|EAS39220.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychromonas sp.
CNPT3]
Length = 429

Score = 439 bits (1130), Expect = e-121, Method: Compositional matrix adjust.
Identities = 227/438 (51%), Positives = 303/438 (69%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ LQPI+++ G + LPGSKSLSNR LLLAALS+GTT + NLL+S+DV +ML AL+ LG
Sbjct: 2 QQLRLQPIRKVQGEINLPGSKSLSNRALLAALSKGTTHTLNLDSDDVAHMLSALQKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V + ++G G F ++ E + LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VKVLSAQKQTCTIIGLGRAFNTEQEMGE-LTLFLGNAGTAMRPLCAALCLGQGD--YVLT 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGT-DCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RM ERPIG LV L+ GA V +LGT + PP+R+ G GL GG +K+ GS+SSQ+L
Sbjct: 119 GEARMFERPIGSLVDALRDAGAKVS-YLGTENYPPLRIQG-QGLKGNKIDGSVSSQFL 176

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+A LM+AP+A D IEII +L+S PY+++TL++M+ FGV+ EH D++ F +KG Q Y
Sbjct: 177 TAFMLSPAMASADTRIEIIGELVSKPYIKITLKIMKDFGVEVEH-DNYQTFIVKGKQTYT 235

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+P + VEGDASSASYFLA AI GG++TV G G S+QGD+ FA+ L+ MGAK+ W +
Sbjct: 236 APGDYLVVEGDASSASYFLAAGAIAGGSITVTGVGKKSIGDIAFADALQAMGAKIEWGDD 295

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + P LKAID++ N +PD AMTLA+VALFA G T IR++ +WRVKET+R
Sbjct: 296 YIKASKGP-----LKAIDMDFNHPIPDAAATLMAVALFAKGTTHIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ EL K+GA V EG DY ITPP+ IDTYDDHR+AM FSL A A+ V+I
Sbjct: 348 LYAMAKELRKVGAEVVEGKDYISITPPKVFKDACIDTYDDHRIAMCFSLVALAKTGVSIN 407

Query: 424 DPGCTRKTFPDYFDVLST 441
DP CT KTFPD+F+ S+
Sbjct: 408 DPQCTSKTFPDFFNKFSS 425

>ref|ZP_01899318.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moritella sp. PE36]
gb|EDM66198.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moritella sp. PE36]
Length = 427

Score = 439 bits (1130), Expect = e-121, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 301/440 (68%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ LQPI ++SGT+ LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 EKLTLQPIGKVSCTINLPGSKSVSNRALLAALAKGTTRLTNLLDSDDIRHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F V E+++LFLGNAG AMR L AA+ + G + L
Sbjct: 62 VQYDLSACKTICTVTGLGRAFSV--NEKLELFLGNAGTAMRPLCAALCLSEGE--FELT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIG LV L+Q GADV D PPV + G G L GG +K+ GS+SSQ+L+
Sbjct: 117 GEPRMEERPIGSLVDSLQAGADVITYLKNEDYPPVLIKGTG-LKGGNIKIDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D IEI+ +L+S PY+E+TL +M++FGV H D++ F IKG Q Y++
Sbjct: 176 AFLMAAPLADNDTTIEIVGELVSKPYIEITLHIMQQFGVTVTH-DNYQTFITKKGKQTYQA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ VEGDASSASYFLA AAI GG + V G G S+QGD++FA+V+E MG K+TW ++
Sbjct: 235 AGDFLVEGDASSASYFLAAAAIKGGKIRVTGIGKKSIGDQIFADVIEAMGGKITWADSY 294

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ L A+D++MN +PD AMT+A ALFA G T IR+V +WRVKET+R+
Sbjct: 295 IEAE-----VGELTAVDMDMNHPIPDAAMTIATTALFAKGTTVIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPP +L IDTY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGHDYIKITPPAQLVHATIDTYNDHRMAMCFSLVALSDPTPTIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
PGCT KTFPDYF+ + V+
Sbjct: 407 PGCTSKTFPDYFERFTGLVQ 426

>ref|YP_003613235.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter cloacae
subsp. cloacae ATCC 13047]
gb|ADF62286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter cloacae
subsp. cloacae ATCC 13047]
Length = 427

Score = 439 bits (1129), Expect = e-121, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 297/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALANGTTVLTNLLSDDDRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG + EE++LFLGNAG AMR L AA+ N VL
Sbjct: 62 VHYTLSDDTRCEVTGNGGAL---RSAAEELFLGNAGTAMRPLAALCLGSNN--IVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGQIDYLEQENYPPLRLRG--GFTGGNVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ ++ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDVTITIKGDLVSKPYIDITLHLMKTFGVEVENQ-AYQRFVVRGAQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW E
Sbjct: 234 PGNYLVEGDASSASYFLAAGAIGGTVKVTGIGRNSVQGDIRFADVLEKMGAVVTWGEDF 293

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY +TPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDYIRVTPPAKLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_003913217.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ferrimonas balearica
DSM 9799]
gb|ADN76143.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ferrimonas balearica
DSM 9799]
Length = 427

Score = 439 bits (1129), Expect = e-121, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 298/440 (67%), Gaps = 14/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L PI + G V LPGSKS+SNR LLLAALSEG T + NLL+S+D+ +ML AL LG
Sbjct: 2 KQLPLPPIAHVEGDVYLPGSKSISNRALLLAALSEGTTLTNLLSDDIRHMLNALALLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + VV G GG P+ ++ + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VSYQWQAEKGEIVVQGRGG--PIANSQALELFLGNAGTAMRPLCAALVVQGQD--YVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ LGA V+ PP+R++ L GG+V + GSISSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRPLGAKVEYLEAEGYPPLRIHA-SQLAGGRVSDIGSISSQFLT 176

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APL + I++ +L+S PY+++TL LM +FGV+ E+ D + +F I GQ+Y S

Sbjct: 177 ALLMTAPLCQDTLTIDVEGELVSKPYIDITLALMAKFGVEVENRD-YRQFVIAAGQRYVS 235

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG +TV G G SLQGD FA+ L MGA++ W + S

Sbjct: 236 PGRFLVEGDASSASYFLAAAAGGGPITVHGVRASLQGDYFADALAAMGAIEWQDES 295

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+T R L ID++MN +PD AMT+A ALFA GPT IR+V +WRVKET+R+

Sbjct: 296 ITAR-----RGELNGIDMDMNHIPDAAMTIATTALFAKGPTTIRNVYNWRVKETDRL 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + P EKL+ AIDTY+DHR+AM FSL A VPVTI D

Sbjct: 348 AAMATELKKVGAVVEEGHDYLRVEPVEKLLHHAIDTYNDHRIAMCFSLLAVGGVPVTIND 407

Query: 425 PGCTRKTFPDYFDVLSFVK 444
PGCT KTFPDYFD L+ +

Sbjct: 408 PGCTAKTFPDYFDRLNALCR 427

>ref|YP_001005833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
enterocolitica subsp. enterocolitica 8081]
sp|P19688.2|AROA_YERE8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAL11617.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
enterocolitica subsp. enterocolitica 8081]
Length = 428

Score = 439 bits (1129), Expect = e-121, Method: Compositional matrix adjust.
Identities = 236/436 (54%), Positives = 301/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI I+GTV LPSKKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLTLHPIALINGTVNLPGSKSVSNRALLAALAEGTTQLNNLLSDDIRHMLNALQAL 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G G G K E + ++LFLGNAG AMR L AA+ G VL
Sbjct: 63 VKYRLSADRTRCEVDGLGGKLVAE---QPLELFLGNAGTAMRPLAALCL--GKNDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPLRIRG--GFRGGKLTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y+S
Sbjct: 176 ALLMTAPLAEQDTEIQIGELVSKPYIDITLHLMKAFGVDVVH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAK++W +
Sbjct: 235 PGIYLVVEGDASSASYFLAAAAGKGTVRVTGIGKQSVQGDTKFADVLEKMGAKISWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGQDYIRVPPAQLIAAEIGTYNDHRMAMCFSLVALSPTPTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFPDYFEQLA 422

>gb|ADZ43082.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
enterocolitica subsp. palearctica 105.5R(r)]
Length = 428

Score = 439 bits (1128), Expect = e-121, Method: Compositional matrix adjust.
Identities = 236/436 (54%), Positives = 301/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESILTLPALINGTVNLPGSKSVSNRALLAALAEAGTTQLNLLDSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G G G E + ++LFLGNAG AMR L AA+ G VL
Sbjct: 63 VKYRLSADTRCEVDGLGGKLVAE---QPLELFLGNAGTAMRPLAALCL--GKNDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRIRG--GFRGGKLTVDGVSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y+S
Sbjct: 176 ALLMTAPLAEQDTEIQIGELVSKPYIDITLHLMKAFGVDVH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAK++W +
Sbjct: 235 PGIYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKSVQGDTKFADVLEKMGAKISWGDDY 294

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGQDYIRVPPAQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFFPDYFQLA 422

>ref|ZP_05945025.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio orientalis CIP
102891]
gb|EEX91832.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio orientalis CIP
102891]
Length = 426

Score = 438 bits (1127), Expect = e-121, Method: Compositional matrix adjust.
Identities = 233/435 (53%), Positives = 301/435 (69%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +++G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESILTLPINKVNGEVNLPGSKSVSNRALLAALASGTTTRLTNLLDSDDIRHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G F DA E ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VNYSLSKDKTVEVEGLGKPF---DAPEALELFLGNAGTAMRPLAALCL--GQGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA+V+ + PP+++ G G L GG V++ GSISQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAEVEYLESNYPPLKIYGTG-LKGGSVIEDGSISQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA DV I I+ +L+S PY+++TL +M +FGV+ E++D + F I+ GQ Y +
Sbjct: 176 AFLMSAPLAQDDVTINIVGELVSKPYIDITLHIMAQFGVEVENND-YQEFVIRKGGQTYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LKA+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGELKAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ++TPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYIVVTPPAKLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439

P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFPDYFDKL 421

>ref|YP_002890011.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thauera sp. MZ1T]
gb|ACR01634.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thauera sp. MZ1T]
Length = 653

Score = 438 bits (1126), Expect = e-121, Method: Compositional matrix adjust.
Identities = 232/444 (52%), Positives = 293/444 (65%), Gaps = 20/444 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P+ +G+V+LPGSKS+SNR+LLLAAL+EG T + +LL S+DV ML ALR LG
Sbjct: 2 EFLDLPMLGAGSVRLPGSKSISNRVLLLAALAEGETDIRDLLSDDVERMLEALRALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + V G GG FPV+ LFLGNAG A R LTAA+ +GG Y L
Sbjct: 62 VDWRRREGDSLNYRVCVGGPFPVKTG---DLFLGNAGTAFRPLTAALALSGGE--YRLS 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L+QLGAD+ C PP+ + PGG V++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDALRQLGADITCTANEGYPPLHLKPATIRPGGVVRVRGDVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL + IE++ +LIS PY+ +TL LM RFGV+ W+RF + GG +Y+S
Sbjct: 176 ALLMALPLTGVETTIEVVGELISKPYIRITLLELMARFGVQVGQQ-GWERFVVPGGARYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT---W 300
P +VEGDASSASYFLA AI GG V VEG G TS+QGDV+FAE LE +GA++T W
Sbjct: 235 PGTVFVEGDASSASYFLAAGAIGGGPVRVEGVGRTSIQGDVRF AEALQLGARITLGDNW 294

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E + G LKA D+++N +PD AMTLAV ALFADGP +R++ASWRVKE
Sbjct: 295 IEAAAPAGG-----VLKAFDLNLHIPDAAMTLAVAALFADGPCRLRNIAASWRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ TEL KLGA VEEG DY ++ P +L AIDTYDDHRMAM FSLA+ V
Sbjct: 346 TDRIAAMATELRKLGAEEVEEGADYLVVQRPPRLQPAIDTYDDHRMAMCFSLASLGGRV 405

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
I DP C KTFP YF+ + +
Sbjct: 406 RINDPKCVNKTFFGYFEAFAQVAR 429

>ref|YP_001176159.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter sp. 638]
sp|A4W8S8.1|ARO_AENT38 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP60108.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter sp. 638]
Length = 427

Score = 438 bits (1126), Expect = e-121, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 300/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALANGTTVLTNLLSDDVHRMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R VVG GG + E++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQFMLSDDRTRCEVVGNGGALK---SATELELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PPVR+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGQIDYLEQKNYPPVRLRG--GFTGGNVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ ++ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTVISIKGDLVSKPYIDITLHLMKTFGVEVENQ-AYQRFVVRGAQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

P N VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGNYLVEGDASSASYFLAAGAIGKGT VKVTGIGRNSVQGDIFADVLEKMGAVVTWGDDF 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T + L A+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----QGELNAVDMDMNHIPDAAMTIATAALFAKGT T TLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY +TPP KL V I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAQVEEGEDYIRVTPPAKLQVAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_003364600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citrobacter rodentium
ICC168]
emb|CBG87756.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citrobacter rodentium
ICC168]
Length = 427

Score = 438 bits (1126), Expect = e-121, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGT VKLPGSKSLSNRILL LLAALSEGTTVDNLLNSEDVHYMLGALRTL G 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ES LTLQPIARVDGTINLPGSKSVSNRALL LLAALAHGTTVLNLLDSDVRHMLNALSAL G 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG + A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 IACTLSADTRCEITGNGGALQAQGA---LELFLGNAGTAMRPLAALCL--GENDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG+V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVEALRQGGAKIDYLEQENYPLRLRG--GFTGGEVTVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA+ D I I +L+S PY+++TL LM+ FGV+ E+ + RF +KGGQ+Y+S
Sbjct: 175 ALLMTAPLAVQDTTISIKGELVSKPYIDITLNLMTFGVEIENQ-RYQRFVVKGGQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGVYLVEGDASSASYFLAAGAIGKGT VKVTGIGRNSMQGDIFADVLEKMGATVTWGDDF 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R LKAID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELKAIDMDMNHIPDAAMTIATAALFAKGT T TLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEEVEEGHDYIRITPPAKLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>emb|CBY27762.1| 5-enolpyruvylshikimate-3-phosphate synthase [Yersinia
enterocolitica subsp. palearctica Y11]
Length = 428

Score = 438 bits (1126), Expect = e-121, Method: Compositional matrix adjust.
Identities = 236/436 (54%), Positives = 300/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGT VKLPGSKSLSNRILL LLAALSEGTTVDNLLNSEDVHYMLGALRTL G 64
E + L PI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ES LTLHPIALINGTVNLPGSKSVSNRALL LLAALAE GTTQLNNLLDSDIRHMLNALQAL G 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G G G E + ++LFLGNAG AMR L AA+ G VL

Sbjct: 63 VKYRLSADTRTRCEVDGVGGKLVAE---QPLELFLGNAGTAMRPLAALCL--GKNDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D PP+R+ G G GGK+ + GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQEHPPLRIRG--GFRGGKLTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y+S

Sbjct: 176 ALLMTAPLAEQDTEIQIGELVSKPYIDITLHLMKAFGVDVVH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAK++W +

Sbjct: 235 PGIYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKKSQGDTKFADVLEKMGAKISWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFADGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 SAMATELRKVGAEVEEGQDYIRVPPAQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 407 PKCTAKTFPDYFEQLA 422

>ref|ZP_03699489.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Luticola nitroferum
2002]
gb|EEG07669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Luticola nitroferum
2002]
Length = 429

Score = 438 bits (1126), Expect = e-121, Method: Compositional matrix adjust.
Identities = 238/445 (53%), Positives = 295/445 (66%), Gaps = 22/445 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+++L P +SGT++LPGSKS+SNR LLLAAL++G T+V LL+S+D+ +MLGALR LG

Sbjct: 2 EQLLSPSPRLSGTIRLPGSKSISNRLLAALAQQKTLVRELLSDDIRHMLGALRL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+++E ++ VV G GG FPV+ A +LFLGNAG A R LTAA+ G Y L

Sbjct: 62 VTIEQVGDSDRFVVGQVGGAFPVKQA---ELFLGNAGTAFRPLTAALALMQGE--YQLS 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RM ERPIGDLV L+ GAD+ PP+ + G + + G++SSQ+L+

Sbjct: 116 GVARMHERPIGDLVDALRVAGADIRYLGAGFPPLAIPATIDAGRVIPVKNVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL V IE++ +LIS PY+E+TL LM RFGVK E W RF I GQ Y S

Sbjct: 176 ALLMALPLTSEAVTIEVVGELISKPYIEITLNLMARFGVKVERQ-GWQRFTIAAGQSYLS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT---W 300
P +VEGDASSASYFLA AI GG V VEG G S+QGDVKFA+ L MGA ++ W

Sbjct: 235 PGEIHVEGDASSASYFLAAGAIAGGPVRVEGVGRDSIQGDVKFADTLREMGATISMGDNW 294

Query: 301 TETSVTVTGPPPEPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E S G LKA+DV++N +PD AMT+AV AL ADG T IR+V SWRVKE

Sbjct: 295 IEASAPAGG-----LKALDVLNHIIPDAAMTIAVAALAADGTTTIRNVESWRVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVP 419
T+R+ A+ TEL K+GA+VEEG DY ITPP L A IDTYDDHRMAM FSL A P

Sbjct: 345 TDRLSAMATELRKVGATVEEGRDYIRITPPAALTPNAEIDTYDDHRMAMCFSLVALMGTP 404

Query: 420 VTIRDPGCTRKTFPDYFDVLSFVK 444
V I DP C KTFPDYF+VL++ +

Sbjct: 405 VVINDPKCVAKTFPDYFEVLASL 429

>ref|YP_001674263.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
halifaxensis HAW-EB4]

sp|B0TT43.1|AROA_SHEHH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ABZ76604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
halifaxensis HAW-EB4]
Length = 426

Score = 437 bits (1125), Expect = e-120, Method: Compositional matrix adjust.
Identities = 225/440 (51%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ L+PIK++SGT+ +PGSKS+SNR LLLA L+ GTT + NLL+S+D+ YML +L+ LG
Sbjct: 2 NQLRLEPIKKVSGTINIPGSKSISNRALLLATLASGTTTLNLLSDDIRYMLASLQ 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + G G +A E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VSYRLSNNTVCELDGLAGPL---NAGEPQTLFLGNAGTAMRPLCAALTL--GQGQFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ + G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGAEVSYLKNEGFPPLNITSTG-LNGGNVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA GDV I+I +L+S PY+++TL LM +FGV+ +++D + F IK GQ+Y S
Sbjct: 176 ALLMVAPLAKGDVNIKIKGELVSKPYIDITLALMAQFGVEVQNN-DYASFKVAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIQGGVEVKVTGVKLSIQGDVKFADVLEQMGADIEWGDDY 294

Query: 305 VTVTGPFPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + LKA+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIR-----QAKLKAVDLDMNHIPDAAMTIATAALFATGTTIRIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V+EG DY +TPP KLN AIDTY+DHRMAM FS+ A A+ +TI +
Sbjct: 347 AAMATELRKVGAIVDEGHDIYSVTPPAKLNTAAIDTYNDHRMAMCFSMMAFADCGITINE 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYF+ +
Sbjct: 407 PECTSKTFPDYFNQFNALAN 426

>ref|NP_797399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus RIMD 2210633]
ref|ZP_01991199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ3810]
ref|ZP_05777410.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus K5030]
ref|ZP_05889312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AN-5034]
ref|ZP_05904302.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus Peru-466]
sp|Q87QX9.1|AROA_VIBPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

dbj|BAC59283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus RIMD 2210633]
gb|EDM58958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ3810]
gb|EFO36532.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus Peru-466]
gb|EFO43356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AN-5034]
gb|EFO50814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus K5030]
Length = 426

Score = 437 bits (1124), Expect = e-120, Method: Compositional matrix adjust.
Identities = 232/438 (52%), Positives = 296/438 (67%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPGSKS+SNR LLL+AL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESRTLQPIKIQGEVNLPGSKSVSNRALLLSALAKGTTRLTNLLSDDIRHMLNALTCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ VV G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VKYTLSADKTECVVEGLGRPFVS---SEPVELFLGNAGTAMRPLAALCV--GQGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GAD++ T+ PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALQKAGADIEYLENTNYPPLKIVGTG-LKAGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G+V I+I L+S PY+++TL +M++FGV+ ++D + F I GQ Y +
Sbjct: 176 AFLMSAPLAEGEVRIKIEGDLVSKPYIDITLHIMKQFGVEVINND-YQEFVIPAGQHYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V G+ LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VI-----SRVGK--LKIDMDYNHIDPDAAMTIATTALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKPVPHLKHAAIDTYDDHRMAMCFSLALSPTPTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKLKAL 424

>ref|YP_004188221.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio vulnificus
MO6-24/O]
gb|ADV86018.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio vulnificus
MO6-24/O]
Length = 428

Score = 437 bits (1124), Expect = e-120, Method: Compositional matrix adjust.
Identities = 233/438 (53%), Positives = 301/438 (68%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPIK+++G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESRTLQPIKQVNGEVLNPGSKSVSNRALLLALAKGTTRLTNLLSDDIRHMLNALTCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E VV G G F +A+E LFLGNAG AMR L AA+ G +VL
Sbjct: 62 VHYELSADKTVCVVEGLGRPFTATEAQE---LFLGNAGTAMRPLAALCL--GKGEFVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA ++ + PP+++N IG L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALREAGAQIEYLENENYPPLKINAIG-LQAGTVNIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V+I I+ +L+S PY+++TL +M++FGV +++++ F I GQ Y S
Sbjct: 176 AFLMAAPLAQGEVKIHIVGELVSKPYIDITLHIMKQFGVDV--NNAYQEFIIIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG + V G G S+QGD+ FA+ LE MGA++ W E
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIHFADALEKMGAEIEWGEDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V GR LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VI-----SRVGR--LKIDMDYNHIDPDAAMTIATTALFAQGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ PP++L AIDTYDDHR+AM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYLIVNPPQLKHAIDTYDDHRIAMCFSLVALSPTPTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442

P CT KTFPDYFD L++
Sbjct: 407 PKCTSKTFPDYFDKLASL 424

>ref|YP_001501926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella pealeana
ATCC 700345]
sp|A8H4A4.1|AROA_SHEPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV87391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella pealeana
ATCC 700345]
Length = 426

Score = 437 bits (1123), Expect = e-120, Method: Compositional matrix adjust.
Identities = 224/438 (51%), Positives = 298/438 (68%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ L+PIK++SGT+ +PGSKS+SNR LLLA L+EGTT + NLL+S+D+ YML +L+ LG
Sbjct: 2 NQLRLEPIKKVSGTINIPGSKSISNRALLLATLAEGTTTLTNLLSDDIRYMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + G G +A E LFLGNAG AMR L AA+T G+ + L
Sbjct: 62 VSYRLSNNNTVCELDGLAGPL---NASEAQTFLFLGNAGTAMRPLCAALTGLQGQD--FTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ ++ G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGAEVSYLKNDFPPLSISSTG-LNGGNVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA DV I+I +L+S PY+++TL LM +FGVK +++D + F IK GQ+Y S
Sbjct: 176 ALLMVAPLAKDDVNIQIKGELVSKPYIDITLALMAQFGVKVQNN-DYASFVIAKAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VL+ MGA++ W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIQGGEVKVTGVGKLSIQGDVKFADVLQMGAEIEWGDDY 294

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IISRG-----AKLTAVDLDMNHIPDAAMTIATTALFATGTTHIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V+EG DY +TPP +LN AIDTY DHRMAM FS+ A A+ +TI +
Sbjct: 347 AAMATELRKVGAIVDEGHDIISVTPPAELNTAAIDTYSDHRMAMCFSMMAFADCGITINE 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYF+ ++
Sbjct: 407 PECTSKTFPDYFNQFNSL 424

>ref|ZP_06038940.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio mimicus MB-451]
gb|EEY38324.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio mimicus MB-451]
Length = 426

Score = 437 bits (1123), Expect = e-120, Method: Compositional matrix adjust.
Identities = 234/440 (53%), Positives = 295/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI ISG V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPINLISGEVNLPGSKSVSNRALLLAALASGTTRLTNLLSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G G F + ++LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VKYRLSADKTTCEVEGLGQAF---QTTQPLELFLGNAGTAMRPLAALCL--GQGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L GG V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQGGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA+V W +
Sbjct: 235 PGNFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAGQVEWGDDY 294

Query: 305 VTVTGPMPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMTTELKVGATVEEGEDFIVITPPAKLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSFVK 444
P CT KTFPDYF+ + +
Sbjct: 407 PKCTSKTFPDYFEKFAQLSR 426

>ref|YP_001438518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cronobacter sakazakii
ATCC BAA-894]
sp|A7MES7.1|AROAS_ENTS8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABU77682.1| hypothetical protein ESA_02436 [Cronobacter sakazakii ATCC BAA-894]
Length = 428

Score = 436 bits (1121), Expect = e-120, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 301/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL LG
Sbjct: 3 ESLTLQPIARVDGTINLPGSKSVSNRALLAALAKGTTTLTNLLDSDVRHMLNALNALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R + G GG F + E++LFLGNAG AMR L AA+ N VL
Sbjct: 63 VHYSLSDDRTRCEIQGGGPF---NTLVELELFLGNAGTAMRPLAALCLGTNNV--VLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV + PP+ + G G GG V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGADVITYLEQENYPPHLKGG--GFTGGNVTVDGSSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA G+ I+I +L+S PY+++TL LM+ FGV+ E+ + + RF I+GGQ+Y+S
Sbjct: 176 ALLMAAPLAPGNTAIDIKGELVSKPYIDITLHLMKTFGVEVENQN-YQRFVIQGGQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 235 PGHYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSVQGDIFADVLEKMGHITWGDDF 294

Query: 305 VTVTGPMPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295 ISCT-----RGELNAIDMDNMNHIPDAAMTIATTALFAKGTTTLRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +TPP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGHDFITVTPPAQLQFADIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFP+YF L+
Sbjct: 407 PKCTAKTFPNYFAQLA 422

>ref|ZP_05926140.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. RC341]
gb|EEX65835.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. RC341]
Length = 426

Score = 435 bits (1119), Expect = e-120, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 15/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI ISG V LKSGKS+SNR LLLAAL+ G T + NLL+S+D+ +ML AL LG

Sbjct: 2 ESLTLQPINLISGEVNLPGSKSVSNRALLLAALASGKTRLTNLLDSDDIRHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F + ++LFLGNAG AMR L AA+ G+ YVL

Sbjct: 62 VKYQLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S

Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +

Sbjct: 235 PGNFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAGQIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+

Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP +L AIDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPAQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYFD L+

Sbjct: 407 PKCTSKTFPDYFDKLA 422

>ref|YP_003209877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cronobacter
turicensis z3032]
emb|CBA29637.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cronobacter
turicensis z3032]
Length = 428

Score = 435 bits (1119), Expect = e-120, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 303/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG

Sbjct: 3 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAKGTTTLTNLLDSDVVRHMLNALKALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + R + G GG F + E++LFLGNAG AMR L AA+ N VL

Sbjct: 63 VNYSLSedrTRCEIQGGGPF---NTLVELELFLGNAGTAMRPLAALCLGTNNV--VLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GAD+ + PP+ + G G GG V + GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGGADIIYLEQENYPPLHLKG--GFSGGNVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA + I+I +L+S PY+++TL LM+ FGV+ E+ + + RF I+GGQ+Y+S

Sbjct: 176 ALLMAAPLAPANTAIDIKGELVSKPYIDITLHLMKTFGVEVENQN-YQRFVIQGGQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V V G G S+QGD++FA+VLE MGA++ W +

Sbjct: 235 PGHYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSVQGDIFADVLEKMGAGQIVWGDDF 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 295 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAQGTTLRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +TPP +L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVEEGHDFITVTPPAQLQFADIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF L+

Sbjct: 407 PKCTAKTFPDYFAQLA 422

>pdb|3FK0|A Chain A, E. Coli Epsp Synthase (Tips Mutation) Liganded With S3p
pdb|3FK1|A Chain A, E. Coli Epsp Synthase (Tips Mutation) Liganded With S3p
And Glyphosate
Length = 427

Score = 435 bits (1119), Expect = e-120, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 297/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E + LQPI + GT+ LKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSKSVSNRALLLAALAHGKTVLTNLLSDDDVRHMLNALTAL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAGIAMRSL AA+ G+ VL
Sbjct: 62 VSYTSLADTRCEIIGNGGPLHAEGA---LELFLGNAGIAMRSLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPRLRQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ--HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_04636035.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia intermedia
ATCC 29909]
gb|EEQ19847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia intermedia
ATCC 29909]
Length = 428

Score = 435 bits (1118), Expect = e-120, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 303/440 (68%), Gaps = 16/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E + LQPI I+GTV LKSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLTLQPIALINGTVNLPGSKSVSNRALLLAALAEGTQLNNLLSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G G A + ++LFLGNAG AMR L AA+ GN+ VL
Sbjct: 63 VNFRLSADRTQCEVDGVGGKLV--ADQPLELFLGNAGTAMRPLAALCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G G G K+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGQIDYLEQENYPPRLRQG--GFRGGKLTVDGSGVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I+I L+S PY+++TL LM+ FGV H +++ F+IK GQ Y++
Sbjct: 176 ALLMTAPLAEQDTDIQIQGDLVSKPYIDITLHLMKAFGVVDVH--ENYQLFHIKSGQTYRT 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGA++W +
Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVTGIGKSVQGDTKFADVLEKMGAKISWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA+GPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFANGPTVIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V EG DY + PP +L I TY+DHMMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVTEGEDYIRVPPAQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYF+ L+ +
Sbjct: 407 PQCTAKTFPDYFEQLANLSQ 426

>ref|NP_935111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio vulnificus
YJ016]
sp|Q7MJ45.1|AROAVIBVY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC95082.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio vulnificus
YJ016]
Length = 428

Score = 435 bits (1118), Expect = e-120, Method: Compositional matrix adjust.
Identities = 232/438 (52%), Positives = 300/438 (68%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPIK+++G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESILTQPIKKVNGEVNLPKSKSVSNRALLLAALAKGTTRLTNLLDSDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E VV G G F +A+E LFLGNAG AMR L AA+ G +VL
Sbjct: 62 VHYELSADKTVCVVEGLGRPFTATEAQE---LFLGNAGTAMRPLAALCL--GKGEFVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA ++ + PP+++N G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALREAGAQIEYLENENYPLKINATG-LQAGTVNIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V+I I+ +L+S PY+++TL +M++FGV ++++ F I GQ Y S
Sbjct: 176 AFLMAAPLAQGEVKIHIVGELVSKPYIDITLHIMKQFGVDVV-NNAYQEFIIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG + V G G S+QGD+ FA+ LE MGA++ W E
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIHFADALEKMGAEIEWGEDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V GR LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VI-----SRVGR--LKGIDMDYNHIDPDAAMTIATTALFAQGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ PP++L AIDTYDDHR+AM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYLIVNPPQQLTHAAIDTYDDHRIAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYFD L++
Sbjct: 407 PKCTSKTFPDYFDKLSL 424

>gb|AA010514.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio vulnificus]
Length = 428

Score = 435 bits (1118), Expect = e-120, Method: Compositional matrix adjust.
Identities = 232/438 (52%), Positives = 300/438 (68%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPIK+++G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESILTQPIKKVNGEVNLPKSKSVSNRALLLAALAKGTTRLTNLLDSDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E VV G G F +A+E LFLGNAG AMR L AA+ G +VL

Sbjct: 62 VHYELSADKTVCVVEGLGRPFTATEAQE---LFLGNAGTAMRPLAALCL--GKGEFVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA ++ + PP+++N G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALREAGAQIEYLENENYPPLKINATG-LQAGTVNIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA G+V+I I+ +L+S PY+++TL +M++FGV +++++ F I GQ Y S

Sbjct: 176 AFLMAAPLAQGEVKIHIIVGELVSKPYIDITLHIMKQFGVDVV-NNAYQEFIIIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG + V G G S+QGD+ FA+ LE MGA++ W E

Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIHFADALEKMGAEIEWGEDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V GR LK ID++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+

Sbjct: 295 VI-----SRVGR--LKIDMDYNHIDPDAAMTIATTALFAQGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ PP++L AIDTYDDHR+AM FSL A ++ PVTI D

Sbjct: 347 SAMATELRKVGAEVEEGEDYLIVNPPQQLRHAADITYDDHRIAMCFLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLS 442
P CT KTFPDYFD L++

Sbjct: 407 PKCTSKTFFPDYFDKLASL 424

>ref|YP_004212257.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rahnella sp. Y9602]
gb|ADW73130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rahnella sp. Y9602]
Length = 427

Score = 435 bits (1118), Expect = e-120, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQP+ ++G++ LPGSKS+SNR LLLAA ++GTT + NLL+S+DV YML AL LG

Sbjct: 2 ESLTLQPVALVNGSINLPGSKSVSNRALLAAFAQGTTRLTNLLDSDDVRYMLTALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G G F +AK ++LFLGNAG AMR L AA+ G VL

Sbjct: 62 VTHRLSASRTECIDGLGTAF--SNAKG-LELFLGNAGTAMRPLAALCL--GEQDVVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLRG--GFSGGDVSVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I+I L+S PY+++TL LM+ FG++ E+ + RF IKG Q Y S

Sbjct: 175 ALLMTAPLADNDTTIQIKGDLVSKPYIDITLNLMTFGIEVENH-KYQRFSSIKGRQHYS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGAYLVEGDASSASYFLAAAAIKGTVRVVTGIGKNSMQGDIRFADVLEKMGATIHWADDY 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L ID++MN +PD AMT+A ALFA+GPT +R++ +WRVKET+R+

Sbjct: 294 IECT-----RGELNGIDMDMNHIDPDAAMTIATAALFAEGPTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG DY I PP+ L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 TAMATELRKVGATVEEGEDYIRIDPPQSLKFAEIGTYNDHRMAMCFLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYFD L+

Sbjct: 406 PKCTAKTFFPDYFDRLA 421

>ref|YP_942554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychromonas
ingrahamii 37]
sp|A1STZ0.1|ARO_A_PSYIN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM02955.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychromonas
ingrahamii 37]
Length = 428

Score = 435 bits (1118), Expect = e-120, Method: Compositional matrix adjust.
Identities = 227/437 (51%), Positives = 305/437 (69%), Gaps = 13/437 (2%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+++LQPI ++ G + LPGSKSLSNR LLLAAL++GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2 EQLLLQPIAKVDGEINLPGSKSLSNRALLLAALAQTTLTNLLSDDIRHMLNALKKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + K K+ VV G G F ++ ++LFLGNAG AMR L AA+ G Y+L
Sbjct: 62 VNYQLSKDKKQCVVEGLGRAFNATAESGL-LELFLGNAGTAMRPLCAALCL--GQGEYILT 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM ERPIG LV L+Q GA V + PP+++ G G L GGK+K+ GS+SSQ+L+
Sbjct: 119 GEARMFERPIGSLVDALQQAGAQTYYLENENYPPLKIKGTG-LKGGKIKIDGSVSSQFLT 177

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAP+A+ D EIEI+ +L+S PY+++TL++M FG+ ++ + ++RF IKG Q Y +
Sbjct: 178 AFLMAAPMAMEDTEIEIVGELVSKPYIKITLQIMHDFGIDVDNHN-FERFIKKGQTYSA 236

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GG + V G G S+QGD++FA+ LE MGAK+ W +
Sbjct: 237 PGHYLVEGDASSASYFLAAGAIAGGCIKVTGIGKKSQGDQIFADALEAMGAKIEWGDDY 296

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + + LKAID++MN +PD AMT+AV ALFA G T IR+V +WRVKET+R+
Sbjct: 297 IKAS-----KGELKAIDMDMNHIPDAAMTIAAALFATGTTKIRNVYNWRVKETDRL 348

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA+V EG D+ +T PEKL IDTYDDHRMAM FSL A VTI D
Sbjct: 349 YAMATELRKVGATVVEGHDFIEVTAPEKLIHAEIDTYDDHRMAMCFSLVALGNTQVTIND 408

Query: 425 PGCTRKTFFPDYFDVLST 441
P CT KTFPDYF+ L++
Sbjct: 409 PKCTSKTFFPDYFEKLAS 425

>ref|ZP_01220232.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Photobacterium profundum 3TCK]
gb|EAS43335.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Photobacterium profundum 3TCK]
Length = 428

Score = 434 bits (1117), Expect = e-120, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 298/436 (68%), Gaps = 15/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +ISG V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2 ESLTLQPISQISGEVNLPGSKSVSNRALLLAALAQTTRLTNLLSDDIRHMLNALKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G F +A + ++L+LGNAG AMR L AA+ + G +VL
Sbjct: 62 VNYQLSADKTVCEVEGLGSAF---NASQALELYLGNAGTAMRPLAALCLSQGE--FVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GADV + PP+ + G G L GG+V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRTAGADVTYLENENYPPLAIKGTG-LNGGEVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAP+A D I I L+S PY+++TL +M +FGV E+ D + F+I GQ Y++
Sbjct: 176 AFLMAAPMATQDVTIRIKGDLVSKPYIDITLHIMAQFVTVENRD-YQEFFIPAGQTYQA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ VEGDASSASYFLA AAI GG V V G G S+QGDV+FA LEMMGA++ W +
Sbjct: 235 AGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSQGDVQFAHALEMMGAIEIWDNY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

V R LKA+D++ N +PD AMT+AV ALFA+G T+IR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELKAVDMDFNHIPDAAMTIAVAALFAEGTTSIRNVYNWRVKETDRL 346
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I PP +L IDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 TAMATELRKVGAEVEEGNDYITIVPPTQLQHATIDTYDDHRMAMCFSLVALSDTPVTIND 406
Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYFD L+
Sbjct: 407 PKCTSKTFPDYFDKLA 422

>ref|YP_269053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Colwellia
psychrerythraea 34H]
sp|Q482G5.1|AROA_COLP3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ27668.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Colwellia
psychrerythraea 34H]
Length = 426

Score = 434 bits (1117), Expect = e-119, Method: Compositional matrix adjust.
Identities = 224/436 (51%), Positives = 296/436 (67%), Gaps = 15/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI +I+G + LPGSKSLSNR LL+AAL+ G T + NLL S+D+++ML AL++LG
Sbjct: 2 EQLTLNPIGKINGEIFLPGSKSLSNRALLIALANGVTKITNLLVSDINHMLNALKSLG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V+G GG F +AK+ ++L+LGNAG AMR L AA+ A+ G ++L
Sbjct: 62 IEYTLSDCGTECTVIGNGGFF--NAKKPLELYLGNAGTAMRPLCAALAASEGE--FILT 116
Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L QL AD++ D PPV++ G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALAQLDADIEYLENKDYPPVKIKG-KALTGNTVTIDGSISSQFLT 175
Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+LM APL + IEI +L+S PY+++TL +M RF V +++D + F + G Q Y++
Sbjct: 176 AILMIAPLLETNTTIEIDGELVSKPYIDITLDIRRFNVSVQNND-YKSFIVNGKQSYQA 234
Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
VEGDASSASYFLA AI GG VTV G G S+QGD FA+VLE MGA++ W + S
Sbjct: 235 LDKYMEVDASSASYFLAAGAIGGGEVTVHGIGKLSVQGDKHFADVLEKMGAEIHWKDES 294
Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TV G P L A+D++MN +PD AMT+A ALFA G T IR++ +WRVKET+R+
Sbjct: 295 ITVIGKP-----LTAVDMDMNHIPDAAMTIATATLAFATGTTTIRNIYNWRVKETDRL 346
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V EG DY ITPP+ L IDTY+DHR+AM FSL A ++ PVTI D
Sbjct: 347 NAMATELRKVGAEVVEGKDYISITPPKSLKHAIDTYNDHRVAMCFSLVALSDTPVTIND 406
Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYFD L+
Sbjct: 407 PKCTAKTFPDYFDKLA 422

>ref|YP_130637.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Photobacterium
profundum SS9]
sp|Q6LPE1.1|AROA_PHOPR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAG20835.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Photobacterium profundum SS9]
Length = 428

Score = 434 bits (1117), Expect = e-119, Method: Compositional matrix adjust.
Identities = 230/436 (52%), Positives = 298/436 (68%), Gaps = 15/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQP+ +I+G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL+ LG

Sbjct: 2 ESLTLQPVSQINGEVNLPGSKSVSNRALLLAALAQGTTRLTNLLDSDDIRHMLNALKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G G F +A + ++L+LGNAG AMR L AA+ + G +VL

Sbjct: 62 VNYQLSTDKTVCVEVGLGSAF--NASQALELYLGNAGTAMRPLAALCLSQGE--FVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GADV + PP+++ G G L GG+V++ GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRTAGADVTYLENENYPPLKITGTG-LYGGEVEIDSGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D I I L+S PY+++TL +M +FGV E+ D + F+I GQ Y+

Sbjct: 176 AFLMAAPLATADTVIRIKGDLVSKPYIDITLHIMAQFGVTVENRD-YQEFFIPAGQTYQG 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ VEGDASSASYFLA AAI GG V V G G S+QGDV+FA LEMMGA++ W +

Sbjct: 235 AGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSQGDVQFAHALEMMGAIEWGDNY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R LKA+D++ N +PD AMT+AV ALFA+G T+IR+V +WRVKET+R+

Sbjct: 295 VIAR-----RGELKAVDMDFNHIPDAAMTIAVAALFAEGTTSIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I PP +L IDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGAEVDEGNDYITIVPTQLQHATIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYFD L+

Sbjct: 407 PKCTSKTFPDYFDKLA 422

>ref|ZP_06189463.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia odorifera
4Rx13]
gb|EFA17765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia odorifera
4Rx13]
Length = 428

Score = 434 bits (1117), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 299/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQP+ ++GTV LPSKKS+SNR LLLAAL+EGTT + NLL+S+DV +ML AL+ LG

Sbjct: 3 DSLTLQPVALVNGTVNLPGSKSVSNRALLLAALAEGTTLTNLLDSDVHRMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + +V G G A E ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 63 VSYQLPDDRTTCIVEGVAGPLV--ASEPLELFLGNAGTAMRPLAALCLGSGDV--VLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D TD PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQTDYPPRLRLG--GFHGGDVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I +L+S PY+++TL LM FGV+ H D++ F I+G Q Y+S

Sbjct: 176 ALLMTAPLAEQDTNIHIKLGELVSKPYIDITLHLMRTFGVEVSH-DNYRVFNIQGRQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGTV V G G S+QGD KFA+VLE MGA++TW +

Sbjct: 235 PGDYLVVEGDASSASYFLAAAAIKGTVRVTGIGKKSQGDTKFADVLEKMGARITWGDDF 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA+GPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELRGIDMDMNHNPDAAMTIAAALFAEGPTTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V+EG DY + PP KL I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGAEVDEGEDYIHVPPVKLFADIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 407 PKCTAKTFPDYFEQLA 422

>ref|ZP_03086030.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4024]
Length = 427

Score = 434 bits (1117), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALANGTTVLTNLLSDSDVRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG + E ++LFLGNAG AMR L AA+ GN VL
Sbjct: 62 VQYALSDDRTRCEVTGNGGAL---HSAEALFLGNAGTAMRPLAALCL--GNNNIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPRLRLG--GFTGGNVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM FGV+ E+ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTVISIKGDLVSKPYIDITLHLMNTFGVEVENQ--SYQRFVVRGAQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGNYLVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIRFADVLEKMGAVVTWGDDF 293

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
+ T L AID++MN +PD AMT+A ALFA G T + ++ +WRVKET+R+
Sbjct: 294 IACT-----HGELNAIDMDMNHIPDAAMTIATAALFAKGTTLGNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEEVEGEDYIRITPPAKLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|ZP_05967101.1| hypothetical protein ENT CAN_05479 [Enterobacter cancerogenus ATCC
35316]
gb|EFC58038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter
cancerogenus ATCC 35316]
Length = 427

Score = 434 bits (1116), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 297/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALANGTTVLTNLLSDSDVRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ K R V G GG + E ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VHYTLKDRTRCDVTGNGGAL---RSSEALFLGNAGTAMRPLAALCLGSGDV--VLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPRLRLG--GFTGGHVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTTIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ--SYQRFVVRGAQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW E
Sbjct: 234 PGHYLVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIRFADVLEKMGAVVTWGENF 293

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----HGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG DY +TPP L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGATVEEGEDYIRVTPPATLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_001477939.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia
proteamaculans 568]
sp|A8GCH1.1|AROASERP5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV40811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia
proteamaculans 568]
Length = 428

Score = 434 bits (1116), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 299/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQP+ ++GTV LKPKSGSK+SNR LLLAAL+EGTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPVAVNGTVNLPKSGSKSVSNRALLAALAEGLTTLTNLLDSDVVRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + V G GG A + ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 63 VSYQLSDDRTTCKVDGVGGPLV---ASKPLELFLGNAGTAMRPLAALCL--GSNDVVLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D TD PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGQIDYLEQTDYPPRLRLRG--GFRGGDVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I +L+S PY+++TL LM FGV+ H D++ F+I G Q Y+S
Sbjct: 176 ALLMTAPLAEQDTHIHIGELVSKPYIDITLHLMRTFGVEVSH-DNYRVFHINGRQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGA++TW +
Sbjct: 235 PGDYLVEGDASSASYFLAAAIAKGGTVRVGTGIGKKSQGDTKFADVLEKMGARITWGDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA+GPT IR++ +WRVKET+R+
Sbjct: 295 IECS-----RGE LRIGIDMDMNHIPDAAMTIATAALFAEGPTTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V+EG DY + PP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVDEGEDYIHVVPPAKLKFADIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPPDYF+ L+
Sbjct: 407 PKCTAKTFFPDYFEQLA 422

>ref|ZP_04404584.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae TMA
21]
gb|EEO12788.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae TMA
21]
Length = 426

Score = 434 bits (1116), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/440 (53%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LKPKSGSK+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIELISGEVNLPGSKSVSNRALLAALASGTTRLTNLLDSDDIRHMLNALTCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+II +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGVKTIKIIGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGDV+FA+ LE MGA++ W +
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDVQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P CT KTFFPDYFD + +
Sbjct: 407 PKCTSKTFFPDYFDKFAQLSR 426

>ref|ZP_08099331.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio brasiliensis
LMG 20546]
gb|EGA64683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio brasiliensis
LMG 20546]
Length = 426

Score = 434 bits (1116), Expect = e-119, Method: Compositional matrix adjust.
Identities = 231/435 (53%), Positives = 299/435 (68%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI +++G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESILTLPINKVNGEVNLPKSKSVSNRALLAALASGTTRLTNLLDSDDIRHMLNALSCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S V G G F DA ++LFLGNAG AMR L AA+ G Y+L
Sbjct: 62 VSYRLSDDKTVCVEGLGKPFQATDA---LELFLGNAGTAMRPLAALCL--GQGEYILT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA V+ + PP+++ G G L GG V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAKVEYLENDNYPPLKIFGTG-LKGGTVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA DV I+I+ +L+S PY+++TL +M +FGV+ E++D + F I+ GQ Y +
Sbjct: 176 AFLMSAPLAQDDVTIKIVGELVSKPYIDITLHIMAQFGVEVENND-YQEFVIRHGQSYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG + V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEIKVTGIGKSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LKA+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGELKAVDMDFNHIPPDAAMTIATTALFAQGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+TPP +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYLIVTPPAQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
P CT KTFFPDYF+ L
Sbjct: 407 PKCTSKTFFPDYFEKL 421

>ref|ZP_02903635.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia albertii
TW07627]
gb|EDS90765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia albertii
TW07627]
Length = 425

Score = 434 bits (1115), Expect = e-119, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 301/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQP+ + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPVARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVVRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ +L
Sbjct: 62 VSYTLTSAEHTRCETIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GHNDIILT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA + + PP+R+ +GG GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKITYQEENYPPRLR--LGGFIGGNVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL +M+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLASQDVTIRIKGDLVSKPYIDITLNMMAKFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AA+ GGTV V G G S+QGD++FA+VLE MGA ++W +
Sbjct: 234 PGSYLVEGDASSASYFLAAAANKGGTVKVTGIGRNSMQGDIRFADVLEKMGATISWGDDY 293

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATTALFAKGTTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGNDFRITPPEKLRFAEIAATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
PGCT KTFPDYF+ L+
Sbjct: 406 PGCTAKTFPDYFEQLA 421

>pdb|3NVS|A Chain A, 1.02 Angstrom Resolution Crystal Structure Of
3-Phosphoshikimate 1- Carboxyvinyltransferase From
Vibrio Cholerae In Complex With Shikimate-3-Phosphate
(Partially Photolyzed) And Glyphosate
Length = 450

Score = 434 bits (1115), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 26 ESLTLQPIELISGEVNLPGSKSVSNRALLLAALASGTRRLTNLLDSDIRHMLNALTCLG 85

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 86 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 140

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 141 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 199

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 200 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 258

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 259 PGQFLVEGDASSASYFLAAAANKGGEVKVTGIGKNSIQGDIQFADALEKMGAIQEWGDDY 318

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 319 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 370

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 371 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 430

Query: 425 PGCTRKTFPDYFDVLSFVK 444
P CT KTFPDYFD + +
Sbjct: 431 PKCTSKTFPDYFDKFAQLSR 450

>ref|YP_001334602.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
subsp. pneumoniae MGH 78578]
sp|A6T701.1|ARO_A_KLEP7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR76372.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
subsp. pneumoniae MGH 78578]
Length = 427

Score = 434 bits (1115), Expect = e-119, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GTV LKPSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVEGTVNLPKSGKSVSNRALLAALARGTTVLNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG P+ A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQYTLSADRTRECVTGNGG--PLRSAAA-LFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +DC + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDCLEQENYPLRLRG--GFQGGNVEVDGSSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ--SYQRFVVRGKQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGDYLVVEGDASSASYFLAAGAIGKGTVKVTGIGRNSVQGDIFADVLEKMGATVTWGDDF 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T LKA+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----HGELKAVDMDMNHIPDAAMTIATAALFAQGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDYIRITPPAKLKYAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_06033632.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio mimicus VM223]
gb|EEY44279.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio mimicus VM223]
Length = 426

Score = 433 bits (1114), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 294/440 (66%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI ISG V LKPSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESITLQPINLISGEVNLPGKSVSNRALLAALASGTTTLNLLDSDDIRHMLNALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G G F + ++LFLGNAG AMR L AA+ G YVL

Sbjct: 62 VKYRLSADKTTCEVEGLGQAF---QTTQPLELFLGNAGTAMRPLAALCL--GQGEYVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S

Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPTGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +

Sbjct: 235 PGNFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAGQIEWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+

Sbjct: 295 VISR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPAKLTHAAIDTYDDHRMAMCFLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSFVK 444
P CT KTFPDYF+ + +

Sbjct: 407 PKCTSKTFFPDYFEKFAQLSR 426

>pdb|2QFS|A Chain A, E.Coli Epsp Synthase Pro101ser Liganded With S3p
pdb|2QFT|A Chain A, E.Coli Epsp Synthase Pro101ser Liganded With S3p And
Glyphosate
Length = 427

Score = 433 bits (1114), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG

Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTLNLLSDDDRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMRSL AA+ G+ VL

Sbjct: 62 VSYTLSDRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRSLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>gb|EGC07735.1| EPSP synthase [Escherichia fergusonii B253]
Length = 425

Score = 433 bits (1114), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 297/436 (68%), Gaps = 16/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + GT+ LPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL+ LG
Sbjct: 2  ESITLQPIARVDGTINLPKSKSVSNRALLAALAHGKTVLTNLLDSDVRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          +S      R ++G GG  E A  ++LFLGNAG AMR L AA+  G+  VL
Sbjct: 62  VSYSLSTDRTRCEIIGNGGPLHAESA---LFLFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV  L+Q GA +  + PP+R+ G  G  GG V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRQGGAGITYLEQENYPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D  I I  L+S PY+++TL LM+ FGV+ E+  + +F +KGGQ Y+S
Sbjct: 175  ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEVENQ-RYQQFVVKGGQSYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P +  VEGDASSASYFLA AAI GGT V V G G  S+QGD+ FA+VLE MGA ++W +
Sbjct: 234  PGSYLVVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIHFADVLEKMGATISWGDDY 293

Query: 305  VVTGTPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          ++ T      R  L AID++MN +PD AMT+A  ALFA G T +R++ +WRVKET+R+
Sbjct: 294  ISCT-----RGELNAIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA VEEG D+  ITPPEKL  I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346  FAMATELRKVGQAQVEEGHDFRITPPEKLFKAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425  PGCTRKTFPDYFDVLS 440
          P CT KTFPDYF+ L+
Sbjct: 406  PKCTAKTFPDYFEQLA 421

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>ref|ZP_04418631.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae
12129(1)]
gb|EEN98501.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae
12129(1)]
Length = 426

```

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

```

Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI+ ISG V LPKSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL  LG
Sbjct: 2  ESITLQPIELISGEVNLPGKSKSVSNRALLAALASGTTTLNLLDSDDIRHMLNALTCLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++      V G G F  + ++LFLGNAG AMR L AA+  G+  YVL
Sbjct: 62  VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV  L+Q GA ++  + PP+R+ G G L  G V + GSISSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGVTIDGSISSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+  + D +  F I  GQ Y S
Sbjct: 176  AFLMSAPLAQGVKTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P      VEGDASSASYFLA AAI GG V V G G  S+QGD++FA+ LE MGA++ W +
Sbjct: 235  PGQLLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEWGGDDY 294

Query: 305  VVTGTPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          V      R  L A+D++ N +PD AMT+A  ALFA G TAIR+V +WRVKET+R+
Sbjct: 295  VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA+VEEG D+ +ITPP KL  AIDTYDDHRMAM FSL A ++ PVTI D

```

Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSFVK 444

P CT KTFPDYFD + +

Sbjct: 407 PKCTSKTFFPDYFDKFAQLSR 426

>ref|ZP_06641049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia odorifera
DSM 4582]

gb|EFE94290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Serratia odorifera
DSM 4582]

Length = 428

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.

Identities = 235/436 (53%), Positives = 299/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

+ + LQP+ ++GTV LPKSKS+SNR LLLAAL+ GTT + NLL+S+DV +ML AL+ LG

Sbjct: 3 DSLTLQPVALVNGTVNLPKSKSVSNRALLAALAAGTTRLTNLLSDDVHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+S + +A R V G P+ AK+ ++LFLGNAG AMR L AA+ GN VL

Sbjct: 63 VSYQL--SADRTVCTVDGVAGPLV-AKQPLELFLGNAGTAMRPLAALCL--GNGEVVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV L+Q GA +D +D PPVR+ G G GG V + GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQSDYPPVRLRG--GFSGGNVSVDSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

ALLM APLA D I I +L+S PY+++TL LM FGV+ H D + F+I+G Q Y S

Sbjct: 176 ALLMTAPLAEQDTHIHKELVSKPYIDITLHLMRTFGVEVSHED-YRVFHIRGQQTYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

P + VEGDASSASYFLA AAI GGT V G GT S+QGD KFA+VL MGA +TW +

Sbjct: 235 PGDYLVVEGDASSASYFLAAAAIKGGTVRVGTGIGTHSVQGDTKFADVLAKMGAHITWGDDF 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

+ R L ID++MN +PD AMT+A ALFA+GPT +R++ +WRVKET+R+

Sbjct: 295 IECH-----RGELNGIDMDMNHIPDAAMTIATAALFANGPTTLRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424

A+ TEL K+GA+V+EG DY + PP KL I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVDEGEDYIHVVPPAKLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440

P CT KTFPDYFD L+

Sbjct: 407 PKCTAKTFFPDYFDQLA 422

>ref|NP_231368.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae O1
biovar El Tor str. N16961]

ref|ZP_01675626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
2740-80]

ref|ZP_01956752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
MZO-3]

ref|ZP_01971738.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae NCTC
8457]

ref|ZP_01975450.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae B33]

ref|ZP_01980597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
623-39]

ref|YP_002810431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
M66-2]

ref|ZP_04397665.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae BX
330286]

ref|ZP_04401080.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae B33]

ref|ZP_04408183.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae RC9]

ref|YP_002878383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
MJ-1236]

ref|ZP_05238199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae MO10]

ref|ZP_05418796.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholera CIRS
101]

ref|ZP_06030889.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae INDRE 91/1]
ref|ZP_07007999.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae MAK 757]
sp|Q9KRB0.1|AROA_VIBCH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|C3LN54.1|AROA_VIBCM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAF94882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae O1 biovar El Tor str. N16961]
gb|EAX59988.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae 2740-80]
gb|EAY41044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae MZO-3]
gb|EAZ72997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae NCTC 8457]
gb|EAZ76912.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae B33]
gb|EDL74646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae 623-39]
gb|ACP05980.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae M66-2]
gb|EEO08404.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae RC9]
gb|EEO16507.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae B33]
gb|EEO20586.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae BX 330286]
gb|ACQ60813.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae MJ-1236]
gb|EET22968.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae MO10]
gb|EET92712.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholera CIRS 101]
gb|EEY47258.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae INDRE 91/1]
gb|EFH78575.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae MAK 757]
Length = 426

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LPKSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIELISGEVNLPGSKSVSNRALLLAALASGTTTLNLLDSDDIRHMLNATKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAQIEWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVLDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDPTVPTIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYFD + +

Sbjct: 407 PKCTSKTFPDYFDKFAQLSR 426

>emb|CBK85480.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter cloacae
subsp. cloacae NCTC 9394]
Length = 427

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALANGTTVLTNLLSDDDRHLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG + E ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQYALSDDRTCEVTGNGGAL---HSAEAELEFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPLRLRG--GFTGGNVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM FGV+ E+ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTSISIKGDLVSKPYIDITLHLMNTFGVEVENQ-SYQRFVVRGAQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGHYLVEGDASSASYFLAAGAIGKGTVKVTGIGRNSVQGDIFADVLEKMGAVVTWGDDF 293

Query: 305 VTVTGPMPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----HGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY +TPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDYIRVTPPAKLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|NP_928909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Photorhabdus
luminescens subsp. laumondii TT01]
sp|Q7N6D5.1|ARO_A_PholL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE13913.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Photorhabdus luminescens subsp.
laumondii TT01]
Length = 428

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/435 (53%), Positives = 292/435 (67%), Gaps = 16/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ ++LQPI I+GT+ LPGSKS+SNR LLLAA ++G T + NLL+S+D+ +ML AL LG
Sbjct: 2 QSLMLQPISYINGTINLPGSKSVSNRALLLAFAKATCLTNLLSDDDRHLNLAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S V G GG + ++LFLGNAG AMR LTAA+ G VL
Sbjct: 62 ISYRLSDDRTCEVDGIGGLITHQGP---IELFLGNAGTAMRPLTAALCL--GKNDVVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+ V G G GGV + G +SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAIEIDYLEQENYPLHVKG--GFVGGKVMVDGRVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D EI I +L+S PY+++TL LM+ FG+ H D + F+IKG Q+Y S

Sbjct: 175 ALLMAAPLAENDSEIHIQGELVSKPYIDITLALMKSFGITINH-DQYQIFHIKGRQQYVS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V V G G SLQGD KFA VLE MGAK+ W +

Sbjct: 234 PGHYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKNSLQGDTKFANVLEKMGAKIRWGDDF 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L ID++MN++PD AMT+A ALFA G T IR++ +WRVKET+R+

Sbjct: 294 VECE-----RGTLTGIDMDMNEIPDAAMTIATTALFAAGETVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP +L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 HAMATELRKVGAEVEEGVDYIRITPPRLLPAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVL 439
PGCT KTFPDYF+ L

Sbjct: 406 PGCTAKTFFPDYFNQL 420

>ref|ZP_04960288.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
AM-19226]
gb|EDN16531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
AM-19226]
Length = 426

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG

Sbjct: 2 ESLTLQPIELISGEVNLPGSKSVSNRALLAALASGTTTLNLLSDDIRHMLNALTCLG 61

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL

Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S

Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +

Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAI EWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+

Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGAAVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P CT KTFPDYFD + +

Sbjct: 407 PKCTSKTFFPDYFDKFAQLSR 426

>gb|ACV91084.1| 5-enolpyruvylshikimate 3-phosphate synthase [Rahnella aquatilis]
Length = 427

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 226/436 (51%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQP+ ++G++ LKSGKS+SNR LLLAA ++GTT + NLL+S+DV +ML AL LG

Sbjct: 2 ESLTLQPVALLVNGSINLPGSKSVSNRALLAFAAQGTTRLNLLSDSDVRHMLTALTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + G G F +AK ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 VTHRLSASRTECEIDGLGTAF--SNAKG-LELFLGNAGTAMRPLAALCL--GEQDVVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLQG--GFSGGDVSVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I+I L+S PY+++TL LM+ FG++ E+ + + RF I+G Q Y S
Sbjct: 175 ALLMTAPLADNDTTIQIKGDLVSKPYIDITLNLMTFGIEVENHE-YQRFISQGRQHYVS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGAYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKNSMQGDIRFADVLEKMGATIHWDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L ID++MN +PD AMT+A ALFA+GPT +R++ +WRVKET+R+
Sbjct: 294 IECT-----RGELNGIDMDMNHIPDAAMTIATAALFAEGPTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG DY I PP+ L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 TAMATELRKVGATVEEGEDYIRIDPPQSLKFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFFPDYFD L+
Sbjct: 406 PKCTAKTFFPDYFDRLA 421

>ref|ZP_04918492.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae V51]
gb|EAS50884.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae V51]
Length = 426

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESILTQPIELISGEVNLPGSKSVSNRALLAALASGTTTLNLLDSDDIRHMLNALTKL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCVEEGLGQAF---HTTQPLEFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIWDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVLDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGDDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSFVK 444
P CT KTFFPDYFD + +
Sbjct: 407 PKCTSKTFFPDYFDKFAQLSR 426

>pdb|3FJX|A Chain A, E. Coli Eps Synthase (T97i) Liganded With S3p
pdb|3FJZ|A Chain A, E. Coli Eps Synthase (T97i) Liganded With S3p And

Glyphosate
Length = 427

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLSDDDRHMLNALTALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +S      R ++G GG  E A  ++LFLGNAGIAMR L AA+  G+  VL
Sbjct: 62  VSYTLSADTRCEIIGNGGPLHAEGA---LELFLGNAGIAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV  L+  GA +  + PP+R+ G G  GG V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALLM APLA  D  I I  L+S PY+++TL LM+ FGV+ E+  + +F +KGGQ Y+S
Sbjct: 175  ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGEIENQ-HYQQFVVKGGQSYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P  VEGDASSASYFLA AAI GGT V G G  S+QGD++FA+VLE MGA + W +
Sbjct: 234  PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305  VVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      ++ T      R  L AID++MN +PD AMT+A  ALFA G T +R++ +WRVKET+R+
Sbjct: 294  ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNINYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA VEEG DY  ITPPEKLN  I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346  FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIAITYNDRMAMCFSLVALSDTPVTILD 405

Query: 425  PGCTRKTFFPDYFDVLS 440
      P CT KTFPDYF+ L+
Sbjct: 406  PKCTAKTFFPDYFQLA 421
```

```
>ref|ZP_01947816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae 1587]
ref|ZP_04410091.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae TM
11079-80]
gb|EAY35615.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae 1587]
gb|EE07218.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae TM
11079-80]
Length = 426
```

Score = 433 bits (1113), Expect = e-119, Method: Compositional matrix adjust.
Identities = 232/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + LQPI+ ISG V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2  ESLTLQPIELISGEVNLPGSKSVSNRALLAALASGTTTLNLLSDDIRHMLNALTKL 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      ++      V G G  F  + ++LFLGNAG AMR L AA+  G+  YVL
Sbjct: 62  VNYRLSADKTTCEVEGLGKAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV  L+Q GA ++  + PP+R+ G G  L  G V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+  + D +  F I  GQ Y S
Sbjct: 176  AFLMSAPLAQGVKTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P  VEGDASSASYFLA AAI GG V V G G  S+QGD++FA+ LE MGA++ W +
Sbjct: 235  PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIWDGDDY 294

Query: 305  VVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
```

V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTAALFAKGTATAIRNVYNWRVKETDRL 346
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406
Query: 425 PGCTRKTFPDYFDVLSFVK 444
P CT KTFPDYFD + +
Sbjct: 407 PKCTSKTFPDYFDKFAQLSR 426

>ref|YP_003777077.1| 5-enolpyruvylshikimate-3-phosphate synthase [Herbaspirillum
seropedicae SmR1]
gb|ADJ65169.1| 5-enolpyruvylshikimate-3-phosphate synthase (EPSP synthase) protein
[Herbaspirillum seropedicae SmR1]
Length = 445

Score = 432 bits (1112), Expect = e-119, Method: Compositional matrix adjust.
Identities = 234/452 (51%), Positives = 296/452 (65%), Gaps = 30/452 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
I L P+ + GTVKLPKSGKS+SNRILLALLALS GTT + +LL S+D ML AL+TLG
Sbjct: 10 RHIDLAPVHHVQGTVKLPKSGKSISNRILLALLAALSGGTTRIFDLLASDDTLVMLMALQTLG 69
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E + + +V G G PV A LF+GNAG A+R LTAA+ GG+ Y L
Sbjct: 70 VKWEQIEGTQDYIVHGVNGVLPVHQA----DLFMGNAGTAIRPLTAALAVLGGD--YTLH 123
Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L +G +D PP+ + G L ++K+ G++SSQ+L+
Sbjct: 124 GVPRMHERPIGDLVDALNAVGMRIDYTGNGPYPLHIRR-GQLTSSRMKVRGNVSSQFLT 182
Query: 185 ALLMAAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKY 242
ALLMAAPL + ++I+++ +LIS PY+E+TL LM RF V+ E D W +F IK GQ Y
Sbjct: 183 ALLMAAPLMAREEAMQIDVVGELISKPYIEITLNLMRFSVEEVER-DGWQQFIKPGQHY 241
Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKAFAEVLEMMGAKVT--- 299
+SP + +VEGDASSASYFLA AITGG + VEG G S+QGDV+F E LE+MGA +T
Sbjct: 242 RSPGSIHVEGDASSASYFLAAGAITGGPIRVEGVGRDSIQGDVRFVEALELMGATIIMGE 301
Query: 300 -WTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRV 358
W E S GP LKA+D + N +PD AMT+AV AL+ADGP+ +R++ASWRV
Sbjct: 302 NWIEASSN--GP-----LKAVDADFNHIPDAAMTIAVAALYADGPSTLRNIASWRV 350
Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
KET+R+ A+ TEL KLGA VEEG DY +TPP ++ IDTYDDHRMAM FSLA+
Sbjct: 351 KETDRLAAMATELRKLGAQVEEGADYLTVTPPAEIGTATIDTYDDHRMAMCFSLASLDGA 410
Query: 419 -----PVTIRDPGCTRKTFPDYFDVLSFVK 445
V I DP C KTFPDYFDV +
Sbjct: 411 LRRGNRVRINDPKCVAKTFPDYFDVFKKIAEQ 442

>dbj|BAI54369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
SE15]
Length = 427

Score = 432 bits (1112), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSGKSVSNRALLAALAHGKTVLTNLLSDSDVRHMLNALTALG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A+E LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRTCEIIGNGGPLHAESARE---LFLGNAGTAMRPLAALCL--GSNDIVLS 116
Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA + + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKITYLEQENYPPLRLQG--GFTGGNVDDVSGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLFKFAEIATYNDHRMAMCFLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFEQLA 421

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>ref|YP_539995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    UTI89]
ref|YP_668835.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli 536]
ref|YP_852039.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli APEC
    O1]
ref|ZP_03033643.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli F11]
ref|YP_002390726.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli S88]
ref|YP_002396960.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    ED1a]
ref|ZP_04001932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    83972]
ref|ZP_04537585.1| AroA [Escherichia sp. 3_2_53FAA]
ref|ZP_07176457.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
    200-1]
ref|ZP_07194885.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
    185-1]
ref|ZP_07446832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    NC101]
sp|Q1RDV0.1|AROAE_COUT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|Q0TJE5.1|AROAE_ECOL5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|A1A9I5.1|AROAE_ECOL1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|B7MHL7.1|AROAE_ECO45 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|B7MS23.1|AROAE_ECO81 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
gb|ABE06464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    UTI89]
gb|ABG68934.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli 536]
gb|ABJ00325.1| AroA [Escherichia coli APEC O1]
gb|EDV67221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli F11]
emb|CAR02268.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
    S88]
emb|CAR07137.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
    ED1a]
emb|CAP75378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    LF82]
gb|EEH84573.1| AroA [Escherichia sp. 3_2_53FAA]
gb|EEJ49345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
    83972]
gb|ADE91223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
```

IHE3034]
gb|EFJ56678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
185-1]
gb|EFJ61497.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
200-1]
gb|EFM53841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
NC101]
gb|ADN45522.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli ABU
83972]
gb|ADN71969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
UM146]
gb|ADR26255.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O83:H1 str. NRG 857C]
gb|EFU46941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
110-3]
gb|EFU55506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
16-3]
gb|EGB49251.1| EPSP synthase [Escherichia coli H252]
gb|EGB53922.1| EPSP synthase [Escherichia coli H263]
gb|EGB79060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
57-2]
gb|EGB82185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
60-1]
Length = 427

Score = 432 bits (1111), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLSDDVHRMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A+E LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAESARE---LFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKITYLEQENYPPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLKFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_01614515.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alteromonadales
bacterium TW-7]
gb|EAW26217.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alteromonadales
bacterium TW-7]
Length = 425

Score = 432 bits (1111), Expect = e-119, Method: Compositional matrix adjust.
Identities = 231/437 (52%), Positives = 306/437 (70%), Gaps = 16/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

Sbjct: 2 E++ L+PI ++G+V LPGSKSLSNRILLLAAL+ GTTVV+NLL+S+D+ +MLGAL LG
EQLRLEPISRVNGSVTLPGSKSLSNRILLLAALANGTTVVENLLSDDIRHMLGALELLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++V ++ A V G GG+F K LFLGNAG A R LTA + A G Y L

Sbjct: 62 VTVTLNEDRTVATVHGVGGEF---KKPNKPLFLGNAGTAYRPLTAVLAAVKGE--YELV 115

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIG LV L+ LG D+ D PP+++ G G + GG+V++ GSISSQ+L+

Sbjct: 116 GEPRMEERPIGHLVDALQALGDDITYTKHKDYPPLKIVG-GQINGGEVEIDGSISSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL GD +I I L+S PY+++TL +M RFG+ EHSD + F +KGGQ+Y+S

Sbjct: 175 ALLMAAPLFGSDTQITIKGTLVSKPYIDITLGVMARFGITVEHSD-YSLFKVKGQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P+ VEGDASSASYF+A AAI GG + ++G G S+QGD+ FA+V+E +GA++ W +

Sbjct: 234 PERIMVEGDASSASYFVAAAAIAGGEIEIKGVGAKSVQGDIGFAKVMQVGAQIDWYDER 293

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V + LK +D++ N +PD AMTLA VALFA GPTAIR++ +WRVKET+R+

Sbjct: 294 LVVR-----KGELKGVDDIDANAIPDAAMTLATVALFAKGPATAIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA V EG D+ ITPP N AIDTYDDHR+AM F++ A P+TI D

Sbjct: 346 YAMSTELRKVGAKVVEGEDFIEITPPLTFNDVAIDTYDDHRIAMCFAMVAVGGKPITIND 405

Query: 425 PGCTRKTFFPDYFDVLST 441
P CT KTFP +F+VL++

Sbjct: 406 PKCTYKTFPTFFNVLAS 422

>ref|ZP_06941240.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
RC385]
gb|EFH75739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
RC385]
Length = 426

Score = 432 bits (1110), Expect = e-119, Method: Compositional matrix adjust.
Identities = 231/440 (52%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI+ ISG V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG

Sbjct: 2 ESLTLQPIELISGEVNLPGSKSVSNRALLLAALASGTTTLNLLSDDIRHMLNALTCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL

Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S

Sbjct: 176 AFLMSAPLAQGVKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +

Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAGQIEWGDDY 294

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+

Sbjct: 295 VIAR-----RGELNAVLDLDFNHIPDAAMTIATTALFAKGTATAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP +L AIDTYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPAQLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P CT KTFPDYFD + +

Sbjct: 407 PKCTSKTFPDYFDKFAQLSR 426

>gb|EGB62579.1| EPSP synthase [Escherichia coli M863]
gb|EGB71793.1| EPSP synthase [Escherichia coli TW10509]
Length = 427

Score = 432 bits (1110), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESRTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVRHMLNALTAL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPRLRQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_07511665.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
TA206]
Length = 427

Score = 431 bits (1109), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESRTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVRHMLNALTAL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A+E LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAESARE---LFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L Q GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALHQGGAKITYLEQENYPPRLRQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

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      ++ T          R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLKFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
      P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

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>ref|YP_002239442.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
342]
ref|YP_003440352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella variicola
At-22]
ref|ZP_06550022.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella sp.
1_1_55]
sp|B5XY87.1|AROA_KLEP3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI11715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
342]
gb|ADC59320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella variicola
At-22]
gb|EFD85366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella sp.
1_1_55]
Length = 427

```

Score = 431 bits (1109), Expect = e-119, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

```

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + LQPI + GTV LKPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVEGTVNLPKSGKSVSNRALLAALARGTTVLNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + R V G GG A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQYTLADTRCEVTGNGGPL---RAAAALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGQIDYLEQENYPPLRLRG--GFQGGNVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTVIAIKGDLVSKPYIDITLHLMKTFGVEVDNQ--SYQRFVVRGKQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
      P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGDYLVEGDASSASYFLAAGAIGKGTVKVTGIGRGSVQGDIFADVLEKMGATVTWGDDF 293

Query: 305 VVTGTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      + T R LKAID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELKAIDMDMNHIPDAAMTIATAALFAQGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDYIRITPPAKLKYAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
      P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

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>ref|ZP_02700430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Newport str. SL317]
gb|EDX49526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Newport str. SL317]
Length = 427

```

Score = 431 bits (1109), Expect = e-119, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 292/437 (66%), Gaps = 18/437 (4%)

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Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + G + LKPKSKS+SNR LLL AL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGAINLPKSKSVSNRALLLALACGKTVLTNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITGNGGPLRASGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGLPGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDSLRLQGGANIDYLEQENYPPRLRLG--GFTGGDIEVDGVSQFILT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
          ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLASKDTIIRVKGELVSKPYIDITLNLMTKTFGVEIANHH--YQQFVVKGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
          SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGPKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          + T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIR 423
          + A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
          DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

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>ref|YP_403921.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella dysenteriae
Sd197]
ref|ZP_07678674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella dysenteriae
1617]
sp|Q32E25.1|AROAS_HIDS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB62430.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella dysenteriae
Sd197]
gb|EFP73636.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella dysenteriae
1617]
Length = 424

```

Score = 431 bits (1109), Expect = e-119, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + GT+ LKPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGTINLPKSKSVSNRALLLAALAHGKTVLTNLLDSDVHRMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          +S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLASDRTRCEIIGNGGSLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGLPGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRLGGAKITYLEQENYPPRLRLQ--GFTGGNVVDGVSQFILT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEIENQ-HYQQFVVKGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIFADVLEKMGATICWGDDY 293

```


Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNINWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_04413226.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae bv.
albensis VL426]
gb|EEO02419.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae bv.
albensis VL426]
Length = 426

Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/440 (52%), Positives = 295/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E + LQPI+ ISG V LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIELISGEVNLPGSKSVSNRALLAALASGTTRLTNLLDSDDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGKVTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIWDGDDY 294

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVDLDFNHPDAAMTIATTALFAKGTTAIRNVNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL IDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHATIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSFVK 444
P CT KTFPDYFD + +
Sbjct: 407 PKCTSKTFPDYFDKFAQLSR 426

>ref|ZP_01680979.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae V52]
ref|YP_001217278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae O395]
ref|ZP_01978926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
MZO-2]
ref|ZP_06037428.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae RC27]
sp|A5F7G5.1|AROAVIBC3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EAX62197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae V52]
gb|ABQ20278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae O395]
gb|EDM54199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae
MZO-2]
gb|ACP09845.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio cholerae O395]
gb|EEY40681.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae RC27]
Length = 426

Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/440 (52%), Positives = 295/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E + LQPI+ ISG V LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIELISGEVNLPGKSVSNRALLAALASGTTTLNLLDSDIRHMLNATKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---HTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q A ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQASQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGVKTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGQFLVEGDASSASYFLAAAIKGEVKVTGIGKNSIQGDIQFADALEKMGAGQIEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYFD + +
Sbjct: 407 PKCTSKTFPDYFDKFAQLSR 426

>ref|YP_003674569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylothera sp.
301]
gb|ADI29992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylothera sp.
301]
Length = 426

Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 227/441 (51%), Positives = 290/441 (65%), Gaps = 17/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E++ L ++ G + LKSGKS+SNR LLLAALSEG T + +LL S+D ML AL+TLG
Sbjct: 2 EQLTLPASHQVQGNITLPGKSSISNRLLALLAALSEGATEIRDLLASDDTSRMLAQLTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + A V GCGG FP ++ ++FLGNAG A R LTA + AGG+ Y L
Sbjct: 62 VKLE-NFAENAWRVTCGCGNFP----NKKAEIFLGNAGTAFRPLTAVLALAGGD--YTLS 114

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV LKQ GAD+ + PP+++ +K+ G +SSQ+L+
Sbjct: 115 GVPRMHERPIGDLVDALKQAGADIQYLANSGFPPLKIAAPNIDLSKSIKIRGDVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL IE++ +LIS PY+E+TL LM +FGV + D W RF I Y S
Sbjct: 175 ALLMALPLTKQKATIEVVGELISKPYIEITLNLMAKFGVNVQR-DGWQRFTIPADSLYIS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
PK +VEGDASSASYFLA AI GG V VEG G S+QGDVKF + L +MG ++++ E
Sbjct: 234 PKQIFVEGDASSASYFLAAGAI-GGNVRVEGLGENSIQGDVKFTDALAIMGGEISYGENH 292

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+T + +K ID++ N +PD AMTLA+VALFA G T +R++ASWRVKET+R+
Sbjct: 293 ITANKAAK-----IKTIDLDCNHIPDAAMTLAIVALFAQGTTLRNIAASWRVKETDRI 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTIR 423

A+ TEL K+GA VEEG DY ITPP +L A IDTYDDHRMAM FSL + VP+TI
Sbjct: 346 AAMATELRKVGAIVEEGADYIKITPPAQLTPNAVIDTYDDHRMAMCFSLVSLGGVPITIN 405

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYF ++ VK

Sbjct: 406 DPKCVNKTFPDYFAQFASIVK 426

>ref|ZP_06080701.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. RC586]
gb|EEY98316.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. RC586]
Length = 426

Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/433 (53%), Positives = 293/433 (67%), Gaps = 15/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI ISG V LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLLTLQPINLISGEVNLPGSKSVSNRALLAALASGTTTLNLLDSDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G F + ++LFLGNAG AMR L AA+ G+ YVL
Sbjct: 62 VNYRLSADKTTCEVEGLGQAF---QTTQPLELFLGNAGTAMRPLAALCLGQGD--YVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G GL G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRQAGAQIEYLEQENFPPLRIQG-SGLQAGTVTIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 176 AFLMSAPLAQGVKTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPAGQSYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGNFLVEGDASSASYFLAAAIAKGGEVKVTGIGKNSIQGDIQFADALEKMGAIQEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMKMPDAMTAVVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ VTI D
Sbjct: 347 AAMATELRKVGATVEEGEDFIVITPPAKLIHAAIDTYDDHRMAMCFSLVALSDTQVTIND 406

Query: 425 PGCTRKTFFPDYFD 437
P CT KTFPDYF+
Sbjct: 407 PKCTSKTFFPDYFE 419

>ref|NP_752973.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
CFT073]
ref|ZP_07174283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
45-1]
sp|Q8FJB6.1|ARO_A_ECOL6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAN79516.1|AE016758_120 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
CFT073]
gb|EFJ93183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
45-1]
gb|EFU50598.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
153-1]
Length = 427

Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLDSDVVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

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+S      R  ++G GG   E A+E   LFLGNAG AMR L AA+   G+   VL
Sbjct: 62 VSYTLSADTRTRCEIIGNGGPLHAESARE---LFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV  L+Q GA  +      + PP+R+ G  G  GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKITYLEQENYPPLRLQG--GFTGGNVDDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA  D  I  I  L+S PY+++TL LM+ FGV+ E+   + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P      VEGDASSASYFLA AAI GGTV V G G  S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          ++ T      R  L AID++MN +PD AMT+A  ALFA G T +R++ +WRVKE++R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKESDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA VEEG D+  ITPPEKL  I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLKFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
          P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFQLA 421

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>ref|YP_069946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 32953]
ref|YP_001401547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 31758]
ref|YP_001721400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis YPIII]
ref|YP_001871945.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis PBI/+ ]
sp|Q66CI8.1|ARO_A_YERPS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A7FJW9.1|ARO_A_YERP3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B1JRD9.1|ARO_A_YERPY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B2KA23.1|ARO_A_YERPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH20655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 32953]
gb|ABS48591.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 31758]
gb|ACA68947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis YPIII]
gb|ACC88488.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis PBI/+ ]
Length = 428

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Score = 431 bits (1108), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/433 (53%), Positives = 297/433 (68%), Gaps = 16/433 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI  ++GTV LPGSKS+SNR LLLAAL+EGTT ++N+L+S+D+ +ML AL+ LG
Sbjct: 3  ESLTLQPIALVNGTVNLPGSKSVSNRALLLAALAEGTTQLNVLDSDDIRHMLNALQALG 62

Query: 65  LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++      V G G GK  A++ + LFLGNAG AMR L A +  GN+  VL
Sbjct: 63  VNFRLSADRTCEVDGLGGKLV---AEQPLSLFLGNAGTAMRPLAAVLCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV  L+Q GA  +D      + PP+R+ G  G  GG++ + G +SSQ+L+

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Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEQENYPPLRLRG--GFRGGELTVDGRVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I+ L+S PY+++TL LM+ FG+ H +++ F+IKGGQ Y+S

Sbjct: 176 ALLMTAPLAEQDTTIRIMGDLVSKPYIDITLHLMKAFGIDVGH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAKVTW +

Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVTVGIGKKSQGDTKFADVLEKMGAKVTWGDDY 294

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFATGPTTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 TAMATELRKVGAEVEEGEDYIRVPPVQLTAADIGTYDDHRMAMCFLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFD 437

P CT KTFPDYF+

Sbjct: 407 PKCTAKTFFPDYFE 419

>ref|NP_286783.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 EDL933]
ref|NP_309018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. Sakai]
ref|NP_415428.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K-12 substr. MG1655]
ref|YP_309883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella sonnei
Ss046]
ref|YP_408593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella boydii
Sb227]
ref|AP_001538.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K-12 substr. W3110]
ref|YP_001462126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
E24377A]
ref|ZP_02782007.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4401]
ref|ZP_02787964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4501]
ref|ZP_02794909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4486]
ref|ZP_02801247.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4196]
ref|ZP_02808826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4076]
ref|ZP_02812344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC869]
ref|ZP_02826416.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC508]
ref|YP_001729886.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K-12 substr. DH10B]
ref|YP_001880897.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella boydii CDC
3083-94]
ref|ZP_03028820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli B7A]
ref|ZP_03045751.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli E22]
ref|ZP_03051687.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
E110019]
ref|ZP_03060913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B171]
ref|ZP_03066649.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella dysenteriae
1012]
ref|ZP_03248841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4206]
ref|ZP_03256366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4045]
ref|ZP_03262808.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4042]
ref|YP_002269580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4115]

ref|YP_002292242.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli SE11]
ref|ZP_03440553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli O157:H7 str. TW14588]
ref|YP_002386407.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli IAI1]
ref|YP_002402048.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli 55989]
ref|YP_002925962.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli BW2952]
ref|YP_003076944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli O157:H7 str. TW14359]
ref|ZP_05434829.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella sp. D9]
ref|ZP_05437256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia sp. 4_1_40B]
ref|YP_003220936.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli O103:H2 str. 12009]
ref|YP_003228090.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli O26:H11 str. 11368]
ref|YP_003233482.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli O111:H- str. 11128]
ref|ZP_05941692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli O157:H7 str. FRIK2000]
ref|ZP_05948699.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli O157:H7 str. FRIK966]
ref|ZP_06661633.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli B088]
ref|ZP_07097208.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 107-1]
ref|ZP_07120879.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 84-1]
ref|ZP_07137442.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 115-1]
ref|ZP_07141300.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 182-1]
ref|ZP_07163709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 116-1]
ref|ZP_07167819.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 175-1]
ref|ZP_07188111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 196-1]
ref|ZP_07208616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 124-1]
ref|ZP_07219216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 78-1]
ref|ZP_07243475.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 146-1]
ref|ZP_07496893.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli H736]
ref|ZP_07591345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli W]
ref|ZP_07689529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 145-7]
sp|P0A6D3.1|AROAEcoli RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|P0A6D4.1|AROAEcoli RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|Q31YU3.1|AROASHIBS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|Q3Z3L4.1|AROASHISS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|A7ZJZ7.1|AROAEcoli RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|B7M836.1|AROAEcoli RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|B1X848.1|AROAEcoli RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|B5YT42.1|AROA_ECO5E RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|B6I8Y0.1|AROA_ECOSE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|B2TUH3.1|AROA_SHIB3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|B7LDA0.1|AROA_ECO55 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|C4ZQ34.1|AROA_ECOBW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

pdb|1G6S|A Chain A, Structure Of Epsp Synthase Liganded With Shikimate-3-
Phosphate And Glyphosate

pdb|1G6T|A Chain A, Structure Of Epsp Synthase Liganded With Shikimate-3-
Phosphate

pdb|1X8R|A Chain A, Epsps Liganded With The (S)-Phosphonate Analog Of The
Tetrahedral Reaction Intermediate

pdb|1X8T|A Chain A, Epsps Liganded With The (R)-Phosphonate Analog Of The
Tetrahedral Reaction Intermediate

pdb|2AA9|A Chain A, Epsp Synthase Liganded With Shikimate

pdb|2AAY|A Chain A, Epsp Synthase Liganded With Shikimate And Glyphosate

pdb|2PQ9|A Chain A, E. Coli Epsps Liganded With (R)-Difluoromethyl Tetrahedral
Reaction Intermediate Analog

gb|AAG55393.1|AE005280_4 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O157:H7 str. EDL933]

dbj|BAA35643.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K12 substr. W3110]

gb|AAC73994.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K-12 substr. MG1655]

dbj|BAB34414.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O157:H7 str. Sakai]

gb|AAZ87648.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella sonnei
Ss046]

gb|ABB66765.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella boydii
Sb227]

gb|ABV17446.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
E24377A]

gb|ACB02108.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
str. K-12 substr. DH10B]

gb|ACD09836.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella boydii CDC
3083-94]

gb|EDU32179.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4196]

gb|EDU67887.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4076]

gb|EDU74354.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4401]

gb|EDU79527.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4486]

gb|EDU85250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4501]

gb|EDU91027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC869]

gb|EDU94837.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC508]

gb|EDV62717.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli B7A]

gb|EDV82344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli E22]

gb|EDV86413.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
E110019]

gb|EDX29868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B171]

gb|EDX33476.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella dysenteriae
1012]

gb|EDZ75906.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4206]

gb|EDZ80523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4045]

gb|EDZ85657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4042]

gb|ACI39126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4115]

gb|ACI85761.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli]

gb|ACI85762.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli]

gb|ACI85763.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli]

gb|ACI85765.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli]

dbj|BAG76491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
SE11]

gb|EEC29114.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14588]

emb|CAU96817.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
55989]

emb|CAQ97812.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
IAI1]

gb|ACR61879.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
BW2952]

gb|ACT70868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14359]

dbj|BAI24350.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O26:H11 str. 11368]

dbj|BAI29802.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O103:H2 str. 12009]

dbj|BAI34931.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O111:H- str. 11128]

gb|ACX40368.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli DH1]

gb|EFE63446.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B088]

gb|EFI88593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
196-1]

gb|EFJ67452.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
175-1]

gb|EFJ88614.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
84-1]

gb|EFJ95304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
115-1]

gb|EFK01796.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
182-1]

gb|EFK14499.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
116-1]

gb|EFK51403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
107-1]

gb|EFK70084.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
124-1]

gb|EFK75198.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
78-1]

gb|EFK92947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
146-1]

gb|EFN38759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli W]

gb|EFO58675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
145-7]

emb|CBJ00484.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli ETEC
H10407]

gb|ADT74520.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli W]

dbj|BAJ42715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli DH1]

gb|EFU37916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
85-1]

gb|EFU99682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
3431]

gb|EFW48458.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Shigella dysenteriae
CDC 74-1112]

gb|EFW56930.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Shigella boydii ATCC
9905]

gb|EFW59073.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Shigella flexneri CDC
796-83]

gb|EFW67247.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Escherichia coli
O157:H7 str. EC1212]

gb|EFW76875.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Escherichia coli


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EC4100B]
gb|EFX07568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. G5101]
gb|EFX12102.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H- str. 493-89]
gb|EFX17013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H- str. H 2687]
gb|EFX21748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. 3256-97 TW 07815]
gb|EFX31439.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. LSU-61]
gb|EFZ43328.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
EPECa14]
gb|EFZ45514.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
E128010]
gb|EFZ51160.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella sonnei 53G]
gb|EFZ60606.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
LT-68]
gb|EFZ61064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
1180]
gb|EFZ70750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
1357]
gb|ADX51515.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
K011]
gb|EGB38989.1| EPSP synthase [Escherichia coli E482]
gb|EGB43311.1| PSP synthase [Escherichia coli H120]
gb|EGB68409.1| EPSP synthase [Escherichia coli TA007]
gb|EGB88303.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
117-3]
gb|EGC11135.1| EPSP synthase [Escherichia coli E1167]
Length = 427

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTLNLLSDDDRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSDRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVDDVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVGKGSYSQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIIATYNDHRMAMCFLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_05971936.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Providencia
rustigianii DSM 4541]
gb|EFB73431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Providencia

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rustigianii DSM 4541]
Length = 424

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 225/436 (51%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI I+GT+ LPGSKS+SNR LLLAA+++GTTV+ NLL+S+D+ +ML AL LG
Sbjct: 2 QSLTLQPISSINGTINLPGSKSVSNRALLAAMAKGTTVLTNLLSDDIRHMLNALSQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + R V G G + E+++FLGNAG AMR LTAA++ + N +L
Sbjct: 62 VSFQLSDDKTRCRVEGINGCLF---HQGELEIFLGNAGTAMRPLTAALSLSNNNI--ILT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA ++ + PP+R+ G G GG++ + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALREGGAHIEYLEQENYPPMRLRG--GFMGGEISVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D I I+ L+S PY+++TL LM+ FGV ++ + +F IKG Q+Y+S
Sbjct: 175 ALLMAAPLAQDQTVITIVGDLVSKPYIDITLALMKTFGVDVDNQ-QYQKFIKGGQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G SLQGD KFA VLE MGA + W +
Sbjct: 234 PGEYLVEGDASSASYFLAAAAIKGGVVRVTGIGRNSLQGDTKFANVLEKMGAIIRWGDDY 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L ID++MN +PD AMT+ VALFA G T IR++ +WRVKET+R+
Sbjct: 294 VECE-----RDTLHGIDMDMNTIPDAAMTIGTVALFAKGETVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ I PP+ L I+TY+DHR+AM FSL A ++ PVTI D
Sbjct: 346 YAMATELRKVGAEVEEGYDFIRIVPPKHLKHADIETYNDHRIAMCFSLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
PGCT KTFPDYF L+
Sbjct: 406 PGCTAKTFPDYFQQLA 421

>ref|ZP_07186821.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
69-1]
gb|EFJ80809.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
69-1]
Length = 427

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLSDDVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--GFTGGNVVDGGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_05722256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio mimicus VM603]
gb|EEW05249.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio mimicus VM603]
Length = 456

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/440 (52%), Positives = 293/440 (66%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
E + LQPI ISG V LP GSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG
Sbjct: 32 ESLTLQPINLISGEVNLPGSKSVSNRALL LLAALASGTTTRLTNLLDSDDIRHMLNALTQLG 91

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G G F + ++LFLGNAG AMR L AA+ G YVL
Sbjct: 92 VKYRLSADKTTCEVEGLGQAF---QTTQPLEFLFLGNAGTAMRPLAALCL--GQGEYVLT 146

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPIG LV L+Q GA ++ + PP+R+ G G L G V + GSISSQ+L+
Sbjct: 147 GEARMKERPIGHLVDALRQAGAQIEYLEQENFPPLRIQGTG-LQAGTVTIDGSISSQFLT 205

Query: 185 ALLMAAPLALGDVEIEI IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ + D + F I GQ Y S
Sbjct: 206 AFLMSAPLAQGVKTIKIVGELVSKPYIDITLHIMEQFGVQVINHD-YQEFVIPTGQSYVS 264

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 265 PGNFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMG AQIEWGDDY 324

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+
Sbjct: 325 VISR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGTTAIRNVYNWRVKETDRL 376

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 377 AAMATELRKVGATVEEGEDFIVITPPAKLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 436

Query: 425 PGCTRKTFFPDYFDVLSFVK 444
P CT KTFPDYF+ + +
Sbjct: 437 PKCTSKTFPDYFEKFAQLSR 456

>ref|ZP_07103774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
119-7]
ref|ZP_07521497.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
TA271]
ref|ZP_07612706.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
H591]
gb|EFK44916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
119-7]
Length = 427

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
E + LQPI + GT+ LP GSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIASVDGTINLP GSKSVSNRALL LLAALAHGKTVLTNLLDSDDVHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADRTCEIIGGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVDDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|NP_706826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella flexneri 2a
str. 301]
ref|NP_836613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella flexneri 2a
str. 2457T]
ref|YP_688435.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella flexneri 5
str. 8401]
sp|Q83RY8.1|AROAS_HIFL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q0SX08.1|AROAS_HIF8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAN42533.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella flexneri 2a
str. 301]
gb|AAP16419.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella flexneri 2a
str. 2457T]
gb|ABF03130.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Shigella flexneri 5
str. 8401]
gb|ADA73251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella flexneri
2002017]
gb|EFS12887.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shigella flexneri 2a
str. 2457T]
Length = 427

Score = 431 bits (1107), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLDSDVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
LS R ++G GG E A ++LFLGNAG AMR L AA+ + VL
Sbjct: 62 LSYTLSADRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCLDSND--IVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVDDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNINWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_08038910.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Serratia symbiotica
str. Tucson]
gb|EFW12641.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Serratia symbiotica
str. Tucson]
Length = 428

Score = 430 bits (1106), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 303/436 (69%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQP+ ++GTV LPKSGK+SNR LLLAAL+EGTT + NLL+S+DV +ML ALR LG
Sbjct: 3 DSLTLQPVALLVNGTVNLPKSGKSVSNRALLLAALAEGTTRLTNLLDSDVVRHMLNALRALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ +A R V G P+ A + ++LFLGNAG AMR L AA+ + G+A VL
Sbjct: 63 VNYRL--SADRTVCQVDGAAGPLA-ADQPLELFLGNAGTAMRPLAALCLSHGDA--VLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D D PPVR+ G G GG + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEQPDYPPVRLRG--GFLGGDITVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I I +L+S PY+++TL LM FGV+ H D + F+++G Q Y+S
Sbjct: 176 ALLMTAPLAPQDTQIHIGKELVSKPYIDITLHLMRSFGVEVSH-DHYRVFHVQGRQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD +FA VLE MGA++TW +
Sbjct: 235 PGDYLVEGDASSASYFLAAAIAKGGTVRVSGIGRKSVQGDQFANVLEKMGARITWGDDF 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + +G L+ ID++MN +PD AMT+A ALFA GPT +R+V +WRVKET+R+
Sbjct: 295 IECS-----YGE--LRGIDMDMNSIPDAAMTIATTALFAKGTTLRNINWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V+EG D + PP KL AIDTY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVDEGKDSIHVVPPAKLKFAAIDTYNDHRMAMCFSLVALSDPTVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PQCTAKTFPDYFEQLA 422

>sp|Q9ZFF7.1|AROA_SHISO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC72854.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Shigella sonnei]
Length = 427

Score = 430 bits (1106), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSGK+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSGKSVSNRALLLAALAHGKTVLTNLLDSDVVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 VSYTLSADTRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMNAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPMPREPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_07506865.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
M718]
Length = 427

Score = 430 bits (1106), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG

Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLSDSDVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 VSYTLSADTRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMTAPLAPKDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPMPREPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTGKTFPDYFEQLA 421

>pdb|2QFQ|A Chain A, E. Coli Eps Synthase Pro101leu Liganded With S3p
pdb|2QFU|A Chain A, E.Coli Eps Synthase Pro101leu Liganded With S3p And
Glyphosate
Length = 427

Score = 430 bits (1106), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLDSDVHRMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTSLADTRCEIIGNGGGLHAEGA---LELFLGNAGTAMRLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_003942408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter cloacae
SCF1]
gb|ADO49124.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterobacter cloacae
SCF1]
Length = 427

Score = 430 bits (1106), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 EFLTLQPIARVDGTINLPGSKSVSNRALLAALARGTTVLTNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG DA E LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VHYTSLADTRCEVTGNGGPLQAGDALE---LFLGNAGTAMRPLAALCL--GHNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGAQIEYLEQENYPLRLKG--GFTGGSVAVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV ++ S+ RF +KGGQ Y+S
Sbjct: 175 ALLMTAPLAEQDTVIAIKGDLVSKPYIDITLHLMKTFGVTVDNQ-SYQRFVVKGGQHYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G +S+QGD++FA+VLE MGA + W
Sbjct: 234 PGSYLVEGDASSASYFLAAAAIKGGTVKVTGIGRSSVQGDIFADVLEKMGATIVWGADF 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424

A+ TEL K+GA VEEG D+ +TPP +LN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDFIRVTPPARLNTAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440

P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|ZP_07501418.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli M605]
Length = 427

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLDSDVVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A+E LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRTRCEIIGNGGPLHAESARE---LFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKINYLEQENYPPRLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGEIENH-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMVDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLFKFAEIATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440

P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>gb|AAA27028.1| 5-enolpyruvylshikimate-3-phosphate synthase, EC 2.5.1.19
[Salmonella enterica subsp. enterica serovar Typhimurium]
emb|CAA71382.1| aroA [Salmonella enterica subsp. enterica serovar Typhimurium]
Length = 427

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 291/437 (66%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL G T + NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLAALPCGKTALTNLLDSDVVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSDTRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRLQGGANIDYLEQENYPPRLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y

Sbjct: 175 ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSQGDKFAEVLEMMGAKVTWTET 303

SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +

Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRSMQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363

+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R

Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIR 423

+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI

Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440

DP CT KTFPDYF+ L+

Sbjct: 405 DPCKTAKTFPDYFEQLA 421

>ref|NP_992569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Microtus str. 91001]
ref|YP_650594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Antiqua]
ref|YP_648515.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]
ref|YP_001163653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Pestoides F]
ref|ZP_01888681.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
CA88-4125]
ref|YP_001606427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Angola]
ref|ZP_02220274.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. F1991016]
ref|ZP_02227497.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. IP275]
ref|ZP_02230741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. E1979001]
ref|ZP_02237787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. B42003004]
ref|ZP_02305362.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. UG05-0454]
ref|ZP_02311658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. MG05-1020]
ref|ZP_02316119.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Mediaevalis str. K1973002]
ref|ZP_02334360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis FV-1]
ref|YP_002346413.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis C092]
ref|ZP_04461519.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. PEXU2]
ref|ZP_04463611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. India 195]
ref|ZP_04511008.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Pestoides A]
ref|ZP_04518269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]
ref|ZP_06204025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis KIM
D27]
ref|YP_003567442.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Z176003]
sp|Q60112.2|AROA_YERPE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q1CA73.1|AROA_YERPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q1CGG5.1|AROA_YERP N RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A4TN18.1|AROA_YERPP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|A9R7I2.1|AROA_YERPG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|AAS61446.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Microtus str. 91001]

gb|ABG18915.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]

gb|ABG12649.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Antiqua]

emb|CAL20042.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis C092]

gb|ABP40680.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Pestoides F]

gb|EDM41096.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
CA88-4125]

gb|ABX84965.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Angola]

gb|EDR31715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. IP275]

gb|EDR40634.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. F1991016]

gb|EDR43540.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. E1979001]

gb|EDR52003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. B42003004]

gb|EDR58667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. MG05-1020]

gb|EDR61960.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. UG05-0454]

gb|EDR66978.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Mediaevalis str. K1973002]

gb|EEO75029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]

gb|EEO81873.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. India 195]

gb|EEO87773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. PEXU2]

gb|EEO88790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Pestoides A]

gb|ACY58142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
D106004]

gb|ACY61600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
D182038]

gb|EFA46232.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis KIM
D27]

gb|ADE64180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
Z176003]

gb|ADV99322.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis
biovar Mediaevalis str. Harbin 35]
Length = 428

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/433 (53%), Positives = 295/433 (68%), Gaps = 16/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI ++GTV LKSKS+SNR LLLAAL+EGTT ++N+L+S+D+ +ML AL+ LG

Sbjct: 3 ESITLQPIALVNGTVNLPGSKSVSNRALLAALAEAGTTQLNNVLDSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G G G K E + + LFLGNAG AMR L A + GN+ VL

Sbjct: 63 VDFRLSADRTCEVDGLGGKLVAE---QPLSLFLGNAGTAMRPLAAVLCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDVDFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + G +SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGGQIDYLEQENYPPLRLRG--GFRGGELTVDGRVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I+ L+S PY+++TL LM+ FG+ H +++ F+IKGGQ Y+S

Sbjct: 176 ALLMTAPLAEQDITIRIMGDLVSKPYIDITLHLMKAFGIDVGH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAKVTW +

Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKKSQGDTKFADVLEKMGAKVTWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFATGPTTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 TAMATELRKVGAEVEEGEDYIRVVPPLQLTAADIGTYDDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFD 437
P CT KTFPDYF+

Sbjct: 407 PKCTAKTFFPDYFE 419

>gb|AAB48057.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Yersinia pestis]
Length = 424

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/433 (53%), Positives = 295/433 (68%), Gaps = 16/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI ++GTV LPKSKS+SNR LLLAAL+EGTT ++N+L+S+D+ +ML AL+ LG

Sbjct: 3 ESITLQPIALVNGTVNLPKSKSVSNRALLLAALAEGLTQLNNVLDSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G GKG E + + LFLGNAG AMR L A + GN+ VL

Sbjct: 63 VDFRLSADRTCCEVDGLGGKLVAE---QPLSLFLGNAGTAMRPLAAVLCL--GNSDIVLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + G +SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLRG--GFRGGELTVDGRVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I+ L+S PY+++TL LM+ FG+ H +++ F+IKGGQ Y+S

Sbjct: 176 ALLMTAPLAEQDITIRIMGDLVSKPYIDITLHLMKAFGIDVGH-ENYQIFHIKGGQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD KFA+VLE MGAKVTW +

Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKKSQGDTKFADVLEKMGAKVTWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+

Sbjct: 295 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFATGPTTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TYDDHRMAM FSL A ++ PVTI D

Sbjct: 347 TAMATELRKVGAEVEEGEDYIRVVPPLQLTAADIGTYDDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFD 437
P CT KTFPDYF+

Sbjct: 407 PKCTAKTFFPDYFE 419

>ref|ZP_06656837.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B185]
gb|EFF07219.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B185]
Length = 427

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG

Sbjct: 2 ESITLQPIARVDGTINLPKSKSVSNRALLLAALAHGKTVLTNLLDSDVHRHMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 VSYTLRADTRCEIIGGGPLHAEGA---LELFLGNAGTAMRPLAAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ-HYQQFVVKGGQPYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFLVALSDPTVITILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_001457748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli HS]
ref|YP_001725644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli ATCC
8739]
ref|ZP_03001521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
53638]
ref|ZP_03070810.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
101-1]
ref|YP_003036894.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
BL21-Gold(DE3)pLysS AG]
ref|YP_003044130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli B
str. REL606]
ref|ZP_07145064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
187-1]
ref|ZP_07785215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
1827-70]
sp|A7ZYL1.1|AROAE_COHS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B1IW23.1|AROA_ECOLC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV05365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli HS]
gb|ACA78317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli ATCC
8739]
gb|EDU64553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
53638]
gb|EDX38355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
101-1]
emb|CAQ31436.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Escherichia coli
BL21(DE3)]
gb|ACT29709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
'BL21-Gold(DE3)pLysS AG']
gb|ACT38594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli B
str. REL606]
gb|ACT42807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
BL21(DE3)]
gb|EFK25932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
187-1]
gb|EFQ01964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
1827-70]
gb|EGB58474.1| EPSP synthase [Escherichia coli H489]
Length = 427

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLSDSDVRHMLNALTGL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTSLADTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGVSQSFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|NP_670084.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia pestis KIM
10]
gb|AAM86335.1|AE013881_5 5-enolpyruvylshikimate-3-phosphate synthetase [Yersinia pestis KIM
10]
Length = 443

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/433 (53%), Positives = 296/433 (68%), Gaps = 16/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI ++GTV LPGSKS+SNR LLLAAL+EGTT ++N+L+S+D+ +ML AL+ LG
Sbjct: 18 ESLLTLQPIALVNGTVNLPGSKSVSNRALLAALAEAGTQLNNVLDSDDIRHMLNALQALG 77

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G GKK A++ + LFLGNAG AMR L A + GN+ VL
Sbjct: 78 VDFRLSADRTCEVDGLGGKLV---AEQPLSLFLGNAGTAMRPLAALVCL--GNSDIVLT 132

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + G +SSQ+L+
Sbjct: 133 GEPRMKERPIGHLVDALRQGGAQIDYLEQENYPPLRLRG--GFRGGELTVDGRVSSQFLT 190

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
E+ L+ I+ L+S PY+++TL LM+ FG+ H +++ F+IKGGQ Y+S
Sbjct: 191 ALLMTAPLAEQDTTIRIMGDLVSKPYIDITLHLMKAFGIDVGH-ENYQIFHIKGGQTYRS 249

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGAKVTW +
Sbjct: 250 PGTYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKKSQGDTKFADVLEKMGAKVTWGDY 309

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+
Sbjct: 310 IECS-----RGELQGIDMDMNHIPDAAMTIATTALFATGPTTIRNIYNWRVKETDRL 361

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY + PP +L I TYDDHRMAM FSL A ++ PVTI D
Sbjct: 362 TAMATELRKVGAEVEEGEDYIRVVPPLQLTAADIGTYDDHRMAMCFSLVALSDTPVTILD 421

Query: 425 PGCTRKTFFPDYFD 437

P CT KTFPDYF+
Sbjct: 422 PKCTAKTFPDYFE 434

>ref|YP_001453724.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citrobacter koseri
ATCC BAA-895]
sp|A8AIH5.1|AROAI_CITK8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV13288.1| hypothetical protein CKO_02164 [Citrobacter koseri ATCC BAA-895]
Length = 427

Score = 430 bits (1105), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSKSVSNRALLAALASGTTVLTNLLDSDDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R + G GG E A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 VSYTSLADTRCEITGQGGVLHAEGA---LELFLGNAGTAMRPLAALCL--GANDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKIDYLEQENYPLRLRG--GFSGGHVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + + RF +KG Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTTIAIKGDLVSKPYIDITLNLMTKTFGVEVENQN-YQRFVVKGEQQYRS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234 PGQYLVEGDASSASYFLAAGAIGGTVKVTGIGRNSMQGDIRFADVLEKMGATITWGDDF 293

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L A+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELNAVMDMDNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG D+ ITPP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPAQLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_002918699.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
NTUH-K2044]
dbj|BAH62632.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
subsp. pneumoniae NTUH-K2044]
Length = 427

Score = 429 bits (1104), Expect = e-118, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GTV LPKSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVEGTVNLPKSKSVSNRALLAALARGTTVLTNLLDSDDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V+G GG P+ A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQYTLADTRCEVIGNGG--PLRSAAA-LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGQIDYLEQENYPLRLRG--GFQGGNVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF ++G Q+Y+S

Sbjct: 175 ALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ-SYQRFVVRGKQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +

Sbjct: 234 PGDYLVEGDASSASYFLAAGAIGKGTVKVTGIGRNSVQGDIFADVLEKMGATVTWGDDF 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T LKA+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 IACT-----HGELKAVDMDMNHIPDAAMTIATAALFAQGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGEDYIRITPPAKLKYAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_725310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia eutropha
H16]
sp|Q0KDH9.1|AROA_RALEH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAJ91942.1| 3-Enolpyruvylshikimate-5-phosphate synthetase [Ralstonia eutropha
H16]
Length = 434

Score = 429 bits (1104), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/441 (52%), Positives = 296/441 (67%), Gaps = 17/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P+ +GTV+LPGSKS+SNR+LLLAAL+ G T V +LL+S+D ML ALRTL

Sbjct: 2 EHLTLGLPLTRANGTVRLPGSKSISNRVLLLAALATGETRVRDLLSDSDTRVMLQALRTL 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + +V G GG FP + A +LF+GNAG A+R LTAA+ GGN Y L

Sbjct: 62 VAWR--QEGDDYIVTGAGGNFPNKS----ELFMGNAGTAIRPLTAALALQGGN--YKLS 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ + G +++ G +SSQ+L+

Sbjct: 114 GVPRMHERPIGDLVDGLRQVGAVIDYLGNEGFPPLHIQPAIRIDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLALGD--VEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM+ P+A D +EIE++ +LIS PY+E+TL L+ RFG++ E W+RF + G

Sbjct: 174 ALLMSLPMAQSDSGRIEIEVGELISKPYIEITLNLARFGIEIERQ-GWERFVLPAGAA 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP +VEGDASSASYFLA AI GG V VEG G S+QGDV+FAE L MGA V

Sbjct: 233 YRSPGEIFVEGDASSASYFLAAGAIGGPPVRVEGVGMASIQGDVRFALNRMGANVMAG 292

Query: 302 ETSVTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V G R+ GR H I+++ N +PD AMTLAV ALFA+G T + ++ASWRVKET

Sbjct: 293 DNWIEVRGTERDD-GR LH--GIELDCNHIPDAAMTLAVAALFAEGTTTLTNIASWRVKET 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL KLGA VEEG DY +TPP+ A I TYDDHRMAM FSLAA +P

Sbjct: 350 DRIAAMATELRKLGAVVEEGADYLRVTPPQWPQTPADGIGTYDDHRMAMCFSLAAFGLP 409

Query: 420 VTIRDPGCTRKTFFPDYFDVLS 440
V I DPGC KTFPDYF V +

Sbjct: 410 VRINDPGCVAKTFFPDYFSVFA 430

>sp|P24497.1|AROA_KLEPN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAA57812.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
Length = 427

Score = 429 bits (1104), Expect = e-118, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

```

Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + GTV LKPKSK+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESILTQPIARVDGTVNLPKSKSVSNRALLAALARGTTVLNLLDSDVHMLNALSALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + R V G GG P++ A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62  VHYVLSDRTRCEVTGTGG--PLQ-AGSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRQGGQIDYLEQENYPLRLRG--GFTGGDVEVDGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLMA+PLA D I I +L+S PY+++TL LM+ FGV+ E+ ++ RF ++G Q+Y+S
Sbjct: 175  ALLMASPLAQDTVIAIKGELVSRPYIDITLHLMKTFGVEVENQ-AYQRFIVRGNQQYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA VTW E
Sbjct: 234  PGDYLVVEGDASSASYFLAAGAIGGTVKVTGIGRNSVQGDIFADVLEKMGATVTWGEDY 293

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          + T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294  IACT-----RGELNAIDMDMNHIPDAAMTIATAALFARGTTTLRNIYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA VEEG DY ITPP L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346  FAMATELRKVGAEVEEGEDYIRITPPLTLQFAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425  PGCTRKTFFPDYFDVLS 440
          P CT KTFPDYF L+
Sbjct: 406  PKCTAKTFFPDYFGQLA 421

```

>pdb|1EPS|A Chain A, Structure And Topological Symmetry Of The Glyphosphate 5-
Enol-Pyruvylshikimate-3-Phosphate Synthase: A
Distinctive Protein Fold
emb|CAA25223.1| unnamed protein product [Escherichia coli]
prf||1006223A synthase,enolpyruvylshikimate
Length = 427

Score = 429 bits (1104), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

```

Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + GT+ LKPKSK++SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESILTQPIARVDGTINLPKSKTVSNRALLAALAHGKTVLTNLLDSDVHMLNALTALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          +S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62  VSYTSLADRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--GFTGGNVVDGGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175  ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234  PGTYLVVEGDASSASYFLAAAAIKGTVKVTGIGRNSMQGDIFADVLEKMGATICWGDDY 293

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          ++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294  ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424

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A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440

P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_001908068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia tasmaniensis Et1/99]

sp|B2VC79.1|AROA_ERWT9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

emb|CAO97190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia tasmaniensis Et1/99]

Length = 428

Score = 429 bits (1103), Expect = e-118, Method: Compositional matrix adjust.
Identities = 236/438 (53%), Positives = 304/438 (69%), Gaps = 20/438 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

+ + LQPI + GTV LPGSKS+SNR LLLAAL+EGTT + NLL+S+DV +ML AL+ +G

Sbjct: 3 DSLTLQPIALVDGTVNLPGSKSVSNRALLAALAEGTTRLTNLLDSDVVRHMLDALKAI 62

Query: 65 L--SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122

+ S+ AD+ +VG GG +AKE ++LFLGNAG AMR L AA+ GN V

Sbjct: 63 VKYLSADRTCCE--IVGQGGPL---NAKEPLELFLGNAGTAMRPLAAALCI--GNGD 115

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQY 182

L G PRM+ERPIG LV L+Q GA+V+ + PP+RV G G GG+V ++GS+SSQ+

Sbjct: 116 LTGEPRMKERPIGHLVDALRQGGAEVEYLEQENYPPLRVKG--GFSGGEVTVNGSVSSQF 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242

L+ALLMAAPLA D I I L+S PY+++TL+LM FGV E++D +D F+I G Q+Y

Sbjct: 174 LTALLMAAPLAPNDTRIVIKGDLVSKPYIDITLKLMTFGVVVENND-YDTFHISGQQQY 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302

++ + VEGDASSASYFLA AAI GGT V V G G S+QGD+ FA+VLE MGA V W +

Sbjct: 233 QATREYLVEGDASSASYFLAAAIKGGTVKVTGIGRNSMQGDIHFADVLEKMGASVEWGD 292

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362

+ T R L A+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+

Sbjct: 293 DYIAC-----RGDLNAVLDLMNHIPDAAMTIATATLFAQGTVMRNIYNWRVKETD 344

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTI 422

R+ A+ TEL K+GA VEEG D+ ITPP K+ I TY+DHRMAM FSL A + PVTI

Sbjct: 345 RLTAMATELRKVGAEVEEGHDFISITPPAKIVFAEIGTYNDHRMAMCFSLVALSSSPVTI 404

Query: 423 RDPGCTRKTFPDYFDVLS 440

DP CT KTFPDYF+ L+

Sbjct: 405 LDPKCTAKTFPDYFEQLA 422

>ref|ZP_04561353.1| 5-enolpyruvylshikimate-3-phosphate synthase [Citrobacter sp. 30_2]

gb|EEH92329.1| 5-enolpyruvylshikimate-3-phosphate synthase [Citrobacter sp. 30_2]

Length = 427

Score = 429 bits (1103), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + LQPI + GT+ LPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG

Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALANGTTVLTNLLDSDVVRHMLNALNALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+S R +VG GG E A V+LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 ISYTLSADTRCEIVGNGGVLHAEGA---VELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG+V++ GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPRLRLG--GFTGGQVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV E+ + + RF +KG Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTTIAIKGDLVSKPYIDITLNLMTFGVVIENQN-YQRFVVKGQQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234 PGAYLVEGDASSASYFLAAGAIGKGTVKVTGIGRNSMQGDIRFADVLEKMGATITWGDDF 293

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L A+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----HGELNAVDMNMNHPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPP L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPATLQFADIATYNDHRMAMCFSLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_002004817.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cupriavidus taiwanensis LMG 19424]
sp|B3R368.1|AROA_CUPTR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAQ68748.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Cupriavidus taiwanensis LMG 19424]
Length = 434

Score = 429 bits (1103), Expect = e-118, Method: Compositional matrix adjust.
Identities = 231/445 (51%), Positives = 297/445 (66%), Gaps = 17/445 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P+ +GTV+LPGSKS+SNR+LLLAAL+ G T V +LL+S+D ML ALRTL
Sbjct: 2 EHLTLGLPLTRATGTVRLPGSKSISNRVLLLAALANGETRVRDLSDDDRVLQALRTL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ D +V G GG FPV+ A +LF+GNAG A+R LTAA+ GG +Y L
Sbjct: 62 VAWRQD--GPDYIVTGAGGNFPVKS----ELFMGNAGTAIRPLTAALALQGG--SYKLS 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ + +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQVGAVIDYLGNEGFPPLHIQPASLRIDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM+ PLA G +EIE++ +LIS PY+E+TL L+ RFG++ E W+RF + G
Sbjct: 174 ALLMSLPLAQASGRIEIEVVGELISKPYIEITLNLARFGIEVERQ-GWERFILPAGTA 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP +VEGDASSASYFLA AI GG V VEG G S+QGDV+FA+ L MGA V
Sbjct: 233 YRSPGEIFVEGDASSASYFLAAGAIGGPPVRVEGVGMASIQGDVRFADALNRMGANVMAG 292

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V G R+ GR H I+++ N +PD AMTLAV ALFA+G T + ++ASWRVKET
Sbjct: 293 DNWIEVRGTERDD-GR LH--GIELDCNHPDAAMTLAVAALFAEGTTTLTNIASWRVKET 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL KLGA VEEG DY +TPP+ A I TYDDHRMAM FSLAA +P
Sbjct: 350 DRIAMATELRKLGA VEEGADYLRVTPPQWPQTPADGIGTYDDHRMAMCFSLAAGFLP 409

Query: 420 VTIRDPGCTRKTFPDYFDVLSFVK 444
V I DPGC KTFPDYF V + +
Sbjct: 410 VRINDPGCVAKTFPDYFSVFAGVTR 434

>ref|ZP_07617960.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli TA280]
Length = 427

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + LQPI + GT+ LKPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESILTLPQIARVDGTINLPGSKSVSNRALLLALLAALAHGKTVLTNLLDSDVRHMLNALLAALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +S      R ++G GG  E A  ++LFLGNAG AMR L AA+  G+  VL
Sbjct: 62  VSYTTLADTRTCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV  L+  GA +  + PP+R+ G  GG V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--SFTGGNVVDVGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALLM APLA D I I  L+S PY+++TL LM+ FGV+ E+  + +F +KGGQ Y+S
Sbjct: 175  ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEIENQ-HYQQFVVKGGSYSQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P  VEGDASSASYFLA AAI GGT V V G G  S+QGD++FA+VLE MGA + W +
Sbjct: 234  PGTYLVEGDASSASYFLAAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      ++ T      R L AID++MN +PD AMT+A  ALFA G T +R++ +WRVKET+R+
Sbjct: 294  ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA VEEG DY  ITPPEKLN  I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346  FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425  PGCTRKTFFPDYFDVLS 440
      P CT KTFPDYF+ L+
Sbjct: 406  PKCTAKTFFPDYFEQLA 421
```

>ref|ZP_01988160.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio harveyi HY01]
gb|EDL67151.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio harveyi HY01]
Length = 426

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/435 (53%), Positives = 295/435 (67%), Gaps = 15/435 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + LQPI +I G V LKPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2  ESILTLPQINKIQGEVNLPKSGKSVSNRALLLALLAKGTTRLTNLLDSDIRHMLNALLTKLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + +  VV G G F V  E V+LFLGNAG AMR L AA+  G+  YVL
Sbjct: 62  VQYQLSEDKTECVVEGLGRPFSV---SEPVELFLGNAGTAMRPLAALCL--GDGEYVLT 116

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV  LK GADV  + PP+++ G G L  G V + GSISSQ+L+
Sbjct: 117  GEPRMKERPIGHLVTALKAAGADVITYLENENYPLKIVGTG-LKSGSVSIDSGSISSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      A LM+APLA GD+ I I  +L+S PY+++TL +M++FGV  ++D +  F I  GQ+Y +
Sbjct: 176  AFLMSAPLAEGDIRINIEGELVSKPYIDITLHIMKQFGVDVINND-YQEFVIPAGQQYVA 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P +  VEGDASSASYFLA AAI GG V V G G  S+QGD++FA+ LE MGA++ W +
Sbjct: 235  PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      V      LK ID++ N +PD AMT+A  ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295  VISR-----VGQLKGIDMDYNHIDPAAMTIATTALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA VEEG DY I+ P  +L  AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347  SAMATELRKVGAEVEEGEDYIIVKVPVQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406
```

Query: 425 PGCTRKTFPDYFDVL 439
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFPDYFDKL 421

>pdb|1MI4|A Chain A, Glyphosate Insensitive G96a Mutant Epsp Synthase Liganded
With Shikimate-3-Phosphate
Length = 427

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVHRMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNA AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAEGA---LELFLGNAATAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIAKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_001474037.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sediminis
HAW-EB3]
sp|A8FVN6.1|AROA_SHESH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV36909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sediminis
HAW-EB3]
Length = 426

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 222/440 (50%), Positives = 296/440 (67%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+PI ++ GT+ +PGSKS+SNR LLLA L++GTT + NLL+S+D+ YML +L+ LG
Sbjct: 2 KQLRLEPINKVQGTINIPGSKSISNRALLLATLAKGTTTLNLLDSDDIRYMLASLKLQ 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + G G E A+ LFLGNAG AMR L AA+T G+ + L
Sbjct: 62 VNYRLSNDNTVCELEGIGAPLNSEQAQ---TLFLGNAGTAMRPLCAALTL--GHGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ +N G L G+V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGANVTYLNKNDGFPPLTINATG-LDAGEVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA GDV I+I +L+S PY+++T+ LM +FGV+ + S++RF IK GQ Y S

Sbjct: 176 ALLMVAPLATGDVNIKIKGELVSKPYIDITIALMAQFGVQVNVH-SYERFEIKAGQGYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +

Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGGEVKVTGVGRMSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPMPREPFGGRKHLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G LKA+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+

Sbjct: 295 IISRG-----STLKAVDLDMNHIPDAAMTIATAALFATGTTHIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA V+EG DY ITPP K + IDTY+DHRMAM FS+ A A+ +TI D

Sbjct: 347 AAMATELRKVGAIVDEGHDIYISITPPTKPTADIDTYNDHRMAMCFMMLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P CT KTFPDYF+ + +

Sbjct: 407 PDCTSKTFFPDYFNQFAALAQ 426

>ref|YP_004068549.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Pseudoalteromonas sp. SM9913]
gb|ADT68398.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Pseudoalteromonas sp. SM9913]
Length = 425

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 230/442 (52%), Positives = 305/442 (69%), Gaps = 20/442 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI +++G+V LKSKSLNRILLALLAALS GTTVV+NL+L+S+D+ +MLGAL+ LG

Sbjct: 2 EQLFLAPISQVNGSVTLPGSKSLNRILLALLAALSNGTTVVNLLDSDDIRHMLGALKHLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
++V + A V G G F P E LFLGNAG A R LTA ++A G Y

Sbjct: 62 VNVTLNTERTVATVEGVSGVFNTPT-----PLFLGNAGTAYRPLTAVLSAAGE--YE 113

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G PRM ERPIG LV L+ LG +V D PP+++ G G + GG+V++ GSISSQ+

Sbjct: 114 LIGEPREMERPIGHLVDALQALGGNVSYLKNKDYPPLKIIG-GQIAGGEVEIDGSISSQF 172

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPL GD I+I L+S PY+++TL +M RFGV EH D++ F++KG Q+Y

Sbjct: 173 LTALLMAAPLFKGDTHIKIKGTLVSKPYIDITLDMARFGVTVEH-DNYTTFFVKGAQQY 231

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
++ + VEGDASSASYF+A AAI GG + ++G G S+QGD+ FA V+E +GAK+ W +

Sbjct: 232 QAVRIMVEGDASSASYFIAAAIAGGEIEIKGVGAKSVQGDIGFANVMEQVGAKIDWYD 291

Query: 303 TSVTVTGPMPREPFGGRKHLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V + L ID++ N +PD AMTLA VALFA GPTAIR++ +WRVKET+

Sbjct: 292 ERLVVR-----KGLNGIDIDANAIPDAAMTLATVALFAKGPTAIRNIYNWRVKETD 343

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
R+ A+ TEL K+GA V EG D+ ITPP+ N A+DTYDDHR+AM F++ A P+TI

Sbjct: 344 RLHAMATELKKVGADVVEGHDFIEITPPKHFNNVAVDITYDDHRIAMCFAMVAVGGKPITI 403

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP CT KTFP +F+VL++ K

Sbjct: 404 NDPACTYKTFPTFFNVLASVSK 425

>ref|ZP_06353542.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citrobacter youngae
ATCC 29220]
gb|EFE08576.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citrobacter youngae
ATCC 29220]
Length = 427

Score = 429 bits (1102), Expect = e-118, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 298/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGKSLSNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESILTQPIARVDGTINLPGSKSVSNRALLAALANGTTVLNLLDSDVRHMLNALNALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R ++G GG E A V+LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 IRYTTLADTRCEIIGNGGALHAEGA--VELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA+++ + PP+R+ G G GG+V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGANIEYLEQENYPPRLRLG--GFTGGQVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I +L+S PY+++TL LM+ FGV+ E+ + + RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTTIAIKGELVSKPYIDITLNLMTFGVEIENQN-YQRFVVQGGQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234 PGAYLVEGDASSASYFLAAGAIKGGTVKVTGIGRYSMQGDIRFADVLEKMGATITWGDFF 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L A+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----HGELNAVMDMNHIPDAAMTIATAALFAKGTTTLRNINWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITTP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFRITPPAKLQFADIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|ZP_04716871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alteromonas macleodii
ATCC 27126]
Length = 427

Score = 428 bits (1101), Expect = e-118, Method: Compositional matrix adjust.
Identities = 230/438 (52%), Positives = 297/438 (67%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI ++SG V +PGSKSLSNR LLLAAL+EG T + NLL+SED+ +ML AL LG
Sbjct: 2 EQLTLDPIAKVSGEVNVPKSGKSLSNRALLAALAEGETELTNLLDSEDIEHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + VV G GG F V E ++LFLGNAG AMR L AA+ A+ N VL
Sbjct: 62 INYRLSEDKTQCVVQNGGAFNV--AEPLFLGNAGTAMRPLCAALAAS--NVDTVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L++ A+V PP+++ G L GG++ + GS+SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALREADAEVTYLKNEGFPPLQIKG-KTLNGGEMSVDSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL GDV I I +L+S PY+++TL M +FGV E+ D++ F + G KY +
Sbjct: 176 ALLMAAPLFGSDVTIRIKGELVSKPYIDITLDTMAKFGVTVEN-DNYQTFVSGDAKYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA V W +
Sbjct: 235 PGKFMVEGDASSASYFLAAGAIKGGTVRVGTGIGQNSIQGDIRFADVLEAMGATVVWNEY 294

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V +TG P LK ++++MN +PD AMT+A ALFA+GPT + ++ +WRVKET+R+
Sbjct: 295 VEITGAP-----LKGVNMDMNHIPDAAMTIATTALFAEGPTTMTNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL KLGA VEEG DY + P + L IDTY+DHR+AM FSL A ++ PVTI D
Sbjct: 347 AAMATELQKLGAKEEGHDYIKVWPTDSLKHAEIDTYNDHRIAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
PGCTRKTFFPDYF T

Sbjct: 407 PGCTRKTFPDYFTRFKTL 424

>sp|O87006.1|AROAS_HIDY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC32745.1| EPSP synthase AroA [Shigella dysenteriae]
Length = 427

Score = 428 bits (1101), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSKSVSNRALLAALAHGKTVLTNLLDSDDVHMLNLAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTSLADTRCEIIGNGGSLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ A + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGRAKITYLEQENYPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIAKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_003746355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia
solanacearum CFBP2957]
emb|CBJ43761.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia
solanacearum CFBP2957]
Length = 435

Score = 428 bits (1101), Expect = e-118, Method: Compositional matrix adjust.
Identities = 235/436 (53%), Positives = 294/436 (67%), Gaps = 14/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GTVKLPKSKS+SNR+LLLAAL+EG TVV +LL+S+D ML AL LG
Sbjct: 2 EHLDVGPLKAARGTVKLPKSKSISNRVLLAALAEGETVVRDLDSDDTRVMLAALDKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E AA VVG GG+FPV+ A LF+GNAG A+R LTAA+ GG Y L
Sbjct: 62 VRCEPLGAANAYRVVGTGGRFPVKS----DLFMGNAGTAIRPLTAALALQGG--AYTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ + +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYAGNAGFPPLAIRAAPVKIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPL--ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
ALLMA PL + G V IE+I +LIS PY+E+TL LM RFGV+ D W F + G +Y
Sbjct: 176 ALLMALPLVESAGQVTIEVIGELISKPYIEITLNLMARFGVQVVR-DGWASFTVPTGVRY 234

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTE 302

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++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V +
Sbjct: 235 RAPGEMFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAGD 294

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET+
Sbjct: 295 NWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKETD 351

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VPV
Sbjct: 352 RLTAMATELRKLGAAVEEGADYIRVTPPSHWTAPAGGIDTYDDHRMAMAFSLAAGFPVPV 411

Query: 421 TIRDPGCTRKTFFPDYF 436
I DP C KTFPDYF
Sbjct: 412 RINDPRCVAKTFFPDYF 427

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>ref|YP_002255766.1| 3-phosphoshikimate 1-carboxyvinyltransferase (epsp synthase)
protein [Ralstonia solanacearum MolK2]
emb|CAQ37568.1| 3-phosphoshikimate 1-carboxyvinyltransferase (epsp synthase)
protein [Ralstonia solanacearum MolK2]
Length = 435

Score = 428 bits (1101), Expect = e-118, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 14/436 (3%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + + P+K GTVKLPGSKS+SNR+LLLAAL+EG TVV +LL+S+D ML AL LG
Sbjct: 2 EHLDVGPLKAARGTVKLPKSKSISNRVLLLAALAEGETVVRDLDSDDTRVMLAALDKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E A VVG GG+FPV+ A LF+GNAG A+R LTAA+ GG Y L
Sbjct: 62 VRCEPLGTANAYRVVGTGGRFPVKA----DLFMGNAGTAIRPLTAALALQGG--AYTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYAGNAGFPPLAIHAAPVKIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
ALLMA PL ++G V IE++ +LIS PY+E+TL LM RFGV+ D W F + G +Y
Sbjct: 176 ALLMALPLVESVGQVTIEVVGELISKPYIEITLNLMARFGVQVAR-DGWASFTVPTGVRY 234

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V +
Sbjct: 235 RAPGEMFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAGD 294

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET+
Sbjct: 295 NWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKETD 351

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VPV
Sbjct: 352 RLTAMATELRKLGAAVEEGTDYIRVTPPSHWTAPAGGIDTYDDHRMAMAFSLAAGFPVPV 411

Query: 421 TIRDPGCTRKTFFPDYF 436
I DP C KTFPDYF
Sbjct: 412 RINDPRCVAKTFFPDYF 427

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>ref|ZP_07949892.1| EPSP synthase [Enterobacteriaceae bacterium 9_2_54FAA]
gb|EFV42326.1| EPSP synthase [Enterobacteriaceae bacterium 9_2_54FAA]
Length = 426

Score = 428 bits (1100), Expect = e-118, Method: Compositional matrix adjust.
Identities = 230/432 (53%), Positives = 293/432 (67%), Gaps = 16/432 (3%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+ + LQPI+ SG + LPGSKS+SNR LLLAAL+ GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPIEHFSGEINLPGSKSVSNRALLLAALASGTTCLHNLLSDSDVRHMLTALKQLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + R + G GG V AK ++LFLGNAG AMR L AA+ G++ +L

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Sbjct: 63 IHFQLSDNHTRCEITGNGG---VLQAKSPLELFLGNAGTAMRPLAAALCL--GDSDIILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG +++ GS+SSQ+L+

Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPLRLRG--GYIGGDIEVDGVSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM FGV E ++++ F I GGQ Y S

Sbjct: 176 ALLMMAPLAQHDTVISIKGDLVSKPYIDITLALMHTFGVNVE-NENYQTFRIAGGQGYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGAK+TW +

Sbjct: 235 PGDYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKNSVQGDIFADVLEKMGAKITWGDDF 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L ID++MN +PD AMT+A ALFAD PT IR++ +WRVKET+R+

Sbjct: 295 IECT-----RGE LHGIDMDMNHIPDAAMTIATTALFADAPTIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP L V I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 347 SAMATELRKVGAEVEEGEDYIRVVPVHLKVAEIGTYNDHRMAMCFSLIALSDTPVTILD 406

Query: 425 PGCTRKTFPDYF 436
P CT KTFPDYF

Sbjct: 407 PKCTAKTFPDYF 418

>ref|ZP_07623317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli H299]
Length = 427

Score = 428 bits (1100), Expect = e-118, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG

Sbjct: 2 ESLTLQPIARVDGTINLPKSKSVSNRALLAALAHGKTVLTNLLSDDDRHMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 VSYTLSADRTCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGE LNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ VTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIIATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFEQLA 421

>gb|AAT45240.1| 5-enol-pyruvylshikimate-phosphate synthase [Sarracenia purpurea]
Length = 265

Score = 428 bits (1100), Expect = e-118, Method: Compositional matrix adjust.

Identities = 220/265 (83%), Positives = 242/265 (91%), Gaps = 1/265 (0%)

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
LRTLGLSVE D KRA+V GCGG FFPV +++++E+ LFLGNAG AMR LTAAVTAAGGN
Sbjct: 1 LRTLGLSVEEDSVIKRAIVEGCGGVFPVGKESRDEIPLFLGNAGTAMRPLTAAVTAAGGN 60

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
++Y+LDGVPRMRERPIGDLV GLKQLGADVDCFLGT+CPPVRV G GGLPGGKVKLSGSI
Sbjct: 61 SSYILDGVPRMRERPIGDLVTGLKQLGADVDCFLGTNCPVRVIGKGLPGGKVKLSGSI 120

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQYL+ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LM+RFGV EH+DSWD+F I+G
Sbjct: 121 SSQYLTALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMKRFVGSVEHTDSWDKFLIRG 180

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLEMMGAKV 298
GQKYKSP +AYVEGDASSASYFLAGAA+TGGT+TVEGCGT+SLQGDVKFAEVLE MGAKV
Sbjct: 181 GQKYKSPGSAYVEGDASSASYFLAGAAVTGGTITVEGCGTSSLQGDVKFAEVLEKMGAKV 240

Query: 299 TWTETSVTVTGPPREPFGRKHLKAI 323
TWTE SVTV GPPR GRKHL+AI
Sbjct: 241 TWTENSVTVRGPPRSSGRKHLRAI 265

>gb|AAA27666.1| 5-enolpyruvylshikimate 3-phosphate synthase (aroA) [Yersinia enterocolitica]
Length = 427

Score = 428 bits (1100), Expect = e-118, Method: Compositional matrix adjust.
Identities = 234/436 (53%), Positives = 297/436 (68%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLTLHPIALINGTVNLPGSKSVSNRALLAALAEAGTTQLNNLLSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GKK E + ++LFLGNAG AMR L AA+ G VL
Sbjct: 63 VKYRLSADRTRCEVDGLGGKLVAE---QPLELFLGNAGTAMRPLAALCL--GKNDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + R GG GKK+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYL---EQENYRRCIAGGFRGGKLTVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D EI+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y+S
Sbjct: 175 ALLMTAPLAEQDTEIQIGELVSKPYIDITLHLMKAFGVDVVH-ENYQIFHIKGGQTYRS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD KFA+VLE MGAK++W +
Sbjct: 234 PGIIYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKQSVQGDTKFADVLEKMGAKISWGDDY 293

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+
Sbjct: 294 IECS-----RGELQGIDMDMNHIPDAAMTIAT'TALFADGPTVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP +L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 SAMATELRKVGAEVEEGQDYIRVPPAQLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_002411854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli UMN026]
ref|ZP_06648207.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli FVEC1412]
ref|ZP_07119723.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS 198-1]
ref|ZP_07516778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli TA143]

sp|B7NAQ7.1|AROA_ECOLU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAR12310.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
UMN026]
gb|EFF01824.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Escherichia coli FVEC1412]
gb|EFJ70826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
198-1]
Length = 427

Score = 427 bits (1099), Expect = e-117, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVHMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSDADRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_002260329.1| 3-phosphoshikimate 1-carboxyvinyltransferase (epsp synthase)
protein [Ralstonia solanacearum IPO1609]
emb|CAQ62266.1| 3-phosphoshikimate 1-carboxyvinyltransferase (epsp synthase)
protein [Ralstonia solanacearum IPO1609]
Length = 435

Score = 427 bits (1099), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 14/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GTVKLPGSKS+SNR+LLLAAL+EG TVV +LL+S+D ML AL LG
Sbjct: 2 EHLDVGPLKAARGTVKLPGSKSISNRVLLLAALAEGETTVVRDLLDSDTRVMLAALDKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E A VVG GG+FPV+ A LF+GNAG A+R LTAA+ GG Y L
Sbjct: 62 VRCEPLGTANAYRVVGTGGRFPVKSAAA---DLFMGNAGTAIRPLTAALALQGG--AYTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYAGNAGFPPLAIHAAPVKIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPL--ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
ALLMA PL ++G V IE++ +LIS PY+E+TL LM RFGV+ D W F + G +Y
Sbjct: 176 ALLMALPLVESVGQVTIEVVGELISKPYIEITLNLMARFGVQVAR--DGWASFAVPTGVRY 234

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V +
Sbjct: 235 RAPGEMFVEGDASSASYFLAAGALGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAGD 294

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET+
Sbjct: 295 NWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKETD 351

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VPV
Sbjct: 352 RLAMATELRLKLGAAVEEGIDYIRVTPPSHWTAPAGGIDTYDDHRMAMAFSLAAGFPVPV 411

Query: 421 TIRDPGCTRKTFPDYF 436
I DP C KTFPDYF
Sbjct: 412 RINDPRCVAKTFPDYF 427

>gb|ADP12127.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia sp. Ejp617]
Length = 428

Score = 427 bits (1099), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI + GTV LKPGSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPIALVDGTVNLPKSGSKSVSNRALLAALAKGTTRLTNLLSDDVHMLAALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R + G GG E A E LFLGNAG AMR L AA+ G+ +L
Sbjct: 63 VQHTLSADTRCEITGQGGALQAEGALE---LFLGNAGTAMRPLAALCI--GSNDIILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV+ D PP+R+ G G GG+V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGADVEYLEQDDYPLRIKG--GFNGGEVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I I L+S PY+++TL+LM FGV +++D + F I+G Q+Y++
Sbjct: 176 ALLMAAPLAQNDSQIIKGDVSKPYIDITLKLMTATFGVVVDNND-YHTFRIRGQQYQA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA V W +
Sbjct: 235 TSEYLVEGDASSASYFLAAAIRGGTVRVVTGIGRNSMQGDIRFADVLEKMGASVEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R LKAID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295 IACT-----RGELKAIDLDMNHIPDAAMTIATLALFAQGTVMRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITTP K+ I TY+DHRMAM FSL A + PVTI D
Sbjct: 347 AAMATELRKVGAEEVEEGHDYIRITPPAKIACAQIGTYNDHRMAMCFSLVALSSTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFPDYFEQLA 422

>gb|EGB34276.1| PSP synthase [Escherichia coli E1520]
Length = 427

Score = 427 bits (1098), Expect = e-117, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPKSGSKSVSNRALLAALAHGKTVLTNLLSDDVHMLNALTEL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLADTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY IT PEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITSPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_003519646.1| AroA [Pantoea ananatis LMG 20103]
gb|ADD76518.1| AroA [Pantoea ananatis LMG 20103]
Length = 434

Score = 427 bits (1098), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/441 (52%), Positives = 298/441 (67%), Gaps = 16/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI ++GTV LKSGKS+SNR LLLAAL+ G T + NLL+S+DV +ML AL+ LG
Sbjct: 9 DSLTLQPIARVNGTVNLPKSGKSVSNRALLAALANGKTRLTNLLSDSDVKHMLNALKALG 68

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G GG P++ A + V+LFLGNAG AMR L AA+ G VL
Sbjct: 69 VDFTLSSDRTVCDVTGKGG--PLQ-ASQPVELFLGNAGTAMRPLAALCL--GEQDVVLT 123

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D TD PPVR+ +GG GG+V + GS+SSQ+L+
Sbjct: 124 GEPRMKERPIGHLVDALRQGAQIDYLENTDYPPVRL--LGGFTGGEVTVDGSVSSQFLT 181

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM FGV+ E+ + F I+G Q+Y+S
Sbjct: 182 ALLMTAPLAQEDTRITIKGDLVSKPYIDITLHLMRCFGVEVENQ-HYQHFLIQGKQYQS 240

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 241 PGEYLVEGDASSASYFLAAAAIKGGTVRVVTGIGRHSVQGDIFADVLEKMGATIEWGDDF 300

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L+AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R+
Sbjct: 301 IACTA-----GKLQAIDMDMNHIPDAAMTIATAALFAEGTTQLRNIYNWRVKETDRL 352

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ +TPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 353 TAMATELRKVGAEVEEGHDFIRVTPPAKLMHADIGTYNDHRMAMCFSLVALSDTPVTILD 412

Query: 425 PGCTRKTFFPDYFDVLSFVKN 445
PGCT KTFPDYF+ L+ N
Sbjct: 413 PGCTAKTFFPDYFEQLAKISHN 433

>ref|YP_001744263.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
SMS-3-5]
ref|YP_002408203.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
IAI39]
sp|B7NM67.1|AROAE07I RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
sp|B1LJV6.1|ARO_A_ECOSM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACB19813.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
SMS-3-5]
emb|CAR18367.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
IAI39]
Length = 427

Score = 427 bits (1098), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV YML AL+ LG
Sbjct: 2 ESLLTLPQIARVDGTINLPKSKSVSNRALLLAALAHGKTVLTNLLDSDDVRYMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRTCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGNNTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLFKFAEIATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>gb|ACA49855.1| enoylpyrovyl-shikimate 3 phosphate synthase [synthetic construct]
Length = 427

Score = 427 bits (1098), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPKSK++SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLPQIAHVDGTINLPKSKTVSNRALLLAALAHGKTVLTNLLDSDDVRYMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRTCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AI ++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIHMDMNHIPDAAMTIATAALFAKGTTRLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_06014214.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
subsp. rhinoscleromatis ATCC 13884]
gb|EEW42735.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae
subsp. rhinoscleromatis ATCC 13884]
Length = 427

Score = 427 bits (1098), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E + LQPI + GTV LKPGSKS+SNR LLLAAL+ GTTV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVEGTVNLPKSGSKSVSNRALLLAALARGTTVLTNLLSDDDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GG P+ A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VQYTLASADRTRCEVTGNGG--PLRSAAA-LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLHVDALRQGGQIDYLEQENYPPLRLRG--GFQGGNVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ F V+ ++ S+ RF ++G Q+Y+S
Sbjct: 175 ALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTF SVEVDNQ--SYQRFVVRGKQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA VTW +
Sbjct: 234 PGDYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIFADVLEKMGATVTWGDDF 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T LKA+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----HGELKAVDMDMNHIPDAAMTIATAALFAQGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGEDYIRITPPAKLKYAEIGTYNDHRMAMCFSLVALSDPTVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_07390463.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS183]
ref|ZP_07582600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
BA175]
gb|EFM17060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS183]
gb|EFN43627.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
BA175]
Length = 426

Score = 427 bits (1097), Expect = e-117, Method: Compositional matrix adjust.
Identities = 221/438 (50%), Positives = 292/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG

Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLDSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG E A+E LFLGNAG AMR L AA+T G + L

Sbjct: 62 VNYRLSQNNVTCELDGLGGVISSESAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLM 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ +N G L GG V+++G +SSQ+L+

Sbjct: 117 GEPRMEERPIGDLVDALRQLGANVVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D + RF I GQ+Y S

Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVTVINHD-YARFEIVAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +

Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+

Sbjct: 295 IIARG-----SQTAVDLDMNHIPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY IITPP +N IDTY+DHRMAM FS+ A A+ +TI D

Sbjct: 347 AAMATELRKVGAEVEEGNDYIIITPPVVINTAEIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYF ++

Sbjct: 407 PDCTSKTFFPDYFKQFASL 424

>ref|YP_003711824.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Xenorhabdus
nematophila ATCC 19061]
sp|Q8RLV9.1|AROAXENNA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAL79610.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xenorhabdus
nematophila]
emb|CBJ89626.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Xenorhabdus
nematophila ATCC 19061]
Length = 428

Score = 427 bits (1097), Expect = e-117, Method: Compositional matrix adjust.
Identities = 228/435 (52%), Positives = 285/435 (65%), Gaps = 16/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI I+GT+ LPGSKS+SNR LLLAA ++GTT + NLL+S+D+ YML AL L

Sbjct: 2 QSLTLQPISRINGTINLPGSKSVSNRALLLAFAKGTTRLTNLLDSDDIRYMLNALTALD 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V G G K ++LFLGNAG AMR L AA+ G+ VL

Sbjct: 62 IPYRLSADRTVCEVEGRSGNIT---GKSGLELFLGNAGTAMRPLAALCL--GDNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+ + G G G GKV + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKIDYIEQENYPPHLIKG--GFSGGKVTVDGSSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA+ + EI I L+S PY+++TL LM+ FGV E+ + FYI+G Q+Y S

Sbjct: 175 ALLMAAPLAVNNTEIHIQGDVSKPYIDITLALMKSFGVTVENH-QYQVFYIRGRQQYLS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G SLQGD KFA VLE MGA + W +

Sbjct: 234 PGQYLVEGDASSASYFLAAAAIKGIVRVGTGIGKNSLQGDTKFANVLEQMGTATIRWGDDF 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L ID++MN +PD AMT+A ALFA G T IR++ +WRVKET+R+

Sbjct: 294 VECE-----RGTLTGIDMDMNAIPDAAMTIATTALFAQGETVIRNIYNWVRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY + PPEK+ I+TY+DHR+AM FSL A + PVTI D

Sbjct: 346 NAMATELRKVGAEVEEGLDYIRVIPPEKIQHAEIETYNDHRVAMCFSLVALSNTPTVITLD 405

Query: 425 PGCTRKTFPDYFDVL 439

PGCT KTFPDYF+ L

Sbjct: 406 PGCTAKTFPDYFNQL 420

>ref|ZP_02195975.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sp. AND4]
gb|EDP59028.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio sp. AND4]
Length = 426

Score = 427 bits (1097), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/439 (53%), Positives = 296/439 (67%), Gaps = 17/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + LQPI +I G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG

Sbjct: 2 ESLTLQPIKIQGEVNLPGSKSVSNRALLAALAKGTTRLTNLLDSDDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+ VV G G F V E V+LFLGNAG AMR L AA+ G YVL

Sbjct: 62 VQYHLSGDKTECVVEGLGRPFVS---SESVLFLGNAGTAMRPLAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV LK GADV + PP+++ G G L G V + GSISSQ+L+

Sbjct: 117 GEPRMKERPIGHLVAALKAAGADVITYLENENYPPLKIVGTG-LKSGSVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

A LM+APLA G++ I I +L+S PY+++TL +M++FGV ++D + F I GQ+Y +

Sbjct: 176 AFLMSAPLAEGELRINIEGELVSKPYIDITLHIMKQFGVDVINND-YQEFVIPAGQQYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TET 303

P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +

Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIRFADALEKMGAEIEWGNDY 294

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363

++ G LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R

Sbjct: 295 VISRVG-----QLKGIDMDYNHIDPAAMTIATATLFAEGTTAIRNVYNWRVKETDR 345

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423

+ A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI

Sbjct: 346 LSAMATELRKVGAEVEEGEDYIIVKVPQLEHAAIDTYDDHRMAMCFSLVALSDTPVTIN 405

Query: 424 DPGCTRKTFPDYFDVLSTF 442

DP CT KTFPDYFD LS+

Sbjct: 406 DPKCTSKTFPDYFDKLSL 424

>ref|ZP_00946822.1| Hypothetical Protein RRSL_00205 [Ralstonia solanacearum UW551]
gb|EAP70677.1| Hypothetical Protein RRSL_00205 [Ralstonia solanacearum UW551]
Length = 435

Score = 427 bits (1097), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/436 (53%), Positives = 295/436 (67%), Gaps = 14/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + + P+K GTVKLPGSKS+SNR+LLLAAL+EG TVV +LL+S+D ML AL LG

Sbjct: 2 EPLDVGLPKAARGTVKLPKSKSISNRVLLLAALAEGETTVVRDLSDSDTRVMLAALDKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+ E A VVG GG+FPV+ A LF+GNAG A+R LTAA+ GG Y L

Sbjct: 62 VRCEPLGTANAYRVVGTGGRFPVKS----DLFMGNAGTAIRPLTAALALQGG--AYTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+L+

Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYAGNAGFPPLAIHAAPVKIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPL--ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242

ALLMA PL ++G V IE++ +LIS PY+E+TL LM RFGV+ D W F + G +Y

Sbjct: 176 ALLMALPLVESVGQVTIEVVGELISKPYIEITLNLMARFGVQVAR-DGWASFAVPTGVRY 234

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302

```

++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V +
Sbjct: 235 RAPGEMFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAGD 294

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET+
Sbjct: 295 NWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKETD 351

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VPV
Sbjct: 352 RLTAMATELRKLGAAVEEGIDYIRVTPPSHWTAPAGGIDTYDDHRMAMAFSLAAFGPVPV 411

Query: 421 TIRDPGCTRKTFPDYF 436
I DP C KTFPDYF
Sbjct: 412 RINDPRCVAKTFPDYF 427

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>ref|YP_003498727.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. CB9615]
gb|ACI85764.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli]
gb|ADD55743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. CB9615]
gb|EFX27375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. USDA 5905]
Length = 427

```

Score = 426 bits (1096), Expect = e-117, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLSDDVHRMLNALTAL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GELRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLTNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

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>ref|ZP_06652861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B354]
gb|EFF12237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
B354]
Length = 427

```

Score = 426 bits (1096), Expect = e-117, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 293/436 (67%), Gaps = 16/436 (3%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

```

Sbjct: 2 E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVRHMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G VL

Sbjct: 62 VSYTLSADRTCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GCNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G GG V + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--SFTGGNVDDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S

Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +

Sbjct: 234 PGTYLVEGDASSASYFLAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+

Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFQLA 421

>ref|ZP_04614864.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia ruckeri ATCC
29473]
gb|EEQ00809.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia ruckeri ATCC
29473]
Length = 438

Score = 426 bits (1095), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LPGSKS+SNR LLLAAL+EGTT + NLL+S+D+ +ML AL++LG

Sbjct: 13 ESLTLQPIALINGTVNLPGSKSVSNRALLLAALAEGTTRLNLLDSDDIRHMLNALKSLG 72

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G GG A ++LFLGNAG AMR L AA+ GN+ VL

Sbjct: 73 VNYRLSADRTQCDVDGLGGPLV---ADKTLELFLGNAGTAMRPLAALCL--GNSDIVLT 127

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + GS+SSQ+L+

Sbjct: 128 GEERMKERPIGHLVDALRQGAQIDYLEQENYPPLRIRG--GFRGGELTVDGSVSSQFLT 185

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D I I L+S PY+++TL LM FGV+ H + + F+I+GGQ Y S

Sbjct: 186 ALLMAAPLATQDTHIRIQGDLVSRPYIDITLHLMRSFGVEVTHQN-YQVFHIQGGQTYHS 244

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGA + W +

Sbjct: 245 PGEYLVEGDASSASYFLAAAIRGGTVRVGTIGKKSQGDTKFADVLEKMGAIHWGDDY 304

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+

Sbjct: 305 IECS-----RGELRGIDMDMNHIPDAAMTIATAALFAKGTIIRNIYNWRVKETDRL 356

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 357 SAMATELRKVGAEVEEGQDYIRVPPAHLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 416

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 417 PKCTAKTFPDYFEQLA 432

```
>ref|YP_339941.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Pseudoalteromonas haloplanktis
TAC125]
sp|Q3ILA2.1|ARO_A_PSEHT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAI86498.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Pseudoalteromonas haloplanktis
TAC125]
Length = 425
```

Score = 426 bits (1095), Expect = e-117, Method: Compositional matrix adjust.
Identities = 230/439 (52%), Positives = 306/439 (69%), Gaps = 20/439 (4%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L+PI ++G+V LKSKSKLSNRILLALLAAL+ GTTVV+NLL+S+D+ +MLGAL+ LG
Sbjct: 2 EQLRLEPISRVNGSVTLKPKSKLSNRILLALLAALANGTTVVENLLDSDDIRHMLGALQLL 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
++V ++ A V G G G F P E LFLGNAG A R LTA + A G Y
Sbjct: 62 VNVSLNQERTVATVQGVGGVFKTPRE-----PLFLGNAGTAYRPLTAVLAAVAGE--YE 113

Query: 123 LDGVPVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G PRM ERPIG LV L+ LG D+ D PP+++ G G + GG+V + GSISSQ+
Sbjct: 114 LIGEPVMEERPIGHLVDALQALGGDITYSKNKDYPPLKIIG-GQINGGEVAIDGSISSQF 172

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMAAPL GD +I I L+S PY+++TL +M RFG++ EHS+ + F +KGGQ+Y
Sbjct: 173 LTALLMAAPLFGNDTKITIKGTLVSKPYIDITLDVMARFGIEVEHSN-YATFTVKGQQY 231

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTE 302
+S + VEGDASSASYF+A AAI GG + ++G G S+QGD+ FA+V+E +GAK+ W +
Sbjct: 232 QSLERINVEGDASSASYFVAAAIAAGIEIEIKGVGAKSVQGDIGFAKVMEQVAKIDWYD 291

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V + L +D++ N +PD AMTLA VALFA GPTAIR++ +WRVKET+
Sbjct: 292 ERLVVR-----KGQLNGVDIDANAIPDAAMTLATVALFAKGPTAIRNIYNWRVKETD 343

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTI 422
R+ A+ TEL K+GA V EG D+ ITPP+ N AIDTYDDHR+AM F++ A P+TI
Sbjct: 344 RLHAMATELRKVGAEVVEGHDFIEITPPKHFNDVAIDTYDDHRIAMCFAMVAVGGKPITI 403

Query: 423 RDPGCTRKTFPDYFDVLST 441
DP CT KTFP +F+VL++
Sbjct: 404 NDPKCTYKTFPTFFNVLAS 422
```

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>ref|ZP_03560897.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Glaciecola sp.
HTCC2999]
Length = 426
```

Score = 426 bits (1095), Expect = e-117, Method: Compositional matrix adjust.
Identities = 228/432 (52%), Positives = 295/432 (68%), Gaps = 15/432 (3%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ LQPI +SGTV +PKSKLSNR LLLAAL++GTT V NLL+S+D+ +ML AL LG
Sbjct: 2 EQLTLQPIASVSGTVNVPKSKLSNRALLAALAKGTTTNTNLLDSDDIRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + VV G G F + E +LFLGNAG AMR L + + N VL
Sbjct: 62 VSYTLSENNTVCVVEGLGDVFTTQ---PESEFLGNAGTAMRPLCGVLATSPINT--VLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIGLV L + AD+ P + + G L GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLDVAALADVADIRYLDEVGYPALDIRG-QRLTGGHIEVDGSVSSQFLT 175
```

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+LMAAPL D EI I L+SIPY+++TL +M++FGV H + + F++KG Q Y +
Sbjct: 176 AILMAAPLFTSDSEIHQGDLSIPYIDITLDIMQKFGVSVTH-NQYKVFHVKGNGSYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
P+ VEGDASSASYFLA AI GGT V G G+ S+QGD++FAEVLE MGAKV++ S
Sbjct: 235 PETYMVEGDASSASYFLAAGAIKGGTVEVTGVGSASVQGDIFAEVLEAMGAKVSYQPN 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+T+TG P L A+D++MN +PD AMT+A ALFA G TAIR++ +WRVKET+R+
Sbjct: 295 ITITGAP-----LTAVDMDMNHIPDAAMTIATTALFAKGTTAIRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA+V EG D+ +TPPE L + IDTYDDHR+AM FSL A + VTI D
Sbjct: 347 HAMATELRKVGATVVEGDDFIEVTPPETLLHSDIDTYDDHRVAMCFSLVALSNTAVTIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PKCTAKTFFPDYF 418

>ref|YP_738101.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. MR-7]
sp|Q0HV11.1|AROA_SHESR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI43044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. MR-7]
Length = 426

Score = 426 bits (1095), Expect = e-117, Method: Compositional matrix adjust.
Identities = 220/432 (50%), Positives = 289/432 (66%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAKGTTTLTNLLDSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + G GG + A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VGYRLSQNNTVCELTGLGGAISADTAQ---TLFLGNAGTAMRPLCAALTL--GRGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV LKQLGA++ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALKQLGANIMYLKNEGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV+ + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVQVINHD-YARFEILAGQQYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGAP-----LTAVDMDMNHIPDAAMTIATAALFAKGTTTIRNIYNWRKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY ITPP LN IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGALVEEGHDYIQTTPPAVLNTAEIDTYNDHRMAMCFSMMAFADCGITIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PDCTSKTFFPDYF 418

>ref|YP_003530703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia amylovora
CFBP1430]
ref|YP_003538424.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia amylovora
ATCC 49946]
emb|CBJ46013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia amylovora
ATCC 49946]
emb|CBA20295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia amylovora

CFBP1430]
Length = 428

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
+ + LQPI + GTV LKSGKSLSNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPIALVDGTVNLPKSGKSVSNRALLAALAKGTTTLNLLSDDDRHMLDALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R + G GG A ++LFLGNAG AMR L AA+ G + +L
Sbjct: 63 VQYSLSADRTRCEITGQGGAL---QADRSLELFLGNAGTAMRPLAALCIGGND--IILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV D PP+RV G G GG++ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGADVLYEQVDYPPLRVKG--GFSGGEITVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I I L+S PY+++TL+LM FGV ++++ + F I+G Q+Y++
Sbjct: 176 ALLMAAPLAKNDSQIIIKGDLVSKPYIDITLKLMAAFGVVVDNNN-YHTFRIRGQQYQA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA V W +
Sbjct: 235 TSEYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGASVEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R LKA+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295 IACT-----RGELKAVDLDNMHNPDAAMTIATTALFAQGTVMRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPP K+ I TY+DHRMAM FSL A + PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGYDFIRITPPAKIACAQIATYNDHRMAMCFSLVALSSTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF L+
Sbjct: 407 PNCTAKTFPDYFTQLA 422

>ref|YP_001366482.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS185]
sp|A6WNN0.1|AROASHEB8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS08419.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS185]
Length = 426

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 220/438 (50%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLNLLSDDIRHMLASLKLQ 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG E A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNTECELDGLGGVISSESAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGLV L+QLGA+V PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGLVDALRQLGANVVYLKNDGFPPLTINATG-LSGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFVTVINHD-YARFEIVAGQQYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVRSLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARG-----SQLTAVDLDNMHIDPAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPVVINTAEIDTYNDHRMAMCFSMLAFADCGITIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFPDYFKQFASL 424

>ref|ZP_06715241.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Edwardsiella tarda
ATCC 23685]
gb|EFE22428.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Edwardsiella tarda
ATCC 23685]
Length = 429

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 219/430 (50%), Positives = 285/430 (66%), Gaps = 16/430 (3%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+ L PI+ +G + LPGSKS+SNR LLLAA + G T + NLL+S+DV YML AL+ LG+
Sbjct: 5 LTLNPIRRFAGEINLPGSKSVSNRALLAAQARGVTRLHNLLDSDVRYMLDALKALGVR 64

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ R V G G PV + LFLGNAG AMR L AA++ G +L G
Sbjct: 65 YQLSDCRTRCEVQGVGDALPVAGV---LSLFLGNAGTAMRPLAAALSL--GRREVILTGE 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM+ERPI LV L+Q GA +D PP+R+ G G GG++ + GS+SSQ+L+AL
Sbjct: 120 PRMKERPIAHLVTALRQGGQIDYLEAEGYPPLRLRG--GFVGGQIAVDGSVSSQFLTAL 177

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAPLA D I I+ L+S PY+++TL +M FGV E+ ++ RF ++G Q Y++
Sbjct: 178 LMAAPLAEQDVTITILGDLVSKPYIDITLMMRAFGVTVENQ-AYQRFVVRGRQSYQAAG 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYFLAGAAI GGTV V G G S+QGD+ FA+VLE MGA + W + +
Sbjct: 237 DYLVGEDASSASYFLAGAAIAGGTVRVTGIGRHSMQGDIHFADVLERMGHIEWGDDYIA 296

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ R L ID++MN +PD AMT+A ALFA+GPT +R++A+WRVKET+R+ A
Sbjct: 297 CS-----RDLRHGIDMDMNTIPDAAMTIATTALFAEGPTTLRNIANWRVKETDRLAA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
+ EL K+GA VEEG D+ I PP +L I TY+DHRMAM FSL A ++ PVTI DPG
Sbjct: 349 MACELRKVGAEVEEGADFLRIEPPAQIQAQIATYNDHRMAMCFSLVALSDTPVTICDPG 408

Query: 427 CTRKTFPDYF 436
CT KTFPDYF
Sbjct: 409 CTAKTFPDYF 418

>ref|ZP_06177435.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio harveyi 1DA3]
gb|EEZ86188.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio harveyi 1DA3]
Length = 426

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/435 (53%), Positives = 294/435 (67%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
E + LQPI +I G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIKIHGEVNLPGSKSVSNRALLAALAKGTTRLTNLLDSDDIRHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + VV G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VQYQLSEDKTECVVEGLGRPFVS---SEPVELFLGNAGTAMRPLAAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM+ERPIG LV L+ GADV + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALQAAGADVITYLENENYPPLKIVGTG-LKSGSVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G++ I I +L+S PY+++TL +M++FGV+ ++D + F I GQ Y +
Sbjct: 176 AFLMSAPLAEGEIRINIEGELVSKPYIDITLHIMKQFGVEVVNND-YQEFVIPAGQHYYA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGQLKGIDMDYNHIDPAAMTIATTALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKVPQLTHAAIDTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKL 421

>ref|YP_296777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia eutropha
JMP134]
sp|Q46Y50.1|AROA_RALEJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ61933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia eutropha
JMP134]
Length = 434

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 230/440 (52%), Positives = 294/440 (66%), Gaps = 17/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P+ +GTV+LPGSKS+SNR+LLLAAL+ G T V +LL+S+D ML AL+TLG
Sbjct: 2 EHLTLGLPLTRAAGTVRLPGSKSISNRVLLLAALAGGETRVRDLSDDTVRMLQALKTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + +V G GG FPV+ A +LF+GNAG A+R LTAA+ GG+ Y L
Sbjct: 62 VAWR--QEGSDYIVTSGSGGNFPVKAA---ELFMGNAGTAIRPLTAALALQGGD--YKLS 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GAD+ PP+ + +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQVGADIGYLANEGFPPLHIRPAQIRIDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM P+A G +EIE++ +LIS PY+E+TL L+ RFG+ E W+RF + G
Sbjct: 174 ALLMTLPMAQAANGKIEIEVVGELISKPYIEITLNLARFGINVERQ-GWERFIVPAGAV 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWT 301
Y+SP YVEGDASSASYFLA AI GG V VEG G +S+QGDV+FAE L MGA V
Sbjct: 233 YRSPGEIYVEGDASSASYFLAAGAIGGPPVRVEGVGMSSIQGDVRFAEALNRMGANVMAG 292

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V G R+ GR H I+++ N +PD AMTLAV ALFA G T + ++ASWRVKET
Sbjct: 293 DNWIEVRGTERDD-GR LH--GIELDCNHIPDAAMTLAVAALFAGGTTTLTNIASWRVKET 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL KLGA+VEEG DY +TPP + A I TYDDHRMAM FSLAA +P
Sbjct: 350 DRISAMATELRKLGATVEEGADYLVKTPPAQWQTPADGIGTYDDHRMAMCFSLAAFGLP 409

Query: 420 VTIRDPGCTRKTFFPDYFDVL 439
V I DPGC KTFPDYF V
Sbjct: 410 VRINDPGCVAKTFFPDYFAVF 429

>ref|XP_003083034.1| 5-enolpyruvylshikimate-3-phosphate (ISS) [Ostreococcus tauri]
emb|CAL56989.1| 5-enolpyruvylshikimate-3-phosphate (ISS) [Ostreococcus tauri]

Length = 316

Score = 426 bits (1094), Expect = e-117, Method: Compositional matrix adjust.
Identities = 216/323 (66%), Positives = 243/323 (75%), Gaps = 14/323 (4%)

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
MRERPI DLV GL QLG +C +GT CPPV++ GLPGG+V+LSGS+SSQYL+ALLM
Sbjct: 1 MRERPIADLVLDGLVQLGVKAECTMTGTGCPPVKIEA-DGLPGGRVELSGSVSSQYLTALLM 59

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAPL G +EI I+D+LIS PYVEMT+ LMERFGVK E S F I+GGQKY SP +A
Sbjct: 60 AAPLCQGSIEIVIVDELISKPYVEMTITLMERFGVKVEKSADLQSFQIQQGQKYVSPGSA 119

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+VEGDASSASYFLAGA ITGGTVTV GCG+ S+QGD FA +E MGA + W SV T
Sbjct: 120 FVEGDASSASYFLAGATITGGTVTVIGCGSESIQGD TNFAYTMEQMGATLEWGPNSVKCT 179

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
GP + LKAIDVNMN MPD AMTLAV ALFADG T IRDVASWRVKETERM+AI
Sbjct: 180 GP-----QGPKAIDVNMNAMPDAAMTLAVAALFADGVTIRDVASWRVKETERMIAIC 233

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPVT 421
TEL KLG V EG DYC+ITPP KLN A IDTYDDHRMAMAF+LAAC +V V
Sbjct: 234 TELRKLGCDVFEGSDYCVITPPHKLNPAPKMRANVDIDTYDDHRMAMAFALAACGVDVVI 293

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVK 444
I DP CT+KTFP YFDVL + V+
Sbjct: 294 INDPTCTKKTFFPTYFDVLKSVVQ 316

>ref|YP_368399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp. 383]
sp|Q39IG1.1|AROA_BURS3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB07755.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp. 383]
Length = 434

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/442 (52%), Positives = 291/442 (65%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL TLG+ +
Sbjct: 6 LGPYSSASGTVRLPGKSSISNRVLLLAALAEGETTITNLLSDDTRVMLDALGTLGVKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVGTGRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYELNEGYPPLRIKPANISVDAPIRVRGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G + +E+ +LIS PY+++T+RLMERFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAADGKIVVEVDGELISKPYIDITIRLMERFGVTVER-DGWQRFVVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPREPFGFRKH--LKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 297 DVRG-----IGHDHGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA +EEGPDY ++TPPEKL AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVGAIIIEGPDYLVVTPPEKLTNAAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>dbj|BAE20403.1| 5-enolpyruvylshikimate-3-phosphate synthase [Lactuca sativa]
Length = 231

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 201/231 (87%), Positives = 217/231 (93%)

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
LSGSISSQYL+ALLMA+PLALGDVEIEIIDKLISIPYVEMTL+LMERFGV EH+DSWDR
Sbjct: 1 LSGSISSQYLTALLMASPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSEHTDSWDR 60

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLEM 293
F+++GGQKYKSP NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL
Sbjct: 61 FFVRGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLGQ 120

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDV 353
MGA+VTWTE SVTV GPPR P GRKHL+A+DVNMNMPDVAMTLAVVAL+ADGPT IRDV
Sbjct: 121 MGAEVTWTENSVTVKGPPRNPGRKHLRAVDVNMNMPDVAMTLAVVALYADGPTTIRDV 180

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDH 404
ASWRVKETERM+AI TEL KLGA+VEEG DY+ITPPEKLNVTADITYDDH
Sbjct: 181 ASWRVKETERMIAICTELRKLGATVEEGADYCVITPPEKLNVAADITYDDH 231

>ref|YP_001050438.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS155]
sp|A3D4A6.1|AROA_SHEB5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABN61569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS155]
Length = 426

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 220/438 (50%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTTLTNLLSDDIRHMLASLKLQ 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG E A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNNTVCELDGLGGVISSESAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGANVVYLKNDGFPPLTINATG-LSGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVTVINHD-YARFEIVAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGKEGVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARG-----SQLTAVDLDMNHIPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEEVEGNDYIKITPPAVINTAEIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFPDYFKQFASL 424

>gb|EGC94707.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia

fergusonii ECD227]
Length = 425

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI + GT+ LPSKSK+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL+ LG
Sbjct: 2 ESLTLHPRIARVDGTINLPKSGKSVSNRALLAALAHGKTVLTNLLSDDDRHLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYSLSTDRTRCEIIGNGGPLHAESA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAGITYLEQENYPPRLRQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEVENQ-RYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD+ FA+VLE MGA ++W +
Sbjct: 234 PGSYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDHIFADVLEKMGATISWGDDY 293

Query: 305 VTVTGPMPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L ID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNGIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITP EKL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPLEKLKFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_02378918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ubonensis Bu]
Length = 434

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 233/444 (52%), Positives = 290/444 (65%), Gaps = 20/444 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGTV+LPSKSK+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EYLDLGPYSSASGTVRLPSKSKSISNRVLLLAALAEGETTITNLLSDDDRVMALDALGKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VRLARD--GDTCVVAGTRGAFARTATA---DLFLGNAGTAVRPLTAALAVNGGD--YRVH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ + + G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAQIDYEQNEGFPPLRIKPASIKVDAPIVVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G + +E+ +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAPDGRIVVEVDGELISKPYIEITIKLMARFGVSVER-DGWQRFVVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
YKSP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YKSPGRIMVEGDASSASYFLAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPMPREPFRGKH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L+AID++ N +PD AMT+AV ALFADGP+ +R++ASWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGKLEAIDMDFNLPDAAMTIAVAALFADGPSTLRNIASWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEV 418

ET+R+ A+ TEL K+GA+VEEGPDY ++TPPEKL AIDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAMATELRKVGATVEEGPDYLVVTPPEKLTPNAAIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTF 442
PV I DP C KTFPDYFD +
Sbjct: 408 PVRINDPKCVGKTFPDYFDRFTAL 431

>emb|CAY74833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia pyrifoliae
DSM 12163]
Length = 434

Score = 425 bits (1093), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI + GTV LPKSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 9 DSLTLQPIALVDGTVNLPKSGKSVSNRALLAALAKGTTRLTNLLDSDDVRHMLDALQALG 68

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R + G GG E A E LFLGNAG MR L AA+ G+ +L
Sbjct: 69 VQHTLSAGRTRCEITGQGGALQAEQALE---LFLGNAGTVMRPLAALCI--GSNDIILT 123

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV+ D PP+R+ G G GG+V + GS+SSQ+L+
Sbjct: 124 GEPRMKERPIGHLVDALRQGGADVLEYEQDDYPPLRIKG--GFNGGEVTVDGSVSSQFLT 181

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I I L+S PY+++TL+LM FGV +++D + F I+G Q+Y++
Sbjct: 182 ALLMAAPLAQNDSQIIKGDVSKPYIDITLKLMAITFGVVVDNND-YHTFRIRGQQYQA 240

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA V W +
Sbjct: 241 TSEYLVVEGDASSASYFLAAAIRGGTVRVGTGIGRNSMQGDIRFADVLEKMGASVEWGDDY 300

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L+AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 301 IACT-----RGELRAIDLDMNHIPDAAMTIATTALFAQGTVMRNIYNWRVKETDRL 352

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP K+ I TY+DHRMAM FSL A + PVTI D
Sbjct: 353 AAMATELRKVGAEVEEGHDYIRITPPAKIACAQIGTYNDHRMAMCFSLVALSSTPVTILD 412

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 413 PKCTAKTFFPDYFEQLA 428

>ref|ZP_01133915.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Pseudoalteromonas tunicata D2]
gb|EAR28107.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Pseudoalteromonas tunicata D2]
Length = 425

Score = 425 bits (1092), Expect = e-117, Method: Compositional matrix adjust.
Identities = 221/437 (50%), Positives = 295/437 (67%), Gaps = 16/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E ++L+ I +++G+V LPKSKSLSNRILLALL EG T VDNLL+S+D+ ML AL LG
Sbjct: 2 ESKLLKAIKNGSVTLPGKSKSLSNRILLALLCEGVTQVDNLLSDDIQRMLEALALLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ VE ++ A+V G GKKF + E LFLGNAG A R LTA + A+ N L
Sbjct: 62 IKVELNETKTALVYGTGGKF----IQPEQALFLGNAGTAFRPLTAVLAAS--NIDTKLT 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIG LV L LGA++ D PP+++ G G+ GG+V++ GSISSQ+L+
Sbjct: 116 GEPRMNERPIGHLVDALDALGANITYLENKDYPPLKIQG-QGIEGGEVEIDGSISSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL I+I +L+S PY+++TL +M+RFGV + D++ F I+ GQ Y+S
Sbjct: 175 ALLMAAPLFTNTTTIKIGELVSKPYIDITLNVMKRFGVVVN-DNYQTFIIEKGQCYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P+ VEGDASSASYF+A AAI GG + + G G +S+QGD+ FA+V+E GAK+TW +
Sbjct: 234 PRQIMVEGDASSASYFIAAAANGGCIENGVGKSSVQGDIAFADVIEQAGAKITWFDNK 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V + L +D + N +PD AMT+A VALFA G TAIR++ +WRVKET+R+
Sbjct: 294 IVVE-----KGQLYGVDFDANAIPDAAMTMATVALFAKGKTAIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V EG D+ ITPP+ + IDTY+DHR+AM FS+ A + I D
Sbjct: 346 NAMATELRKVGAIIVEGHDFIEITPPDVIEFATIDTYNDHRIAMCFMSVAVGGHDIVIND 405

Query: 425 PGCTRKTFFPDYFDVLST 441
P CT KTFP YF+ L+T
Sbjct: 406 PKCTHKTFPTYFETLAT 422

>gb|AAP94212.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli]
Length = 427

Score = 425 bits (1092), Expect = e-117, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 293/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVHRMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG A R L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAEGA---LELFLGNAGTATRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLHVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVDDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIAKGGTVKVTGIVRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>gb|AAT45238.1| 5-enol-pyruvylshikimate-phosphate synthase [Helianthus
salicifolius]
Length = 264

Score = 424 bits (1091), Expect = e-117, Method: Compositional matrix adjust.
Identities = 221/264 (83%), Positives = 241/264 (91%), Gaps = 1/264 (0%)

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
RTLGL VE D A KRA+V GCGG FPV ++AK+E+QLFLGNAG +MR LTAAVTAAGGN+
Sbjct: 1 RTLGLRVEEDGAIKRAIVEGCGGVFPVGKEAKDEIQLFLGNAGTSMRPLTAAVTAAGGNS 60

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+Y+LDGVPRMRERPIGDLV GLKQLGADVDCFLGT+CPPVRV G GGLPGGKVKLSGSIS
Sbjct: 61 SYILDGVPRMRERPIGDLVTGLKQLGADVDCFLGTNCPVRVVGGLPGGKVKLSGSIS 120

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQYL+ALLMA+PLALGDVEIEIIDKLISIPYV+MT++LMERFGV EHSDSWDRF+IKGG
Sbjct: 121 SQYLTALLMASPLALGDVEIEIIDKLISIPYVDMTIKLMERFGVSVHSDSWDRFFIKGG 180

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLMMGAKVT 299
QKYKSP NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL MGA+VT
Sbjct: 181 QKYKSPGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLQMGA EVT 240

Query: 300 WTETSVTVTGPPREPFGRKHLKAI 323
WTE SVTV GPPR GRKHL A+
Sbjct: 241 WTENSVTVRGPPRNASGRKHLHAV 264

>ref|YP_002649277.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia pyrifoliae
Ep1/96]
emb|CAX56053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia pyrifoliae
Ep1/96]
Length = 428

Score = 424 bits (1091), Expect = e-116, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI + GTV LPGSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPIALVDGTVNLPGSKSVSNRALLAALAKGTTRLTNLLDSDVHRMLDALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R + G GG E A E LFLGNAG MR L AA+ G+ +L
Sbjct: 63 VQHTLSAGRTRCEITGQGGALQAEGALE---LFLGNAGTVMRPLAALCI--GSNDIILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GADV+ D PP+R+ G G GG+V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGADVEYLEQDDYPPLRIK--GFNGGEVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I I L+S PY+++TL+LM FGV +++D + F I+G Q+Y++
Sbjct: 176 ALLMAAPLAQNDSQIIIKGDLVSKPYIDITLKLMTFGVVVDNND-YHTFRIRGQQYQA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT+TVEGCGTSSLQGDVKFAEVLMMGAKVTWTETS 304
VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA V W +
Sbjct: 235 TSEYLVVEGDASSASYFLAAAIRGGT+TVEGCGTSSLQGDVKFAEVLMMGAKVTWTETS 294

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L+AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295 IACT-----RGELRAIDLDMNHIPDAAMTIATTALFAQGTVMRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP K+ I TY+DHRMAM FSL A + PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGHDYIRITPPAKIACAQIGTYNDHRMAMCFSLVALSSTPVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 407 PKCTAKTFPDYFEQLA 422

>emb|CBJ38069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia
solanacearum CMR15]
Length = 436

Score = 424 bits (1091), Expect = e-116, Method: Compositional matrix adjust.
Identities = 232/437 (53%), Positives = 293/437 (67%), Gaps = 15/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GTVKLPGSKS+SNR+LLAAL+EG TVV +LL+S+D ML AL TLG
Sbjct: 2 EHLDVGPLKAARGTVKLPGSKSISNRVLLAALAEGETVVRDLDSDDTRVMLAALDTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

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      + E   A   V G GG+FPV+ A   LF+GNAG A+R LTAA+   GG   Y L
Sbjct: 62 VPCEPLGTANAYRVGTGTGGRFPVKSA----DLFMGNAGTAIRPLTAALALQGGE--YTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      GVPRM ERPIGDLV GL+Q+GA +D   PP+ +   +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYTGNEGFPPLAIRAAAIRIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      ALLMA PL G+ V IE++ +LIS PY+E+TL LM RFGV+ E + W F + G
Sbjct: 176 ALLMALPLVEGNRPVTIEVVGELISKPYIEITLNLMARFGVQVERT-GWASFSVPTGVA 234

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
      Y++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 235 YRAPGEIFVEGDASSASYFLAAGALGGGPVRVEGVMSSIQGDVRFADALNRMGANVMAG 294

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
      + + V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET
Sbjct: 295 DNWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKET 351

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
      +R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VP
Sbjct: 352 DRLTAMATELRKLGA+VEEGTDYIRVTPPSHWTAAPAGGIDTYDDHRMAMAFSLAAFGPVP 411

Query: 420 VTIRDPGCTRKTFPDYF 436
      V I DP C KTFP+YF
Sbjct: 412 VRINDPRCVAKTFPEYF 428

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>ref|YP_562758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
denitrificans OS217]
sp|Q12NE1.1|AROAS_HEDO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABE55035.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
denitrificans OS217]
Length = 428

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Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 223/432 (51%), Positives = 284/432 (65%), Gaps = 15/432 (3%)

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Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      +++ L+PI I G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ YML +L LG
Sbjct: 2 KQLHLEPIACIDGIEINIPGSKSISNRALLLATLAKGTTTLTNLLSDDIRYMLASLEQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + E R V G GG A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VQFELSDDKTRCTVQGMGGAVSASTAQ---TLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM ERPIGDLV L+QLGA V PP+ +N G L GG V ++G +SSQ+L+
Sbjct: 117 GEPRMERPIGDLVDALRQLGASVTYLKNDGFPPLTINATG-LNGGDVDIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALLM APLA G V I I +L+S PY+++TL LM +FGV ++ D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGVNINIKGELVSKPYIDITLALMAQFGVDVQNH-D-YARFEINPGQYLS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P VEGDASSASYFLA AI GG+V V G G S+QGDVKFA+ LE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIAGGSVKVTGVGRLSIQGDVKFADALEKMGADIEWGDDF 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      + L ID++MN +PD AMT+A ALFA+G T +R++ +WR+KET+R+
Sbjct: 295 IIARS-----AKLSGIDMDMNHIPDAAMTIATAALFAEGETCLRNINWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIRD 424
      A+ TEL K+GA VEEG D+ ITPP K+N AIDTY+DHRMAM FSL A A+ +TI D
Sbjct: 347 HAMATELRKVGAVVEEGHDFIRITPPVKMNTAAIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFPDYF 436
      P CT KTFP YF
Sbjct: 407 PDCTSKTFPSYF 418

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>ref|ZP_06052274.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Grimontia hollisae CIP 101886]
gb|EEY72340.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Grimontia hollisae CIP 101886]
Length = 427

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 231/438 (52%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ LQPI +I G V LKSGKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 EQLTLQPIKIHGEVNLPGSKSVSNRALLAALAKGTTRLTNLLDSDIRHMLNALGKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + + VV G G F E ++LFLGNAG AMR L AA+ GN YVL
Sbjct: 62 VSYQLSEDKTECVVEGLGSPFKT---SEPMELFLGNAGTAMRPLAALCLGEGN--YVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG L+ ++ +GADV PP+++ + GG V++ GSISQ+L+
Sbjct: 117 GEPRMKERPIGHLIDAMRTVGADVTYLENEHYPLKIAS-KAIQGGDVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APL GD I I L+S PY+++TL +M +FGV+ ++D + F +KG Q Y +
Sbjct: 176 ALLMTAPLFGSDTHIRIKGDLVSKPYIDITLHIMAQFGVQVNNND-YKTFDVKGNQTYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGDVKFA+ L MGA + W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSQGDVKFADALAAMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R LKA+D++ N +PD AMT+A ALFA G T IR+V +WRVKET+R+
Sbjct: 295 VIAR-----RGELKAVDMDFNHIPDAAMTIATTALFAQGTTVIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITP L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGADVEEGEDYIKITPTANLKHAADITYDDHRMAMCFSLVALSDPTVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYFD LS
Sbjct: 407 PTCTSKTFPDYFDKLSAL 424

>ref|YP_869612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. ANA-3]
sp|A0KWN7.1|AROAS_HESA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK48206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. ANA-3]
Length = 426

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 220/432 (50%), Positives = 289/432 (66%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAKGTTTLTNLLDSDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + G G + A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VEYRLSQNNNTVCELTGLGGVSSDTAQ---TLFLGNAGTAMRPLCAALTL--GRGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV LKQLGA++ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALKQLGANIVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV+ + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVQVINHD-YARFEIPAGQYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGKEVGVKTVGVRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGAP-----LTAVDLDMNHIPDAAMTIATAALFAKGTITIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP LN IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGALVEEGHDYIQITPPVVLNTAEIDTYNDHRMAMCFSMMAFADCGITIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PDCTSKTFFPDYF 418

>ref|YP_734053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. MR-4]
sp|Q0HIX1.1|AROA_SHEM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI38996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp. MR-4]
Length = 426

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 219/432 (50%), Positives = 288/432 (66%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAKGTTTLTNLLSDDIRHMLASLQQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + +G GG + A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VEYRLSQNNTVCELIGLGGASADTAQ---TLFLGNAGTAMRPLCAALTL--GRGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV LKQLGA++ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALKQLGANIVYLKNEGFPPLAINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA V I + +L+S PY+++TL LM +FGV+ + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKDSVNIHVKGELVSKPYIDITLALMAQFGVQVINHD-YARFEIPAGQQYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGKEVGVKTVGVRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGAP-----LTAVDLDMNHIPDAAMTIATAALFAKGTITIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP LN IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGALVEEGHDYIQITPPAVLNTAEIDTYNDHRMAMCFSMMAFANCGITIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PDCTSKTFFPDYF 418

>ref|YP_003524676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sideroxydans
lithotrophicus ES-1]
gb|ADE12289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sideroxydans
lithotrophicus ES-1]
Length = 647

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 233/438 (53%), Positives = 295/438 (67%), Gaps = 18/438 (4%)

Query: 1 MAGAEIIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ E + L P+ GTV+LPGSKS+SNR+LLLAAL++G T V +LL+S+D ML AL
Sbjct: 1 MSQQEFLELPLMSARGTVRLPGSKSISNRVLLLAALAQAQATTVRDLLHSDDTERMLDAL 60

Query: 61 RTLGLSVE--ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
RTLG+ VE D A + + GCGG FP ++AK LFLGNAG A R LTAA+ +GG
Sbjct: 61 RTLGVEVEQLGDNAYR---ITGCGGNFPNKNKAK----LFLGNAGTAFRPLTAALALSGG- 112

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+Y L GVPRM ERPIGDLV L+QLGAD+ PP++++ L G V++ G +
Sbjct: 113 -SYELSGVPRMHERPIGDLVDALRQLGADIRYLGNEGFPLQISP-AKLAGDTVQVRGDV 170

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQ+L+ LLMA PL V++E++ +LIS PY+ +TL +M RF V E D W F ++
Sbjct: 171 SSQFLTGLLMALPLLNRITVKVEVLGELISQPYIAITLTMMARFLVVVERED-WHSFTVRA 229

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
G Y P YVEGDASSASYFLA AI G V VEG G+ S+QGDV FA L+ MGA+V
Sbjct: 230 GSCYVPNEIYVEGDASSASYFLAAGAIGKGPVRVEGVGSNSVQGDVHFAHELKKMGAEV 289

Query: 299 TWTETSVTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
W + S+ GP LKA+D++ N +PD AMTLAV ALFADG T +R++ASWRV
Sbjct: 290 EWGDNLSLVAKG-----ASGKLKAVDLDCNHIPDAAMTLAVAALFADGTTTLRNIAASWRV 344

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
KET+R+ A+ TEL K+GA+VEEG D+ ITPP ++ AIDTYDDHRMAM FSLAA
Sbjct: 345 KETDRIAAMATELRKVGVATVEEGADFIRITPPAQIKHAAIDTYDDHRMAMCFSLAAFGGA 404

Query: 419 PVTIRDPGCTRKTFPDYF 436
V I DP C KTFP+YF
Sbjct: 405 GVRINDPKCVAKTFPEYF 422

>ref|ZP_07152402.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
21-1]
gb|EFK20872.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli MS
21-1]
Length = 427

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 230/436 (52%), Positives = 293/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTLNLLSDDVHRMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLASEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346 FAMATELRKVGAEEVEEGHDFIRITPPEKLFKFAEIATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_002382216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia
fergusonii ATCC 35469]
emb|CAQ88582.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia
fergusonii ATCC 35469]
Length = 434

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPSKKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL+ LG
Sbjct: 11 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDVRHMLNALKALG 70

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 71 VSYSLSTDRTRCEIIGNGGPLHAESA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 125

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 126 GEPRMKERPIGHLVDALRQGGAGITYLEQENYPPRLRQG--GFTGGNVVDGSGVSSQFLT 183

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 184 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEVENQ-RYQQFVVKGGQSYQS 242

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD+ FA+VLE MGA ++W +
Sbjct: 243 PGSYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIHFADVLEKMGATISWGDDY 302

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L ID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 303 ISCT-----RGELNGIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 354

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITP EKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 355 FAMATELRKVGAEVEEGHDFIRITPLEKLFKFAEIATYNDHRMAMCFSLVALSDTAVTILD 414

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 415 PKCTAKTFPDYFEQLA 430

>ref|YP_001183564.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
putrefaciens CN-32]
sp|A4Y732.1|AROASHEPC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP75765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
putrefaciens CN-32]
Length = 426

Score = 424 bits (1090), Expect = e-116, Method: Compositional matrix adjust.
Identities = 218/438 (49%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLDSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNNVTCELDGIGGVISASAE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGLV L+QLGA++ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGLVDALRQLGANIVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++T+ LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITIALMAQFGVNVINHD-YARFEIVAGQRYIS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGSP-----LTAVDLDNMNHPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVINTAEIDTYNDHRMAMCFMSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFFPDYFKQFASL 424

>ref|NP_717994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella oneidensis
MR-1]
sp|Q8EEH8.1|AROASHEON RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAN55438.1|AE015681_2 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella oneidensis
MR-1]
Length = 426

Score = 424 bits (1089), Expect = e-116, Method: Compositional matrix adjust.
Identities = 220/432 (50%), Positives = 286/432 (66%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLDSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + G GG V +K+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VEYRLSHNNTVCELALGG---VMSSKQAQTLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA++ PP+ +N G L GG V++ G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGANIVYLKNDGFPPLTINATG-LNGGDVEIVGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGVK + + RF I GQ Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVKVINH-HYARFEIPAGQHYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGAP-----LTAVDLDNMNHPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP LN IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVLNTAQIDTYNDHRMAMCFMSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PDCTSKTFFPDYF 418

>ref|YP_205144.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio fischeri
ES114]
sp|Q5E3Z0.1|AROAVIBF1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW86256.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Vibrio fischeri
ES114]
Length = 426

Score = 424 bits (1089), Expect = e-116, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 292/436 (66%), Gaps = 17/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI +I+G + LKSGKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2  ESITLQPIKINGQINLPGSKSVSNRALLAALASGTTKLTNLLDSDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + + V G G F + E ++LFLGNAG AMR L AA+ G +VL
Sbjct: 62  VEYKLSANKTECEVTGLGRAF---EPNEALELFLGNAGTAMRPLAALCL--GQGEFVLT 116

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV LK GADV+ + PP+++ G G L GG V++ GSISSQ+L+
Sbjct: 117  GEPRMKERPIGHLVTALKAAAGADVEYLENENYPPLKIKGTG-LHGGTVEIDGSISSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          A LMAAPL+ + I+I+ L+S PY+++TL +M FGK E+ + + F + Q Y +
Sbjct: 176  AFLMAAPLSTQETTIKIVGDLVSKPYIDITLDMATFGVKIENQN-YQTFVVPANQTYVA 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P + VEGDASSASYFLA AAI GG V V G G S+QGDV+FA+ L MG ++ W +
Sbjct: 235  PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSQGDVQFADALAAMGTEIEWGDDY 294

Query: 305  VVTGTGPPREPFGGRK-HLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          V RK L AID++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R
Sbjct: 295  V-----IARKGELNAIDMDFNHIDPAAMTIATAALFAKGTTIRNVYNWRVKETDR 345

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIR 423
          + A+ TEL K+GA VEEG DY ITPP L +IDTYDDHRMAM FSL A ++ PVTI
Sbjct: 346  LAAMATELRKVGAVVEEGEDYITITPPASLQHASIDTYDDHRMAMCFSLVALSDTPVTIN 405

Query: 424  DPGCTRTFPDYFDVL 439
          DPGCT KTFPDYFD L
Sbjct: 406  DPGCTSKTFPDYFDKL 421

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>emb|CBX80205.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia amylovora
ATCC BAA-2158]
Length = 428

Score = 423 bits (1088), Expect = e-116, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          + LQPI + GTV LKSGKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3  HSLTLQPIALVDGTVNLPKSGKSVSNRALLAALAKGTTRLNLLDSDVVRHMLDALQALG 62

Query: 65  LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + R + G GG A ++LFLGNAG AMR L AA+ G + +L
Sbjct: 63  VQYSLSADRTRCEITGQGGAL---QADRSLELFLGNAGTAMRPLAALCIGGND--IILT 117

Query: 125  GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GADV D PP+RV G G GG++ + GS+SSQ+L+
Sbjct: 118  GEPRMKERPIGLVDALRQGGADVLYEQVDYPLRVKG--GFSGGEITVDGSVSSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLMAAPLA D +I I L+S PY+++TL+LM FGV ++++ + F I+G Q+Y++
Sbjct: 176  ALLMAAPLAKNDSQIIIKGDLVSKPYIDITLKLMAAFGVVDNNN-YHTFRIRGQQYQA 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA V W +
Sbjct: 235  TSEYLVEGDASSASYFLAAAAIKGTVKVTGIGRNSMQGDIRFADVLEKMGASVEWGGDY 294

Query: 305  VVTGTGPPREPFGRKLKKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          + T R LKA+D++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295  IACT-----RGELKAVDLDNMNHPDAAMTIATTALFAQGTVMRNIYNWRVKETDRL 346

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPVTIRD 424
          A+ TEL K+GA VEEG D+ ITPP K+ I TY+DHR+AM FSL A + PVTI D
Sbjct: 347  AAMATELRKVGAEVEEGYDFIRITPPAKIACAQIATYNDHRIAMCFSLVALSSTPVTILD 406

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Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF L+
Sbjct: 407 PNCTAKTFPDYFTQLA 422

>ref|YP_157512.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Aromatoleum aromaticum EbN1]
emb|CAI06611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aromatoleum
aromaticum EbN1]
Length = 646

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/443 (51%), Positives = 295/443 (66%), Gaps = 22/443 (4%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I L P+ + +G V+LPGSKS+SNR LLLAAL+EG T + +LL S+DV ML ALRTLGS+
Sbjct: 6 IDLPPLMDATGQVRLPGSKSISNRTLLLAALAEGRTEIRDLLASDDVERMLDALRTLGV 65

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ + V G G FPV+ A LFLGNAG A R LTAA+ +GG Y L GV
Sbjct: 66 WAREGSDHYRVDGVRGPFVVKAA---DLFLGNAGTAFRPLTAALALSGGE--YRLTGV 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
RM ERPIGDLV GL+Q+GA+V +LG + PP+ + PGG +++ G +SSQ+L+A
Sbjct: 120 ARMHERPIGDLVDGLRQVGANVR-YLGVGFPPLHILPAAIRPGGMLRVRGDVSSQFLTA 178

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLMA PL IE++ +LIS PY+ +TL LM RFGV+ + + W RF + GG +Y+SP
Sbjct: 179 LLMALPLTGTQTTEVVGELISKPYISITLDMARFGVEVQR-EGWTRFTVPGGARVRS 237

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV----TWT 301
+VEGDASSASYFLA AI GG V VEG G +S+QGDV+FAE L +GA+V W
Sbjct: 238 GTLFVEGDASSASYFLAAGAIGGGPVRVEGVGRSSIQGDVRFAEALAEALGARVDIGDNWI 297

Query: 302 ETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPATAIRDVASWRVKET 361
E +G LKA D+++N +PD AMTLAV ALFADGP +R++ASWRVKET
Sbjct: 298 EARAPESG-----RLKAFDLDLNHPDAAMTLAVAALFADGPCTLRNIASWRVKET 348

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPT 421
+R+ A+ EL K+GA+VEEG D+ +TPP KL AIDTYDDHRMAM FSL + V
Sbjct: 349 DRIAAMAKELRKVGAAVEEGADFLRVTPPAKLVPAAIDTYDDHRMAMCFSLVSLGGCRVR 408

Query: 422 IRDPGCTRKTFPDYFDVLSFVK 444
I +P C KTFP YF+ ++ +
Sbjct: 409 INEPKCVNKTFTPTFEFCFASITR 431

>ref|ZP_01077391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinomonas sp.
MED121]
gb|EAQ64621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinomonas sp.
MED121]
Length = 430

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 221/436 (50%), Positives = 296/436 (67%), Gaps = 17/436 (3%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+ L P+ +G +++PGSKSLSNRILLALLAAL++G T + NLL+S+D+ +ML AL +LG+S
Sbjct: 4 LTLGPLSNANGEIQIPGSKSLSNRILLALLAALAKGETKITNLLSDDIRHMLDALTSLGVS 63

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEV---QLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ V G G P+ +A + LFLGNAG AMR LTAA+ G Y+L
Sbjct: 64 YQLSDNGTSCVTQGVAG--PLSNATDNTISADLFLGNAGTAMRPLTAALCL--GKGEYLL 119

Query: 124 DGVRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM ERPIGDLV+ L+QLGADV+ + PP+++ G+ GG+V + G+ISSQ+L
Sbjct: 120 HGEPRMHERPIGDLVIALRQLGADVEYQGEENYPPLKIRA-NGIQGGEVSIKGNISSQFL 178

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+A+LM+APLA D+ I + +L+S PY+++TL +M+++FGV E+ + + F +KG Q Y
Sbjct: 179 TAILMSAPLAQNDLTIHVDGELVSKPYIDITLHVMKQFGVDVENQN-YQSFVVKGNTYV 237

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AAI GGT+ V G GT S+QGDVKFAEVL MGA +++
Sbjct: 238 SPGEIMVEGDASSASYFLAAAAIAGGTIKVHGIGTDSVQGDVKFAEVLAAAMGANISY--- 294

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
GP + L +D++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R
Sbjct: 295 -----GPTWVKASKGELNGVDLDMNHIPDAAMTIATTALFAKGPTRIRNIYNWRVKETDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL KLGA+V+EG DY + P + AIDTY+DHR+AM FSL A + VTI
Sbjct: 350 LNAMATELRKLKATVDEGEDYIYVEPLADVQHAAIDTYNDHRIAMCFSLVAFSNSQVTIN 409

Query: 424 DPGCTRKTFPDYFDVL 439
DPGCT KTFP YFD+
Sbjct: 410 DPGCTSKTFPTYFDLF 425

>ref|YP_002311816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
piezotolerans WP3]
sp|B8CMH2.1|AROA_SHEPW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACJ29229.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
piezotolerans WP3]
Length = 426

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 220/432 (50%), Positives = 290/432 (67%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
++ L+PI++++GT+ +PGSKS+SNR LLLA L+EGTT + NLL+S+D+ YML +L+ LG
Sbjct: 2 NQLRLEPIEKVNGTINIPGSKSISNRALLLATLAEGTTTLTNLLSDDIRYMLASLQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ V G G + A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLTNNTTVEVDGIAGVLNADTAQ---TLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGADV PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVSLRQLGADVSYLKNDGFPPLTINATG-LSGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA GDV I+I +L+S PY+++TL LM +FGV +++ + F IK GQ+Y S
Sbjct: 176 ALLMVAPLAKGDVNIKIGELVSKPYIDITLALMAQFGVNVNTNNN-YVSFEIKTGQRYIS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VL MGA + W +
Sbjct: 235 PGKLLVEGDASSASYFLAAGAIGGEVKVTGVGKLSIQGDVKFADVLAQMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARG-----SKLNAVLDLMNHIPDAAMTIATAALFATGTTHIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA V+EG DY +TPP K + IDTY+DHRMAM FS+ A A+ +TI +
Sbjct: 347 AAMATELRKVGAIVDEGHDIYSVTPPVKPHATANIDTYNDHRMAMCFSMALAFADCGITINE 406

Query: 425 PGCTRKTFPDYF 436
P CT KTFPDYF
Sbjct: 407 PECTSKTFPDYF 418

>ref|YP_002357991.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS223]
sp|B8EA95.1|AROA_SHEB2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACK46568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS223]
Length = 426

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 219/438 (50%), Positives = 290/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++G T + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVPVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG E A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQDNTVCELDGLGGVISSESAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA+V PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGANVVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVTVINH-DYARFEIVAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IARG-----SQLTAVDLDMNHIPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITTP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVINTAEIDTYNDHRMAMCFMSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFFPDYFKQFASL 424

>ref|YP_001554826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS195]
sp|A9L2X7.1|ARO_A_SHEB9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX49566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS195]
gb|ADT94550.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella baltica
OS678]
Length = 426

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 219/438 (50%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVPVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG E A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNNTVCELDGLGGVISSESAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
PRM ERPIGDLV L+QLGA+V PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 CEPRMEERPIGDLVDALRQLGANVVYLKNDGFPPLTINATG-LSGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITLALMAQFGVTVINH-DYARFEIVAGQRYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA++ W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVGRLSIQGDVKFADVLEKMGAEIEWGDDY 294

Query: 305 VVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARG-----SQLTAVDLDNMNHPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITTP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVINTAEIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFFPDYFKQFASL 424

>gb|ADV54422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
putrefaciens 200]
Length = 426

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 217/438 (49%), Positives = 290/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLSDDIRHMLASLQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG A+E FLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNNTVCELDGLGGVISSASAQE---FFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA++ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGANIVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++T+ LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITIALMAQFGVNVINH-DYARFEIVAGQRYIS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGKEGVKVTGVRLSIQGDVKFADVLEKMGADIEWDDY 294

Query: 305 VVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGSP-----LTAVDLDNMNHPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITTP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVINTAEIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYF ++
Sbjct: 407 PDCTSKTFFPDYFKQFASL 424

>ref|YP_004115204.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pantoea sp. At-9b]
gb|ADU68648.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pantoea sp. At-9b]
Length = 428

Score = 423 bits (1087), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 299/436 (68%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI + GTV LPSKGS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 DSLTLQPIARVDGTVNLPGSKSVSNRALLAALAKGTTRLTNLLSDSVKHMNLNALKALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S +A R V G P+ +++ ++LFLGNAG AMR L AA+ G + VL
Sbjct: 63 VSYTL--SADRTVCEVIGNAGPLH-SEQPLELFLGNAGTAMRPLAALCL--GQQSIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ TD PP+ + G G GG V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAKIEYLEQTDYPLLLKG--GFNGGDVTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM FGV ++ + + RF +KG Q+Y+S
Sbjct: 176 ALLMTAPLAQQDTTISIKGDLVSKPYIDITLHLMRCFGVDVDNQN-YQRFVVKGKQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 235 PGDYLVEGDASSASYFLAAAAIKGGTVRVVTGIGRNSVQGDIRFADVLEKMGASIEWGDDY 294

Query: 305 VVTGTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R+
Sbjct: 295 IACT-----RGS LNAIDMDMNHIPDAAMTIATTALFANGTTLMRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG D+ ITPP +L I TY+DHRMAM F+L A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGHDFIRITPPAQLQHADIGTYNDHRMAMCFALVALSDPTVTILD 406

Query: 425 PGCTRKTFPDYFDVLS 440
PGCT KTFPDYF L+
Sbjct: 407 PGCTAKTFPDYFQQLA 422

>ref|NP_519028.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia solanacearum GMI1000]
sp|Q8Y0Y6.1|AROA_RALSO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD14609.1| probable 3-phosphoshikimate 1-carboxyvinyltransferase (epsp synthase) protein [Ralstonia solanacearum GMI1000]
Length = 436

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 231/437 (52%), Positives = 291/437 (66%), Gaps = 15/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GTVKLPKSGKS+SNR+L LLAAL+EG TVV +LL+S+D ML AL TLG
Sbjct: 2 EHLVDVGLPKAARGTVKLPKSGKSISNRVLLLAALAEGETTVVRDLSDSDTRVMLAALDTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E A V G GG+FP + A LF+GNAG A+R LTAA+ GG Y L
Sbjct: 62 VRCEPLGTANAYRVGTGGRFPAKSA---DLFMGNAGTAIRPLTAALALQGGE--YTLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ + +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYTGNEGFPPLAIRAASIRIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLMA PL G V IE++ +LIS PY+E+TL LM RFGV+ E + W F + G
Sbjct: 176 ALLMALPLVEGSGRPVTIEVVGELISKPYIEITLNLMARFGVQVER-NGWASFSVPTGVA 234

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 235 YRAPGEIFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAG 294

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET
Sbjct: 295 DNWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKET 351

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A--IDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VP
Sbjct: 352 DRLTAMATELRKLGA+VEEGTDYIRVTPPSHWTPAGGIDTYDDHRMAMAFSLAAGFPVP 411

Query: 420 VTIRDPGCTRKTFPDYF 436
V I DP C KTFP+YF
Sbjct: 412 VRINDPRCAKTFPEYF 428

>ref|YP_662038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoalteromonas atlantica T6c]
sp|Q15T04.1|AROA_PSEA6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG40984.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoalteromonas
atlantica T6c]
Length = 429

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 222/439 (50%), Positives = 294/439 (66%), Gaps = 15/439 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ + ++L PI ISGTV +PGSKSLSNR LLLAA++ G T + NLL+SED+ +ML AL
Sbjct: 1 MSRSAPLLNLPISAISGTVNVPGSKSLSNRALLAAVANGETHLTNLLDSEDIRHMLKAL 60

Query: 61 RTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LG++ V G G F V++ + LFLGNAG AMR L A + + G
Sbjct: 61 TQLGVNYRLSDDKTECWVQGLGRGFSVDNLE---TLFLGNAGTAMRPLCAVLATSIGE-- 115

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ L G PRM ERPIG LV L+Q GA + PP+++ G+ L GG + + G++SS
Sbjct: 116 FELTGEPRMEERPIGALVDSLQAGAQITYLKNEGYPPLKMGMA-LKGGNISVEGAVSS 174

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+L+ALLMAAPL D I I+ +L+S PY+++TL M +FG+ E+++ + F +KG Q
Sbjct: 175 QFLTALLMAAPLFEHDSVINIVGELVSKPYIDITLNTMAQFGITVENNN-YQSFTVKGNQ 233

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y++ + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA+TW
Sbjct: 234 QYQAAGDFLVEGDASSASYFLAAGAIAKGGTVRVTGVGKKSIGDIRFADVLEKMGAKITW 293

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ + VTG P L A+D++MN +PD AMT+A ALFA+G T+IR++ +WRVKE
Sbjct: 294 GDDYIEVTGAP-----LTAVDMDMNHIPDAAMTIATTALFAEGTTSIRNIYNWRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ EL K+GA V EG DY ITPP L T IDTYDDHR+AM FSL A ++ PV
Sbjct: 346 TDLRAAMACELRKVGAEVIEGQDYITITPPNLTIQTDIDTYDDHRVAMCFSLVALSDTPV 405

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
TI DP CT KTFPDYF L
Sbjct: 406 TINDPDCTAKTFFPDYFTRL 424

>ref|ZP_06181709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio alginolyticus
40B]
gb|EEZ82030.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio alginolyticus
40B]
Length = 426

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/438 (52%), Positives = 293/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPGSKS+SNR LLLAAL++G T + NLL+S+D+ +ML AL LG
Sbjct: 2 ESRTLQPIKIQGEVNLPGSKSVSNRALLLAALAKGRTRLTNLLDSDIRHMLNALTKLG 61

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + +V G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VQYQLSEDKTECLVEGLGRPFVS---SEPVELFLGNAGTAMRPLAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GA+V+ + PP+++ G G L G V + GSISQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALKDAGANVEYMENENFPPLKIIGTG-LKAGTVSIDSGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G++ I I L+S PY+++TL +M++FGV ++D + F I GQ+Y +
Sbjct: 176 AFLMSAPLAEGEIRINIEGDLVSKPYIDITLHIMKQFGVDVINND-YQEFVIPAGQQYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE TERM 364

V LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGQLKGIDMDYNHIDPAAMTIATTAALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKPVSQLKHAADITYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKLKAL 424

>ref|YP_003740883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia billingiae
Eb661]
emb|CAX59032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erwinia billingiae
Eb661]
Length = 428

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 231/436 (52%), Positives = 295/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQP+ + GTV LPGSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL+ L
Sbjct: 3 ESLTLQPVALLVDGTVNLPKSGSVSNRALLAALAKGTTRLTNLLDSDDVRHMLTALKALN 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S V G GG A+ V+LFLGNAG AMR L AA+ G+ VL
Sbjct: 63 VSYSLSDDRTVCEVTGQGGPL---HAEGPVFLFLGNAGTAMRPLAALCL--GSNDIVLT 117

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA+V TD PP+ + G G GG+V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAEVSYLEQTDYPPHLHLKG--GFSGGEVSVDGVSQSFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I I L+S PY+++TL LM FGV+ ++ D++ F+I G Q+Y S
Sbjct: 176 ALLMTAPLAPNDTKIVIKGDLVSKPYIDITLNLMTFGVEVKN-DNYREFHIAAGNQYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 235 PGEYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEQMGAVIEWGDDY 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 295 ISCT-----RGDLNAIDLDMNHIPDAAMTIATAALFAKGTVMRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY +TPP+ L I TY+DHRMAM FSL A + PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGHDYIRVTPPQTLKFAEIGTYNDHRMAMCFSLVALSSTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLS 440
PGCT KTFPDYF+ L+
Sbjct: 407 PGCTAKTFFPDYFEQLA 422

>ref|YP_002156583.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio fischeri MJ11]
sp|B5FG60.1|AROA_VIBFM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACH66919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio fischeri MJ11]
Length = 426

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 291/436 (66%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G + LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2 ESLTLQPIKIDQINLPGSKSVSNRALLAALASGTTKLTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F + E ++LFLGNAG AMR L AA+ G +VL
Sbjct: 62 VEYKLSADKTECEVTGLGRAF---EPNEALELFLGNAGTAMRPLAALCL--QGGEFVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GADV+ + PP+++ G G L GG V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALKAAAGADVEYLENENYPPLKIKGTG-LHGGTVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPL+ + I+I+ L+S PY+++TL +M FGVK E+ + + F + Q Y +
Sbjct: 176 AFLMAAPLSTQETTIKIVGDLVSKPYIDITLDIMATFGVKIENQN-YQTFVVPANQTYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGDV+FA+ L MG ++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKTGIGKKSIGGDVQFADALAAMGTEIEWGDDY 294

Query: 305 VVTGTGPPREPFGGRK-HLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V RK L AID++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R
Sbjct: 295 V-----IARKGELNAIDMDFNHIPDAAMTIATAALFAKGTTsirNVYNWRVKETDR 345

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP L +IDTYDDHRMAM FSL A ++ PVTI
Sbjct: 346 LAAMATELRKVGA VEEGEDYITITPPASLQHASIDTYDDHRMAMCFSLVALSDTPVTIN 405

Query: 424 DPGCTRKTFPDYFDVL 439
DPGCT KTFPDYFD L
Sbjct: 406 DPGCTSKTFPDYFDKL 421

>ref|YP_856510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromonas hydrophila
subsp. hydrophila ATCC 7966]
gb|ABK38353.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromonas hydrophila
subsp. hydrophila ATCC 7966]
Length = 455

Score = 422 bits (1086), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/433 (52%), Positives = 292/433 (67%), Gaps = 16/433 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L+PI ++G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG+ +
Sbjct: 34 LEPISR VAGEVNLPGSKSVSNRALLAALARGTTTRLTNLLDSDDIRHMLAALTQLGVKYK 93

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V G G F V KE V LFLGNAG AMR L AA+ G+ Y L G PR
Sbjct: 94 LSADKTECTVHGLGRSFAV---KEPVNLFLGNAGTAMRPLCAALCL--GSGEYTLGGEPR 148

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIG LV L++ GA + PP+ V+ GL GG V + GS+SSQ+L+A LM
Sbjct: 149 MEERPIGHLVDALREAGAHIQYLKKGYPPLVVDA-KGLWGGDVHVDGSVSSQFLTAFLM 207

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAP+A GD I I +L+S PY+++TL +M++FGV EH D++ FYIKG Q Y SP +
Sbjct: 208 AAPMAAGDTRIIHKELVSKPYIDITLHIMKQFGVVIEH-DNYKLFYIKGNQSYVSPGDF 266

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGDASSASYFLA AI G V V G G S+QGD+ FA+VLE MGA++TW + +
Sbjct: 267 LVEGDASSASYFLAAGAIKG-KVRVTGIGKHSIQGDIHFADVLEKMGARITWGDDFIEAE 325

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P L ID++MN +PD AMT+AV ALFA+GPT+IR++ +WRVKET+R+ A+
Sbjct: 326 QAP-----LHGIDMDMNHIPDAAMTIAVAALFAEGPTSIRNIYNWRVKETDRLHAMA 377

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
TEL KLG VEEG D+ +TPP +L AIDTY+DHR+AM FSL A ++ VTI DPGCT
Sbjct: 378 TELRKLGVVEVEGRDFTVTPPAQLKHAADTYNDHRIAMCFSLVALSDTAVTINDPGCT 437

Query: 429 RKTFFPDYFDVLST 441
KTFFPDYFD L++
Sbjct: 438 SKTFFPDYFDKLAS 450

>ref|YP_002892566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tolomonas auensis DSM
9187]
sp|C4LEG3.1|AROATOLAT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACQ92980.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tolomonas auensis DSM
9187]
Length = 427

Score = 422 bits (1085), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/430 (53%), Positives = 292/430 (67%), Gaps = 15/430 (3%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ L+PI + GTV LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL+TLG+S
Sbjct: 4 LTLEPIARVEGTVNLPGSKSVSNRALLAALARGTTRLTNLLDSDDIRHMLNALKTLGVS 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E V G G F + E V LFLGNAG AMR L AA+ + G + L G
Sbjct: 64 YELSANKTECTVHGLGRAF---SSSEPVNLPFGNAGTAMRPLCAALCLSNGE--FTLTGE 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM ERPI LV L+Q GA V PP+ + G GL GG+V + GS+SSQ+L+A
Sbjct: 119 PRMEERPIAHLVDALRQAGAHVHYLKKDGYPLTIEG-KGLWGGEVVIDGSVSSQFLTAF 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAPLA GDV I I +L+S PY+++TL +M++FGV EH D + FY++G Q Y SP
Sbjct: 178 LMAAPLASGDVIRIRIGELVSKPYIDITLHIMKQFGVTVEHDD-YQVFYVRGNQTYVSPG 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VEGDASSASYFLA AI G V V G G S+QGD++FA+VLE MGAK+TW + +
Sbjct: 237 TFLVEGDASSASYFLAAGAIG-KVRVTGIGKNSIQGDIRFADVLEKMGAKITWGDDFI- 294

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
E L+A+D++MN++PD AMT+A ALFA+G TAIR++ +WRVKET+R+ A
Sbjct: 295 -----EAENVGELQAVDLDMNQIPDAAMTIATAALFANGKTAIRNIYNWRVKETDRLTA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ TEL K+GA V EG D+ ITTP +L AIDTY+DHR+AM FSL A ++ VTI DPG
Sbjct: 349 MATELRKVGAEVVEGHDFIETPPAQKHAIDTYNDHRIAMCFSLVALSDTKVTINDPG 408

Query: 427 CTRKTFPDYF 436
CT KTFPDYF
Sbjct: 409 CTSKTFPDYF 418

>emb|CBG33822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli 042]
Length = 427

Score = 422 bits (1085), Expect = e-116, Method: Compositional matrix adjust.
Identities = 230/436 (52%), Positives = 292/436 (66%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESILTQPIARVDGTINLPGSKSVSNRALLAALAHGKTVL/TNLLDSDVHRMLNALAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTSLADRTCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+ + G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLHLQG--SFTGGNVVDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIRGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_001444769.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio harveyi ATCC BAA-1116]
sp|A7N1K3.1|AROA_VIBHB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABU70542.1| hypothetical protein VIBHAR_01572 [Vibrio harveyi ATCC BAA-1116]
Length = 426

Score = 422 bits (1085), Expect = e-116, Method: Compositional matrix adjust.
Identities = 232/438 (52%), Positives = 293/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 2 ESITLQPIKIQGEVNLPGSKSVSNRALLAALAKGTTRLTNLLDSDDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + VV G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VQYQLSEDKTECVVEGLGRPFVS---SEPVELFLGNAGTAMRPLAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GADV + PP+++ G G PG V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVKALKAAAGADVTYLENENYPPLKIVGTGLKPG-SVSIIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA GD+ I I +L+S PY+++TL +M++FGV ++D + F I GQ+Y +
Sbjct: 176 AFLMSAPLAEGDIRINIEGELVSKPYIDITLHIMKQGVVDVINND-YQEFVIPVGQYVA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA + W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAIAKGEVVKVTGIGKNSIQGDIQFADALEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA+G T+IR+V +WRVKET+R+
Sbjct: 295 VISR-----VGQLKGIDMDYNHIDPDAAMTIATTALFAEGTTSIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKVPVQLTHAAIDTYDDHRMAMCFSLVALSDKPVITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTF 442
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKLKAL 424

>ref|ZP_04578078.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Oxalobacter formigenes
OXCC13]
gb|EE029051.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Oxalobacter formigenes
OXCC13]
Length = 440

Score = 422 bits (1085), Expect = e-116, Method: Compositional matrix adjust.
Identities = 223/438 (50%), Positives = 292/438 (66%), Gaps = 21/438 (4%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+K +SGTV+LPGSKS+SNR LLL+AL++G T++ +LL S+D ML AL++LG+
Sbjct: 11 LLPVKHVSgtVRLPGSKSISNRTLLLSALADGKTLIKDLLFSDDTQVMLEALKSLGIQWN 70

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 128
A V G G+ P ++E LFLGNAG A+R LTAA+ A GG ++L GV R

Sbjct: 71 ETGVANEYEVNGANGRLP---RQEADLFLGNAGTAIRPLTAALALGG-GDFLLHGVKR 125

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L GA+++ PP+R++ G + + + G++SSQ+L+ALLM

Sbjct: 126 MHERPIGDLVDALNDAGAEIETENQGYPPIRIHA-GNIDRHDHVKGNVSSQFLTALLM 184

Query: 189 AAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
AAPL DV I +I +LIS PY+E+TL LM FGV+ E D W F ++ GQ Y+SP

Sbjct: 185 AAPLMARSHDVTIHVIGELISKPYIEITLNLMSRFGVEIEQ-DGWKSFTLRKGQVYRSPG 243

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
A+VEGDASSASYFLA AAI GG V VEG G S+QGD++FA+VLE MGA V + + +

Sbjct: 244 VAHVEGDASSASYFLAAAAIAGGPVRVEGVGKYSIQGDIFADVLEKMGANVYGDNYIE 303

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V+ LKAID + N +PD AMT+A++AL+ADG + +R++ SWRVKET+R+ A

Sbjct: 304 VSHSGA-----LKAIDEDFNLPDAAMTAVAILALYADGTSVLRNIGSWRVKETDRIAA 356

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP-----VT 421
+ TEL KLGASVE G D+ ITPPE +N AIDTYDDHRMAM FSLA+ +

Sbjct: 357 METELKKLGASVESGEDWLKITPPEHINDAIDTYDDHRMAMCFSLASLCTEKGATIR 416

Query: 422 IRDPGCTRKTFPDYFDVL 439
I DP C KTFP+YF

Sbjct: 417 INDPQCVSKTFPEYFQAF 434

>ref|YP_050684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
atrosepticum SCRI1043]
sp|Q6D401.1|AROEA_ERWCT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAG75492.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
atrosepticum SCRI1043]
Length = 429

Score = 422 bits (1085), Expect = e-116, Method: Compositional matrix adjust.
Identities = 232/439 (52%), Positives = 300/439 (68%), Gaps = 21/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PIK I+GT+ LPGSKS+SNR LLLAALSEG T + NLL+S+DV +ML AL LG

Sbjct: 3 ESLTLHPKIKLINGTLNLPGSKSVSNRALLAALSEGKTRLTNLLSDDVHRMLTALTALG 62

Query: 65 LSVEADKAAKRAV--VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE ++ R V ++G GG F A + ++LFLGNAG AMR L AA+ G+ V

Sbjct: 63 --VEYHLSSDRTVCEIIGLGGAFA---ASQPLELFLGNAGTAMRPLAALCLTDGD--IV 115

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G PRM+ERPIG LV L+Q GA +D + PP+R++G G GG++ + GS+SSQ+

Sbjct: 116 LTGEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPRLRHG--GFQGGGEISVDGSVSSQF 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLM APLA D +I I L+S PY+++TL +M+ FG+ H +++ RF++ G Q+Y

Sbjct: 174 LTALLMTAPLAAQDTQISIQGDLVSKPYIDITLHMMKAFGIDVRH-ENYQRFVAGRQQY 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+SP + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+VLE MGA V W E

Sbjct: 233 RSPGDYLVEGDASSASYFLAAAAIKGGVVRVTGVGRNSVQGDIFADVLEKMGAIWRWE 292

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADG-PTAIRDVASWRVKET 361
+ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET

Sbjct: 293 DYIECE-----RGELHAIDMDMNHIPDAAMTIATAALFAQGGTTTLRNINWRVKET 344

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ EL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVT

Sbjct: 345 DRLAAMAIELRKVGAEEVEEGNDYIRITPPAKLKAAEIGTYNDHRMAMCFSLVALSDTPVT 404

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I DP CT KTFPDYF+ L+

Sbjct: 405 ILDPKCTAKTFPDYFEQLA 423

>gb|AAT45239.1| 5-enol-pyruvylshikimate-phosphate synthase [Helianthus
salicifolius]
Length = 264

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 217/264 (82%), Positives = 237/264 (89%), Gaps = 1/264 (0%)

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
R LGL+VE + KRA V GCGG FPV ++AK+E+QLFLGNAG AMR LTAAVTAAGGN+
Sbjct: 1 RALGLNVEENGEIKRATVEGCGGVFPVGKEAKDEIQLFLGNAGTAMRPLTAAVTAAGGNS 60

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+Y+LDGVPRMRERPIGDLV GLKQLGADVDCFLGT+CPPVRV GGLPGGKVKLSGSIS
Sbjct: 61 SYILDGVPRMRERPIGDLVTGLKQLGADVDCFLGTNCPVRVAANGGLPGGKVKLSGSIS 120

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQYL+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EHSDSWD+FY++GG
Sbjct: 121 SQYLTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSVHSDSWDKFYVRGG 180

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTSSLQGDVKFAEVLEMMGAKVT 299
QKYKSP NAYVEGDASSASYFLAGAAITGGTGTVEGCGT+SLQGDVKFAEVL MGA+VT
Sbjct: 181 QKYKSPGNAYVEGDASSASYFLAGAAITGGTGTVEGCGTSSLQGDVKFAEVLQMGAEVT 240

Query: 300 WTETSVTVTGPPREPFGGRKHLKAI 323
WTE SVTV GPPR GR HL+ +
Sbjct: 241 WTENSVTVRGPPRNASGRGHLRPV 264

>ref|YP_963357.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp.
W3-18-1]
sp|AlRJF8.1|AROA_SHEW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM24803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella sp.
W3-18-1]
Length = 426

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 218/438 (49%), Positives = 291/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++ G + +PGSKS+SNR LLLA L++GTT + NLL+S+D+ +ML +L+ LG
Sbjct: 2 KQLRLEPVVQVRGEINIPGSKSISNRALLLATLAQGTTLTNLLDSDDIRHMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G GG A+E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSQNNTVCELDGLGGVISSASAQE---LFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L++LGA+V PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRKLGANVVYLKNDGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++T+ LM +FGV + D + RF I GQ+Y S
Sbjct: 176 ALLMVAPLAKGSVNIHVKGELVSKPYIDITIALMAQFGVNVINHD-YARFEIVAGQRYIS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PCKVLVEGDASSASYFLAAGAIKGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G P L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IIARGSP-----LTAVDLDNMNHIPDAAMTIATAALFAKGTTVIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITTP +N IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAEVEEGNDYIKITPPAVINTAEIDTYNDHRMAMCFSMFAFADCGITIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYF ++

Sbjct: 407 PDCTSKTFPDYFKQFASL 424

>ref|YP_003286576.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. Ex25]
gb|ACY52111.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio sp. Ex25]
Length = 426

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/438 (52%), Positives = 293/438 (66%), Gaps = 15/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPSKKS+SNR LLLAAL++G T + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLTLQPIKIQGEVNLPGSKSVSNRALLLAALAKGRTRLTNLLSDDIRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + +V G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VQYQLSEDKTECLVEGLGRPFVS---SEPVELFLGNAGTAMRPLAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GA V+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALKDAGAKVEYMENENFPPLKIVGTG-LKAGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G++ I I +L+S PY+++TL +M++FGV ++D + F I GQ+Y +
Sbjct: 176 AFLMSAPLAEGEIRINIEGELVSKPYIDITLHIMKQFGVDVINND-YQEFVIPAGQQYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGQLKGIDMDYNHHPDAAMTIATTALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKPVSQLKHAADITYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFPDYFDKLKAL 424

>ref|YP_002114029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Schwarzengrund str. CVM19633]
sp|B4TRT9.1|AROASALSV RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF92120.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Schwarzengrund str. CVM19633]
Length = 427

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 295/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPSKKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLSDDVHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG++++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDSLQGGANIDYLEQENYPPLRLRG--GFTGGEIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTTIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSMTQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL+ I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLHHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_002328464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
O127:H6 str. E2348/69]
ref|ZP_07783233.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
2362-75]
sp|B7UMZ4.1|AROAE027 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAS08449.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Escherichia coli
O127:H6 str. E2348/69]
gb|EFRL4341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
2362-75]
gb|EFW71221.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Escherichia coli
WV_060327]
Length = 427

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 292/436 (66%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTLNLLSDDDRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSDRTRCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVDDVGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCM-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNINYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDFIRITPPEKLFABEATYNDHRMAMCFSLVALSDTAVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_003333837.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii
Ech586]
gb|ACZ77132.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii

Ech586]
Length = 429

Score = 422 bits (1084), Expect = e-116, Method: Compositional matrix adjust.
Identities = 226/442 (51%), Positives = 297/442 (67%), Gaps = 17/442 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E + LQPI I GT+ LKSGKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL LG
Sbjct: 3 ESLTLQPISLIDGTINLPGSKSVSNRALLAALAKGTTTLNLLSDDDVRHMLNALSALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + +VG GG F A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 63 VEYHLSASRTECDIVLGGGFT--ASAPLELFLGNAGTAMRPLAALCLTDGD--IVLT 117

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGARIDYLEQENYPPLRLRG--GFQGGESVDSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA+ D +I I L+S PY+++TL +M+ FG+ ++++ F + G Q Y+S
Sbjct: 176 ALLMTAPLAVQDTQITIKGDLVSKPYIDITLHMMQTFGITVT--NNNYQTFVAGNQHYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA+V W +
Sbjct: 235 PGHYLVEGDASSASYFLAAAAIRGGTVRVTVGVRNSVQGDIFADVLEKMGAVRWGDAY 294

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ R L AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R
Sbjct: 295 IECQ-----RGLHAIDMDMNHIPDAAMTIATAALFAEGGTTTTLRNIYNWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP++L I TY+DHRMAM FSL A ++ PVTI
Sbjct: 347 LAAMATELRKVGAEVEEGHDYIRITPPKQLKAAEIGTYNDHRMAMCFSLVALSDTPVTIL 406

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
DP CT KTFPDYF L ++
Sbjct: 407 DPKCTAKTFPDYFQQLERLSQH 428

>gb|AAT45235.1| 5-enol-pyruvylshikimate-phosphate synthase [Asimina triloba]
Length = 264

Score = 421 bits (1083), Expect = e-116, Method: Compositional matrix adjust.
Identities = 204/264 (77%), Positives = 230/264 (87%)

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
L+TLGL+VE D AA +A V GCGG+FPV +++QLFLGNAG AMR LTA AV AAGG +
Sbjct: 1 LQTLGLNVEEDSAANKATVEGCGGQFPVGKDAKDIQLFLGNAGTAMRPLTAAVVAAGGKS 60

Query: 120 TYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSI 179
YVLDGVPRMRERPIGDLV GLKQL ADVDC LGT+CPPV +N GGL GGVKLSG++S
Sbjct: 61 RYVLDGVPRMRERPIGDLVGLKQLDADVDCVLGTNCPVSVINANGGLRGKVKLSGTL 120

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+++LMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV AEHS SWDRF ++GG
Sbjct: 121 SQFLTSLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVSAEHSWSWDRFLVRGG 180

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
QKYKSP A+VEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGAKV+
Sbjct: 181 QKYKSPGTAFVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEKMGAKVS 240

Query: 300 WTETSVTVTGPPREPFRGKHLKAI 323
WTE SVTVTGPP +P +K L I
Sbjct: 241 WTENSVTVTGPPLDPSRKKRLHGI 264

>gb|EFZ75997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
RN587/1]
Length = 427

Score = 421 bits (1083), Expect = e-116, Method: Compositional matrix adjust.

Identities = 229/436 (52%), Positives = 291/436 (66%), Gaps = 16/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + GT+ LKPSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLSDDDRHLNLTALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          +S R ++G GG AK ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62  VSYTLSDRTRCEIIGNGGPL---HAKSALELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--GFTGGNVDDGSGVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175  ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234  PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305  VTVTGPPEPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          ++ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET R+
Sbjct: 294  ISCM-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRLNIYNWRVKETNRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA VEEG D+ ITPPEKL I TY+DHRMAM FSL A ++ VTI D
Sbjct: 346  FAMATELRKVGAEVEEGHDFIRITPPEKLFKFAEIATYNDHRMAMCFLVALSDTAVTILD 405

Query: 425  PGCTRKTFPDYFDVLS 440
          P CT KTFPDYF+ L+
Sbjct: 406  PKCTAKTFPDYFEQLA 421

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>ref|YP_001571007.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
      subsp. arizonae serovar 62:z4,z23:-- str. RSK2980]
sp|A9MHX5.1|AROASALAR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX21865.1| hypothetical protein SARI_01985 [Salmonella enterica subsp.
      arizonae serovar 62:z4,z23:--]
      Length = 427

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Score = 421 bits (1083), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 296/436 (67%), Gaps = 16/436 (3%)

```

Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + G + LKPSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGAINLPGSKSVSNRALLAALACGKTVLTNLLSDDDRHLNLTALSALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + R ++G GG A +++LFLGNAG AMR L AA+ G N T VL
Sbjct: 62  IDYTLSDRTRCDIIGNGGAL---RAPGDLELFLGNAGTAMRPLAAL-CLGQNET-VLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDSLQGGANIDYLEQENYPLRLRG--GFTGGDIEVDGSGVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D I + +L+S PY+++TL LM+ FGV+ + + +F +KGGQ+Y S
Sbjct: 175  ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIMNH-HYQQFVVKGGQYHS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234  PGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQMGDIRFADVLEKMGATITWGDDF 293

Query: 305  VTVTGPPEPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          + T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294  IACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 345

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Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL+ I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGDDYIRITPPAKLHHADIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|ZP_01262195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio alginolyticus
12G01]
gb|EAS74503.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio alginolyticus
12G01]
Length = 426

Score = 421 bits (1082), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/435 (52%), Positives = 292/435 (67%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G V LPGSKS+SNR LLLAAL++G T + NLL+S+D +ML AL LG
Sbjct: 2 ESLTLQPIKIQGEVNLPGSKSVSNRALLAALAKGRTRLTNLLDSDTRHMLNALT 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + +V G G F V E V+LFLGNAG AMR L AA+ G YVL
Sbjct: 62 VQYQLSEDKTECLVDGLGRPFVS---SEPVELFLGNAGTAMRPLAALCL--GEGEYVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GA+V+ + PP+++ G G L G V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVTALKDAGANVEYEMENENFPPLKIIGTG-LKAGTVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LM+APLA G++ I I L+S PY+++TL +M++FGV ++D + F I GQ+Y +
Sbjct: 176 AFLMSAPLAEGEIRINIEGDLVSKPYIDITLHIMKQFGVDVINND-YQEFVIPAGQQYIA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ LE MGA++ W +
Sbjct: 235 PGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADALEKMGAEIEWGDDY 294

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V LK ID++ N +PD AMT+A ALFA+G TAIR+V +WRVKET+R+
Sbjct: 295 VISR-----VGQLKGIDMDYNHHPDAAMTIATTALFAEGTTAIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY I+ P +L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGEDYIIVKPVSQLKHAADTYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKL 421

>ref|YP_003556821.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella violacea
DSS12]
dbj|BAJ02043.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella violacea
DSS12]
Length = 426

Score = 421 bits (1081), Expect = e-115, Method: Compositional matrix adjust.
Identities = 219/440 (49%), Positives = 290/440 (65%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+PI ++ GT+ +PGSKS+SNR LLLA L++GTT + NLL+S+D+ YML +L+ LG
Sbjct: 2 KQLRLEPISKVQGTINIPGSKSISNRALLATLAKGTTTTLTNLLDSDDIRYMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + G G E A+ LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSENNTVCELEGTGAPLNAELAQ---TLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA V PP+ +N G L G V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGASVTYLNKNEGFPLTINATG-LNAGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G+V I+I +L+S PY+++T+ LM +FGVK + D + F IK GQ Y S
Sbjct: 176 ALLMVAPLAKGEVNIKIGELVSKPYIDITIALMAQFGVKVINHD-YQAFEIKAGQTYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA++ W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGGEVKVTGVGRLSIQGDVKFADVLEKMGAEIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ L +D++MN +PD AMT+A ALFA GPT IR++ +WR+KET+R+
Sbjct: 295 IISR-----VAKLNGVDLDMNHIPDAAMTIATAALFATGPTTIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA V+EG DY ITPP K + IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAIIVDEGHDIISITPPSPKPTAEIDTYNDHRMAMCFSLALADCGITIND 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P CT KTFPDYF + +
Sbjct: 407 PDCTSKTFFPDYFQFAALAQ 426

>ref|ZP_04939314.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
cenocepacia PC184]
gb|EAY62485.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
cenocepacia PC184]
Length = 479

Score = 421 bits (1081), Expect = e-115, Method: Compositional matrix adjust.
Identities = 231/442 (52%), Positives = 288/442 (65%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLNSSEVDHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 51 LGPYSSASGTVRLPGSKSISNRVLLAALAEGETTTTNLLDSDDTRVMDALGKLGVKLA 110

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 111 RD--GDTCVVGTGRGAF+TAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 162

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 163 MHERPIGDLVDGLRQIGAQIDYELNEGYPPLRIKPATISVDAPIRVRGDVSSQFLTALLM 222

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +E+ +LIS PY+++T+RLM RFGV E D W RF + G +YKSP
Sbjct: 223 TLPLVKAkdGRTVVEVDGELISKPYIDITIRLMARFGVTVER-DGWQRFVVPAGVRYKSP 281

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 282 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 341

Query: 306 TVTGPPEPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 342 DVRG-----IGHDHGKLEPIDMDFNLPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 396

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA VEEGPDY ++TPPEKL AIDTYDDHRMAM FSL + VPV I
Sbjct: 397 IAAMATELRKVGAIIVEEGPDYLVVTPPEKLTNPAAIDTYDDHRMAMCFSLVSLGGVPVRI 456

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 457 NDPKCVGKTFFPDYFDRFAALAK 478

>ref|YP_002145896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Agona str. SL483]
sp|B5F161.1|AROASALA4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACH51017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Agona str. SL483]

Length = 427

Score = 421 bits (1081), Expect = e-115, Method: Compositional matrix adjust.
Identities = 230/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LKPKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLLTLQPIARVDGAINLPKSKSVSNRALLAALACGKTVLMNLLDSDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADRTCDITGNGGALHAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPRLRLRG--GFTGGDIEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQKY
Sbjct: 175 ALLMTAPLAPEDTIIIRVKELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQKYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSMDQDIRFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGELHAIDMDMNHIPDAAMTIATATLFAKGTTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|ZP_03841175.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Proteus mirabilis
ATCC 29906]
gb|EEI48015.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Proteus mirabilis
ATCC 29906]
Length = 428

Score = 421 bits (1081), Expect = e-115, Method: Compositional matrix adjust.
Identities = 226/438 (51%), Positives = 292/438 (66%), Gaps = 16/438 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I GT+ LKPKSKS+SNR LLLAAL++G T + NLL+S+D+ +ML AL LG
Sbjct: 2 ESLLTLQPIVHIEGTINLPKSKSVSNRALLAALAKGKTRLTNLLDSDIRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + G G F ++ ++LFLGNAG AMR L AA++ G VL
Sbjct: 62 VQYQLSNNTVCDIEGLAGSF---HPQQPLELFLGNAGTAMRPLAALSL--GEHDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D TD PP+RV GG GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKIDYLEQTDYPPPLRV--CGGFGSGSVSDVDSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I +L+S PY+++TL L+ FG + E+ + + RF IKGGQ+Y+S
Sbjct: 175 ALLMMAPLAQDQTTITIKGELVSKPYIDITLALINTFGGEIENQN-YQRFMIKGGQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G SLQGD+ FA VLE MGA + W +
Sbjct: 234 PGKYLVEGDASSASYFLAAAAIKGIVRVGTGIGKNSLQGDHIFASVLEKMGATIRWGDDY 293

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ R LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R+
Sbjct: 294 IECE-----RGKLKGIDMDMNTIPDAAMTIATTALFAEGETTIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424

A+ TEL K+GA V+EG DY + PP++L I TY+DHR+AM FSL A + P+TI D

Sbjct: 346 SAMATELRKVGAMVDEGRDYLTVIPPKQLTTAEIKTYNDHRIAMCFSLVALSNTPTITILD 405

Query: 425 PGCTRKTFPDYFDVLSTF 442

PGCT KTFPDYF+ L++

Sbjct: 406 PGCTAKTFPDYFEKLASI 423

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>gb|EFY13317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 315996572]
gb|EFY16533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 495297-1]
gb|EFY19491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 495297-3]
gb|EFY26570.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 495297-4]
gb|EFY29229.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 515920-1]
gb|EFY33725.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 515920-2]
gb|EFY38076.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 531954]
gb|EFY42612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str.
    NC_MB110209-0054]
gb|EFY46033.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. OH_2009072675]
gb|EFY50419.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str.
    CASC_09SCPH15965]
gb|EFY54890.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 19N]
gb|EFY59687.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 81038-01]
gb|EFY66361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. MD_MDA09249507]
gb|EFY67579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 414877]
gb|EFY72880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 366867]
gb|EFY78757.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 413180]
gb|EFY82399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 446600]
gb|EFZ81107.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 609458-1]
gb|EFZ84861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 556150-1]
gb|EFZ87801.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 609460]
gb|EFZ93973.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 507440-20]
gb|EFZ96351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 556152]
gb|EGA02718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. MB101509-0077]
gb|EGA04400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. MB102109-0047]
gb|EGA10904.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. MB110209-0055]
gb|EGA13928.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. MB111609-0052]
gb|EGA17126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 2009083312]
gb|EGA24807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 2009085258]
gb|EGA27102.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. 315731156]
gb|EGA33658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Montevideo str. IA_2009159199]
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gb|EGA36609.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008282]
gb|EGA38592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008283]
gb|EGA43636.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008284]
gb|EGA51470.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008285]
gb|EGA53287.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008287]
Length = 427

Score = 420 bits (1080), Expect = e-115, Method: Compositional matrix adjust.
Identities = 227/436 (52%), Positives = 293/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LKSGK+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSGKSVSNRALLAALACGKTVLTNLLDSDVHRMLNALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPRLRLG--GFTGGDIEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ + + +F +KGGQ+Y S
Sbjct: 175 ALLMTAPLAPETTTIRVKGELVSKPYIDITLNLMTKTFGVEITNH-HYQQFVVKGGQYHS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234 PGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDDF 293

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL+ I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPAKLHHADIGTYNDHRMAMCFLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFFPDYFEQLA 421

>ref|YP_003017310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium carotovorum subsp. carotovorum PC1]
sp|C6DF65.1|ARO_A_PCECP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACT12774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium carotovorum subsp. carotovorum PC1]
Length = 429

Score = 420 bits (1080), Expect = e-115, Method: Compositional matrix adjust.
Identities = 232/439 (52%), Positives = 301/439 (68%), Gaps = 21/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPIK I+GT+ LKSGK+SNR LLLAALSEG T + NLL+S+DV +ML AL LG
Sbjct: 3 ESLTLQPIKLINGTLNLPKSGKSVSNRALLAALSEGKTRLTNLLDSDVHRMLTALAALG 62

Query: 65 LSVEADKAAKRAV--VVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE ++ R V + G GG F A + ++LFLGNAG AMR L AA+ G+ V
Sbjct: 63 --VEYHLSSDRITVCEITGLGGAFT---ASQPLELFLGNAGTAMRPLAALCLTDGD--IV 115

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G PRM+ERPIG LV L+Q GA +D + PP+R++G G GG++ + GS+SSQ+
Sbjct: 116 LTGEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPRLRHG--GFQGGIEISVDGVSQSF 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLM APLA D +I I L+S PY+++TL +M+ FG++ + +++ RF++ G Q+Y
Sbjct: 174 LTALLMTAPLAAQDTQISIQGDLVSKPYIDITLHMMKAFGIEVRN-ENYQRFVAGRQQY 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+SP + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+VLE MGA V W E
Sbjct: 233 RSPGDYLVEGDASSASYFLAAAIKGGVVRVTGVGRNSVQGDIFADVLERMGAIVRWGE 292

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG-PTAIRDVASWRVKET 361
+ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET
Sbjct: 293 DYIECE-----RGELHAIDMDMNHIPDAAMTIATAALFAQGGTTTLRNIYNWRVKET 344

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ EL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVT
Sbjct: 345 DRLAAMAEI LRKVGAEVEEGNDYIRITPPAKLKAAEIGTYNDHRMAMCFSLVALSDTPVT 404

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I DP CT KTFPDYF+ L+
Sbjct: 405 ILDPKCTAKTFPDYFEQLA 423

>ref|ZP_02834918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Weltevreden str. HI_N05-537]
gb|EDZ27500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Weltevreden str. HI_N05-537]
Length = 427

Score = 420 bits (1080), Expect = e-115, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPSKSK+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSKSVSNRALLAALACGKTVLTLNLLSDDDRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGLVVLGKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG L+ L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLIDSLRQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTTIRVKGELVSKPYIDITLNLMTKTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACF-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_001118812.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
vietnamiensis G4]
sp|A4JCH4.1|ARO_A_BURVG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABO53977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
vietnamiensis G4]

Length = 434

Score = 420 bits (1080), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/442 (51%), Positives = 287/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGETTITNLLDSDDTVRMLDALGKLGVRLT 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D A VV G G F A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--ADTCVVAGTRGAFTARTA----DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPPRLRIKPAAITVDAPIRVGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G + +E+ +LIS PY+++T+RLMERFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAADGKIVVEVDGELISKPYIDITIRLMERFGVTVER-DGWQRFFVVPAGVYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA V+ + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVSMGDDWI 296

Query: 306 TVTGPPPREPFGKRH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L ID++ N +PD AMT+AV ALFA G + +R++ASWRVKET+R
Sbjct: 297 EVRG-----IGHDHGKLDPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL KLGA VEEGPDY ++TPP++L A IDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKLGA VEEGPDYLVVTPPQRLTPNATIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>ref|ZP_03220991.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Javiana str. GA_MM04042433]
gb|EDZ06165.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Javiana str. GA_MM04042433]
Length = 427

Score = 420 bits (1080), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLDSDDVHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADTRCDITGNGGPLRASGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTIIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_151047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Paratyphi A str. ATCC 9150]
ref|YP_002142532.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Paratyphi A str. AKU_12601]
sp|Q5PGG5.1|AROA_SALPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B5BBP9.1|AROA_SALPK RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAV77735.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Paratyphi A str. ATCC 9150]
emb|CAR59885.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Paratyphi A str. AKU_12601]
Length = 427

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 294/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSGKSVSNRALLAALACGKTVLTNLLSDDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITGNGGPLRASGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRQGGANIDYLEQENYPPLRLRG--GFIGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTIIRVKELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQMGDIRFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL+ I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLHHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_620450.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia AU 1054]
sp|Q1BY28.1|AROA_BURCA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF75477.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia AU 1054]
Length = 434

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.

Identities = 230/440 (52%), Positives = 288/440 (65%), Gaps = 16/440 (3%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
          L P      SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6  LGPYSSASGTVRLPGSKSISNRVLLLAALAEGETTITNLLSDDDRTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
          D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
          M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVGLRQIGAQIDYELSEGYPPLRIKPATISVDAPIRVRGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
          PL G +E+ +LIS PYV++T+RLM RFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAQKGDQAVVEVDGELISKPYVDITIRLMARFGVTVER-DGWQRFVVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSV 305
          VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
          V G + R L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R+
Sbjct: 297 DVRGIGHD--RGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDRIA 353

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA VEEGPDY ++TPPEKL AIDTYDDHRMAM FSL + VPV I D
Sbjct: 354 AMATELRKVGAIIVEEGPDYLVVTPPEKLTNPAAIDTYDDHRMAMCFLSVSLGGVPVRIND 413

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
          P C KTFPDYFD + K
Sbjct: 414 PKCVGKTFFPDYFDRFAALAK 433
```

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>ref|YP_215919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Choleraesuis str. SC-B67]
ref|YP_001588751.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Paratyphi B str. SPB7]
ref|ZP_02685504.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Hadar str. RI_05P066]
ref|YP_002636585.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Paratyphi C strain RKS4594]
sp|Q57R23.1|AROASALCH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
  AltName: Full=5-enolpyruvylshikimate-3-phosphate
  synthase; Short=EPSP synthase; Short=EPSPS
sp|A9N7V6.1|AROASALPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
  AltName: Full=5-enolpyruvylshikimate-3-phosphate
  synthase; Short=EPSP synthase; Short=EPSPS
sp|C0PXU4.1|AROASALPC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
  AltName: Full=5-enolpyruvylshikimate-3-phosphate
  synthase; Short=EPSP synthase; Short=EPSPS
gb|AA64838.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Salmonella enterica
  subsp. enterica serovar Choleraesuis str. SC-B67]
gb|ABX67918.1| hypothetical protein SPAB_02538 [Salmonella enterica subsp.
  enterica serovar Paratyphi B str. SPB7]
gb|EDZ34457.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Hadar str. RI_05P066]
gb|ACN45144.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
  subsp. enterica serovar Paratyphi C strain RKS4594]
gb|EFZ05542.1| 5-enolpyruvylshikimate-3-phosphate synthase [Salmonella enterica
  subsp. enterica serovar Choleraesuis str. A50]
Length = 427
```

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
          E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLSDDDRHMLNALSALG 61
```

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRLQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQMGGDIRFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_834691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia HI2424]
sp|A0K5M1.1|ARO_A_BURCH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK07798.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia HI2424]
Length = 434

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 231/442 (52%), Positives = 288/442 (65%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGKSSISNRVLLLAALAEGETTITNLLSDDDRTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYELSEGYPPLRIKPATISVDAPIRVRGVDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +E+ +LIS PYV++T+RLM RFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAKDGQAVVEVDGELISKPYVDITIRLMARFGVTVER-DGWQRFVVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPREPFGFRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 297 DVRG-----IGHDHGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA VEEGPDY ++TPPEKL AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVGAIVEEGPDYLVVTPPEKLTNPAAIDTYDDHRMAMCFSLSVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
DP C KTFPDYFD + K

Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>ref|YP_003753110.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia solanacearum PSI07]
emb|CBJ51843.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia solanacearum PSI07]
Length = 436

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 230/437 (52%), Positives = 292/437 (66%), Gaps = 15/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P++ GTVKLPKSGKS+SNR+LLLAAL+EG TVV +LL+S+D ML AL LG
Sbjct: 2 EHLEVGLPRAARGTVKLPKSGKSISNRVLLLAALAEGETTVVRDLLSDDTRVMLAALDRLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E A V G GG+FPV+ A LF+GNAG A+R LTAA+ GG Y L
Sbjct: 62 VRCEPLGTANAYRVAGTGGFRFPVKS-----DLFMGNAGTAIRPLTAALALQGGE--YALH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDGLRQVGARIDYTGNEGFPPLAIHAGAIRIDAPIRVRGDVSSQFLT 175

Query: 185 ALLMAAPLALGD--VEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLMA PL G V IE++ +LIS PY+E+TL LM RFGV+ E + W F + G
Sbjct: 176 ALLMALPLVEGGGRPVITIEVVGELISKPYIETLNLMARFGVQVER-NGWASFSVPTGVA 234

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y++P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 235 YRAPGEIFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAG 294

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ SWRVKET
Sbjct: 295 DNWIEVRGVERDD-GKLH--ALELDCNHIPDAAMTLAVAALFADGTTTLTNIGSWRVKET 351

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL KLGA+VEEG DY +TPP A IDTYDDHRMAMAFSLAA VP
Sbjct: 352 DRLTAMATELRKLGATVEEGADYIRVTPPSHWTPADGIDTYDDHRMAMAFSLAAGPVP 411

Query: 420 VTIRDPGCTRKTFPDYF 436
V I DP C KTFP+YF
Sbjct: 412 VRINDPRCVAKTFPEYF 428

>ref|YP_002040176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
sp|B4T142.1|AROASALNS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF65036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
Length = 427

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPKSGKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSGKSVSNRALLAALACGKTVLTLNLLSDSDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSDRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y

Sbjct: 175 ALLMTAPLAPEDTIIRVKGELVSKPYIDITLNLTKTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +

Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQMDIRFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R

Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI

Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFFPDYFDVLS 440
DP CT KTFPDYF+ L+

Sbjct: 405 DPKCTAKTFFPDYFEQLA 421

>ref|YP_001764303.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia MC0-3]
sp|B1JXR9.1|AROA_BURCC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACA90181.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia MC0-3]
Length = 434

Score = 420 bits (1079), Expect = e-115, Method: Compositional matrix adjust.
Identities = 231/442 (52%), Positives = 288/442 (65%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLNSQDVHMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +

Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGETTTNLLDSDDTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR

Sbjct: 66 RD--GDTCCVVTGTRGAF TAKTA----DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM

Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYELNEGYPPLRIKPATISVDAPIRVRGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP 245
PL G +E+ +LIS PY+++T+RLM RFGV E D W RF + G +YKSP

Sbjct: 178 TLPLVKAKDGRVTVEVDGELISKPYIDITIRLMARFGVTVER-DGWQRFVVPAGVRYKSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +

Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPREPFRGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R

Sbjct: 297 DVRG-----IGHDHGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA VEEGPDY ++TPPEKL AIDTYDDHRMAM FSL + VPV I

Sbjct: 352 IAAMATELRKVGAEVEEGPDYLVVTPPEKLT PNA AIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYFD + K

Sbjct: 412 NDPKCVGKTFFPDYFDRFAALAK 433

>ref|YP_002150479.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Proteus mirabilis
HI4320]
sp|B4ET25.1|AROA_PROMH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAR41667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Proteus mirabilis
HI4320]

Length = 428

Score = 419 bits (1078), Expect = e-115, Method: Compositional matrix adjust.
Identities = 225/438 (51%), Positives = 292/438 (66%), Gaps = 16/438 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI I GT+ LPGSKS+SNR LLLAAL++G T + NLL+S+D+ +ML AL LG
Sbjct: 2  ESILTQPIVHIEGTINLPGSKSVSNRALLLAALAKGKTRLTNLLDSDDIRHMLNALTAL 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + + + G G F ++ ++LFLGNAG AMR L AA++ G VL
Sbjct: 62  VQYQLSNNNTVCDIEGLAGSF---HPQQPLELFLGNAGTAMRPLAALSL--GEHDIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA +D TD PP+RV GG GG V + G++SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDLRQGGAKIDYLEQTDYPPPLRV--CGGFSGGSVDDGTVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          ALLM APLA D I I +L+S PY+++TL L+ FG + E+ + + RF IKGGQ+Y+S
Sbjct: 175  ALLMMAPLAQQDTTITIKGELVSKPYIDITLALINTFGGEIENQN-YQRFMIKGGQYQS 233

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
          P VEGDASSASYFLA AAI GG V V G G SLQGD+ FA VLE MGA + W +
Sbjct: 234  PGKYLVEGDASSASYFLAAAAIKGGIVRVGTGIGKNSLQGDHFAVLEKMGATIRWGDDY 293

Query: 305  VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          + R LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R+
Sbjct: 294  IECE-----RGKLKGIDMDMNTIPDAAMTIATTALFAEGETTIRNIYNWRVKETDRL 345

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
          A+ TEL K+GA V+EG DY + PP++L I TY+DHR+AM FSL A + P+TI D
Sbjct: 346  SAMATELRKVGAMVDEGRDYLTVIPPQQLTTAEIKTYNDHRIAMCFSLVALSNTPTITILD 405

Query: 425  PGCTRKTFPDYFDVLSTF 442
          PGCT KTFPDYF+ L++
Sbjct: 406  PGCTAKTFPDYFEKLASI 423
```

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>ref|ZP_03217375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
      subsp. enterica serovar Virchow str. SL491]
gb|EDZ01755.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
      subsp. enterica serovar Virchow str. SL491]
Length = 427
```

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESILTQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLDSDVHRHMLNALSAL 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62  INYTLASDRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPPLRLRG--GFIGGDIEVDGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
          ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175  ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGQYH 232

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
          SP VEGDASSASYFLA AI GGT V V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233  SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304  SVTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          + T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293  FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNIYNWRVKETDR 344
```

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|ZP_04657086.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Tennessee str. CDC07-0191]
Length = 427

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 292/437 (66%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSGKSVSNRALLAALACGKTVLTNLLSDDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADTRCITGNGGPLRASGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APL D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLGPEDTTIRVKGELVSKPYIDITLNLMTKTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|NP_455465.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
ref|NP_805721.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. Ty2]
ref|ZP_03347320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E00-7866]
ref|ZP_03351734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E01-6750]
ref|ZP_03357378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E02-1180]
ref|ZP_03369581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E98-2068]
ref|ZP_03379422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. J185]
ref|ZP_03381542.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. M223]
ref|ZP_06534828.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. AG3]
ref|ZP_06545027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E98-3139]
sp|P19786.2|AROASALTI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

```

    synthase; Short=EPSP synthase; Short=EPSPS
pir|AH0613 3-phosphoshikimate 1-carboxyvinyltransferase [imported] -
    Salmonella enterica subsp. enterica serovar Typhi
    (strain CT18)
emb|CAD05378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Typhi]
gb|AA069570.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Typhi str. Ty2]
Length = 427

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 230/437 (52%), Positives = 295/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLDSDDVHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG P+ A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITGNGG--PLR-ASGTLELFLGNAGTAMRPLAALCL--QNEIVLT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFIGGDIEVDGVSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIGGTVKVTGIGRKSQGDIRFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGELHAIDMDMNHIPDAAMTIAATALFAKGTTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|YP_002214902.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Dublin str. CT_02021853]
ref|YP_002225986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Gallinarum str. 287/91]
ref|YP_002243020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Enteritidis str. P125109]
sp|P22299.1|AROA_SALGL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|B5FQ51.1|AROA_SALDC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|B5QYQ8.1|AROA_SALEP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
sp|B5R8J5.1|AROA_SALG2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
gb|AAA27223.1| 5-enolpyruvylshikimate 3-phosphate synthase [Salmonella enterica
    subsp. enterica serovar Gallinarum]
gb|ACH77880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Dublin str. CT_02021853]
emb|CAR36810.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
    subsp. enterica serovar Gallinarum str. 287/91]
emb|CAR32465.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica

```

subsp. enterica serovar Enteritidis str. P125109]
Length = 427

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLAALACGKTVLTNLLSDDDRHLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSDRTRCDITNGGGLRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFIGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGELHAIDMDMNHIPDAAMTIATLALFAGTTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSPTVITL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|ZP_02156189.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella benthica
KT99]
gb|EDQ02202.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella benthica
KT99]
Length = 426

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 219/440 (49%), Positives = 290/440 (65%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+PI ++ GT+ +PGSKS+SNR LLLA L++GTT + NLL+++D+ YML +L+ LG
Sbjct: 2 KQLRLEPISKVQGTINIPGSKSISNRALLLATLAKGTTTLTNLLDADDIRYMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + G G +AK LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNYRLSDNNTVCELEGIGAPL---NAKLAQTLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGA V PP+ + G L G V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGASVTYLNKNEGFPLTIKATG-LNAGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G+V I+I +L+S PY+++T+ LM +FGV+ + D + RF IK GQ Y S
Sbjct: 176 ALLMVAPLAKGEVNIKIGELVSKPYIDITIALMAQFGVEVINHD-YRRFEIKAGQTYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVGRLSIQGDVKFADVLEKMGADIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G LK +D++MN +PD AMT+A VALFA G T IR++ +WR+KET+R+
Sbjct: 295 IISRGA-----KLKGVLDMDMNHIPDAAMTIATVALFATGTTTIRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP K + IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAIVEEGHDYISITPPSKPHTAEIDTYNDHRMAMCFSLAFADCGITIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFP+YF + +
Sbjct: 407 PDCTSKTFPNYFQQFAALAQ 426

>ref|ZP_02665765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Heidelberg str. SL486]
ref|YP_002044970.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Heidelberg str. SL476]
sp|B4TD38.1|AROA_SALHS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF67954.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Heidelberg str. SL476]
gb|EDZ26886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Heidelberg str. SL486]
Length = 427

Score = 419 bits (1077), Expect = e-115, Method: Compositional matrix adjust.
Identities = 227/436 (52%), Positives = 292/436 (66%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITNGGGLRASGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYQEENYPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ + + +F +KGGQ+Y S
Sbjct: 175 ALLMTAPLAPEDTTIRVKGELVSKPYIDITLNLMTFGVEITNH-HYQQFVVKGQQQYHS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 234 PGRYLVEGDASSASYFLAAGAIGKGTVKVTGIGRKSMTQDIRFADVLEKMGATITWGDDF 293

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 IACT-----RGELHAIDMDMNHIPDAAMTIAT'TALFAKGT'TTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_02655933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Kentucky str. CDC 191]
ref|ZP_03076807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Kentucky str. CVM29188]
gb|EDX46026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Kentucky str. CVM29188]
gb|EDZ21576.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Kentucky str. CDC 191]
Length = 427

Score = 419 bits (1076), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 294/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVDGAINLPGSKSVSNRALLLALACGKTVLTNLLSDDDRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG++++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRQGGANIDYQEQENYPLRLRG--GFIDGEIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINRWVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>ref|ZP_02344102.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Saintpaul str. SARA29]
gb|EDZ12498.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Saintpaul str. SARA29]
Length = 427

Score = 418 bits (1075), Expect = e-115, Method: Compositional matrix adjust.
Identities = 229/437 (52%), Positives = 292/437 (66%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVDGAINLPGSKSVSNRALLLALACGKTVLTNLLSDDDRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADRTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQDEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG ++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLRQGGANIDYLEQENYPLRLRG--GFIGDIEADGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTTIRVKGELVSKPYIDITLNLMTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI GGT V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSQGDIFADVLEKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTLRNINRWVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFFPDYFEQLA 421

>ref|YP_002980821.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia pickettii
12D]
gb|ACS62149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia pickettii
12D]
Length = 434

Score = 418 bits (1075), Expect = e-115, Method: Compositional matrix adjust.
Identities = 232/438 (52%), Positives = 295/438 (67%), Gaps = 19/438 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GT+KLPKSGKS+SNR+LLLAAL++G TVV +LL+S+D ML AL LG
Sbjct: 2 EHLVDVGLKRTARGTIKLPKSGKSISNRVLLLAALAQGETVVRDLDSDTRVMLEALGKLG 61

Query: 65 LSVEA--DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+SVE D A + V G G+FP + A LF+GNAG A+R LTAA+ GG Y
Sbjct: 62 VSVEGLGDNAYR--VTGTAGRFPNKSA---DLFMGNAGTAIRPLTAALALQGGE--YT 112

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQY 182
L GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+
Sbjct: 113 LHGVPRMHERPIGDLVDGLRQVGARIDYTGNEGYPPLAIHAAPVKIDAPIRVRGDVSSQF 172

Query: 183 LSALLMAAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
L+ALLMA PL + G+V IE++ +LIS PY+E+TL LM RFGV+ D W F + G
Sbjct: 173 LTALLMALPLVESAGNVTIEVVGELISKPYIEITLNLMARFGVQVAR-DGWASFTVPTGV 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 232 AYKAPGEIFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMA 291

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ASWRVKE
Sbjct: 292 GGNWIEVRGAERDD-GKLH--AVELDCNHIPDAAMTLAVAALFADGTTTTLTNIASWRVKE 348

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEV 418
T+R+ A+ TEL KLGA VEEG DY +TPP + A IDTYDDHRMAMAFSLAA V
Sbjct: 349 TDRLSAMATELRKLGAEEVEEGADYIRVTPPSQWTPPAGGIDTYDDHRMAMAFSLAAFGPV 408

Query: 419 PVTIRDPGCTRKTFPDYF 436
PV I DP C KTFP+YF
Sbjct: 409 PVRINDPRCAKTFPEYF 426

>ref|NP_459953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. LT2]
ref|ZP_02575816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar 4,[5],12:i:- str. CVM23701]
sp|P07637.2|AROA_SALTY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAL19912.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Salmonella enterica
subsp. enterica serovar Typhimurium str. LT2]
gb|EDZ14224.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar 4,[5],12:i:- str. CVM23701]
emb|CBG23998.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. D23580]
gb|ACY87600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. 14028S]
emb|CBW17011.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. SL1344]
dbj|BAJ35938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. T000240]
gb|EFX48370.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Salmonella enterica
subsp. enterica serovar Typhimurium str. TN061786]
gb|ADX16673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhimurium str. 4/74]
Length = 427

Score = 418 bits (1075), Expect = e-115, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 292/437 (66%), Gaps = 18/437 (4%)

```

Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + G + LPGSKS+SNR LLLAAL+ G T + NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTALTNLDSDDVRHMLNALSALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++          R + G GG          A ++LFLGNAG AMR L AA+          G VL
Sbjct: 62  INYTLSADTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA++D          + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFTGGDIEVDGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
          ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175  ALLMTAPLAPKDTIIRVKGELVSKPYIDITLNLMTKTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
          SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233  SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSMTQGDIFADVLEKMGATITWGDD 292

Query: 304  SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          + T          R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293  FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTTLRNIYNWRVKETDR 344

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
          + A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345  LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424  DPGCTRKTFFPDYFDVLS 440
          DP CT KTFPDYF+ L+
Sbjct: 405  DPKCTAKTFFPDYFEQLA 421

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>ref|ZP_03163351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Saintpaul str. SARA23]
gb|EDY24152.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Saintpaul str. SARA23]
Length = 427

Score = 418 bits (1075), Expect = e-115, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2  ESLTLQPIARVDGAINLPGSKSVSNRALLLAALACGKTVLTNLLDSDDVRHMLNALSALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++          R + G GG          A ++LFLGNAG AMR L AA+          G VL
Sbjct: 62  INYTLSADTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G PRM+ERPIG LV L+Q GA++D          + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117  GEPRMKERPIGHLVDSLQGGANIDYLEQENYPPLRLRG--GFIGGDIEVDGSVSSQFLT 174

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
          ALLM AP+A D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175  ALLMTAPMAPEDTIIRVKGELVSKPYIDITLNLMTKTFGVEIANHH--YQQFVVKGGQQYH 232

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
          SP VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW +
Sbjct: 233  SPGRYLVEGDASSASYFLAAGAIKGGTVKVTGIGRKSMTQGDIFADVLEKMGATITWGDD 292

Query: 304  SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          + T          R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293  FIACT-----RGELHAIDMDMNHIPDAAMTIATTALFAKGTTTLRNIYNWRVKETDR 344

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423

```

+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404
Query: 424 DPGCTRKTFFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFFPDYFEQLA 421

>ref|ZP_06155071.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Photobacterium
damselae subsp. damsela CIP 102761]
gb|EEZ40768.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Photobacterium
damselae subsp. damsela CIP 102761]
Length = 426

Score = 418 bits (1075), Expect = e-115, Method: Compositional matrix adjust.
Identities = 225/432 (52%), Positives = 286/432 (66%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+G V LPKSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2 ESLLTLQPINLINGEVNLPKSGKSVSNRALLAALAAGTTRLTNLLDSDDIRHMLNALQQLG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V G G F V+D L+LGNAG AMR L AA+ G + L
Sbjct: 62 VQYQLSADKTECTVEGLGQPFVSKDF---TCLYLGNAGTAMRPLAALCL--GQGEFELT 116
Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GAD+ PP+++ G G L GG+V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRSAGADITYLENEHYPLKIKGTG-LDGEVSIIDGSISSQFLT 175
Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D I I L+S PY+++TL +M +FGV+ E+ + + +F + GQ Y+S
Sbjct: 176 AFLMAAPLAKSDTTILIKGDLVSKPYIDITLIMAQFGVQVENQN-YQKFIVPAGQVYQS 234
Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGD++FA+ LE MGA++ W E
Sbjct: 235 PGEFLVEGDASSASYFLAAGAIGKEGVKVTGIGKNSIQGDIQFADALEAMGAIEIWGEDY 294
Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + L AID++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R+
Sbjct: 295 IIR-----HRQLNAIDMDFNHIDPDAAMTIATAALFAPGTTISIRNVYNWRVKETDRL 346
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL KLGA VEEG DY ITPP +L AIDTYDDHRMAM FSL A ++ VTI D
Sbjct: 347 HAMATELRKLGDVEEGDDYITITPPTQLKHAIDTYDDHRMAMCFSLVALSDTAVTIND 406
Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PKCTSKTFFPDYF 418

>ref|YP_001094077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella loihica
PV-4]
sp|A3QEC0.1|AROASHELP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABO23818.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella loihica
PV-4]
Length = 426

Score = 418 bits (1074), Expect = e-115, Method: Compositional matrix adjust.
Identities = 219/432 (50%), Positives = 285/432 (65%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++ L PI ++ GTV +PGSKS+SNR LLLA L+EG T + NLL+S+D+ +ML AL+ LG
Sbjct: 2 KQLRLNPIKSVHGTVNIPKSGKSLSNRALLLATLAEGKTRLTNLLDSDDIRHMLTALKQLG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + V G G + A+ LFLGNAG AMR L AA+T G+ + L
Sbjct: 62 VNYQLSDNNRVEVEGLSGVINSDTAQ---TLFLGNAGTAMRPLCAALTL--GSGEFTLT 116
Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G PRM ERPIGDLV L LGAD+ PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMERPIGDLVDALNALGADIRYLKQPGFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM PLA V I+I +L+S PY+++T+ LM +FGV + D + RF I GQKY S
Sbjct: 176 ALLMVTPLAKAQVNIKIGELVSKPYIDITIALMAQFGVTVINHD-YQRFEIPAGQKYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFAEVLE MGA++ W +
Sbjct: 235 PGTVLVEGDASSASYFLAAGAIQGGEVKVTGVGLKSIQGDVKFAEVLEAMGAQIEWGDDF 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P L +D++MN +PD AMT+A ALFA G T +R++ +WR+KET+R+
Sbjct: 295 IIARSAP-----LHGVLDLMNHIPDAAMTIATAALFATGTTTLRNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY +T P +LN IDTY+DHRMAM FSL A A+ +TI D
Sbjct: 347 AAMATELRKVGAEEVEEGHDYIRVTAPQLNTADIDTYNDHRMAMCFSLMAFADCGITIND 406

Query: 425 PGCTRKTFFPDYF 436
P CT KTFPDYF
Sbjct: 407 PDCTSKTFFPDYF 418

>ref|ZP_04753511.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus minor
NM305]
gb|EER47103.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus minor
NM305]
Length = 432

Score = 418 bits (1074), Expect = e-114, Method: Compositional matrix adjust.
Identities = 231/439 (52%), Positives = 292/439 (66%), Gaps = 17/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI I G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLAPISRIEGEINLPGSKSLSNRALLAALAQQTTQVTNLLDSDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E V G GG F ++ + LFLGNAG AMR LTAA+ G A VL
Sbjct: 62 VKYELSADKTICTVEGVGGAFQWQNG---LSLFLGNAGTAMRPLTAALCLKGKEEAEEVVL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA + PPV + G L GGVK+ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAQIQYLENEGYPVVAIRNTG-LTGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEII +L+S PY+++TL +M+ FGV H + + F++KG Q Y
Sbjct: 178 TALLMSAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVTVSHQN-YQTFVKGQQSYV 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237 SPEKYMVEGDASSASYFLAAGAIK-NVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ R LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----RGELKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P ++ I+TY+DHR+AM FSL A + PVT
Sbjct: 348 LTAMATELRKVGAEEVEEGEDFIRIQPLALDQFQHAIEITYNDRHVAMCFSLVALSNTPVT 407

Query: 422 IRDPGCTRKTFFPDYFDVLS 440
I DP CT KTFP YFD L+
Sbjct: 408 ILDPKCTAKTFPTYFDELA 426

>ref|YP_001760683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella woodyi
ATCC 51908]
sp|B1KF47.1|AROA_SHEWM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ACA86588.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella woodyi
ATCC 51908]
Length = 426

Score = 417 bits (1073), Expect = e-114, Method: Compositional matrix adjust.
Identities = 219/433 (50%), Positives = 291/433 (67%), Gaps = 15/433 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
      +++ L+ I ++ GTV +PGSKS+SNR LLLA L++GTT + NLL+S+D+ YML +L+ LG
Sbjct: 2  KQLRLETINKVQGTVNIPGSKSISNRALLLATLAKGTTTLNLLDSDDIRYMLASLKQLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      ++      +      + G G      A+      LFLGNAG AMR L AA+T      G      ++L
Sbjct: 62  VNYRLESDKTVCELDGLGAPINSNVAQ---TLFLGNAGTAMRPLCAALTL--GEGEFILT 116

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM ERPIGDLV L+QLGA+V      PP+ +N G L G V+++G +SSQ+L+
Sbjct: 117  GEPRMEERPIGDLVDALRQLGAEVTYLKSEGFPLTINATG-LNAGDVEIAGDLSSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALLM +PLA GDV I+I +L+S PY+++TL LM +FGVK + D ++RF IK GQ Y S
Sbjct: 176  ALLMVSPLAKGDVNIKIKGELVSKPYIDITLALMAQFGVKVINHD-YERFEIKSGQSYVS 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P      VEGDASSASYFLA AI GG V V G G S+QGDVKFA+VLE MGA++ W +
Sbjct: 235  PGKVLVEGDASSASYFLAAGAIGGEVKVTGVGRLSIQGDVKFADVLEKMGAEIEWGDDY 294

Query: 305  VTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      +      L A+D++MN +PD AMT+A ALFA G T IR++ +WR+KET+R+
Sbjct: 295  IISR-----VAKLNAVLDLNMHNPDAAMTIATAALFATGTTHIRNIYNWRIKETDRL 346

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+ TEL K+GA V+EG DY +TPP K + IDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347  AAMATELRKVGAIVDEGHDIISVTPPTKPHNTANIDTYNDHRMAMCFMMLAFADCGITIND 406

Query: 425  PGCTRKTFPDYFD 437
      P CT KTFPDYF+
Sbjct: 407  PDCTSKTFPDYFE 419

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>ref|YP_001898360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia pickettii
12J]
sp|B2U886.1|AROARALPJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD25928.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia pickettii
12J]
Length = 434

Score = 417 bits (1073), Expect = e-114, Method: Compositional matrix adjust.
Identities = 230/436 (52%), Positives = 292/436 (66%), Gaps = 15/436 (3%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + + P+K GT+KLPKSGSKS+SNR+LLLAAL++G TVV +LL+S+D ML AL LG
Sbjct: 2  EHLVDVGLKLTARGETIKLPKSGSKSISNRVLLLAALAQGETTVVRDLLDSDTRVMDALGKLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +SVE +      V G GG+FP A      LF+GNAG A+R LTAA+      GG      Y L
Sbjct: 62  VSVEG-QGENAYRVGTGGRFPNTSA----DLFMGNAGTAIRPLTAALALQGGE--YTLH 114

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      GVPRM ERPIGDLV GL+Q+GA +D      PP+ ++      +++ G +SSQ+L+
Sbjct: 115  GVPRMHMERPIGDLVDGLRQVGARIDYTGNEGYPPLAIHAAPVKIDAPIRVRGDVSSQFLT 174

Query: 185  ALLMAAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
      ALLMA PL + G+V IE++ +LIS PY+E+TL LM RFGV+      D W F + G Y
Sbjct: 175  ALLMALPLVESAGNVITIEVVGELISKPYIEITLNLMARFGVQVAR-DGWSSFTVPTGVAY 233

Query: 243  KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 234  TAPGEIFVEGDASSASYFLAAGALGGPVRVEGVGMSSIQGDVRFADALNRMGANVMAGG 293

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Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ASWRVKET+
Sbjct: 294 NWIEVRGAERDD-GKLH--AVELDCNHIPDAAMTLAVAALFADGTTTLTNIASWRVKETD 350

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL KLGA VEEG DY +TPP + A IDTYDDHRMAMAFSLAA VPV
Sbjct: 351 RLSAMATELRKLGAEEVEEGADYIRVTPPSQWTPPAGIDTYDDHRMAMAFSLAAFGVPV 410

Query: 421 TIRDPGCTRKTFPDYF 436
I DP C KTFP+YF
Sbjct: 411 RINDPRCVAKTFPEYF 426

>ref|YP_750809.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
frigidimarina NCIMB 400]
sp|Q081U4.1|AROASHEFN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI71971.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
frigidimarina NCIMB 400]
Length = 426

Score = 417 bits (1073), Expect = e-114, Method: Compositional matrix adjust.
Identities = 219/440 (49%), Positives = 288/440 (65%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L PI I+G + +PGSKS+SNR+LLLA L+ G+T + NLL+S+D+ YML +L+ LG
Sbjct: 2 KQLRLNPINCINGEINIPGSKSISNRVLLLATLARGSTTLTNLLDSDDIRYMLASLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + VV G G P+ A + LFLGNAG AMR L AA+T G + L
Sbjct: 62 IQYTLSEDKTECVVEGNEG--PISSASVQ-SLFLGNAGTAMRPLCAALTL--GQGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGDLV L+QLGADV PP+ +N G L GG V+++G +SSQ+L+
Sbjct: 117 GEPRMEERPIGDLVDALRQLGADVITYLKNDFPPLTINATG-LNGGDVEIAGDLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APL V I+I +L+S PY+++T+ LM++FGV+ + + RF IK GQ Y S
Sbjct: 176 ALLMVAPLTKDSVNIKIGELVSKPYIDITIALMKQFGVEVINH-QYQRFEIKAGQHYS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGDVKFA+ L MGA + W +
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIKGEVKVTGVRLSIQGDVKFADALQMGADIEWGDDY 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ L AI+++MN +PD AMT+A ALFA G T + ++ +WR+KET+R+
Sbjct: 295 IIR-----KSTLTAIEMDMNHIPDAAMTIATAALFATGTTKLTNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPP +LN AIDTY+DHRMAM FS+ A A+ +TI D
Sbjct: 347 AAMATELRKVGAIVEEGHDYITITPPAELNTAAIDTYNDHRMAMCFSMMAFADCGITIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYF + K
Sbjct: 407 PDCTSKTFPDYFAQFTQLAK 426

>ref|YP_002263584.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aliivibrio
salmonicida LF11238]
sp|B6EIX8.1|AROALISL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAQ79903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aliivibrio
salmonicida LF11238]
Length = 427

Score = 417 bits (1073), Expect = e-114, Method: Compositional matrix adjust.
Identities = 224/435 (51%), Positives = 287/435 (65%), Gaps = 14/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI +I G + LPGSKS+SNR LLLAAL+ G T + NLL+S+D+ +ML AL+ LG
Sbjct: 2 ESLTLQPIKIDGQINLPGSKSVSNRALLAALASGKTTLTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + V G G F + E ++LFLGNAG AMR L AA+ G ++L
Sbjct: 62 VDYKLSKEDKTVEVNGLGQAF--KSTTEALELFLGNAGTAMRPLAALCL--GEGEFILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV LK GADV+ + PP+++ G G L GG V + GSISSQ+L+
Sbjct: 118 GEPRMKERPIGHLVTALKAGADVEYLENENYPLKIKGTG-LKGGNVLDIDGSISSQFLT 176

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPL+ + I I+ L+S PY+++TL +M FGV E+ + + F + Q Y +
Sbjct: 177 AFLMAAPLSSQETTINIVGDLVSKPYIDITLDMATFGVVVLENKE-YKTFVVPANQSYIA 235

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG+V V G G S+QGDV+FA+ L MGA++ W +
Sbjct: 236 PGEFLVEGDASSASYFLAAAIAKGGSVKVTGIGKKSIGQDVQFADALAAMGAIEWGGDY 295

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V + L AID++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R+
Sbjct: 296 VIAH-----KGELNAIDMDFNHIPPDAAMTIATTALFAKGTTISIRNVYNWRVKETDRL 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITTP L IDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 348 AAMATELRKVGAEVEEGEDYITITPPAMLRHATIDTYDDHRMAMCFSLVALSDTPTVIND 407

Query: 425 PGCTRKTFPDYFDVL 439
PGCT KTFPDYFD L
Sbjct: 408 PGCTSKTFPDYFDKL 422

>ref|YP_001141683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromonas salmonicida
subsp. salmonicida A449]
sp|A4SM13.1|ARO_AERS4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABO89935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromonas salmonicida
subsp. salmonicida A449]
Length = 427

Score = 417 bits (1072), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/433 (51%), Positives = 291/433 (67%), Gaps = 16/433 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG+ +
Sbjct: 6 LEPIRSRVAGEVNLPGSKSVSNRALLAALARGTTTLTNLLSDDIRHMLAALTQLGVKYK 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V G G F V V LFLGNAG AMR L AA+ G+ Y+L G PR
Sbjct: 66 LSADKTECTVHGLGRSFAV---SAPVNLFLGNAGTAMRPLCAALCL--GSGEYMLGGEPR 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIG LV L++ GA + PP+ V+ GL GG V + GS+SSQ+L+A LM
Sbjct: 121 MEERPIGHLVDALREAGAHIQYLKKGYPPLVVDA-KGLWGGDVHVDGSVSSQFLTAFLM 179

Query: 189 AAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAP+A GD I I +L+S PY+++TL +M++FGV EH D++ FYIKG Q Y SP +
Sbjct: 180 AAPMAAGDTRIIHIGELVSKPYIDITLHIMKQFGVVIEH-DNYKLFYIKGNQSYVSPGDF 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGDASSASYFLA AI G V V G G S+QGD+ FA+VLE MGA++TW + +
Sbjct: 239 LVEGDASSASYFLAAGAIKG-KVRVTGIGKHSIQGDIHFADVLERMGARITWGDDFIEAE 297

Query: 309 GPPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P L +D++MN +PD AMT+AV ALFA+GPT+IR++ +WRVKET+R+ A+
Sbjct: 298 QGP-----LHGVDMDMNHIPPDAAMTIAVAALFAEGPTSIRNIYNWRVKETDRLHAMA 349

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
TEL KLG VEEG D+ +TPP +L IDTY+DHR+AM FSL A +++ VTI DPGCT

Sbjct: 350 TELRKLGEVEEGHDFITVTPPTQLKHAEIDTYNDHRIAMCFSLVALSDIAVTINDPGCT 409

Query: 429 RKTFPDYFDVLST 441

KTFPDYFD L++

Sbjct: 410 SKTFPDYFDKLAS 422

>ref|YP_932575.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Azoarcus sp. BH72]
emb|CAL93688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Azoarcus sp. BH72]
Length = 653

Score = 417 bits (1072), Expect = e-114, Method: Compositional matrix adjust.
Identities = 227/441 (51%), Positives = 283/441 (64%), Gaps = 20/441 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P+ G V+LPGSKS+SNR LLLAAL+EG T + +LL S+DV ML AL+ LG
Sbjct: 4 EFLDLPMLAARGQVRLPGSKSISNRSLLLAALAEGETDIRDLLASDDVERMLEALQALG 63

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ V G GG FPV+ LFLGNAG A R LTAA+ +GG+ Y L
Sbjct: 64 VRWSREEGTDNRYRVHVGVPVKKG---DLFLGNAGTAFRPLTAALALSAGD--YRLS 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
GV RM ERPIGDLV L+Q GAD++ PP+ + PGG +K+ G +SSQ+L+
Sbjct: 118 GVARMHERPIGDLVDALRQAGADIEYVGNFPPHLPATIRPGGVKVRGVDVSSQFLT 177

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL + IE++ +LIS PY+ +TL LM RFGV D W RF + GG +Y+S
Sbjct: 178 ALLMALPLTGVETTIEVVGELISKPYIAITLDMARFGVDVRED-WQRFVTPGGARYRS 236

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT---W 300
P YVEGDASSASYFLA AI GG V VEG G S+QGDV+FA+ L +GA +T W
Sbjct: 237 PGVLYVEGDASSASYFLAAGAIGGGPVRVEGVGRDSIQGDVRFADALAQLGAVITVGDNW 296

Query: 301 TETSVTVTGPPREPFRGKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E + G L+A D+++N +PD AMTLAV ALFADGP +R++ASWRVKE
Sbjct: 297 IEAAAPAGG-----RLRAFDLNLHIPDAAMTLAVAALFADGPCTLRNIASWRVKE 347

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ TEL K+GA VEEG DY I PP L AIDTYDDHRMAM FSL + V
Sbjct: 348 TDRIAAMATELRKVGAEVEEGADYLRIMPPAVLRPAIDTYDDHRMAMCFSLSLGGCRV 407

Query: 421 TIRDPGCTRKTFPDYFDVLST 441
I DP C KTFP YF+ +T
Sbjct: 408 RINDPRCVNKTFFPSYFEAFAT 428

>ref|ZP_07378948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pantoea sp. ab]
gb|EFM19586.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pantoea sp. ab]
Length = 428

Score = 417 bits (1072), Expect = e-114, Method: Compositional matrix adjust.
Identities = 229/432 (53%), Positives = 289/432 (66%), Gaps = 16/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI + GTV LPKSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL LG
Sbjct: 3 DSLTLQPISRVDGTVNLPKSKSVSNRALLAALAKGTRTLNLLSDDVKHMLNALTALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S V G G +A + + LFLGNAG AMR L AA+ G L
Sbjct: 63 VSYTSLSDRTVCEVTGNAGPL---NASQPLSLFLGNAGTAMRPLAALCL--GEHDIELT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA ++ + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGLVDALRQGGATIEYLENENYPPLRLRG--GFTGGDVSVDSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV E+ S+ RF IKG Q+Y+S
Sbjct: 176 ALLMTAPLAQQDTCITIKGDLVSKPYIDITLNLMQCFGVDVENQ-SYQRFLIKGQQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 235 PGDYLVEGDASSASYFLAAAAIKGGTVRVGTIGRQSMQGDIFADVLEKMGAAIEWGDDY 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L+AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R+
Sbjct: 295 IACTA-----GKLQAIDMDMNHIPDAAMTIATTALFAEGTTQLRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY ITPP L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGHDYIRITPPATLKHADIGTYNDRMAMCFSLVALSDPTVTILD 406

Query: 425 PGCTRKTFPDYF 436
PGCT KTFPDYF
Sbjct: 407 PGCTAKTFPDYF 418

>ref|YP_004028375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
rhizoxinica HKI 454]
emb|CBW74231.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
rhizoxinica HKI 454]
Length = 445

Score = 417 bits (1072), Expect = e-114, Method: Compositional matrix adjust.
Identities = 231/446 (51%), Positives = 291/446 (65%), Gaps = 16/446 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P +GTV+LPGSKS+SNR+LLLAAL+EG T +DNLL+S+D ML AL LG
Sbjct: 9 EYLDLGPYTRATGTVRLPGSKSISNRVLLLAALAEVTTIDNLLSDSDTRVMLAALQLG 68

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++++ D A R V G G FPV+ A LFLGNAG A+R LTAA+ GG Y L
Sbjct: 69 VTLQHDAAQWRCVTGTGAGSVFPVKRAA----LFLGNAGTAVRPLTAALAVMGGE--YRLH 122

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+QLGA +D PP+ V+ +++ G +SSQ+L+
Sbjct: 123 GVPRMHERPIGDLVDGLRQLGARIDYEGNPGYPPLL VHPASLRANAPIRVRGDVSSQFLT 182

Query: 185 ALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI--KGG 239
ALL+ PL A G +E+ +LIS PYVE+T+RLMERFGV + D W RF + G
Sbjct: 183 ALLITLPLVETAGGEAVVEVEGELISKPYVEITIRLMERFGVHVQR-DGWRRFIVPAAGC 241

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+Y+SP VEGDASSASYFLA A+ G V VEG G S+QGDV+FA+ L MGA V
Sbjct: 242 ARYRSPGRIVVEGDASSASYFLAAGALAHGVPVRVEGVGRASIQGDVQFADALVRMGANVM 301

Query: 300 WTETSVTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G + GR L+ +D++ N +PD AMT+AV ALFA G T +R++ SWRVK
Sbjct: 302 IGDDWIEVRGVESDD-GR--LQPLDMDCNLIPDAAMTIAAALFASGMTTLRNIGSWRVK 358

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL KLGA VEEG DY + PP L AIDTYDDHRMAM FSL + V
Sbjct: 359 ETDRIAMATELRKLGAVHEEGADYLRVAPPAALTPNAAIDTYDDHRMAMCFSLVSLGHV 418

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I DP C KTFPDYFD + +
Sbjct: 419 PVRIHDPSCVGKTFPDYFDRFAAATR 444

>gb|EGC99608.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
TJ149]
Length = 434

Score = 417 bits (1071), Expect = e-114, Method: Compositional matrix adjust.
Identities = 230/442 (52%), Positives = 286/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAALSEG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALSEGDTTITNLLSDSDTRVMLDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

Sbjct: 66 D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
RD--GDTCVVTGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM

Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGYPPLRIKPATISVDAPIRVRGVDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +EI +LIS PY+++T+RLMERFGV E D W RF + G +Y+SP

Sbjct: 178 TLPLVKAKDGRSVVEIDGELISKPYIDITIRLMERFGVNVER-DGWQRFFVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +

Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVGEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA G + +R++ASWRVKET+R

Sbjct: 297 EVRG-----IGHDHGKLEPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA+VEEGPDY ++TPP L AIDTYDDHRMAM FSL + VPV I

Sbjct: 352 IAAMATELRKVATVEEGPDYLVVTPPPALTPNAAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLFSTFVK 444
DP C KTFPDYFD + K

Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>ref|YP_003259387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
wasabiae WPP163]
gb|ACX87780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
wasabiae WPP163]
Length = 429

Score = 416 bits (1070), Expect = e-114, Method: Compositional matrix adjust.
Identities = 230/439 (52%), Positives = 299/439 (68%), Gaps = 21/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PIK I+GT+ LPGSKS+SNR LLLAALSEG T + NLL+S+DV +ML AL LG

Sbjct: 3 ESLTLHPILKINGTLNLPGSKSVSNRALLAALSEGKTRLNLLDSDVHRMLTALTALG 62

Query: 65 LSVEADKAAKRAV--VVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE ++ R + + G GG F A + ++LFLGNAG AMR L AA+ G+ V

Sbjct: 63 --VEYHLSSDRTICEITGLGGAFT---ATQPLELFLGNAGTAMRPLAALCLTAGD--IV 115

Query: 123 LDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G PRM+ERPIG LV L+Q GA +D + PP+R++G G GG++ + GS+SSQ+

Sbjct: 116 LTGEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPRLRHG--GFQGEISVDGVSQF 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLM APLA D I I L+S PY+++TL +M+ FG++ +++++ RF+I G Q+Y

Sbjct: 174 LTALLMTAPLATQDTHISIQGDLVSKPYIDITLHMMKAFGIEVR-NENYQRFIAGRQY 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
SP + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+VLE MGA V W +

Sbjct: 233 HSPGDYLVGEGDASSASYFLAAAAIKGGVVRVTGVGRNSVQDIRFADVLEKMGAIVRWGD 292

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG-PTAIRDVASWRVKET 361
+ R L+AID++MN +PD AMT+A ALFA G T +R++ +WRVKET

Sbjct: 293 DYIECE-----RGELRAIDMDMNHIPDAAMTIATAALFAQGGTTTLRNIYNWRVKET 344

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ EL K+GA VEEG DY ITTP KL I TY+DHRMAM FSL A ++ PVT

Sbjct: 345 DRLAAMAIELRKVGAEVEEGNDYIRITPPVKLKAAEIGTYNDHRMAMCFSLVALSDTPVT 404

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I DP CT KTFPDYF+ L+

Sbjct: 405 ILDPKCTAKTFPDYFEQLA 423

>ref|YP_002232052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia

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cenocepacia J2315]
sp|B4EB42.1|AROA_BURCJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
  AltName: Full=5-enolpyruvylshikimate-3-phosphate
  synthase; Short=EPSP synthase; Short=EPSPS
emb|CAR53255.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
cenocepacia J2315]
Length = 434

Score = 416 bits (1070), Expect = e-114, Method: Compositional matrix adjust.
Identities = 229/442 (51%), Positives = 287/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGETTITNLLDSDDTVRMLDALGKLGVKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
      D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      M ERPIGDLV GL+Q+GA +D L PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYELNEGYPPLRIKPATISVDAPIRVGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSP 245
      PL G +E+ +LIS PY+++T+RLM RFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAKDGRITVVEVDGELISKPYIDITIRLMARFGVTVER-DGWQRFFVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFGKRH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 297 DVRG-----IGHDHGKLEPIDMDFNLPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEPVPTI 422
      + A+ TEL K+GA VEEGPDY ++TPP KL AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVGAIVEEGPDYLVVTPPAKLTNPAAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
      DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

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>ref|YP_003882820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii
3937]
gb|ADM98263.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii
3937]
Length = 435

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Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/433 (51%), Positives = 291/433 (67%), Gaps = 17/433 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
      E + LQPI I+GT+ LPGSKS+SNR LLLAAL+ GTT + NLL+S+DV +ML AL LG
Sbjct: 9 ESLTLQPISLINGTINLPGSKSVSNRALLAALARGTTRLTNLLDSDDVHMLNALSALG 68

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + +VG GG A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 69 VEYRLSDSRTECEIVGGGGALT---ASTPLELFLGNAGTAMRPLAALCLTDGD--IVLT 123

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG + + GS+SSQ+L+
Sbjct: 124 GEPRMKERPIGHLVDALRQGGARIDYLEQENYPPLRLQG--GFTGGDISVDGSVSSQFLT 181

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKS 244
      ALLM APLA+ D I I L+S PY+++TL +ME FG+ ++D + F + G Q Y+S
Sbjct: 182 ALLMTAPLAVQDTRISIKGDLVSKPYIDITLHMMETFGITVINND-YQTFVVAGNQHYQS 240

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 304
      P + VEGDASSASYFLA AAI GGTV V G G S+QGD++FA+VLE MGA++ W +

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Sbjct: 241 PGHYLVEGDASSASYFLAAAAIRGGTVRVTVGVRHSVQGDIFADVLEKMGAEIRWGDDY 300

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ R +L AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R

Sbjct: 301 IECQ-----RGNLHAIDMDMNHIPDAAMTIATAALFAEGGTTTLRNIYNWRVKETDR 352

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITPP +L I TY+DHRMAM FSL A ++ PVTI

Sbjct: 353 LAAMATELRKVGAEEVEEGHDYIRITPPTQLKAAEIGTYNDHRMAMCFSLVALSDTPVTIL 412

Query: 424 DPGCTRKTFFPDYF 436
DP CT KTFPDYF

Sbjct: 413 DPKCTAKTFFPDYF 425

>ref|YP_582874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cupriavidus metallidurans CH34]
gb|ABF07605.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Cupriavidus metallidurans CH34]
Length = 452

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 229/449 (51%), Positives = 299/449 (66%), Gaps = 22/449 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L P+ SGT+LPGSKS+SNR+LLL+AL+ G T V +LL+S+D ML AL+ LG

Sbjct: 17 EQLTLGLPLTRASGTVRLPGSKSISNRVLLLSALATGETRVRLDSDTRVMLEALKVLG 76

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + +V G GG FP + A LF+GNAG A+R LTAA+ GG TY L

Sbjct: 77 VAWR--REGNCIVSGVGGNFPSKAA---DLFMGNAGTAIRPLTAALALQGG--TYKLS 128

Query: 125 GVPRMRERPIGDLVVLGLKQLGADVDCFLGT-DCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
GV RM ERPIGDLV GL+Q+GA VD +LGT PP+++N +++ G +SSQ+L

Sbjct: 129 GVQRMHERPIGDLVDGLRQVGASVD-YLGTGYPPLQINPAQIRIDAPIRVRGDVSSQFL 187

Query: 184 SALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ALLM P+A G +EIE++ +LIS PY+E+TL L+ RFG+ E W+RF + G

Sbjct: 188 TALLMTLPMAQAQSGRIEIEVVGELISKPYIEITLNLSSRFGIAVERQ-GWERFILPAGA 246

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y+SP YVEGDAS+ASYFLA AI GG V VEG G S+QGDV+FA+ L MGA V

Sbjct: 247 RYRSPGEIYVEGDASTASYFLAAGAIGGGPVRVEGVGMASIQGDVRFADALNRMGANVMA 306

Query: 301 TETSVTVTGPPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ + V G R+ GR L I+++ N +PD AMTLAV ALFA+G T + ++ASWRVKE

Sbjct: 307 GDNWIEVRGTERDD-GR--LNGIELD CNHIPDAAMTLAVAALFAEGTTTLTNIASWRVKE 363

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPE-----KLNVTADITYDDHRMAMAFSLAAC 415
T+R+ A+ TEL KLGA VEEG DY +TPP + I TYDDHRMAM FSLAA

Sbjct: 364 TDRISAMATELRKLGAEEVEEGADYLVKTPPTSPATWQTPDAGIGTYDDHRMAMCFSLA AF 423

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
+PV I DPGC KTFP+YF+V + +

Sbjct: 424 GPLPVKINDPGCAKTFPEYFEVFAGVAR 452

>ref|YP_003296223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Edwardsiella tarda EIB202]
gb|ACY85012.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Edwardsiella tarda EIB202]
gb|ADM42075.1| 5-Enolpyruvylshikimate-3-phosphate synthase AroF [Edwardsiella tarda FL6-60]
Length = 428

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 223/438 (50%), Positives = 285/438 (65%), Gaps = 16/438 (3%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ L P++ SG + LPGSKS+SNR LLLAA + G T + NLL+S+DV YML AL+ LG+

Sbjct: 5 LTLHPVRRFSGEINLPGSKSVSNRALLAAQARGVTRLHNLLDSDDVRYMLDALKALGVR 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ R V G GG A + LFLGNAG AMR L AA++ G +L G
Sbjct: 65 YQLSDCRTRCEVQGLGGLTSAHGA---LTLFLGNAGTAMRPLAAALSL--GQRDMILTGE 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM+ERPI LV L+Q GA VD PPVR+ G G GG + + GS+SSQ+L+AL
Sbjct: 120 PRMKERPIAHLVTALRQGGAHVDYLEDGYPPVRLRG--GFNGGDISVDGSVSSQFLTAL 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAP+A + I I+ +L+S PY+ +TL +M FGV+ EH ++ F ++GGQ Y++P
Sbjct: 178 LMAAPMAAEETRITILGELVSKPYIAITLAMMRTFGVEVEHH-AYRHFVVRGGQTYQAPG 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYFLAGAAI GGT V G G S+QGD+ FA+ LE MGA + W + +
Sbjct: 237 DYLVEGDASSASYFLAGAAIAGGTVRVTGIGRHSMQGDIHFADALEKMGAHIEWGDDYIA 296

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
T R L ID++MN +PD AMTLA ALFA GPT +R++ +WRVKET+R+ A
Sbjct: 297 CT-----RDSLHGIDMDMNAIPDAAMTLATTALFATGPTTLRNIYNWRVKETDRLAA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ EL K+GA VEEGPD+ I PP +L I TY+DHRMAM FSL A ++ PVTI DPG
Sbjct: 349 MACELQKVGAVVEEGPDFLRIEPPAQLRAAQIATYNDHRMAMCFSLVALSDTPVTICDPG 408

Query: 427 CTRKTFPDYFDVLSTFVK 444
CT KTFPDYF S
Sbjct: 409 CTAKTFPDYFSQFSALCH 426

>ref|ZP_04577990.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Oxalobacter formigenes
HOxBLS]
gb|EEO28952.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Oxalobacter formigenes
HOxBLS]
Length = 439

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 226/444 (50%), Positives = 296/444 (66%), Gaps = 24/444 (5%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L P+K +SGTV+LPGSKS+SNR LLL+AL++G TV+ +LL S+D ML AL+ LG+S
Sbjct: 8 IDLSPVKNVSGTVRLPGSKSISNRTLLLSALADGKTVIKDLLASDDTTVMLQALQDLGIS 67

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ VV G G PV++A LFLGNAG A+R LTAA+ GGN ++L G+
Sbjct: 68 WLQETGDACVVTGTRGNLPVKEA----DLFLGNAGTAIRPLTAALAVLGGN--FLLHGI 121

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM ERPIGDLV L + GA+++ PP+R+ G + +K+ G++SSQ+L+AL
Sbjct: 122 KRMHERPIGDLVDALNESGANIEYVENRGYPPIRIRD-GHIHSHDLKVRGNVSSQFLTAL 180

Query: 187 LMAAPLA--LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LMA+PL DV I ++ +LIS PY+E+TL LM FGV+ E D W+ F +K GQ YKS
Sbjct: 181 LMASPLMARTHDTVITHVVGELISKPYIEITLNLMRVFGVEVER-DGWESFTLKKGQTYKS 239

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P +VEGDASSASYFLA AAI GG V VEG G S+QGDV+F +VLE MGAKV + +
Sbjct: 240 PGTVHVVEGDASSASYFLAAAAIAGGPVRVEGIGRNSIQGDVRFVDVLERMGAKVVYGDNF 299

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V+ LK ID + N +PD AMT+A++A++ADGP+ +R++ SWRVKET+R+
Sbjct: 300 IEVSSG-----GSLKHIDEFNLIPDAAMTVAMLAVYADGPSVLNRNIGSWRVKETDRI 352

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP----- 419
VA+ TEL KLGA VE G D+ ITP +++ IDTYDDHRMAM FSL AC P
Sbjct: 353 VAMATELKKLGAGVEAGEDWLKITPGKRIFDAEIDTYDDHRMAMCFSL-ACLCSPNRMGA 411

Query: 420 -VTIRDPGCTRKTFPDYFDVLSTF 442
+ I DP C KTFP+YF V S

Sbjct: 412 KIRINDPRCVSKTFPEYFQVFSAL 435

>pdb|1Q36|A Chain A, Epsp Synthase (Asp313ala) Liganded With Tetrahedral
Reaction Intermediate
Length = 427

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 232/436 (53%), Positives = 294/436 (67%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LKSGK+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLSDDDRHLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSDRTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKTFGEIENQ--HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +P AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPAAAMTIATAALFAKGTTLRLNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDPTPTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+
Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|YP_927609.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
amazonensis SB2B]
sp|A1S6D3.1|AROASHEAM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABL99939.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Shewanella
amazonensis SB2B]
Length = 428

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 221/440 (50%), Positives = 286/440 (65%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ L+P+ ++G V +PGSKS+SNR LLLA L+ G T + NLL+S+D+ +ML AL++LG
Sbjct: 2 DQLRLEPVSrvngvvnipgsksisnralllatlasgettlnllsdDIRHMLNALKSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + G GG + A E LFLGNAG AMR L AA+T G + L
Sbjct: 62 VNFTLSDDKTVCTNLNGLGGPIQTDKAFE---LFLGNAGTAMRPLCAALTL--GTGEFTLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM ERPIGLV L+QLGAD+ PP+ +N G L GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMEERPIGLVDALRQLGADIRYKNDGFPPLTINATG-LAGGVVEIDGSLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA G V I + +L+S PY+++TL LM +FGV + D++ RF I GQ Y S
Sbjct: 176 ALLMVAPLAKGAVTIAVKGELVSKPYIDITLDMKFGVTVVN-DNYQRFEIASGQHYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G ++QGDVKFA+ L MGA + W E
Sbjct: 235 PGKVLVEGDASSASYFLAAGAIGGGEVKVTGVGR LAVQGDVKFADALAAMGADIEWGEDY 294

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ G L ID++MN +PD AMT+A ALFA+G T + ++ +WR+KET+R+
Sbjct: 295 IARG-----SKLHGIDMDMNHIPDAAMTIATAALFAEGTTRMSNIYNWRIKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY ITPP K IDTY+DHRMAM FSL A A+ VTI D
Sbjct: 347 AAMATELRKVGAKVEEGHDYIQITPPVKPVHAEIDTYNDHRMAMCFSLLAFADCGVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
PGCT KTFPDYF+ + K
Sbjct: 407 PGCTSKTFPDYFNRFANLAK 426

>sp|Q8VP65.1|AROA_PASPI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAL47682.1| 5-enolpyruvylshikimate-3-phosphate synthase [Photobacterium
damselfae subsp. piscicida]
Length = 426

Score = 416 bits (1069), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/440 (51%), Positives = 287/440 (65%), Gaps = 15/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
E + LQPI I+G V LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL+ LG
Sbjct: 2 ESLTLQPINLINGEVNLP GSKSVSNRALLLAALA QGTTRLTNLLDSDDIRHMLNALQQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA AVTAAGGNATYVLD 124
+ + V G G F V+D L+LGNAG AMR L AA+ G + L
Sbjct: 62 VQYQLSADKTECTVEGLGQPF SVKDF---TCLYLG NAGTAMRPLAALCL--GQGEFELT 116

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTD CPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GAD+ PP+++ G G L GG+V + GSISSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRSAGADITYLENEHYPLKIKGTG-LD GGEVSIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKA EHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D I I L+S PY+++TL +M +FGV+ E+ + + +F + GQ Y+S
Sbjct: 176 AFLMAAPLAKSDTTILIKGDLVSKPYIDITL NIMAQFGVQVENQN-YQKFIVPAGQVYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V G G S+QGD++FA+ LE MGA++ W E
Sbjct: 235 PGFVLVEGDASSASYFLAAGAIGGGEVKVTGIGKNSIQGDIQFADALEAMGAEIEWGEDY 294

Query: 305 VTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + L AID++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R+
Sbjct: 295 IIR-----HRQLNAIDMDFNHIPDAAMTIATAALFAPGTT SIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL KLGA VEEG DY IT P +L AIDTYDDHRMAM FSL A ++ VTI D
Sbjct: 347 HAMATELRKLGAEEVEEGDDYITITSPTQLKHVAIDTYDDHRMAMCFSLVALSDTAVTIND 406

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P CT KTFPDYF L +
Sbjct: 407 PKCTSKTFPDYFTKLEQLSR 426

>ref|YP_003004662.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya zeae Ech1591]
gb|ACT07183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya zeae Ech1591]
Length = 429

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/442 (50%), Positives = 295/442 (66%), Gaps = 17/442 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
E + LQPI I+GT+ LPGSKS+SNR LLLAAL++GTT + NLL+S+D+ +ML AL LG
Sbjct: 3 ESLTLQPISLINGTINLP GSKSVSNRALLLAALAKGTHLTNLLDSDDIRHMLNALSALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +VG G A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 63 VEYRLSANRTECEIVGLGTPLT---ASAPLELFLGNAGTAMRPLAALCLTEGD--IVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R++G G GG++ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGARIDYLEQENYPPLRLSG--GFQGGEISVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA+ D I I +L+S PY+++TL +ME FG+ +D + F + G Q+Y+S
Sbjct: 176 ALLMAAPLAVQDTRISIKGELVSKPYIDITLHMMETFGITVL-NDDYQTFVAVAGNQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD+ FA+VLE MGA++ W +
Sbjct: 235 PGHYLVEGDASSASYFLAAAIRGGTVRVTVGGRNSVQGDILFADVLEKMGARIGWGDDY 294

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ R L AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R
Sbjct: 295 IECQ-----RGELHAIDMDMNHIPDAAMTIATAALFAEGGTTTTLRNIYNWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL K+GA VEEG DY ITTP +L I TY+DHRMAM FSL A ++ PVTI
Sbjct: 347 LAAMATELRKVGAEVEEGHDYIRITPPTQLKAAEIGTYNDHRMAMCFSLVALSDTPVTIL 406

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
DP CT KTFPDYF L ++
Sbjct: 407 DPKCTAKTFPDYFQQLERLSQH 428

>ref|ZP_07675781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia sp.
5_7_47FAA]
gb|EFP65768.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ralstonia sp.
5_7_47FAA]
Length = 434

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 231/438 (52%), Positives = 295/438 (67%), Gaps = 19/438 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P+K GT+KLPGSKS+SNR+LLLA L++G TVV +LL+S+D ML AL LG
Sbjct: 2 EHLVDVGLKLTARGTIKLPKSGSISNRVLLAVLAQGETTVVRDLSDSDTRVMLEALGKLG 61

Query: 65 LSVEA--DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+SVE D A + V G GG+FP + A LF+GNAG A+R LTAA+ GG Y
Sbjct: 62 VSVEGLGDNAYR---VTGTGGRFPNKS----DLFMGNAGTAIRPLTAALALQGGE--YT 112

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L GVPRM ERPIGDLV GL+Q+GA +D PP+ ++ +++ G +SSQ+
Sbjct: 113 LHGVPRMHERPIGDLVDGLRQVGARIDYTGNEGYPPLAIHAAPVKIDAPIRVRGDVSSQF 172

Query: 183 LSALLMAAPL--ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
L+ALLMA PL + G+V IE++ +LIS PY+E+TL LM RFGV+ D W F + G
Sbjct: 173 LTALLMALPLVESAGNVITIEVVGELISKPYIEITLNLMARFGVQVVR-DGWSSFTVPTGV 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+P +VEGDASSASYFLA A+ GG V VEG G +S+QGDV+FA+ L MGA V
Sbjct: 232 VYKAPGEIFVEGDASSASYFLAAGALGGGPVRVEGVGMSSIQGDVRFADALNRMGANVMA 291

Query: 301 TETSVTVTGPPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V G R+ G+ H A++++ N +PD AMTLAV ALFADG T + ++ASWRVKE
Sbjct: 292 GGNWIEVRGVERDD-GKLH--AVELDCNHIPDAAMTLAVAALFADGTTTLTNIASWRVKE 348

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEV 418
T+R+ A+ TEL KLGA VEEG DY +TPP + + A IDTYDDHRMAMAFSLAA V
Sbjct: 349 TDRLTAMATELRKLGAEVEEGADYIRVTPPSQWTLTPAGGIDTYDDHRMAMAFSLAAFGPV 408

Query: 419 PVTIRDPGCTRKTFPDYF 436
V I DP C KTFP+YF
Sbjct: 409 SVRINDPRCVGKTFPEYF 426

>emb|CAA38417.1| unnamed protein product [Salmonella enterica subsp. enterica
serovar Typhi]
Length = 427

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 293/437 (67%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVDGAINLPGSKSVSNRALLAALACGKTVLTNLLDSDVHRMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG P+ A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLASDRTRCDITNGG--PLR-ASGTLELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA++D + PP+R+ G G GG +++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDSLQGGANIDYLEQENYPLRLRG--GFIGGDIEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
ALLM APLA D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y
Sbjct: 175 ALLMTAPLAPEDTIIRVKGELVSKPYIDITLNLTKTFGVEIANHH--YQQFVVKGGQYH 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA I GGTV V G G S+QGD++FA+VL MGA +TW +
Sbjct: 233 SPGRYLVEGDASSASYFLAAGGIKGGTVKVTGIGGKSMQGDIFADVLHKMGATITWGDD 292

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 293 FIAC-----RGLHAIDMDMNHIPDAAMTIATALTALFAKGTTLRNIYNWRVKETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA VEEG DY ITPP KL I TY+DHRMAM FSL A ++ PVTI
Sbjct: 345 LFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDHRMAMCFSLVALSDTPVTIL 404

Query: 424 DPGCTRKTFFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 405 DPKCTAKTFPDYFEQLA 421

>sp|Q93ED4.1|AROA_YERRU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK97382.1|AF360730_1 5-enolpyruvylshikimate-3-phosphate synthase [Yersinia ruckeri]
Length = 427

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 293/436 (67%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LPGSKS+SNR LLLAAL+EGTT + NLL+S+D+ +ML AL++LG
Sbjct: 3 ESITLQPIALINGTVNLPGSKSVSNRALLAALAEGTTRLHNLLDSDDIRHMLNALKSLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G GG A ++LFLGNAG AMR L AA+ G + VL
Sbjct: 63 VNYRLSADRTQCDVDGLGGPLV---ADKTLELFLGNAGTAMRPLAALCL--GYSDIVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPIG LV L+ GA +D + PP+R+ G G GG++ + GS+SSQ+L+
Sbjct: 118 GEERMKERPIGHLVDALEG-GAQIDYLEQENYPLLRIG--GFRGGELTVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D I I L+S PY+++TL LM FGV+ H + + F+I+GGQ Y S
Sbjct: 175 ALLMAAPLATQDTHIRIQGDLVSRPYIDITLHLMRSFGVEVTHQN-YQVFHIQGGQTYHS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGTV V G G S+QGD KFA+VLE MGA + W +
Sbjct: 234 PGEYLVEGDASSASYFLAAAAIKGGTVRVVTGIGKKSVDGDKFADVLEKMGAIHWGDDY 293

Query: 305 VTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L+ ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+

Sbjct: 294 IECS-----RGELRDIDMDMNHIPDAAMTIATAALFAKGPTIIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG DY + PP L I TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 SAMATELRKVGAEVEEGQDYIRVVPAPHLIAAEIGTYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFPDYFDVLS 440
P CT KTFPDYF+ L+

Sbjct: 406 PKCTAKTFPDYFEQLA 421

>ref|ZP_01115017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Reinekea sp. MED297]
gb|EAR08948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Reinekea sp. MED297]
Length = 437

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 223/437 (51%), Positives = 286/437 (65%), Gaps = 14/437 (3%)

Query: 9 LQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L +K G V +PGSKSLNRILLALLAAL GTT + NLL+S+DV +ML AL+ LG+S

Sbjct: 15 LPKLKRAQGEVTIPGSKSLNRILLALLAALCRGTTTITNLLSDDDRHMLTALKQLGVSYT 74

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ G GG +++ LFLGNAG AMR L AA+ G T+ L G R

Sbjct: 75 LSDDRTYCTLEGKGPLAT---GQDISLFLGNAGTAMRPLAALCI--GQGTFLHVTGEER 129

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDL+ ++ LG DV+ PP+ + L K+++ GSISQ+L+ALLM

Sbjct: 130 MFERPIGDLIEAMRPLGIDVNYDGEPPPLTIRA-QSLKAAKLQIDGSISQFLTALLM 188

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAPL ++IE+I +L+S PY+++TL +M RFGV E+ + + F + Q+Y+SP

Sbjct: 189 AAPLLKSRIDIEVIGELVSKPYIDITLDVMARFGVTVENHN-YQTFVTPADQQYQSPGRI 247

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGDASSASYFLA AI G V V G GT S+QGDV+FAEVLE MGA V W+E + V+

Sbjct: 248 QVEGDASSASYFLAAGAIGQGPVRVHGTGTASVQGDVRFQAEVLEQMGANVNWSEHWIEVS 307

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L+A+D+++N +PD AMT+AV ALFADG T IR++ +WRVKET+R+ A+

Sbjct: 308 ASQR-----LQAVDLNLNHPDAAMTIAVAALFADGTTIRIRNIYNWRVKETDRIHAMA 360

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
EL KLGA VEEG DY ITPPE L AIDTY+DHR+AM FSLAA + I DPGCT

Sbjct: 361 AELRKLGAEEVEEGDDYLQITPPETLTPAAIDTYNDHRIAMCFSLAAGTDLVINDPGCT 420

Query: 429 RKTFFPDYFDVLSSTFVKN 445
KTFPDYFD ++

Sbjct: 421 AKTFPDYFDRFASITDQ 437

>ref|ZP_01237049.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
angustum S14]
gb|EAS62815.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
angustum S14]
Length = 426

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/435 (51%), Positives = 289/435 (66%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E I LQPI +I+G V LPSKGS+SNR LLLAAL+ GTT + NLL+S+D+ +ML L+ LG

Sbjct: 2 ESITLQPIAKINGEVNLPKSGSKSVSNRALLAALATGTTTLNLLSDDIRHMLNGLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + V G G F E ++L+LGNAG AMR L AA+ GG +VL

Sbjct: 62 VNYQLSEDKTVCEVEGLGRAF---SPNEPLELYLGNAGTAMRPLAALCLGGGE--FVL 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA++ + PP+++ G G L GG+V++ GSISQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRSAGANITYLENENYPPLKIMGTG-LKGGEVEIDGSISQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D I I L+S PY+++TL +M +FGV+ E+ + + F ++G Q Y S
Sbjct: 176 AFLMAAPLAQSDTVIRIKGDLVSKPYIDITLHIMAQFGVEVENRN-YQEFVVRGNQTVYS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD++FA+ L MGA + W +
Sbjct: 235 PGELLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSIGQDIQFADALAAMGADIEWGDDY 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V L A+D++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R+
Sbjct: 295 VIARC-----GDLSAVDMDFNHIPDAAMTIATTALFAKGTTSIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG DY I PP L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEVEEGEDYITIVPPTLQHAAIDTYDDHRMAMCFSLVALSDPTVTIND 406

Query: 425 PGCTRKTFFPDYFDVL 439
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFFPDYFDKL 421

>ref|ZP_04946247.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia dolosa
AU0158]
gb|EAY69418.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia dolosa
AU0158]
Length = 434

Score = 415 bits (1067), Expect = e-114, Method: Compositional matrix adjust.
Identities = 227/442 (51%), Positives = 287/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLNSSEVDHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEAGDTTITNLLDSDDTRVMLDALAKLGVKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D+ VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RDR--DTCVVGTGRGAFATKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGARIDYEQNAGYPPLRIRPATIAVDASIRVRGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G + +E+ +LIS PY+++T+RLMERFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAADGKIVVEVDGELISKPYIDITIRLMERFGVVVER-DGWRFTVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA G + +R++ASWRVKET+R
Sbjct: 297 EVRG-----IGHDHGKLEPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA+VEEG DY ++TPP L AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVATVEEGADYLVVTPPAALTPNAAIDTYDDHRMAMCFSLSLGGVPVRI 411

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFFPDYFDRFAALAK 433

>ref|YP_002897748.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
MSHR346]
gb|ACQ95462.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
MSHR346]
Length = 749

Score = 415 bits (1066), Expect = e-114, Method: Compositional matrix adjust.
Identities = 229/439 (52%), Positives = 284/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDDDTRVMLDALTKLG 376

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 377 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 429 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPLRIRPATISVDAPIRVRGDVSSQFLT 488

Query: 185 ALLMAAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 489 ALLMTLPLVKAKDGASVVEIDGELISKPYIETIKLMARFGVTVER-DGWQRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AVVALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG----IGHDHGLRAPIDMDFNLIPDAAMTIAVVALFADGPSTLNRIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 722

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 723 PVRINDPKCVGKTFPDYFD 741

>ref|YP_002987848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii
Ech703]
gb|ACS86026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dickeya dadantii
Ech703]
Length = 429

Score = 415 bits (1066), Expect = e-114, Method: Compositional matrix adjust.
Identities = 225/442 (50%), Positives = 294/442 (66%), Gaps = 17/442 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQ+ +GT+ LPGSKS+SNR LLLAAL+EGTT + NLL+S+DV +ML AL+ LG
Sbjct: 3 ESLLTLQPVSLVNGTINLPGSKSVSNRALLLAALAEGTTRLTNLLSDDDVRHMLNALKALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S + G G F + E ++LFLGNAG AMR LTAA+ G+ VL
Sbjct: 63 VSYTLLSDRTVCEITGLGHAF---ETSERLELFLGNAGTAMRPLTAALCLTAGD--IVLT 117

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAGIDYLEQENYPPLRLRG--GFVGGDISVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL +M+ FGV +++ + F I G Q Y++
Sbjct: 176 ALLMTAPLAPQDTRITIQGDLVSKPYIDITLHMMKAFGVVDVTNAE-YRTFAIAGNQHYRA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGTV V G G S+QGDV+FA+VLE MGA++ W +
Sbjct: 235 PGDYLVEGDASSASYFLAAAAIRGGTVRVTVGVRKSVQGDVRFADVLEKMGAIQIRWGDDY 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 295 IECQ-----RGELHAIDMDMNHIPDAAMTIATTALFAQGGTTTLRNIYNWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIR 423

+ A+ EL K+GA VEEG DY ITPP++L I TY+DHRMAM FSL A ++ PVTI
Sbjct: 347 LAAMAIELRKVGAEVEEGHDYICITPPKQLQAAEIGTYNDHRMAMCFSLVALSDTPVTIL 406

Query: 424 DPGCTRTKTFPDYFDVLSTFVK 445
DP CT KTFPDYF L ++

Sbjct: 407 DPKCTAKTFPDYFQQLERLSRH 428

>ref|YP_001981148.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellvibrio japonicus Ueda107]

sp|B3PJM0.1|AROA_CELJU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ACE85131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellvibrio japonicus Ueda107]
Length = 428

Score = 415 bits (1066), Expect = e-114, Method: Compositional matrix adjust.
Identities = 231/445 (51%), Positives = 289/445 (64%), Gaps = 25/445 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E I L P G V+LPGSKS+SNR LLLAAL++G T + +LL S+D ML AL +LG

Sbjct: 2 EFIDLAPSAHARGAVQLPGSKSISNRLLLLAALAQGETQIRDLLKSDDTDRMLEALTSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+++ +VG GG FP +E LFLGNAG A R LTAA+ +GG TY L

Sbjct: 62 VTL-TRTGENDYHVLGTGGSF-----HKEADLFLGNAGTAFRPLTAALAFSGG--TYKLH 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYL 183
GVPRM ERPIGDLV L+Q+GAD+ +LG + PP+ + G +K+ G +SSQ+L

Sbjct: 115 GVPRMHERPIGDLVDALRQVGADI-TYLGQEGFPPLLIKPAHIAAQSGIKIRGDVSSQFL 173

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMA P+ + IE++ +LIS PY+E+TLRLM +FGV+ + D W+RF + Y

Sbjct: 174 TALLMALPMTGKETHIELVSELISKPYIEITLRLMAQFGVEVQR-DGWERFTVPAASGYV 232

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT---- 299
SP YVEGDASSASYFLA A+ GG V V+G G S+QGDV FA+ LE +G +T

Sbjct: 233 SPGTVYVEGDASSASYFLAAGALGGPVRVQVGAKSIQGDVAFADALEAIGVTITKGDN 292

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E S P+ P LKA + + N +PD AMTLAVVALF DGP+ + ++ASWRVK

Sbjct: 293 WIEASA-----PQLP-----LKAFNRDFNHIPDAAMTLAVVALFCDGPSRLTNIASWRVK 342

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVA-IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL KLGA VEEG D+ +TP LN IDTYDDHRMAM FSLA V

Sbjct: 343 ETDRIAMATELRKLGAIVEEGEDWLQVTPVPTLNAQVPIDTYDDHRMAMCFSLATFGGV 402

Query: 419 PVTIRDPGCTRTKTFPDYFDVLSTFV 443
PV I DP CT KTFP YFDV S V

Sbjct: 403 PVRINDPQCTAKTFPTYFDVFSQVV 427

>ref|YP_718825.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus somnus 129PT]

sp|Q0I320.1|AROA_HAES1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ABI24890.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus somnus 129PT]
Length = 432

Score = 414 bits (1065), Expect = e-113, Method: Compositional matrix adjust.
Identities = 231/444 (52%), Positives = 292/444 (65%), Gaps = 17/444 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI I G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ YML AL+ LG

Sbjct: 2 EKLTLSPISRIDGEINLPGSKSLSNRALLLAALAKGTTQVTNLLSDDIRYMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
++ + VV G GG F ++ + LFLGNAG AMR L AA+ G + V L

Sbjct: 62 VNYQLSDDKTVCVVEGIGGAFQWQNG---LSLFLGNAGTAMRPLAAALCLKGDTSEVIL 118

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA++ PP+ + G+ GGV++ GSISQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQTGANIQYLENEGYPPLAIRN-QGIFGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPL GD+EIEI+ +L+S PY+++TL +M+ FG+ EH + + RF IKG Q Y

Sbjct: 178 TALLMAAPLGECDMEIEIILGELVSKPYIDITLAMMKDFGINVEHYN-YQRFLIKGQYYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AAI G V V G G S+QGD FA+VL MGAKVTW E

Sbjct: 237 SPQTYLVEGDASSASYFLAAAAIKG-KVKVTGIGRNSIQGDRLFADVLAQMGAKVTWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V + LK ID++MN +PD AMT+A+ ALFA G T IR++ +WRVKET+R

Sbjct: 296 FIQVE-----KSELKGIDMDMNHIPDAAMTIAITALFAQGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+ AI TEL KLGA VEEG D+ I P +K I TY+DHR+AM FSL A ++ VT

Sbjct: 348 LTAIATELRKLGAEEVEGEDFIRIQPLALDKFKHAEIATYNDHRIAMCFSIALSDTSVT 407

Query: 422 IRDPGCTRKTFFDYFDVLSTFVKN 445
I DP CT KTFP YF KN

Sbjct: 408 ILDPACTAKTFPTYFSEFEKISK 431

>ref|ZP_03611660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus minor
202]
gb|EEF16122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus minor
202]
Length = 432

Score = 414 bits (1064), Expect = e-113, Method: Compositional matrix adjust.
Identities = 229/439 (52%), Positives = 291/439 (66%), Gaps = 17/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ L PI I G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKLTLNPISRIEGEINLPGSKSLSNRALLAALAAGTTQVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E V G GG F ++ + LFLGNAG AMR LTAA+ G A VL

Sbjct: 62 VKYELSADKTICTVEGVGGAQWQNG---LSLFLGNAGTAMRPLTAALCLKGKEEAEEVVL 118

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA + PPV + G L G KVK+ GSISQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAQIQYLENEGYPVAIRNTG-LTGDKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPL GD+EIEII +L+S PY+++TL +M+ FGV H + + F++KG Q Y

Sbjct: 178 TALLMSAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVTVSHQN-YQTFVKGQQSYV 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 SPEKYMVEGDASSASYFLAAGAIKG-NVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----QGELKGIDMDMNHIPDAAMTIAITALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P ++ I+TY+DHR+AM FSL A + PVT

Sbjct: 348 LTAMATELRKVGAEVEEGEDFIRIQPLALDQFQHAIEIETYNDRHVAMCFSVALSNTPV 407

Query: 422 IRDPGCTRKTFFDYFDVLS 440
I DP CT KTFP YFD L+

Sbjct: 408 ILDPKCTAKTFPTYFDELA 426

>ref|YP_001784296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus somnus
2336]

sp|BOUT47.1|AROA_HAES2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACA32650.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus somnus
2336]
Length = 432

Score = 414 bits (1064), Expect = e-113, Method: Compositional matrix adjust.
Identities = 231/444 (52%), Positives = 292/444 (65%), Gaps = 17/444 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ L PI I G + LPSKSLSNR LLLAAL++GTT V NLL+S+D+ YML AL+ LG
Sbjct: 2 EKLTLSPISRIDGEINLPGSKSLSNRALLLAALAKGTTQVTNLLSDDIRYMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
++ + VV G GG F ++ + LFLGNAG AMR L AA+ G + V L
Sbjct: 62 VNYQLSDDKTVCVVEGIGGAFQWQNG---LSLFLGNAGTAMRPLAALCLKGDTSEVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA++ PP+ + G+ GGKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQTGANIQYLENDGYPLAIRN-QGIFGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPL GD+EIEI+ +L+S PY+++TL +M+ FG+ EH + + RF IKG Q Y
Sbjct: 178 TALLMAAPLGEGDMEIEILGELVSKPYIDITLMMKDFGINVEHYN-YQRFILKKGQYYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AAI G V V G G S+QGD FA+VL MGAKVTW E
Sbjct: 237 SPQTYLVEGDASSASYFLAAAAIKG-KVKVTGIGRNSIQGDRLFADVLAQMGAKVTWGED 295

Query: 304 SVTVTGPPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V + LK ID++MN +PD AMT+A+ ALFA G T IR++ +WRVKET+R
Sbjct: 296 FIQVE-----KSELKGIDMDMNHIPDAAMTIAITALFAQGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPVT 421
+ AI TEL KLGA VEEG D+ I P +K I TY+DHR+AM FSL A ++ VT
Sbjct: 348 LTAIATELRKLGAEEVEEGEDFIRIQPLALDKFKHAEIATYNDHRIAMCFSLIALSDTSVT 407

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVK 445
I DP CT KTFP YF KN
Sbjct: 408 ILDPACTAKTFFTYFSEFEKISK 431

>ref|ZP_04902010.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
S13]
gb|EDS85022.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
S13]
Length = 749

Score = 414 bits (1063), Expect = e-113, Method: Compositional matrix adjust.
Identities = 229/439 (52%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPSKSLSNR+LLLAALSEG T V NLL+S+D ML AL LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALSEGTTVTNLLSDDIRVMDALTKLG 376

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 377 VKLSRDGGT--CVVGTRGAFATAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 429 GVPFRMHERPIGDLVDLGRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDIVSSQFLT 488

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 489 ALLMTLPLVAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWT 301

Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVALFADGPSTLRNIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 722

Query: 419 PVTIRDPGCTRKTFFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 723 PVRINDPKCVGKTFFPDYFD 741

>ref|ZP_02889490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria IOP40-10]
gb|EDT04925.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria IOP40-10]
Length = 434

Score = 414 bits (1063), Expect = e-113, Method: Compositional matrix adjust.
Identities = 230/447 (51%), Positives = 288/447 (64%), Gaps = 30/447 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGDTTITNLLSDDDTRVMLDALGKLGVKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG-----GKVKLSGSIS SQYL 183
M ERPIGDLV GL+Q+GA +D PP+R+ PG +++ G +SSQ+L
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPLRIK-----PGTIAVDAPIRVRGDVSSQFL 172

Query: 184 SALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQ 240
+ALLM PL G +EI +LIS PY+++T+RLMERFGV E D W RF + G
Sbjct: 173 TALLMTPLPLVKAKDGRTVVEIDGELISKPYIDITIRLMERFGVTVER-DGWQRFVVPAGV 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA V+
Sbjct: 232 RYRSPGRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVSM 291

Query: 301 TETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ + V G G H L ID++ N +PD AMT+AVVALFA G + +R++ASWRV
Sbjct: 292 GDNWIEVRG-----IGHDHGKLDPIDMDFNLIPDAAMTIAVVALFASGTSTLRNIASWRV 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAE 417
KET+R+ A+ TEL K+GA VEEG DY ++TPP++L AIDTYDDHRMAM FSL +
Sbjct: 347 KETDRIAAMATELRKVGAIVEEGADYLVVTPPQRLTPNAAIDTYDDHRMAMCFSLVSLGG 406

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
VPV I DP C KTFPDYFD + K
Sbjct: 407 VPVRINDPKCVGKTFFPDYFDRFAALAK 433

>ref|YP_284501.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Dechloromonas aromatica RCB]
gb|AAZ46031.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dechloromonas
aromatica RCB]
Length = 643

Score = 413 bits (1062), Expect = e-113, Method: Compositional matrix adjust.
Identities = 232/434 (53%), Positives = 287/434 (66%), Gaps = 26/434 (5%)

Query: 16 SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SGTV+LPGSKS+SNR+LLLAALS G T V +LL S+D ML AL+ LG+ V+ +
Sbjct: 13 SGTVRLPGSKSISNRVLLLAALSGGETEVRDLLGSDDTERMLEALKALGVGVQ-HLGGEN 71

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ GCGG FVPV+ +++LFLGNAG A R LTAA+ AGG+ YVL GV RM ERPIG
Sbjct: 72 WSIKCGGHHFPVK----QIELFLGNAGTAFRPLTAALALAGGD--YVLKGVARMHERPIG 125

Query: 136 DLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
DLV GL+QLGAD+ +LG + PP+ + LP G V + G +SSQ+L+ LLMA PL
Sbjct: 126 DLVDGLRQLGADI-TYLGNEGFPPLHLKPASILPNGVVTVRGDVSSQFLTGLLMALPLTG 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
V +E++ +LIS PY+E+TL M RFGV E + W RF + G +Y SP +VEGDA
Sbjct: 185 ETVVVEVLGELISKPYIEITLATMARFGVIVER-EGWQRFTVLAGSRYVSPGTIFVEGDA 243

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV---TWTETSVTVTGP 310
SSASYFLA AI GG V VEG G S+QGDVKFAE L MGA++ W E G
Sbjct: 244 SSASYFLALGAIGGGPVRVEGVGRDSIQGDVKFAEALVKMGAQIEMGPNWMEARAPQAG- 302

Query: 311 PREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L A+D++ N +PD AMTLA ALFA G T +R++ASWRVKET+R+ A+ TE
Sbjct: 303 -----LVAVDLCNHIPDAAMTLATTALFAKGTTLRNIAASWRVKETDRIAAMATE 353

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
L KLGA V+EG DY +TP + L AIDTYDDHRMAM FSLAA P+ I DP C K
Sbjct: 354 LRKLGAUVDEGDDYIRVTPAD-LKPAIDTYDDHRMAMCFSLAAGF-TPLRINDPKCVAK 411

Query: 431 TFPDYFDVLSTFVK 444
TFPDYF+ + K
Sbjct: 412 TFPDYFERFAGVTK 425

>ref|ZP_07396143.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Candidatus Regiella
insecticola LSR1]
gb|EFL91171.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Candidatus Regiella
insecticola LSR1]
Length = 429

Score = 413 bits (1062), Expect = e-113, Method: Compositional matrix adjust.
Identities = 224/439 (51%), Positives = 296/439 (67%), Gaps = 17/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTVKLPGSKS+SNR+LLLAAL+ GTT +DNLL+S+D +ML AL TLG
Sbjct: 3 ESLRLQPIPLINGTVKLPGSKSISNRVLLLAALASGTTQIDNLLSDSTRHMLKALTTLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ A + + G G + K +LFLGNAG +R LTA + GN+ +L
Sbjct: 63 VKYRLSADATQCEIDGLSGLMHTDKGK---KLFLGNAGTVLRPLTAILCL--GNSEVILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG + L GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEQHNYPPLRLKG--GFSGGTLTLDGSLSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+AAPLA+ D +I+I L+S PY+++TL LM+ FGV+ + + FYIKG Q Y+S
Sbjct: 176 ALLLAAPLAIQDTDIQIQGNLVSKPYIDITLHLMKIFGVEVRRKN-YQHFYIKGRQTYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
PK ++EGDASSASYFLA AAI GG V V+G G S+QGD++FA VL+ MGA + W +
Sbjct: 235 PKKYWIEGDASSASYFLAAAAIKGGKVRVKGIGKKSQGDIEFANVLQRMGATIHWHDDY 294

Query: 305 VTVTGPMPREPFRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ R L+ ID++MN PDVAMTLA+ ALFA G T IR++ +WR+KET+R+
Sbjct: 295 IECC-----RGQLQGIDIDMNHPTDVAMTLAITALFATGSTTIRNIYNWRIKETDRI 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ TEL K+GA V G D+ I PP+KL T I+TY+DHRMAM FSL A ++ P+TI
Sbjct: 347 YAMTTELEKVGAKVMAGKDHICIVPPQKLIFTTKINTYNDHRMAMCFSLALSDNPITIL 406

Query: 424 DPGCTRKTFPDYFDVLSTF 442
+P C KTFPDYF L+
Sbjct: 407 NPNCVTKTFPDYFHNLTAL 425

>ref|ZP_01160582.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Photobacterium sp. SKA34]
gb|EAR55730.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Photobacterium sp. SKA34]
Length = 426

Score = 413 bits (1062), Expect = e-113, Method: Compositional matrix adjust.
Identities = 226/435 (51%), Positives = 290/435 (66%), Gaps = 15/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E I LQPI +I+G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML L+ LG
Sbjct: 2 ESITLQPIAKINGEVNLPGSKSVSNRALLAALATGTRLANLLDSDDIRHMLNGLKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + + V G G F D+ ++L+LGNAG AMR L AA+ GG +VL
Sbjct: 62 VNYKLSDEKTVCEVEGLGRAFPNDSD---LELYLGNAGTAMRPLAALCLGGGE--FVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA++ + PP+++ G G L GG+V++ GSISSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRGAGANITYLENENYPPLKIIGTG-LKGGEVEIDGSISSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A LMAAPLA D I I L+S PY+++TL +M +FGV+ E+ + + F ++G Q Y S
Sbjct: 176 AFLMAAPLAQADTVIRIKGDLVSKPYIDITLHIMAQFGVEVENRN-YQEFVVRGKIYVS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G S+QGD+KFA+ L MGA + W +
Sbjct: 235 PGELLVEGDASSASYFLAAAAIKGGEVKVTGIGKKSIGDIFADALAAMGADIEWGDDY 294

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
V L A+D++ N +PD AMT+A ALFA G T+IR+V +WRVKET+R+
Sbjct: 295 VIARC-----GDLSAVDMDFNHIDPAAMTIATTALFAKGTTSIRNVYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
A+ TEL K+GA VEEG DY I PP L AIDTYDDHRMAM FSL A ++ PVTI D
Sbjct: 347 AAMATELRKVGAEEVEGDDYITIVPPTTLQHAADITYDDHRMAMCFSLVALSDTPVTIND 406

Query: 425 PGCTRKTFPDYFDVL 439
P CT KTFPDYFD L
Sbjct: 407 PKCTSKTFPDYFDKL 421

>gb|ABA50570.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1710b]
Length = 714

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 282 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLDSDTRVMLDALTKLG 341

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 342 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 393

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 394 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 453

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 454 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 512

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 513 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 572

Query: 302 ETSVTVTGTPPREPFGRKH--LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASVRVK 359

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      + + V G      G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 573 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 627

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
      ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 628 ETDRIAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 687

Query: 419 PVTIRDPGCTRKTFPDYFD 437
      PV I DP C KTFPDYFD
Sbjct: 688 PVRINDPKCVGKTFPDYFD 706

```

>emb|CAH36524.1| putative bifunctional protein: 3-phosphoshikimate
1-carboxyvinyltransferase/prephenate dehydrogenase
[Burkholderia pseudomallei K96243]
Length = 753

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

```

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 321 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDDDRVMMLDALTKLG 380

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 381 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 432

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 433 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 492

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 493 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWRFTVPAGVR 551

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWT 301
      Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 552 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGAFANALMQMGANVTMG 611

Query: 302 ETSVTVTGPPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
      + + V G      G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 612 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 666

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
      ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 667 ETDRIAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 726

Query: 419 PVTIRDPGCTRKTFPDYFD 437
      PV I DP C KTFPDYFD
Sbjct: 727 PVRINDPKCVGKTFPDYFD 745

```

>ref|YP_001856979.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia phymatum
STM815]
sp|B2JF04.1|AROA_BURP8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACC69933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia phymatum
STM815]
Length = 434

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 226/439 (51%), Positives = 286/439 (65%), Gaps = 20/439 (4%)

```

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EHLDLGPFSSRASGTVRLPGSKSISNRVLLLAALAEGETTITNLLSDDDRVMMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + D VV G G P A LFLGNAG A+R LTAA+ GG+ Y +

```

Sbjct: 62 VKFKRD--GDTCVVTGTRGALPAARA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+

Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAKIDYEENEGFPPLRIRPAQISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G+ +E+ +LIS PY+E+T+RLMERFG+K E W+RF I G +

Sbjct: 174 ALLMTLPLVKTESGETIVEVSGELISKPYIEITIRLMERFGIKVERF-GWERFTIPSGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT

Sbjct: 233 YQSPGKIMVEGDASSASYFLAAGALGGPLRVEGVGRASIQGDVGFATALMKMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG T +R++ SWRVK

Sbjct: 293 DDWIEVRG----VGNDHGKLDPIIDMFNLIPDAAMTIAAALFADGTTTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL+K+GA V+ G D+ ++TPPE+L AIDTYDDHRMAM FSL + V

Sbjct: 348 ETDRIAAMATELSKVGAKVQAGEDFLVVTPPEQLTPNAAIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYF+

Sbjct: 408 PVRINDPKCVGKTFPDYFE 426

>ref|ZP_04814100.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1106b]

ref|ZP_04898518.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
Pasteur 52237]

ref|ZP_04950382.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1710a]

ref|YP_001059903.2| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
668]

gb|EDO95605.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
Pasteur 52237]

gb|EES24725.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1106b]

gb|EET07401.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1710a]

gb|ABN83250.2| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
668]

Length = 753

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG

Sbjct: 321 EHLDLGPFSHAQGTVRVLPGSKSISNRVLLLAALAEGETTVTNLLDSDTRVMLDALTKLG 380

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +

Sbjct: 381 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 432

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+

Sbjct: 433 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 492

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +

Sbjct: 493 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 551

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 552 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 611

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 612 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 666

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 667 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 726

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 727 PVRINDPKCVGKTFPDYFD 745

>ref|YP_109113.2| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
K96243]
ref|YP_334375.2| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1710b]
Length = 673

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 241 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLDSDTRVMLDALTKLG 300

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 301 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 352

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 353 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 412

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 413 ALLMTLPLVKAKD GASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 471

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 472 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 531

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 532 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 586

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 587 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 646

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 647 PVRINDPKCVGKTFPDYFD 665

>ref|YP_001067192.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1106a]
ref|ZP_01763882.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
305]
ref|ZP_03793382.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
Pakistan 9]

gb|ABN90360.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
1106a]
gb|EBA50896.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
305]
gb|EEH26009.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
Pakistan 9]
Length = 749

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDDTRVMLDALTKLG 376

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 377 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 429 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 488

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 489 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGAFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG----IGHDHGRLAPIDMDFNLIPDAAMTIAAALFADGPSTLNRIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 722

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 723 PVRINDPKCVGKTFPDYFD 741

>ref|YP_102243.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei ATCC
23344]
gb|AAU48805.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei ATCC
23344]
Length = 673

Score = 413 bits (1061), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 241 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDDTRVMLDALTKLG 300

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 301 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 352

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 353 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 412

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241

ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 413 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 471

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT

Sbjct: 472 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 531

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK

Sbjct: 532 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 586

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V

Sbjct: 587 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 646

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD

Sbjct: 647 PVRINDPKCVGKTFPDYFD 665

>ref|ZP_04963077.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
406e]
gb|ED082684.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
406e]
Length = 740

Score = 412 bits (1060), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG

Sbjct: 308 EHLDLGPFSHAQGTVRPLPGSKSISNRVLLLAALAEGETTVTNLLSDSDTRVMLDALTKLG 367

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +

Sbjct: 368 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 419

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+

Sbjct: 420 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 479

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +

Sbjct: 480 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 538

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT

Sbjct: 539 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 598

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK

Sbjct: 599 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 653

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V

Sbjct: 654 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 713

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD

Sbjct: 714 PVRINDPKCVGKTFPDYFD 732

>ref|ZP_03452380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
gb|EEC36304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
Length = 749

Score = 412 bits (1060), Expect = e-113, Method: Compositional matrix adjust.

Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

```

Query: 5   EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + L P      GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D   ML AL  LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTTVNLDSDDTRVMLDALTKLG 376

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + + D      VV G G F + A      LFLGNAG A+R LTAA+   GG  Y +
Sbjct: 377 VKLSRDGGT--CVVGGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          GVPRM ERPIGDLV GL+Q+GA +D      PP+R+      +++ G +SSQ+L+
Sbjct: 429 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 488

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
          ALLM  PL      G +EI +LIS PY+E+T++LM RFGV  E D W RF + G +
Sbjct: 489 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
          Y+SP      VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
          + + V G      G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAAALFADGPSTLRNIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
          ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L  A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLSLGGV 722

Query: 419 PVTIRDPGCTRKTFFPDYFD 437
          PV I DP C KTFPDYFD
Sbjct: 723 PVRINDPKCVGKTFFPDYFD 741

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>ref|ZP_04887685.1| prephenate dehydrogenase/3-phosphoshikimate
      1-carboxyvinyltransferase [Burkholderia pseudomallei
      1655]
gb|EDU08669.1| prephenate dehydrogenase/3-phosphoshikimate
      1-carboxyvinyltransferase [Burkholderia pseudomallei
      1655]
Length = 749

```

Score = 412 bits (1060), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

```

Query: 5   EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + L P      GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D   ML AL  LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTTVNLDSDDTRVMLDALTKLG 376

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          + + D      VV G G F + A      LFLGNAG A+R LTAA+   GG  Y +
Sbjct: 377 VKLSRDGGT--CVVGGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          GVPRM ERPIGDLV GL+Q+GA +D      PP+R+      +++ G +SSQ+L+
Sbjct: 429 GVPRMHERPIGDLVDGLRQVGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 488

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
          ALLM  PL      G +EI +LIS PY+E+T++LM RFGV  E D W RF + G +
Sbjct: 489 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
          Y+SP      VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
          + + V G      G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAAALFADGPSTLRNIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418

```

ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 722

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD

Sbjct: 723 PVRINDPKCVGKTFPDYFD 741

>gb|AC092617.1| AroA [Edwardsiella tarda]
Length = 428

Score = 412 bits (1060), Expect = e-113, Method: Compositional matrix adjust.
Identities = 222/438 (50%), Positives = 283/438 (64%), Gaps = 16/438 (3%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ L P++ SG + LPGSKS+SNR LLLAA + G T + NLL+S+DV YML AL+ LG+
Sbjct: 5 LTLHPVRRFSGEINLPGSKSVSNRALLAAQARGVTRLHNLLDSDDVRYMLDALKALGVR 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ R V G GG A + LFLGNAG AMR L AA++ G +L G
Sbjct: 65 YQLSDCHTRCEVQGLGGTSLAHGA---LTLFLGNAGTAMRPLAAALSL--GQRDVILTGE 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM+ERPI LV L+Q GA VD PPVR+ G G GG + + GS SSQ+L+AL
Sbjct: 120 PRMKERPIAHLVTALRQGGAHVDYLEDGYPPVRLRG--GFNGGDISVDGSASSQFLTAL 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAP+A + I I+ +L+S PY+ +TL +M FGV+ EH ++ F ++GGQ Y++P
Sbjct: 178 LMAAPMAAEEETRITILGELVSKPYIAITLMMRTFGVEVEHH-AYRHFVVRGGQTYQAPG 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYFLAGAAI GGTV V G G S+QGD+ FA+ LE MGA + W + +
Sbjct: 237 DYLVEGDASSASYFLAGAAIAGGTVRVTGIGRHSMQGDIHFADALEKMGAHIEWGDDYIA 296

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
T R L ID++MN +PD AMTLA ALFA GPT +R++ +WRVKET+R+ A
Sbjct: 297 CT-----RDSLHGIDMDMNAIPDAAMTLATTALFATGPTTLRNIYNWRVKETDRLAA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTVIRDPG 426
+ EL K+GA VEEGPD+ I PP +L I TY+DHRMAM FSL A ++ PVTI DPG
Sbjct: 349 MACELQKVGAVVEEGPDFLRIEPPAQLRAAQIATYNDHRMAMCFSLVALSDTPVTICDPG 408

Query: 427 CTRKTFPDYFDVLSTFVK 444
CT KT PDYF S
Sbjct: 409 CTAKTLPDYFQSFSALCH 426

>ref|ZP_02905400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria MEX-5]
gb|EDT43480.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria MEX-5]
Length = 434

Score = 412 bits (1059), Expect = e-113, Method: Compositional matrix adjust.
Identities = 227/442 (51%), Positives = 285/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGDTTITNLLDSDDTVRMLDALGKLGVKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPPLRIKPAAIAVDAPIRVGDVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +EI +LIS PY+++T+RLMERFGV E D W RF + G +Y+SP
Sbjct: 178 TLPLVKAKDGRVTVEIDGELISKPYIDITIRLMERFGVTVER-DGWRQFVVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA V+ + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVSMGDDWI 296

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L ID++ N +PD AMT+AV ALFA G + +R++ASWRVKET+R
Sbjct: 297 EVRG-----IGHDHGKLDPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA VEEG DY ++TPP++L AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVGAIVEEGADYLVVTPPQQLTPNAAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>ref|YP_001341243.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinomonas sp.
MWYL1]
sp|A6VXX9.1|AROAMARMS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR71308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinomonas sp.
MWYL1]
Length = 425

Score = 412 bits (1059), Expect = e-113, Method: Compositional matrix adjust.
Identities = 223/435 (51%), Positives = 297/435 (68%), Gaps = 16/435 (3%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L P+ + +G +++PGSKSLNRILLALLA L++GTT + NLL+S+D+ ML +L LG+S
Sbjct: 4 ITLGPLSKANGEIQIPGSKSLNRILLALLATLAKGTTKITNLLSDDIRRMLESITKLGV 63

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ V+ G GG P++ + LFLGNAG AMR LTAA+ G ++L G
Sbjct: 64 YSLEDNGTTCVLEGLG--PIQ--ADFGDLFLGNAGTAMRPLTAALCL--GKGEFLLHGE 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM ERPIGDLV L+ LG D+ + PP+R+ GL GG+V + G+ISSQ+L+A+
Sbjct: 118 PRMHERPIGDLVDALQALGVDITYEGEKNYPLRIKA-NGLSGGEVSIKGNISSQFLTAI 176

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM+APLA D+ I++ +L+S PY+++TL M++FGV+ E+ + + F +KG Q Y+SP
Sbjct: 177 LMSAPLAKSDLTIKVDGELVSKPYIDITLHAMKQFGVEVENQN-YQAFVVKGQQTQYQSPG 235

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VEGDASSASYFLA AAI GG + V G GT S+QGDVKFA+VL MGAK+T+
Sbjct: 236 EIMVEGDASSASYFLAAAAIAGGKIKVHGVGTDSVQGDVKFADVLAQMGAITY----- 289

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
GP R L ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+ A
Sbjct: 290 --GPSWIEAERNELNGIDMDMNHIPDAAMTIATTALFAKGPPTTIRNIYNWRVKETDRLYA 347

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ TEL KLGA V EG D+ +TP L AIDTY+DHR+AM FSL A ++ PVTI DPG
Sbjct: 348 MATELKKLGADVIEGKDFITVTPVANLKHAIDTYNDHRIAMCFSLVAFSDTPVTINDPG 407

Query: 427 CTRKTFPDYFDVLST 441
CT KTFP YF++ +T
Sbjct: 408 CTSKTFPTYFELFNT 422

>ref|YP_993876.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei SAVP1]
ref|YP_001026939.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei NCTC
10229]
ref|YP_001079774.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei NCTC
10247]

ref|ZP_00441668.2| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei GB8 horse
4]
ref|ZP_04819907.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei PRL-20]
ref|ZP_04883315.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei ATCC
10399]
ref|ZP_04910287.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei FMH]
ref|ZP_04915255.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei JHU]
ref|ZP_04976308.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|ABM49601.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei SAVPl]
gb|ABN03887.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei NCTC
10229]
gb|ABO07042.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei NCTC
10247]
gb|EDK52519.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei FMH]
gb|EDK57852.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei JHU]
gb|EDK87183.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|EDP87669.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei ATCC
10399]
gb|EEP87569.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei GB8 horse
4]
gb|EES46409.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia mallei PRL-20]
Length = 749

Score = 412 bits (1059), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 317 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTTVTNLLSDSDTRVMDALTKLG 376

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 377 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 428

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 429 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGVDVSSQFLT 488

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 489 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 547

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 548 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 607

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 608 DDWIEVRG----IGHDHGRLAPIDMFNLIPDAAMTIAAALFADGPSTLRNIGSWRVK 662

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 663 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLSVSLGGV 722

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 723 PVRINDPKCVGKTFPDYFD 741

>ref|ZP_02403904.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
DM98]
ref|ZP_02448541.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei 91]
ref|ZP_02472272.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
B7210]
ref|ZP_02490944.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
NCTC 13177]
ref|ZP_02499079.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
112]
Length = 434

Score = 412 bits (1058), Expect = e-113, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 2 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDDTVMLEALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 62 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAAAVNGGE--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YRSPGTIMVEGDASSASYFLAAGALGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVA-IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 408 PVRINDPKCVGKTFPDYFD 426

>ref|ZP_03268141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
H160]
gb|EAA00283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
H160]
Length = 434

Score = 411 bits (1057), Expect = e-113, Method: Compositional matrix adjust.
Identities = 224/446 (50%), Positives = 290/446 (65%), Gaps = 20/446 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P +GTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFSSRAAGTVRLPGSKSISNRVLLLAALAEGDTTITNLLSDDTVMLEALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

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+ ++ D      VV G  G F      A      LFLGNAG A+R LTAA+  GG+  Y +
Sbjct: 62  VRLKRD--GDTCVVVTGRGAFTARTA----DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
          GVPRM ERPIGDLV GL+Q+GA +D      PP+R+      +++ G +SSQ+L+
Sbjct: 114  GVPRMHERPIGDLVDGLRQIGAKIDYEQNEGFPPLRIRPAQIAADAPIRVRGDVSSQFLT 173

Query: 185  ALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
          +LLM PL  A G      +++ +LIS PY+E+TL+LMERFG+K E      W +F +  GQ+
Sbjct: 174  SLLMTLPLLRRTASGVTTVQVDGELISKPYIEITLKLMEFRGKVERH-GWHQFVVPAGQR 232

Query: 242  YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
          Y+SP      VEGDASSASYFLA A+ GG + VEG G  S+QGDV FA+ L  MGA V
Sbjct: 233  YQSPGAIMVEGDASSASYFLAAGALGGGGLKVEGVGRASIQGDVGFADALIKMGANVQMG 292

Query: 302  ETSVTVTGPPPREPFGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
          +  + V G      G H L  ID++ N +PD AMT+AV ALFADG T +R++ASWRVK
Sbjct: 293  DDWIEVRG-----VGNDHGKLDPIDMDFNLIPDAAMTIAVAALFADGTTTLRNIASWRVK 347

Query: 360  ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEV 418
          ET+R+ A+ TEL K+GA V+EG D+ ++TPPEKL  AIDTYDDHRMAM FSL +  V
Sbjct: 348  ETDRIAAMATELRKVGAKVQEGEDFLVVTPEKLIPNAAIDTYDDHRMAMCFSVLVSLGGV 407

Query: 419  PVTIRDPGCTRKTFPDYFDVLSTFVK 444
          P+ I DP C  KTFPDYF+  +  +
Sbjct: 408  PIRINDEPKCVGKTFPDYFERFTALAQ 433

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>ref|YP_002933862.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative
[Edwardsiella ictaluri 93-146]
sp|Q9X4H2.1|AROA_EDWI9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAD28375.1|AF110153_2 5-enolpyruvylshikimate-3-phosphate synthase [Edwardsiella ictaluri
93-146]
gb|ACR69627.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative
[Edwardsiella ictaluri 93-146]
Length = 428

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Score = 411 bits (1057), Expect = e-113, Method: Compositional matrix adjust.
Identities = 223/438 (50%), Positives = 288/438 (65%), Gaps = 16/438 (3%)

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Query: 7  IVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
          + LQP++ SG + LPGSKS+SNR LLLAA + G T + NLL+S+DV YML AL+ LG+
Sbjct: 5  LTLQPVRRFSGEINLPKSKSVSNRALLAAQARGVTRLHNLLDSDDVRYMLDALKALGVR 64

Query: 67  VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
          +      R V G GG      A + LFLGNAG AMR L AA++ G      +L G
Sbjct: 65  YQLSDCRTCRCVQGLGGTSLAHGA---LTLFLGNAGTAMRPLAAALSL--GLRDVILTGE 119

Query: 127  PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
          PRM+ERPI LV L+Q GA VD      PPVR++G G GG++ + GS+SSQ+L+AL
Sbjct: 120  PRMKERPIAHLVTALRQGAQVDYLEDGYPVRLHG--GFNGGEISVDGSVSSQFLTAL 177

Query: 187  LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
          LMAAP+A + I I+ +L+S PY+ +TL +M FGV+ E + ++ F ++GGQ Y++P
Sbjct: 178  LMAAPMAAEETRITILGELVSKPYIAITLAMMRAFGVEVE-NHAYRHFVVRGGQVYQAPS 236

Query: 247  NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
          + VEGDASSASYFLAGAAI GGTV V G G S+QGD+ FA+VLE MGA+V W      +
Sbjct: 237  DYLVVEGDASSASYFLAGAAIAGGTVRVTGIGRHSMQGDHFAADVLEKMGAVQVEWGNNDYIA 296

Query: 307  VTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
          T      R L  ID++MN +PD AMT+A ALFA GPT +R++ +WRVKET+R+ A
Sbjct: 297  CT-----RDSLHGIDMDMNAIPDAAMTIATTALFAKGPTTLRNIYNWRVKETDRLAA 348

Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPG 426
          + +EL K+GA VEEG D+ I PP +L I TY+DHRMAM FSL A + PVTI DPG
Sbjct: 349  MASELRKVGAVVEEGTDFLRLEPPAQLQAAQIATYNDHRMAMCFSVLVSLSGTPVTICDPG 408

Query: 427  CTRKTFPDYFDVLSTFVK 444

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CT KTFPDYF S
Sbjct: 409 CTAKTFPDYFRQFSALCH 426

>ref|ZP_02482755.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
7894]
ref|ZP_02507070.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei
BCC215]
Length = 434

Score = 411 bits (1057), Expect = e-112, Method: Compositional matrix adjust.
Identities = 228/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 2 EHLDLGPFSHAQGTVRLLPGSKSISNRVLLAALAEGETTNTLLDSDTRVMDALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG Y +
Sbjct: 62 VKLSRDGGT--CVVGGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGE--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQVGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 408 PVRINDPKCVGKTFPDYFD 426

>gb|AAT45242.1| 5-enol-pyruvylshikimate-phosphate synthase [Plantago lanceolata]
Length = 265

Score = 411 bits (1056), Expect = e-112, Method: Compositional matrix adjust.
Identities = 222/265 (83%), Positives = 240/265 (90%), Gaps = 1/265 (0%)

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
LRTLGL VE DKA +RA V GCGG FPV +++K+E+QLFLGNAG AMR LTA AV AAGG+
Sbjct: 1 LRTLGLDVEEDKANQRTAVGGCGGLFPVSKESKDEIQFLGNAGTAMRPLTAAVVAAGGD 60

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI 178
ATYVLDGVPRMRERPIGDLV GLKQLGAD+DCFLGT CPPVRV G GGLPGGKVKLSGSI
Sbjct: 61 ATYVLDGVPRMRERPIGDLVTLKQLGADIDCFLGTCPPVRVIGKGLPGGKVKLSGSI 120

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQYL+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LMERFGV EH+DSWDRF ++G
Sbjct: 121 SSQYLTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMERFGVVEHTDSWDRFLVRG 180

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
GQKYKSP AYVEGDASSASYFLAGAA+TGGTVTVEGCGT+SLQGDVKFAEVLE MGA+V
Sbjct: 181 GQKYKSPGKAYVEGDASSASYFLAGAAVTGGTVTVEGCGTSSLQGDVKFAEVLEKMGAEV 240

Query: 299 TWTETSVTGTGPPREPFGRKHLKAI 323

TWTE SVTV GPPR GRKHL+AI
Sbjct: 241 TWTE SVTVKGPPRNSSGRKHLRAI 265

>ref|YP_002468613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola str. Tuc7 (Acyrtosiphon pisum)]
sp|B8D7K3.1|AROA_BUCAT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ACL30118.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola str. Tuc7 (Acyrtosiphon pisum)]
Length = 427

Score = 411 bits (1056), Expect = e-112, Method: Compositional matrix adjust.
Identities = 214/433 (49%), Positives = 291/433 (67%), Gaps = 17/433 (3%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++GTV LPGSKS+SNR+LLL++++GTT + NLLNS D +ML AL+ LG+
Sbjct: 7 LKPISHVNGTVCLPGSKSISNRVLLSSIAKGTTCCLTNLLNSHDTQHMLNALKKLGVRYN 66

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V G G G F + +A + L+LGNAG A+R L + ++ N +L+G R
Sbjct: 67 LSDDKKTCHVQIGGPFHLSEA---ISLYLGNAGTAIRPLLSVLSLHKNNI--LLNGDDR 121

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L Q GA ++ PP+ G G GG + L+G+ISSQ+L++LL+
Sbjct: 122 MHERPIGDLVDALIQGGAVIEYKKNKGYPPICTKG--GFLGGSIFLNGNISSQFLTSLLI 179

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ PLAL D I I L+S PY+++TL L++ FGV EH DS++ FYIKG Q+YK+P
Sbjct: 180 STPLALKDITTFIKGNLVSKPYIDITLNLKIFGVNIEH-DSYNVFYIKGQKYKTPGKY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVT 308
+EGDASSASYFLA AAI GG+V V G G S+QGD++FA +LE MGA + W + S+T T
Sbjct: 239 TIEGDASSASYFLAAAAIKGGSVKVTGKGKSIQGDIEFANILEKMGATIFWEDYSITCT 298

Query: 309 GPPREPFGKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L AID++MN +PD AMT+A++ALF+ G T IR++ +WRVKET+R+ A+
Sbjct: 299 -----RNKLNAIDLDMNHIPDAAMTVAILALFSGGTTIIRNIYNWRVKETDRLSMT 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
EL K+GA VEEG D+ I+PP ++I+TY+DHRMAM FSL + + V V I +P C
Sbjct: 351 IELRKIGAIVEEGRDFLSISPPIFFQYSSIETYNDRMAMCFSLISLSGVGVNINLPNCI 410

Query: 429 RKTFFPDYF-DVLS 440
KTFP YF D LS
Sbjct: 411 SKTFPSYFKDFLS 423

>gb|ADP66703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola str. TLW03 (Acyrtosiphon pisum)]
Length = 427

Score = 411 bits (1056), Expect = e-112, Method: Compositional matrix adjust.
Identities = 214/433 (49%), Positives = 291/433 (67%), Gaps = 17/433 (3%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++GTV LPGSKS+SNR+LLL++++GTT + NLLNS D +ML AL+ LG+
Sbjct: 7 LKPISHVNGTVCLPGSKSISNRVLLSSIAKGTTCCLTNLLNSHDTQHMLNALKKLGVRYN 66

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V G G G F + +A + L+LGNAG A+R L + ++ N +L+G R
Sbjct: 67 LSDDKKTCHVQIGGPFHLSEA---ISLYLGNAGTAIRPLLSVLSLHKNNI--LLNGDDR 121

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L Q GA ++ PP+ G G GG + L+G+ISSQ+L++LL+
Sbjct: 122 MHERPIGDLVDALIQGGAVIEYKKNKGYPPICTKG--GFLGGSIFLNGNISSQFLTSLLI 179

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ PLAL D I I L+S PY+++TL L++ FGV EH DS++ FYIKG Q+YK+P
Sbjct: 180 STPLALKDITTFIKGNLVSKPYIDITLNLKIFGVNIEH-DSYNVFYIKGQKYKTPGKY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+EGDASSASYFLA AAI GG+V V G G S+QGD++FA +LE MGA + W + S+T T
Sbjct: 239 TIEGDASSASYFLAAAAIKGGSVKVTGVGKKSIQGDIEFANILEKMGATIFWEDYSITCT 298

Query: 309 GPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L AID++MN +PD AMT+A++ALF+ G T IR++ +WRVKET+R+ A+
Sbjct: 299 -----RNKLNAIDLDMNHIPDAAMTVAILALFSKGTTIIRNIYNWRVKETDRLSMT 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
EL K+GA VEEG D+ I+PP ++I+TY+DHRMAM FSL + + V V I +P C
Sbjct: 351 IELRKIGAIVEEGRDFLSISPPIFFQYSSIETYNDRMAMCFSLSLSGVGVNINLPNCI 410

Query: 429 RKTFFPDYF-DVLS 440
KTFF YF D LS
Sbjct: 411 SKTFPSYFKDFLS 423

>gb|ADP66131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. LL01 (Acyrtosiphon pisum)]
Length = 427

Score = 411 bits (1056), Expect = e-112, Method: Compositional matrix adjust.
Identities = 213/433 (49%), Positives = 291/433 (67%), Gaps = 17/433 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++GTV LPGSKS+SNR+LLL++++GTT + NLLNS D +ML AL+ LG+
Sbjct: 7 LKPISHVNGTVCLPGSKSISNRVLLSSIAKGTTCCLTNLLNSHDTQHMLNALKKLGVRYN 66

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K + G GG F + +A + L+LGNAG A+R L + ++ N +L+G R
Sbjct: 67 LSDDKKTCHIQIGGPFHLSEA---ISLYLGNAGTAIRPLLVLSLHKNNI--LLNGDDR 121

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L Q GA ++ PP+ G G GG + L+G+ISSQ+L++LL+
Sbjct: 122 MHERPIGDLVDALIQGGAIVIEYKKNKGYPPICTKG--GFLGGSIFLNGNIISSQFLTSLLI 179

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKNA 248
+ PLAL D I I L+S PY+++TL L++ FGV EH DS++ FYIKG Q+YK+P
Sbjct: 180 STPLALKDITIFIKGNLVSKPYIDITLNLKIFGVNIEH-DSYNVFIYIKGQYKTPGKY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+EGDASSASYFLA AAI GG+V V G G S+QGD++FA +LE MGA + W + S+T T
Sbjct: 239 TIEGDASSASYFLAAAAIKGGSVKVTGVGKKSIQGDIEFANILEKMGATIFWEDYSITCT 298

Query: 309 GPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L AID++MN +PD AMT+A++ALF+ G T IR++ +WRVKET+R+ A+
Sbjct: 299 -----RNKLNAIDLDMNHIPDAAMTVAILALFSKGTTIIRNIYNWRVKETDRLSMT 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
EL K+GA VEEG D+ I+PP ++I+TY+DHRMAM FSL + + V V I +P C
Sbjct: 351 IELRKIGAIVEEGRDFLSISPPIFFQYSSIETYNDRMAMCFSLSLSGVGVNINLPNCI 410

Query: 429 RKTFFPDYF-DVLS 440
KTFF YF D LS
Sbjct: 411 SKTFPSYFKDFLS 423

>ref|NP_240133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. APS (Acyrtosiphon pisum)]
ref|YP_002468060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. 5A (Acyrtosiphon pisum)]
ref|ZP_05635364.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. LSR1 (Acyrtosiphon pisum)]
sp|P57396.1|AROA_BUCAI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B8D9A1.1|AROA_BUCA5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
pir||C84966 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)

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[imported] - Buchnera sp. (strain APS)
dbj|BAB13019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. APS (Acyrtosiphon pisum)]
gb|ACL30672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. 5A (Acyrtosiphon pisum)]
gb|ADP67285.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. JF99 (Acyrtosiphon pisum)]
Length = 427

Score = 411 bits (1056), Expect = e-112, Method: Compositional matrix adjust.
Identities = 213/433 (49%), Positives = 291/433 (67%), Gaps = 17/433 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++GTV LPGSKS+SNR+LLL++++GTT + NLLNS D +ML AL+ LG+
Sbjct: 7 LKPISHVNGTVCLPGSKSISNRVLLSSIAKGTTCCLTNLLNSHDTQHMLNALKKLGVRYN 66

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V G GG F + +A + L+LGNAG A+R L + ++ N +L+G R
Sbjct: 67 LSDDKKTCHVQIGGPFHLSEA---ISLYLGNAGTAIRPLLSVLSLHKNNI--LLNGDDR 121

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L Q GA ++ PP+ G G GG + L+G+ISSQ+L++LL+
Sbjct: 122 MHERPIGDLVDALIQGGAIVIEYKKNKGYPICTKG--GFLGGSIFLNGNISSQFLTSLLI 179

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ PLAL D I I L+S PY+++TL L++ FGV EH DS++ FYIKG Q+YK+P
Sbjct: 180 STPLALKDITIFIKGNLVSKPYIDITLNLKIFGVNIEH-DSYNVFIYKKGQYKTPGKY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+EGDASSASYFLA AAI GG++ V G G S+QGD++FA +LE MGA + W + S+T T
Sbjct: 239 TIEGDASSASYFLAAAAIKGSIKVTGVGKKSIGDIEFANILEKMGATIFWEDYSITCT 298

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L AID++MN +PD AMT+A++ALF+ G T IR++ +WRVKET+R+ A+
Sbjct: 299 -----RNKLNADLDMNHIPDAAMTVAILALFSGGTTIIRNIYNWRVKETDRLSMT 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
EL K+GA VEEG D+ I+PP ++I+TY+DHRMAM FSL + + V V I +P C
Sbjct: 351 IELRKIGAIVEEGRDFLSISPPIFFQYSSIETYNDRMAMCFSLISLSGVGVNINLPNCI 410

Query: 429 RKTFFPDYF-DVLS 440
KTFP YF D LS
Sbjct: 411 SKTFPSYFKDFLS 423

>ref|YP_003930386.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Pantoea vagans C9-1]
gb|AD008937.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Pantoea vagans C9-1]
Length = 428

Score = 410 bits (1055), Expect = e-112, Method: Compositional matrix adjust.
Identities = 230/441 (52%), Positives = 294/441 (66%), Gaps = 16/441 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+ + LQPI + GTV LPGSKS+SNR LLLAAL++GTT + NLL+S+DV +ML AL LG
Sbjct: 3 DSLTLQPIARVDGTVNLPGSKSVSNRALLLAALAKGTTRLTNLLSDDDVKHMLNALTALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + R V G P+ A + + LFLGNAG AMR L AA+ G L
Sbjct: 63 --VNYTLSGDRITVCEVTGNAGPLH-ASQPLSLFLGNAGTAMRPLAALCL--GEHDIELT 117

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGLVDALRQGGAIIDYLENENYPPLRLRG--GFIGGDVSVDSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV E+ + + RF IKG Q+Y+S
Sbjct: 176 ALLMTAPLAQQDTCITIKGDLVSKPYIDITLNLMQCFGVDVENQN-YQRFLIKGQQYQS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 304
P + VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 235 PGDYLVEGDASSASYFLAAAAIKGTVRVGTIGRQSVQGDIFADVLERMGAVIEWGDDY 294

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Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ T L+AID++MN +PD AMT+A ALFA+G T +R++ +WRVKET+R+
Sbjct: 295 IACTA-----GKLQAIDMDMNHIPDAAMTIAT'TALFAEGTTQLRNIYNWRVKETDRL 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA VEEG D+ ITPP L I TY+DHRMAM FSL A ++ PVTI D
Sbjct: 347 SAMATELRKVGAEVEEGHDFIRITPPASLIHADIGTYNDHRMAMCFSLVALSDTPVTILD 406

Query: 425 PGCTRKTFFPDYFDVLSTFVK 445
PGCT KTFPDYF L+ ++
Sbjct: 407 PGCTAKTFPDYFVQLAKISQH 427

>ref|YP_002910765.1| Prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia glumae BGR1]
gb|ACR28061.1| Prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia glumae BGR1]
Length = 432

Score = 410 bits (1053), Expect = e-112, Method: Compositional matrix adjust.
Identities = 227/446 (50%), Positives = 290/446 (65%), Gaps = 21/446 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + + P +SGTV+LPGSKS+SNR+LLLAALSEG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDIGPYSRVSGTVRLPGSKSISNRVLLLAALSEGVTITNLLSDSDTRVMLAALEALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + A VV G G FP + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VRLE--RHADTCVVNGTRGAFPAKTA---DLFLGNAGTAVRPLTAAALAVNGGD--YRVH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAVIDYEQNEGYPPLRIQAGTIAVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + +
Sbjct: 174 ALLMTLPLVGKKGASVVEIDGELISKPYEITIKLMARFGVTVER-DGWQRFSVPAA-R 231

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + +EG G S+QGDV FA L MGA V+
Sbjct: 232 YQSPGTMVEGDASSASYFLAAGALGGGPLRIEGVGRASIQGDVGFATALMQMGANVSMG 291

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVK
Sbjct: 292 DDWIEVRG-----IGHDHGKLEPIDMDFNLIPDAAMTI AVALFAEGTSTLRNIASWRVK 346

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA+VEEG DY ++TPP KL AIDTYDDHRMAM FSL + V
Sbjct: 347 ETDRIAAMAAELRKLGA+VEEGADYLVVTPPAKLVPNAIDTYDDHRMAMCFSLSLGGV 406

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
PV I DP C KTFPDYFD + +
Sbjct: 407 PVRINDPKCVAKTFFPDYFDRFTALAR 432

>ref|ZP_03317918.1| hypothetical protein PROVALCAL_00838 [Providencia alcalifaciens DSM
30120]
gb|EEB47129.1| hypothetical protein PROVALCAL_00838 [Providencia alcalifaciens DSM
30120]
Length = 425

Score = 410 bits (1053), Expect = e-112, Method: Compositional matrix adjust.
Identities = 228/436 (52%), Positives = 292/436 (66%), Gaps = 16/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + LQPI ISGT+ LPGSKS+SNR LLLA+++GTTV+ NLL+S+D+ +ML AL LG
Sbjct: 2 QSLTLQPISSISGTINLPGSKSVSNRALLLAAMAKGTTVLNLLSDSDIRHMLNALSLLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + R V G G K E+++FLGNAG AMR LTAA++ N +L

Sbjct: 62 VKYQLSADKTRCEVEGIDGCL---SHKGELEIFLGNAGTAMRPLTAALSLCPNNI--ILT 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L++ GA++D + PP+R+ G G GG + + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALREGGAEIDYLEQENYPPMRLKG--GFVGGHISVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D I I L+S PY+++TL LM+ FGV E+ + +F IKG Q+Y S

Sbjct: 175 ALLMAAPLAAQDTVISIAGDLVSKPYIDITLALMKTFGVDVENH-QYQKFVIKGGQQYLS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GG V V G G SLQGD KFA VLE MGA + W +

Sbjct: 234 PGEYLVEGDASSASYFLAAAAIKGGVVRVTGIGRNSLQGDTKFANVLEKMGAIIRWGDDY 293

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L ID++MN +PD AMT+ VALFA G T IR++ +WRVKET+R+

Sbjct: 294 VECE-----RGTLNGIDMDMNAIPDAAMTIGTVALFAKGETVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL K+GA VEEG D+ +TPP++L I+TY+DHR+AM FSL A + PVTI D

Sbjct: 346 YAMATELRKVGAEVEEGHDFIRVTPPKQLKHAIEIETYNDHRIAMCFSLVALSNTPTVITLD 405

Query: 425 PGCTRKTFFPDYFDVLS 440
PGCT KTFPDYF L+

Sbjct: 406 PGCTAKTFFPDYFQQLA 421

>ref|YP_772814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria AMMD]
sp|Q0BH93.1|AROA_BURCM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI86480.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria AMMD]
Length = 434

Score = 410 bits (1053), Expect = e-112, Method: Compositional matrix adjust.
Identities = 228/447 (51%), Positives = 287/447 (64%), Gaps = 30/447 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +

Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGDTTITNLLDSDTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR

Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPG-----GKVKLSGSISSQYL 183
M ERPIGDLV GL+Q+GA +D PP+R+ PG +++ G +SSQ+L

Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPLRIK-----PGTISVDAPIRVRGDVSSQFL 172

Query: 184 SALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ALLM PL G +EI +LIS PY+++T+RLMERFGV E D W RF + G

Sbjct: 173 TALLMTLPLVKAKDGRTVVEIDGELISKPYIDITIRLMERFGVTVER-DGWQRFVVPAGV 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA V+

Sbjct: 232 RYRSPGRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVSM 291

Query: 301 TETSVTVTGPPEPFRGRK--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ + V G G H L ID++ N +PD AMT+AV ALFA G + +R++ASWRV

Sbjct: 292 GDDWIEVRG-----IGHDHGKLDPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRV 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAE 417
KET+R+ A+ TEL K+GA VEEG DY ++TPP++L AIDTYDDHRMAM FSL +

Sbjct: 347 KETDRIAAMATELRKVGAEVEEGADYLVVTPPQRLTPNAAIDTYDDHRMAMCFSLVSLGG 406

Query: 418 VPVITIRDPGCTRKTFFPDYFDVLSTFVK 444
VPV I DP C KTFPDYF+ + K

Sbjct: 407 VPVRINDPKCVGKTFFPDYFNRFALAK 433

>ref|YP_442173.2| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
E264]
Length = 673

Score = 410 bits (1053), Expect = e-112, Method: Compositional matrix adjust.
Identities = 227/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 241 EYLDLGPFSHARGTVRLPGSKSISNRVLLAALAEGETTTVNNLLSDSDTRVMDALTKLG 300

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 301 VKLSRD--GDTCCVVGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 352

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 353 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 412

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 413 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 471

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 472 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 531

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG + +R++ SWRVK
Sbjct: 532 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAVAALFADGTSTLRNIGSWRVK 586

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 587 ETDRIAAMATELRKIGATVEEGADYLVVTPPARLTPNASIDTYDDHRMAMCFSLVSLGGV 646

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 647 PVRINDPKCVGKTFPDYFD 665

>gb|ABC39479.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
E264]
Length = 805

Score = 410 bits (1053), Expect = e-112, Method: Compositional matrix adjust.
Identities = 227/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 373 EYLDLGPFSHARGTVRLPGSKSISNRVLLAALAEGETTTVNNLLSDSDTRVMDALTKLG 432

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 433 VKLSRD--GDTCCVVGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 484

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 485 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 544

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 545 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 603

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 604 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 663

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359

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      + + V G      G H L ID++ N +PD AMT+AV ALFADG + +R++ SWRVK
Sbjct: 664 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAVAALFADGTSTLRNIGSWRVK 718

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
      ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 719 ETDRIAMATELRKIGATVEEGADYLVVTPPARLTPNASIDTYDDHRMAMCFSLVSLGGV 778

Query: 419 PVTIRDPGCTRKTFPDYFD 437
      PV I DP C KTFPDYFD
Sbjct: 779 PVRINDPKCVGKTFPDYFD 797

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>ref|YP_003007701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
aphrophilus NJ8700]
gb|ACS97614.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
aphrophilus NJ8700]
Length = 441

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Score = 409 bits (1052), Expect = e-112, Method: Compositional matrix adjust.
Identities = 228/442 (51%), Positives = 288/442 (65%), Gaps = 20/442 (4%)

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Query: 1  MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVNLLNSEDVHYMLGAL 60
      M A I L PI+ I GT+ LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL
Sbjct: 1  MQHAISITLNPRIHIEGTINLPGSKSLSNRALLLAALAHGTTKVTNLLDSDDIRHMLNAL 60

Query: 61  RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
      + LG+ V G GG F D + LFLGNAG AMR L AA+ A A+
Sbjct: 61  KQLGVQYSLSDDKSVCEVQGLGGAFFQWHDG---LALFLGNAGTAMRPLAALCLAREGAS 117

Query: 121 ----YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
      +L G PRM+ERPI LV L Q GAD+ PP+ + G L GG +K+ G
Sbjct: 118 AQNEVILTGEPRMKERPIQHLVDALLQAGADIRYLENEGFPPIAIRNTG-LRGGTIKIDG 176

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
      SISSQ+L+ALLMAAPLA GD EIEII +L+S PY+++TL +M+ FGV+ E+ + + RF +
Sbjct: 177 SISSQFLTALMAAPLAEGDSEIEIIGELVSKPYIDITLNMKIFGVEVENQN-YQRFIV 235

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGA 296
      KG Q Y+SP + VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA
Sbjct: 236 KKGQSYQSPGSFLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMG 294

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
      K+TW E + P L +D++MN +PD AMT+A ALFA+G T IR++ +W
Sbjct: 295 KITWGEDFIEAEQAP-----LHGVDMDNMNHPDAAMTIATTALFAEGETVIRNIYNW 346

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT- IDTYDDHRMAMAFSLAA 414
      RVKET+R+ A+ TEL K+GA VEEG D+ I P P + I+TY+DHRMAM F+L A
Sbjct: 347 RVKETDRLTAMATELRKVGAEEVEGEDFIRIQPLKPTFKAEEIETYNDHRMAMCFALIA 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYF 436
      ++ PVTI DP CT KTFP +F
Sbjct: 407 LSDTPVTILDPNCTAKTFPTFF 428

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>ref|NP_245776.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pasteurella multocida
subsp. multocida str. Pm70]
sp|Q04570.2|ARO_A_PASMU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK02923.1| AroA [Pasteurella multocida subsp. multocida str. Pm70]
Length = 440

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Score = 409 bits (1052), Expect = e-112, Method: Compositional matrix adjust.
Identities = 220/447 (49%), Positives = 295/447 (65%), Gaps = 23/447 (5%)

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Query: 4  AEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVNLLNSEDVHYMLGALRTL 63
      A I L PI I G V+LPGSKSLSNR LLL+AL++G T + NLL+S+DV +ML AL+ L
Sbjct: 5  ATAITLNPISYIEGEVRLPGSKSLSNRALLLSALAKGKTTLTNLLDSDVVRHMLNALKEL 64

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---GNA 119
      G++ + + + G G F + + LFLGNAG AMR LTAA+ + G

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Sbjct: 65 GVTYQLSEDKSVCEIEGLGRAFEWQSG--LALFLGNAGTAMRPLTAALCLSTPNKEGKN 121

Query: 120 TYVLDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSIS 179
VL G PRM+ERPI LV L Q GA++ PP+ + G L GG++++ GS+S

Sbjct: 122 EIVLTGEPRMKERPIQHLVDALCQAGAEIQYLEQEGYPPIAIRNTG-LKGGRIQIDGSVS 180

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMAAP+A D EIEII +L+S PY+++TL++M+ FGV+ E+ ++ RF +KG

Sbjct: 181 SQFLTALLMAAPMAEADTEIEIIGELVSKPYIDITLKMMTQTFGEVENQ-AYQRFVLKGH 239

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Q+Y+SP VEGDASSASYFLA AAI G V V G G S+QGD FA+VLE MGA +T

Sbjct: 240 QQYQSPHRFLVEGDASSASYFLAAAAIKG-KVKVTGVGKNSIQGDRFLFADVLEKMGAHIT 298

Query: 300 WTETSVTVTGPPREPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W + + V + +LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVK

Sbjct: 299 WGDDFIQVE-----KGNLKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVK 350

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPE--KLNVT AIDTYDDHRMAMAFSLAACAE 417
ET+R+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM F+L A ++

Sbjct: 351 ETDRLTAMATELRKVGAEEVEGEDFIRIQPLNLAQFQHAIEIETYNDRMAMCFALIALSQ 410

Query: 418 VPVTIRDGPCTRKTFPDYFDVLSTFVK 444
VTI DP CT KTFP +FD TF++

Sbjct: 411 TSVTILDPSCTAKTFPTFFD---TFLR 434

>ref|YP_001807632.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria MC40-6]
sp|B1YV33.1|ARO_A_BURA4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACB63416.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
ambifaria MC40-6]
Length = 434

Score = 409 bits (1052), Expect = e-112, Method: Compositional matrix adjust.
Identities = 229/447 (51%), Positives = 286/447 (63%), Gaps = 30/447 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +

Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEGDTTITNLLDSDTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR

Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPG-----GKVKLSGSISSQYL 183
M ERPIGDLV GL+Q+GA +D PP+R+ PG +++ G +SSQ+L

Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPLRIK-----PGTISVDAPIRVRGDVSSQFL 172

Query: 184 SALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ALLM PL G +EI +LIS PY+++T+RLMERFGV E D W RF G

Sbjct: 173 TALLMTLPLVKAKDGRVTVEIDGELISKPYIDITIRLMERFGVTVER-DGWQRVFVAPAGV 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA V+

Sbjct: 232 RYRSPGRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVSM 291

Query: 301 TETSVTVTGPPREPFRGKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ + V G G H L ID++ N +PD AMT+AV ALFA G + +R++ASWRV

Sbjct: 292 GDDWIEVRG-----IGHDHGKLDPIDMDFNLPDAAMTIAVAALFASGTSTLRNIASWRV 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAE 417
KET+R+ A+ TEL K+GA VEEG DY ++TPP++L AIDTYDDHRMAM FSL +

Sbjct: 347 KETDRIAAMATELRKVGAIVEEGADYLVVTPPQRLTPNAAIDTYDDHRMAMCFSLVSLGG 406

Query: 418 VPVTIRDGPCTRKTFPDYFDVLSTFVK 444
VPV I DP C KTFPDYFD + K

Sbjct: 407 VPVRINDPKCVGKTFPDYFDRFAALAK 433

>ref|YP_003605803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1002]
gb|ADG16292.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1002]
Length = 434

Score = 409 bits (1051), Expect = e-112, Method: Compositional matrix adjust.
Identities = 221/446 (49%), Positives = 290/446 (65%), Gaps = 20/446 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFSRASGTVRPLPGSKSISNRVLLLAALAEGETTITNLLSDDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D VV G G F A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VRLKRD--GDTCVVTGTRGAFTARTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ + +++ G +SSQ+L+
Sbjct: 114 GVPRMHMERPIGDLVDGLRQIGAKIDYEQNEGYPPLRIRPAQIMADAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LLM PL A G +++ +LIS PY+E+T++LM RFG++ E W +F + GQ+
Sbjct: 174 SLLMTLPLLRRTASGVTTVQVDGELISKPYIEITIKLMARFGIEVERH-GWHQFVVPAGQR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA+ L MGA +
Sbjct: 233 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFDALIKMGANLQMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG T +R++ASWRVK
Sbjct: 293 DDWIEVRG----VGNDHGKLDPIDMDFNLIPDAAMTIAAALFADGTTTLRNIAVSRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA V+EG D+ ++TPPEKL AIDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAMATELRKVGAKVQEGEDFLVVTPEKLIIPNAAIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
P+ I DP C KTFPDYF+ + +
Sbjct: 408 PIRINDPKCVGKTFFPDYFERFTALAQ 433

>ref|ZP_01788712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 3655]
gb|EDJ93201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 3655]
Length = 432

Score = 409 bits (1051), Expect = e-112, Method: Compositional matrix adjust.
Identities = 225/436 (51%), Positives = 288/436 (66%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPGSKSLSNRALLLAALAKGTTKVNTLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G GG F +++ + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEIEGLGGAFNMQN---NLSLFLGNAGTAMRPLTAALCLKGNHEVEIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGVK+ GSISSQ+L
Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +FYIK Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFYIKGNQSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237 SPKNYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + L +ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QAELENSIDMDMNHIPDAAMTIATTALFANGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P + I TY+DHRMAM FSL A + PVT
Sbjct: 348 LTAMATELRKVGAEEVEGEDFIRIQPLALNQFKHANIKTYNDRMAMCFSLIALSNTPTVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|ZP_02478328.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus parasuis
29755]
gb|EDS24566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus parasuis
29755]
Length = 437

Score = 409 bits (1050), Expect = e-112, Method: Compositional matrix adjust.
Identities = 222/436 (50%), Positives = 291/436 (66%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LKPKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLNPIARVEGEINLPGSKSLSNRALLLAALAQQTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
++ + V G GG F ++ + LFLGNAG AMR LTAA+ G A +L
Sbjct: 62 VNYQLSDDKTVCVTEGVGGAFQWQNG---LSLFLGNAGTAMRPLTAAALCLKGEQAEVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L Q GA V PP+ + +G + GGK+++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALLQAGASVQYLENEGYPPPIAIRNLG-IQGGKIQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEI+ +L+S PY+++TL +M+ FGV +++ + F++KG Q Y
Sbjct: 178 TALLMSAPLASGDMEIEIVGELVSKPYIDITLAMMKDFGVTVSYNN-YQTFVKGNGHYV 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPQKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGELKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P +K I+TY+DHRMAM FSL A + P+T
Sbjct: 348 LTAMATELRKVGAEEVEGEDFIRIQPLALDKFQHAETIETYNDRMAMCFSLVALSNTPLT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP YFD
Sbjct: 408 ILDPKCTAKTFPTYFD 423

>ref|YP_454671.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sodalis glossinidius
str. 'morsitans']
sp|Q2NUA9.1|AROASODGM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE74266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sodalis glossinidius
str. 'morsitans']
Length = 435

Score = 409 bits (1050), Expect = e-112, Method: Compositional matrix adjust.
Identities = 218/439 (49%), Positives = 286/439 (65%), Gaps = 17/439 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + L PI + GT+ LKPKSKS+SNR LLLAA + GTT + NLL+S+DV +ML AL LG
Sbjct: 3 DSLTLNPIARVDGTLNLPKSKSVSNRALLLAQAQNGTTRLTNLLDSDVVRHMLTALGQLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + G GG A E + LFLGNAG AMR L AA+ + T L
Sbjct: 63 VNYRLSADRSCIEDLGGPL--RADEALTFLGNAGTAMRPLAALCLQAQDVT--LT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D PP+R+ G G GG + + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAQIDYLEHEHYPLRLRG--GYQGGDITVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA + I I +L+S PY+++TL LM+ FG++ H D++ FY+ GG Y+S
Sbjct: 176 ALLMMAPLAPQNSCIKIGELVSRPYIDITLALMKSFGIEVRH-DNYQVFYLTGGSVYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W
Sbjct: 235 PGEYLVEGDASSASYFLAAAIRGGTVRVVTGIGRHSVQGDIRFADVLESMTGATIRWGN DY 294

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ + R L ID++MN +PD AMT+A ALFA G T +R++A+WRVKET+R
Sbjct: 295 IECS-----RASLHTIDMDMNHIPDAAMTIATTALFASGGTTTLRNIANWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ TEL K+GA+V EG DY +TP +L+ I TY+DHRMAM F+L A ++ PVTI
Sbjct: 347 LTAMATELRKVGATVIEGEDYLTVP SARLSAARIGTYNDHRMAMCFALVALSDTPVTIL 406

Query: 424 DPGCTRKTFPDYFDVLSTF 442
DP CT KTFPD+F LS
Sbjct: 407 DPQCTHKTFPDFFARLSAL 425

>ref|ZP_07336590.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
ref|ZP_07338548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. 4226]
ref|ZP_07529714.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. S1536]
ref|ZP_07534151.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
gb|EFL79031.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. 4226]
gb|EFL80876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
gb|EFM88003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. S1536]
gb|EFM92192.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
Length = 432

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 229/435 (52%), Positives = 289/435 (66%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISRVEGEINLPGSKSLSNRALLLAALAKGTTKVTNLLDSDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G A VL
Sbjct: 62 VNYSLSEDKTVCTVEGVGGAF--NWKNGLALFLGNAGTAMRPLTAALCLKGATEAEVVL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGVK E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVKVENRN-YQTFVVKGNQSYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGA+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFANVLEAMGAKITWDDD 295

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGELKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA+VEEG D+ I P + I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LAAMATELRKVGATVEEGEDFIRIQPLPLTQFQHAETIATYNDHRMAMCFSLIALSDTPVT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP YF
Sbjct: 408 ILDPNCTAKTFPTYF 422

>ref|ZP_02373925.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
TXDOH]
ref|ZP_02387760.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
Bt4]
ref|ZP_05586624.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
E264]
Length = 434

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 227/439 (51%), Positives = 283/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 2 EYLDLGFPSHARGTVRLPGSKSISNRVLLLAALAEGETTVTNLLSDSDTRVMLDALTKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VKLSRD--GDTCVVGTRGAFTAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG + +R++ SWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAVAALFADGTSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ADITYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMATELRKIGATVEEGADYLVVTPPARLTPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 408 PVRINDPKCVGKTFPDYFD 426

>ref|YP_003048947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium mobilis
JLW8]
gb|ACT48420.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium mobilis
JLW8]
Length = 426

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 216/435 (49%), Positives = 281/435 (64%), Gaps = 21/435 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L + GT+ LPGSKS+SNR LLLAAL+ GTT + ++L S+D ML AL L

Sbjct: 2 EQLTLAASHQAQGTTLTLPKSGKSISNRTLLLAALANGTTEIRDVLASDDTSRMLEALEALD 61

Query: 65 LSVE--ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ +E AD A + V GCGG FP ++ LFLGNAG A R LTAA+ AGGN Y

Sbjct: 62 VQLENFADNAWR--VTGCGGNFP----NKQADLFLGNAGTAFRPLTAALALAGGN--YQ 112

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L GV RM ERPIGDLV LKQ GAD+ PP+++ ++K+ G +SSQ+

Sbjct: 113 LSGVARMHERPIGDLVDALKQAGADIQYLANDGYPLKIAAPQLDLKRIKIRGDVSSQF 172

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMA PL IE+I +LIS PY+E+TL LM +FGV+ + W F I Y

Sbjct: 173 LTALLMALPLTKQQATIEVIGELISKPYIEITLNLMAKFGVQVAR-NGWQSFTIPANSSY 231

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ +VEGDASSASYFLA AI G VTV+G G S+QGDV+FA+ L +MG +++ +

Sbjct: 232 TAPQEIFVEGDASSASYFLAGAI-AGNVTVQGLGKDSIQGDVRFADALALMGNISSYAD 290

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+T + + + ID++ N +PD AMTLA++ALFA G + +R++ASWRVKET+

Sbjct: 291 NHITASKA-----EQIHTIDLDCNHIPDAAMTLAILALFAKGTSTLRNIASWRVKETD 343

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVT 421
R+ A+ TEL K+GA VEEG DY ITPP L AIDTYDDHRMAM FSL + VP+

Sbjct: 344 RIAAMATELRKVGAIVEEGADYITITPPATLTPNAAIDTYDDHRMAMCFSLVSLGGVPPII 403

Query: 422 IRDPGCTRKTFFDYF 436
I DP C KTFP+YF

Sbjct: 404 INDPNCVAKTFPNYF 418

>ref|YP_545038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacillus
flagellatus KT]
ref|YP_545182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacillus
flagellatus KT]
gb|ABE49197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacillus
flagellatus KT]
gb|ABE49341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacillus
flagellatus KT]
Length = 429

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 225/443 (50%), Positives = 284/443 (64%), Gaps = 19/443 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + L ++ GTVKLPKSGKS+SNR LLLAAL++G T + LL S+D ML ALR LG

Sbjct: 2 ESITLPAVRHAYGTVKLPKSGKSISNRTLLLAALAQGDTEIHELLASDDTQRMLDALRILG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + V G G+FPV+ A LFLGNAG A R LTAA+ + GN Y L

Sbjct: 62 VKLE-QTGLHQVQVHGTCGEFPVKQAA----LFLGNAGTAFRPLTAALALSHGN--YELS 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G+ RM ERPIGDLV L GA ++ PP+ + +++ G +SSQ+L+

Sbjct: 115 GIARMHERPIGDLVDTLNAAAGAAIEYLQNPFGPPLHIRPATLNTSEALRVRGDVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKA--EHSDSWDRFYIKGGQKY 242
ALLMA PL + IE+I +LIS PY+++TL LM +FG++ EH W F I G +Y

Sbjct: 175 ALLMALPLTGEEARIEVIGELISKPYIDITLNLMRQFGIEVLREH---WRTFTIPAGSRY 231

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
KSP +VEGDASSASYFLA AI G VTVEG G S+QGDV+F E LE MGA V +

Sbjct: 232 KSPGIVHVEGDASSASYFLAAGAIGQGPVTVEGVGRNSIQGDVRFVEALERMGADVNTGD 291

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ V P + LKA+D++ N +PD AMTLA++ALFADG + +R++ASWRVKET+

Sbjct: 292 HWIKVHSTPGK-----LKALDMDCNHIPDAAMTLAILALFADGTSTLRNIASWRVKETD 345

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVT 421
R+ A+ TEL K+GA VEEG DY ITPP+ L A IDTYDDHRMAM FSL A VP+

Sbjct: 346 RLAAMATELRKVGAVVEEGNDYLRITPPDALTPNACIDTYDDHRMAMCFSLVALGGVPPIV 405

Query: 422 IRDPGCTRKTFPDYFDVLSFVK 444
I DP C KTFPDYF+ S V
Sbjct: 406 INDPNCVAKTFPDYFERFSALVH 428

>ref|ZP_03825646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. brasiliensis PBR1692]
Length = 429

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 228/437 (52%), Positives = 297/437 (67%), Gaps = 17/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + LQPIK I+GT+ LKPSKS+SNR LLLAAL+EG T + NLL+S+DV +ML AL LG
Sbjct: 3 ESLTLQPIKLINGTLNLPKSKSVSNRALLAALAEGKTRLTNLLSDSDVRHMLTALTALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ G GG F A + ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 63 VDYHLSDDRTVCEITGLGGFT--ASQPLELFLGNAGTAMRPLAALCLTDGD--IVLT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R++G G GG++ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPRLRHG--GFQGGESVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I I L+S PY+++TL +M+ FG++ +++ RF++ G Q+Y+S
Sbjct: 176 ALLMTAPLAAQDTQISIQGDLVSKPYIDITLHMMKAFGIEVR-NENYQRFVTGRQQYRS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA+VLE MGA V W E
Sbjct: 235 PGDYLVEGDASSASYFLAAAAIKGGVVRVTGVGRKSVQGDIRFADVLEKMGATVRWGEDY 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADG-PTAIRDVASWRVKETER 363
+ R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R
Sbjct: 295 IECE-----RGELHAIDMDMNHIPDAAMTIATAALFAQGGTTTLRNIYNWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ EL K+GA VEEG DY ITPP KL V I TY+DHRMAM FSL A ++ PVTI
Sbjct: 347 LAAMAIELRKVGAEEVEEGNDYIRITPPTKLKVAEIGTYNDHRMAMCFSLVALSDTPVTIL 406

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFPDYF+ L+
Sbjct: 407 DPKCTAKTFPDYFEQLA 423

>ref|YP_001580441.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
ref|YP_001945462.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
sp|A9ADV6.1|AROABURM1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX15944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
dbj|BAG42926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
Length = 434

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 226/442 (51%), Positives = 285/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLAALAEGDTTITNLLSDSDTRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVGTGRTGAFKTA----DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPPLRIRPATISVDAPIRVRGDIVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +EI +LIS PY+++T+RLM RFGV E + W RF + G +Y+SP
Sbjct: 178 TLPLVKAkdGRSIVEIDGELISKPYIDITIRLMARFGVNVER-EGWQRFTVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFALHMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 297 EVRG-----IGHDHGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA+VEEG DY ++TPP L AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVATVEEGADYLVVTPPAALTTPNAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFPDYFDVLTSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFPDYFDRFAALAK 433

>ref|ZP_03574299.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD2M]
ref|ZP_03579300.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD2]
ref|ZP_03586542.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD1]
gb|EED98829.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD1]
gb|EEE06030.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD2]
gb|EEE11516.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia multivorans
CGD2M]
Length = 434

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 226/442 (51%), Positives = 285/442 (64%), Gaps = 20/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG+ +
Sbjct: 6 LGPYSSASGTVRLPGSKSISNRVLLLAALAEEDTTITNLLSDDTVRVMDALGKLGKLA 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D VV G G F + A LFLGNAG A+R LTAA+ GG+ Y + GVPR
Sbjct: 66 RD--GDTCVVTGTRGAFTAKTA----DLFLGNAGTAVRPLTAALAINGGD--YRVHGVPR 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 118 MHERPIGDLVDGLRQIGAQIDYEQNEGFPPLRIRPATISVDAPIRVRGDIVSSQFLTALLM 177

Query: 189 AAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
PL G +EI +LIS PY+++T+RLM RFGV E + W RF + G +Y+SP
Sbjct: 178 TLPLVKAkdGRSIVEIDGELISKPYIDITIRLMARFGVSVER-EGWQRFTVPAGVRYRSP 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT + +
Sbjct: 237 GRIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMGDDWI 296

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V G G H L+ ID++ N +PD AMT+AV ALFA+G + +R++ASWRVKET+R
Sbjct: 297 EVRG-----IGHDHGKLEPIDMDFNLIPDAAMTIAVAALFANGTSTLRNIASWRVKETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTI 422
+ A+ TEL K+GA+VEEG DY ++TPP L AIDTYDDHRMAM FSL + VPV I
Sbjct: 352 IAAMATELRKVGATVEEGADYLVVTPPAALTPNAAIDTYDDHRMAMCFSLVSLGGVPVRI 411

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
DP C KTFPDYFD + K
Sbjct: 412 NDPKCVGKTFFPDYFDRFAALAK 433

>ref|ZP_02356546.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia oklahomensis
EO147]
Length = 434

Score = 408 bits (1049), Expect = e-112, Method: Compositional matrix adjust.
Identities = 227/446 (50%), Positives = 284/446 (63%), Gaps = 20/446 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 2 EHLDLGPFSHAQGTVRLPGSKSISNRVLLAALAEGETTVTNLLSDDTVRMLDALAKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D A VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VKLSRDGDA--CVVGGTRGAFTAKSA----DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPAAISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +E+ +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAKDGASVVEVDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YRSPGTIMVEGDASSASYFLAAGALGGGPLRVGEVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG + +R++ SWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAAALFADGSSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMAAELRKVGATVEEGADYLVVTPPAQLVPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
PV I DP C KTFPDYFD K
Sbjct: 408 PVRINDPKCVGKTFFPDYFDRFLALAK 433

>gb|ABY53228.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus parasuis]
Length = 437

Score = 408 bits (1048), Expect = e-111, Method: Compositional matrix adjust.
Identities = 222/436 (50%), Positives = 289/436 (66%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLNPIARVEGEINLPGSKSLSNRALLAALAQGTQVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
++ + V G GG F ++ + LFLGNAG AMR LTAA+ G A +L
Sbjct: 62 VNYQLSDNKTCTVEGVGGAFQWQNG---LSLFLGNAGTAMRPLTAALCLKGEQAEVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L Q GA V PP+ + +G + GKK+++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALLQAGASVQYLENEGYPPIAIRNLG-IQGGKIQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEI+ +L+S PY+++TL +M+ FGV H++ + F++KG Q Y
Sbjct: 178 TALLMSAPLASGDMEIEIVGELVSKPYIDITLAMMKDFGVTVSHNN-YQTFVKGNGHYV 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPQKYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGELKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P +K I+TY+DHRMAM F L A + VT
Sbjct: 348 LTAMATELRKVGAEVEEGEDFIRIQPLALDKFQHAIEIETYNDHRMAMCFPLVALSNTSVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP YFD
Sbjct: 408 ILDPKCTAKTFPTYFD 423

>ref|ZP_07538500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 10 str. D13039]
gb|EFM96673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 10 str. D13039]
Length = 432

Score = 407 bits (1047), Expect = e-111, Method: Compositional matrix adjust.
Identities = 229/435 (52%), Positives = 290/435 (66%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTL 64
E+I L PI + G + LPGSKLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISRVEGEINLPKSKLSNRALLAALAKGTTKVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G + A VL
Sbjct: 62 VNYSLESDKTVCTVEGVGGAF--NWKNGLALFLGNAGTAMRPLTAAALCLKGSSEAEVVL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGV++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPPVVIRN-SGLKGKGVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGVK E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVKVENRN-YQTFVVKGNSQYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGAK+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFANVLEAMGAKITWGDD 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGLKGVMDMNHIPDAAMTIATAALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA+VEEG D+ I P + I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LTAMATELRKVGATVEEGEDFIRIQPLPLTQFQHAIEIATYNDHRMAMCFSLIALSDTPVT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP YF
Sbjct: 408 ILDPKCTAKTFPTYF 422

>ref|ZP_00134045.2| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase
[Actinobacillus pleuropneumoniae serovar 1 str. 4074]
ref|YP_001053404.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae L20]
ref|ZP_07527643.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 1 str. 4074]
ref|ZP_07531881.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
ref|ZP_07536347.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 9 str. CVJ13261]
ref|ZP_07540700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus

pleuropneumoniae serovar 11 str. 56153]
sp|A3N063.1|AROACTP2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABN73799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 5b str. L20]
gb|EFM85833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 1 str. 4074]
gb|EFM90178.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
gb|EFM94519.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 9 str. CVJ13261]
gb|EFM98850.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 11 str. 56153]
Length = 432

Score = 407 bits (1047), Expect = e-111, Method: Compositional matrix adjust.
Identities = 229/435 (52%), Positives = 290/435 (66%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + G + LPGSKSLNRI LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISRVEGEINLPGSKSLNRIALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G + A VL
Sbjct: 62 VNYSLSDEKTVCTVEGVGGAF---NWKNGLALFLGNAGTAMRPLTAAALCLKGSSEAEVVL 118

Query: 124 DGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGK E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVKVENRN-YQTFVVGKNQSYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGAK+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRFLFANVLEAMGAKITWGDD 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGKLGVDMDMNHIPDAAMTIATAALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADTYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA+VEEG D+ I P + I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LTAMATELRKVGATVEEGEDFIRIQPLPLTQFQHAETATYNDHRMAMCFSLIALSDTPVT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP YF
Sbjct: 408 ILDPKCTAKTFPTYF 422

>ref|ZP_01791397.1| outer-membrane lipoprotein carrier protein precursor [Haemophilus
influenzae PittAA]
gb|EDK07034.1| outer-membrane lipoprotein carrier protein precursor [Haemophilus
influenzae PittAA]
Length = 432

Score = 407 bits (1047), Expect = e-111, Method: Compositional matrix adjust.
Identities = 225/436 (51%), Positives = 286/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPGSKSLNRI LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPGSKSLNRIALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + V G GG F ++D + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEVEGLGGTFNIQD---NLSLFLGNAGTAMRPLTAAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGVK+ GSISQ+L

Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGVK E+ + +F +KG Q Y

Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIK-GKVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPDAAMTIATTALFANGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM FSL A + PVT

Sbjct: 348 LTAMATELRKIGAEVEEGEDFIRIQPLPLNQFKHANIETYNDHRMAMCFSLIALSNTPVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+

Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|YP_001651710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 3 str. JL03]
ref|YP_001968535.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 7 str. AP76]
ref|ZP_07544959.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 13 str. N273]
sp|B0BNY1.1|AROA_ACTPJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B3GXD4.1|AROA_ACTP7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABY69266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 3 str. JL03]
gb|ACE61393.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 7 str. AP76]
gb|EFN03129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 13 str. N273]
Length = 432

Score = 407 bits (1046), Expect = e-111, Method: Compositional matrix adjust.
Identities = 229/435 (52%), Positives = 289/435 (66%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+I L PI + G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKITLAPISRVEGEINLPGSKSLSNRALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G A VL

Sbjct: 62 VNYSLSSEDKTCTVEGVGGAF--NWKNGLALFLGNAGTAMRPLTAALCLKGATEAEVVL 118

Query: 124 DGVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGKV++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPPVAIRN-SGLKGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGVK E+ + + F +KG Q Y

Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVKVENRN-YQTFVVKGNQSYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGAK+TW +

Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIK-GKVKVTGIGKNSIQGDRLFANVLEAMGAKITWGDD 295

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----QGKLGVDMDMNHIPDAAMTIATAALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT 421

+ A+ TEL K+GA+VEEG D+ I P + I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LTAMATELRKVGATVEEGEDFIRIQPLPLTQFQHAETATYNDHRMAMCFSLIALSPTVPT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP YF

Sbjct: 408 ILDPKCTAKTFPTYF 422

>gb|AAA24943.1| enolpyruvylshikimatephosphatesynthase [Haemophilus influenzae]
emb|CBW29957.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Haemophilus
influenzae 10810]
Length = 432

Score = 407 bits (1045), Expect = e-111, Method: Compositional matrix adjust.
Identities = 223/436 (51%), Positives = 286/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKITLAPISAVEGTINLPGSKSLSNRALLLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G GG F ++D + LFLGNAG AMR LTAA+ G + +L

Sbjct: 62 VRYQLSDDKTICEIEGLGGAFFNIQD---NLSLFLGNAGTAMRPLTAALCLKGNHEVEIIL 118

Query: 124 DGVPFRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGKVK+ GSISQ+L

Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +F +KG Q Y

Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIK-GKVKTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALF++G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPDAAMTIATTALFNSGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM FSL A + PVT

Sbjct: 348 LTAMATELRKVGAEVEEGEDFIRIQPLALNQFKHANIETYNDRMAMCFSLIALSNTPTV 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+

Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|ZP_02363666.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
l-carboxyvinyltransferase [Burkholderia oklahomensis
C6786]
Length = 434

Score = 406 bits (1044), Expect = e-111, Method: Compositional matrix adjust.
Identities = 226/446 (50%), Positives = 283/446 (63%), Gaps = 20/446 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E + L P G V+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG

Sbjct: 2 EHLDLGPFSHAQGAURLPGSKSISNRVLLLAALAEGETTVTNLLSDDTRVMLDALAKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D A VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +

Sbjct: 62 VKLSRDGDA--CVVGGTRGAFTAKSA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+

Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPAAISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +E+ +LIS PY+E+T++LM RFGV E D W RF + G +

Sbjct: 174 ALLMTLPLVKAKDGASVVEVDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT

Sbjct: 233 YRSPGTMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFADG + +R++ SWRVK

Sbjct: 293 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAVAALFADGSSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V

Sbjct: 348 ETDRIAAMAAELRKVGATVEEGADYLVVTPPAQLVPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I DP C KTFPDYFD K

Sbjct: 408 PVRINDPKCVGKTFFPDYFDRFLALAK 433

>ref|YP_004229109.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1001]
gb|ADX56049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1001]
Length = 434

Score = 406 bits (1044), Expect = e-111, Method: Compositional matrix adjust.
Identities = 223/439 (50%), Positives = 286/439 (65%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGTV+LPGSKS+SNR+LLLAAL+E T + NLL+S+D ML AL LG

Sbjct: 2 EFLDLGPFSRASGTVRLPGSKSISNRVLLLAALAESETTITNLLSDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D VV G G F A LFLGNAG A+R LTAA++ GG+ Y +

Sbjct: 62 VRIKRD--GDTCVVTGTRGAFTARTA---DLFLGNAGTAVRPLTAALSVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+

Sbjct: 114 GVPRMHERPIGDLVDGLRQIGARIDYEENEGYPPLRIRPAQISAEAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LLM PL A G +++ +LIS PY+E+T++LM RFG+ E W +F + GQ+

Sbjct: 174 SLLMTLPLVRTASGVSTVQVDGELISKPYIEITIKLMARFGINVERH-GWHQFVVPAGQR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA + GG V VEG G +S+QGDV FA+ L MGA +

Sbjct: 233 YQSPGTMVEGDASSASYFLAAGVLGGGPVKVEGVGRSSIQGDVGFADALIKMGANLQMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
E + V G G H L ID++ N +PD AMT+AV ALFADG T +R++ASWRVK

Sbjct: 293 EDWIEVRG-----VGNDHGKLPIDMDFNLIPDAAMTIAVAALFADGTTTLRNIAASWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA VEEG D+ ++TPPEKL A IDTYDDHRMAM FSL + V

Sbjct: 348 ETDRIAAMATELRKVGAKVEEGEDFLMVTPEKLIPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYF+

Sbjct: 408 PVRINDPKCVGKTFFPDYFE 426

>ref|ZP_01783517.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 22.1-21]
ref|ZP_01795501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittII]
gb|EDJ89150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 22.1-21]
gb|EDK10909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittII]
gb|ADO81064.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Haemophilus
influenzae R2866]

Length = 432

Score = 406 bits (1044), Expect = e-111, Method: Compositional matrix adjust.
Identities = 224/436 (51%), Positives = 286/436 (65%), Gaps = 17/436 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKITLAPISAVEGTINLPKSKSLSNRALLLAALAKGTTKVTNLLDSDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ + + G GG F +++ + LFLGNAG AMR LTAA+ G + + L
Sbjct: 62  VRYQLSDDKTICEIEGLGGAFNIQN---NLSLFLGNAGTAMRPLTAALCLKGKTESEITL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GKKVK+ GSISQ+L
Sbjct: 119  TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +FYIKG Q Y
Sbjct: 178  TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENQ-HYQKFYIKGNQSYI 236

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237  SPNKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304  SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA G T IR++ +WRVKET+R
Sbjct: 296  FIQAE-----HAELNGIDMDMNHIPDAAMTIATATLAFASGETVIRNIYNWRVKETDR 347

Query: 364  MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHR+AM FSL A + PVT
Sbjct: 348  LTAMATELRKIGAEVEEGEDFIRIQLPLNQFKHANIETYNDHRIAMCFSLIALSNTPV 407

Query: 422  IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408  ILDPKCTAKTFPTFFN 423
```

```
>ref|ZP_04465725.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 6P18H1]
gb|EEP47169.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 6P18H1]
Length = 432
```

Score = 406 bits (1044), Expect = e-111, Method: Compositional matrix adjust.
Identities = 224/436 (51%), Positives = 287/436 (65%), Gaps = 17/436 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKITLAPISAVEGTINLPKSKSLSNRALLLAALAKGTTKVTNLLDSDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G GG F +++ + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62  VRYQLSDDKTICEIEGLGGAFNMQN---NLSLFLGNAGTAMRPLTAALCLKGNHEVEIIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GKKVK+ GSISQ+L
Sbjct: 119  TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +FYIKG Q Y
Sbjct: 178  TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKIENH-HYQKFYIKGNQSYI 236

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237  SPNKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304  SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296  FIQAE-----YAEELNGIDMDMNHIPDAAMTIATATLAFANGETVIRNIYNWRVKETDR 347
```

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHR+AM FSL A + PVT
Sbjct: 348 LTAMATELRKIGAEVEEGEDFIRIQPLPLNQFKHANIETYNDHRIAMCFSLIALSNTFPVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|ZP_07542841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 12 str. 1096]
gb|EFN00948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 12 str. 1096]
Length = 432

Score = 406 bits (1043), Expect = e-111, Method: Compositional matrix adjust.
Identities = 228/435 (52%), Positives = 289/435 (66%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + G + LPSKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISRVEGEINLPSKSKSLSNRALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G + A VL
Sbjct: 62 VNYSLSDEKTVCTVEGVGGAF--NWKNGLALFLGNAGTAMRPLTAALCLKGSSEAEVVL 118

Query: 124 DGVPFRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGV E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVNVENQN-YQTFVVKGNQSYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGAK+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFANVLEAMGAKITWGDD 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGKLGVDMDMNHIPDAAMTIATAALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA+VEEG D+ I P + I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LTAMATELRKVGATVEEGEDFIRIQPLPLTQFQHAIEIATYNDHRMAMCFSLIALSDTPVT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP YF
Sbjct: 408 ILDPKCTAKTFPTYF 422

>sp|A4G861.2|AROA_HERAR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAL62698.2| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Herminiimonas arsenicoxydans]
Length = 442

Score = 405 bits (1042), Expect = e-111, Method: Compositional matrix adjust.
Identities = 220/444 (49%), Positives = 283/444 (63%), Gaps = 22/444 (4%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQP G V+LPSKSKS+SNR LLLAAL++GTT + +LL S+D H ML AL+ +G+ E
Sbjct: 11 LQFAMHAKGVVRLPGSKSISNRTLLLAALADGTTQIRDLLASDDTHVMLMALQKIGVKWE 70

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ VV G G FPV A LF+GNAG A+R LTAA+ GG+ Y L GV R
Sbjct: 71 QIGESQDYVHVGVNGAFPVHQAD----LFMGNAGTAIRPLTAALAVTGGD--YTLHGVSR 124

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

M ERPIGDLV L +G ++ PP+ + G + +++++ G++SSQ+L+ALLM
Sbjct: 125 MHERPIGDLVDALNAIGTHIEYTGEPGYPLHIQR-GRIHAQRMQVRGNVSSQFLTALLM 183

Query: 189 AAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
AAPL DV I+++ +LIS PY+E+TL LM RFGV+ + D W F I GQ+Y SP
Sbjct: 184 AAPLMAREQDVTIDVVGELISKPYIEITLNLMMRRFGVEVQ-RDGWQSFTIAAGQRYISPG 242

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+VEGDASSASYFLA AI GG V VEG G S+QGDV+F E L+ MGA +T + +
Sbjct: 243 IIVVEGDASSASYFLAAGAIAGGPVRVEGVGKNSIQGDVRFVESLQQMGATITMGDNWI- 301

Query: 307 VTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
E L+AID + N +PD AMT+AV AL+ADG + +R++ SWRVKET+R+ A
Sbjct: 302 -----EAKSNGALRAIDADFNHIDPAAMTIAVAALYADGTSTLRNIGSWRVKETDRISA 355

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEV-----PVT 421
+ EL KLGASVEEG DY ITPP + AIDTYDDHRMAM FSLA +
Sbjct: 356 MTIELRLKLGASVEEGEDYLRITPPAVIQPAIDTYDDHRMAMCFSLATLDGAIRKGSKIR 415

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVK 445
I DP C KTFPDYF + ++
Sbjct: 416 INDPQCVAKTFPDYFTAFKVTED 439

>ref|ZP_01873490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lentisphaera araneosa
HTCC2155]
gb|EDM29094.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lentisphaera araneosa
HTCC2155]
Length = 424

Score = 405 bits (1042), Expect = e-111, Method: Compositional matrix adjust.
Identities = 220/440 (50%), Positives = 286/440 (65%), Gaps = 17/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+I L I I GTVKLPGSKS+SNR LLLAAL EG ++N+L+S DV M AL+TL
Sbjct: 2 EKITLPKISSIQGTVKLPGSKSISNRSLLLAALGEGQITLENVLSNDVDVDMFEALQTLN 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + + GC G P D L+L NAG A+RS++AA+ A+ GN YV+D
Sbjct: 62 IPCSRNVEERTVELQGCAGPLPNGD----FNLYLENAGTAVRSMSAAICASKGN--YVID 115

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RMRERPI DLV L++L D+ TDCPP+ + G+ GG ++GS+SSQY++
Sbjct: 116 GNARMRERPIKDLVDALQKLNIDISYEFNTDCPPLNIKA-NGIKGGVTSVNGSVSSQYIT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+A+PLA V I I +L S PYV+MT+ LM++FGV + D++ F + QKY +
Sbjct: 175 ALLASPLAEDVTINIDGELTSKPYVDMTIGLMKKFGVDVTN-DNYQTFTVPAPQKYIN 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VEGDA SASYFL AAI G V V GCG S+QG+ FA V+ MGA+VT+ +
Sbjct: 234 PCNFIVEGDAGSASYFLGAAAIING-HVKVYCGKDSIQGESGFAGVMQMGAEVTYGDNF 292

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V L ID++MN M D MTLAVVA+FA G T IR++A+W+VKETER+
Sbjct: 293 IEVKS-----NGTLNGIDIDMNTMTDTGMTLAVVAMFAKGTITIRNIANWQVKETERI 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL + GASVEEGPDY +I PPEK+ I+TYDDHRMAMAF++ + +TI D
Sbjct: 346 TAVATELKRAGASVEEGPDYLVINPPEKILNCEIETYDDHRMAMAFAILSLG-TEITILD 404

Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
P C +KTFPDYF V VK
Sbjct: 405 PLCKKTFPDYFTVREGLVK 424

>ref|YP_001896621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
phytofirmans PsJN]
sp|B2T630.1|AROA_BURPP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ACD17397.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
phytofirmans PsJN]
Length = 434

Score = 405 bits (1042), Expect = e-111, Method: Compositional matrix adjust.
Identities = 224/449 (49%), Positives = 289/449 (64%), Gaps = 26/449 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGT++LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFPSRASGTIRLPGSKSISNRVLLLAALAEGETTITNLLDSDDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D VV G G F A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VRLKRD--GDTCVVTGTRGAPTARTA---DLFLGNAGTAVRPLTAAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG-----GKVKLSGSIS 179
GVPRM ERPIGDLV GL+QLGA +D PP+R+ PG + + G +S
Sbjct: 114 GVPRMHERPIGDLVDGLRQLGARIDYEENEGYPPLRIR-----PGQINADAPITVRGDVS 168

Query: 180 SQYLSALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SQ+L++LLM PL G +++ +LIS PY+E+T++LMERFG+K E W +F +
Sbjct: 169 SQFLTSLMLTLPLLRTESGVSTVQVDGELISKPYIEITIKLMERFGIKVERH-GWHQFVV 227

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GQ+Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA+ L MGA
Sbjct: 228 PAGQRYQSPGTIMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFADALIKMGA 287

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
+ + + V G + L+ ID++ N +PD AMT+AV ALFADG T +R++ASW
Sbjct: 288 NLQMGGDWIEVRGVGHD---SGKLEPIDMDCNLIPDAAMTIAVAALFADGATTLRNIAW 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAAC 415
RVKET+R+ A+ TEL K+GA V+EG DY +I PPEKL AIDTYDDHRMAM FSL +
Sbjct: 345 RVKETDRLAAMATELRKVGAKVQEGEDYLVIEPPEKLTNPAAIDTYDDHRMAMCFSLVSL 404

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
VPV I DP C KTFPDYF+ + +
Sbjct: 405 GGVPVRINDPKCVGKTFPDYFERFTALAQ 433

>ref|ZP_04978293.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica PHL213]
gb|EDN74689.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica PHL213]
Length = 432

Score = 405 bits (1042), Expect = e-111, Method: Compositional matrix adjust.
Identities = 226/436 (51%), Positives = 288/436 (66%), Gaps = 18/436 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGV++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAEGDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNYLVEGDASSASYFLASGAIKG-KVKVTGIGKKSIGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V

Sbjct: 348 RLTAMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTTEV 407

Query: 421 TIRDPGCTRKTTFPDYF 436
TI DP CT KTFP YF

Sbjct: 408 TILDPNCTAKTFPTYF 423

>ref|ZP_05991014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. OVINE]
sp|P54220.2|AROA_PASHA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAB86439.1| AroA [Mannheimia haemolytica]
gb|EEY11040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. OVINE]
Length = 432

Score = 405 bits (1042), Expect = e-111, Method: Compositional matrix adjust.
Identities = 226/436 (51%), Positives = 287/436 (65%), Gaps = 18/436 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G A +L

Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGAETAQIIL 118

Query: 124 DGVPFRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGKV++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y

Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 APQGNLYVEGDASSASYFLASGAIKG-KVKVTGIGKKSIIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V

Sbjct: 348 RLTAMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTTEV 407

Query: 421 TIRDPGCTRKTTFPDYF 436
TI DP CT KTFP YF

Sbjct: 408 TILDPNCTAKTFPTYF 423

>sp|P52310.1|AROA_HAESO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAA85091.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Histophilus somni]
Length = 432

Score = 405 bits (1041), Expect = e-111, Method: Compositional matrix adjust.
Identities = 228/444 (51%), Positives = 290/444 (65%), Gaps = 17/444 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI I G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ YML AL+ LG

Sbjct: 2 EKLTLSPISRIDGEINLPGSKSLSNRALLAALAKGTTQVTNLLDSDDIRYMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123

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      ++ +          VV G GG F ++ + LFLGNAG AMR L AA+ G + V L
Sbjct: 62 VNYQLSDDKTVCVVEGIGGAFQWQNG---LSLFLGNAGTAMRPLAALCLKGDTESEVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GA++ PP+ + G+ GGKV++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQTGANIQYLENDGYPLAIRN-QGIFGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLMAAPL GD+EIEI+ +L+S PY+++T +M+ FG+ + + + RF IKG Q Y
Sbjct: 178 TALLMAAPLGEEDMEIEILGELVSKPYIDITPAMMKDFGINVDDYN-YQRFLIKQKQYYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      SP+ VEGDASSASYFLA AAI G V V G G S+QGD FA+VL MGAKVTW E
Sbjct: 237 SPQTYLVEGDASSASYFLAAAAIKG-KVKVTGIGRNSIQGDRLFADVLAQMGAKVTWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      + V + LK ID++MN +PD AMT+A+ ALFA G T IR++ +WRVKET+R
Sbjct: 296 FIQVE-----KSELKGIDMDMNHIPDAAMTIAITALFAQGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT 421
      + AI TEL KLGA VEEG D+ I P +K I TY+DHR+AM FSL A ++ VT
Sbjct: 348 LTAIATELRLKLGAEVEEGEDFIRIQPLALDKFKHAEIATYNDHRIAMCFSLIALSDTSVT 407

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 445
      I DP CT KTFP YF KN
Sbjct: 408 ILDPACTAKTFTFYFSEFEKISK 431

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>gb|ADZ27779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosomonas sp.
AL212]
Length = 440

Score = 405 bits (1041), Expect = e-111, Method: Compositional matrix adjust.
Identities = 230/438 (52%), Positives = 287/438 (65%), Gaps = 17/438 (3%)

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Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADK 71
      K+ GT++LPGSKS+SNRILLLAAL++GTT + +LL S+D +ML AL LG+ V + +K
Sbjct: 10 KKAQGTIRLPGSKSISNRILLLAALAAGTTQIHDLASDDTGHMLDALIQLGVMVTQTEK 69

Query: 72 AAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      R + G G FPV DA LFLGNAG A R L A ++ G+ Y L GVPRM E
Sbjct: 70 NNYR--ICGINGTFFVIDA----DLFLGNAGTAFRPLVAVLSLMHGH--YRLSGVPRMHE 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK---VKLSGSISSQYLSALLM 188
      RPI DLV L+QLGA+++ PP+ + G V + G +SSQ+L+ LLM
Sbjct: 122 RPIADLVDTLRQLGANINYLGNPGFPPEIKPFTPHIIGDTYAVTVKGDVSSQFLTGLLM 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      A PL+ IE+ LIS PY+E+TL M FGV+AEH+ W +F I QKY++P +
Sbjct: 182 ALPLSGKKSIIIEVTTGLISQPYIELTLAQMRHFGVQAEHT-GWRQFVIPAEQKYRTPGHL 240

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      VEGDASSASYFLA AI G V VEG G S+QGDV+FA LE MGAK++ E + +
Sbjct: 241 SVEGDASSASYFLAAGAIGNGPVRVEGVGCNSVQGDVRFAAALEQMGAKISMGENWIEAS 300

Query: 309 GPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      P G K L+AID++ N +PD AMTLAV+ALFA+G T +R++ASWR+KET+R+ A+
Sbjct: 301 SPNSGNSG-KFLRAIDLDCNHIPDAAMTLAVIALFAEGATMLRNIAWRLKETDRLAAMS 359

Query: 369 TELTKLGASVEEGPDYCIITPP-EKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
      EL KLGASVEEG DY ITPP L A IDTYDDHRMAM FSL AC PV I DP
Sbjct: 360 AELRLKLGASVEEGADYLRITPPIHGLTPHATIDTYDDHRMAMCFSL-ACLGAPVRINDPE 418

Query: 427 CTRKTFPDYFDVLSTFVK 444
      C KTFPDYF+ LS V
Sbjct: 419 CVAKTFPDYFERLSQLVH 436

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>ref|ZP_02467913.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia thailandensis
MSMB43]

Length = 434

Score = 405 bits (1040), Expect = e-111, Method: Compositional matrix adjust.
Identities = 226/439 (51%), Positives = 281/439 (64%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P GTV+LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG
Sbjct: 2 EHLDLGPFSHAQGTVRLPGSKSISNRVLLLAALAEGETTVTNLLDSDTRVMDALAKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V+ + VV G G F + A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 --VKLSRNGDTCVVGTRGAF TAKTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGAQIDYEGNEGFPPLRIRPAAISVDAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
ALLM PL G +EI +LIS PY+E+T++LM RFGV E D W RF + G +
Sbjct: 174 ALLMTLPLVKAKDGASVVEIDGELISKPYIEITIKLMARFGVTVER-DGWRFTVPAGVR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA L MGA VT
Sbjct: 233 YRSPGAMVEGDASSASYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQMGANVTMG 292

Query: 302 ETSVTVTGPPPREPFGRKH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + V G G H L ID++ N +PD AMT+AV ALFA G + +R++ SWRVK
Sbjct: 293 DDWIEVRG-----IGHDHGKLAPIDMDFNLIPDAAMTIAVAALFAGGTSTLRNIGSWRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMAELRKLKATVEEGADYLVVTPPAQLAPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYFD
Sbjct: 408 PVRINDPKCVGKTFPDYFD 426

>emb|CBA28839.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Curvibacter putative
symbiont of Hydra magnipapillata]
Length = 665

Score = 405 bits (1040), Expect = e-111, Method: Compositional matrix adjust.
Identities = 226/444 (50%), Positives = 292/444 (65%), Gaps = 30/444 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ +G V LPGSKS+SNR+LLLAAL+SEGTT + +LL+S+D ML ALRTLGL +VE
Sbjct: 9 LPPLAHAAGAVTLPGSKSISNRVLLLAAMSEGTTTIHDLSDSDTRVMLIALRTLGCAGE 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A + + G G G K P A QLFLGNAG AMR LTAA+ GG+ + L GVPR
Sbjct: 69 QSGAIVK--ITGLGGKLPNGSA---QLFLGNAGTAMRPLTAALAVVGGD--FELSGVPR 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L+QLG +D PP+++ +K+ G +SSQ+L+ALLM
Sbjct: 121 MHERPIGDLVDALRQLGCAIDYLGNEGYPPLKLTGPALQLDAPIKVRGDVSSQFLTALLM 180

Query: 189 AAPL-ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
A PL A D+ IE++ +LIS PY+E+TL L+ RFGVK D W+RF I G K +SP +
Sbjct: 181 ALPLVASKDIVIEVVGELISRPIEITLNLARFGVKVRR-DGWERFTIPAGAKLRSPGD 239

Query: 248 AYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+VE DASSASYF+A A++ G + ++G G S+QGD++F E + MGAK+
Sbjct: 240 IHVEADASSASYFIALGALSTGANGHNGIKIQGVGADSIQGDIFRMEAAQAMGAKIE--- 296

Query: 303 TSVTVTGPPPREPFGRKH--LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+GP R LKAID++ N +PD AMTLAV+AL+ADG T +R++ASWRVKE
Sbjct: 297 -----SGPNWLHIQRGAWPLKAIDLDCNHIPDAAMTLAVMALYADGTTNLRNIASWRVKE 351

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTADTYDDHRMAMAFSLAAC-- 415
T+R+ A+ TEL KLGA+V EG DY +TPP + +I TYDDHR+AM FSLAA

Sbjct: 352 TDRIAAMATELRKLGATVVEGQDYIQVTPPAGIADWKAASIHTYDDHRVAMCFSLAAFNP 411

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVL 439

A+VPV I DP C KTFPDYF+ L

Sbjct: 412 AQVPVRIEDPKCVAKTFPDYFEAL 435

>ref|YP_314712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiobacillus
denitrificans ATCC 25259]
sp|Q3SK83.1|AROA_THIDA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ96907.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiobacillus
denitrificans ATCC 25259]
Length = 428

Score = 405 bits (1040), Expect = e-111, Method: Compositional matrix adjust.
Identities = 224/431 (51%), Positives = 283/431 (65%), Gaps = 17/431 (3%)

Query: 16 SGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75

SGTV+LPGSKS+SNR+LLLAAL+EG T V ++L+S+D YML AL+ LG+ VE D+

Sbjct: 13 SGTVRLPGSKSISNRVLLLAALAEGVTDVYDVLDSDDTRYMLAALQALGVGVE-DRGDNH 71

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPIG 135

V G G FP A +LFLGNAG A R LTA + +GG+ YVLDGV RM ERPIG

Sbjct: 72 WRVTGVAGAFPARQA----ELFLGNAGTAFRPLTAVLALSGGD--YVLDGVARMHERPIG 125

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKV-KLSGSISSQYLSALLMAAPLAL 194

DLV L+QLG +D PP+ V+ G V + G++SSQ+L+ LLMA PL

Sbjct: 126 DLVDAFLRQLGGRIDYRGTGLGFPPLHVHPPQA--GADVAHIRGNVSSQFLTGLLMALPLRR 183

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254

+E++ +LIS PY+E+TL ++ RFGV+ D W F + Y+SP+ YVEGDA

Sbjct: 184 LRTRVEVVGELISKPYIEITLAMLRRFGVEVAR-DGWQAFSVAADACYRSPREIYVEGDA 242

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314

SSASYFLA AI GG V VEG G S+QGDV FA+ L MGA++ + P +

Sbjct: 243 SSASYFLAAGAIGGGPVRVEGVGRDSVQGDVGFADALAAMGARIAMGPNWIEACAPAQ-- 300

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374

GR LKAID++ N +PD AMTLAV ALFADG T +R++ASWRVKET+R+ A+ TEL K+

Sbjct: 301 -GR--LKAIDLDCNAIPDAAMTLAVAALFADGTTTLRNIAASWRVKETDRIAAMATELRKV 357

Query: 375 GASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433

GA+VEEG D+ +TPPE L A IDTYDDHRMAM SL + V V I DPGC KTFP

Sbjct: 358 GATVEEGDDFLRVTPPETLRAGAVIDTYDDHRMAMCLSLVSLGGVAVRINDPGCVAKTFP 417

Query: 434 DYFDVLSTFVK 444

YF+ + +

Sbjct: 418 GYFNAFAEIR 428

>ref|YP_560019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
xenovorans LB400]
sp|Q13VC2.1|AROA_BURXL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABE31967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
xenovorans LB400]
Length = 434

Score = 404 bits (1039), Expect = e-110, Method: Compositional matrix adjust.
Identities = 225/442 (50%), Positives = 288/442 (65%), Gaps = 26/442 (5%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64

E + L P SGT++LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG

Sbjct: 2 EFLDLGPFPSRSGTIRLPGSKSISNRVLLLAALAEGETTITNLLSDSDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+ ++ D VV G G F A LFLGNAG A+R LTAA+ GG+ Y +

Sbjct: 62 VRLKRD--GDTCVVTGTRGAFRTARTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG-----GKVKLSGSIS 179
GVPRM ERPIGDLV GL+QLGA +D PP+R+ PG + + G +S
Sbjct: 114 GVPRMHERPIGDLVDGLRQLGAKIDYEENEGYPPLRIR-----PGQINADAPITVRGDVS 168

Query: 180 SQYLSALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SQ+L++LLM PL G +++ +LIS PY+E+TL+LMERFG+K E W +F +
Sbjct: 169 SQFLTSLMLTLPLVRTGSGVSTVQVDGELISKPYIEITLKLMEFVGKVERH-GWHQFVV 227

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GQ+Y+SP + VEGDASSASYFLA A+ GG + VEG G S+QGDV FA+ L MGA
Sbjct: 228 PAGQRYQSPGSIMVEGDASSASYFLAAGALGGGPLKVEGVGRASIQGDVGFADALIRMGA 287

Query: 297 KVTWTETSVTGTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
+ + + V G + L+ ID++ N +PD AMT+AV ALFADG T +R++ASW
Sbjct: 288 NLQMGGDWIEVRGVGH---SGKLEPIDMDCNLIPDAAMTIAVAALFADGATTLRNIAW 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAAC 415
RVKET+R+ A+ TEL K+GA V+EG D+ II PPEKL AIDTYDDHRMAM FSL +
Sbjct: 345 RVKETDRLAAMATELRKVGAKVKEGEDFIIIEPPEKLIPNAAIDTYDDHRMAMCFSLVSL 404

Query: 416 AEPVPTIRDPGCTRKTFPDYFD 437
VPV I DP C KTFPDYF+
Sbjct: 405 GGVPRINDPKCVGKTFPDYFE 426

>ref|ZP_01793472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittHH]
gb|EDK08922.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittHH]
Length = 432

Score = 404 bits (1039), Expect = e-110, Method: Compositional matrix adjust.
Identities = 224/435 (51%), Positives = 284/435 (65%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTISLPGSKSLSNRALLLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + V G GG F ++D + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEVEGLGGAFFNIQD---NLSLFLGNAGTAMRPLTAAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGVK+ GSISSQ+L
Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGVK E+ + +F +KG Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA A + G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPNKYLVEGDASSASYFLA-AGVIKGVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTGTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET R
Sbjct: 296 FIQAE-----HAEIENGIDMDMNHIPDAAMTIATTALFANGETVIRNIYNWRVKETNR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM FSL A + PVT
Sbjct: 348 LTAMATELRKIGAEVEEGEDFIRIQPLPLNQFKHANIETYNDHRMAMCFSLIALSNTPVT 407

Query: 422 IRDPGCTRKTFPDYF 436
I DP CT KTFP +F
Sbjct: 408 ILDPKCTAKTFPTFF 422

>ref|ZP_05849995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae NT127]
gb|EEW78727.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus

influenzae NT127]
Length = 432

Score = 404 bits (1039), Expect = e-110, Method: Compositional matrix adjust.
Identities = 222/436 (50%), Positives = 285/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPKSKSLSNRALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G GG F ++D + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEIEGLGGAFFNIQD---NLSLFLGNAGTAMRPLTAAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGKVK+ GSISQ+L
Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGV E+ + +F +KG Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVHVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPKNYLVEGDASSASYFLAAGAIK-GVKVGTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPDAAMTIATTALFANGETIIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA +EEG D+ I P + I+TY+DHRMAM FSL A + PVT
Sbjct: 348 LTAMATELRKIGAEIEEGEDFIRIQPLPLNQFKHANIETYNDHRMAMCFSLIALSNTPVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|NP_841981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosomonas europaea
ATCC 19718]
sp|Q82TD4.1|AROANITEU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD85875.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Nitrosomonas europaea ATCC 19718]
Length = 431

Score = 404 bits (1039), Expect = e-110, Method: Compositional matrix adjust.
Identities = 229/436 (52%), Positives = 283/436 (64%), Gaps = 27/436 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS-V 67
L ++ G V+LPKSKS+SNRILL+AL+EGTT+V NLL S+D ML ALR LG++ V
Sbjct: 6 LPHVQRAQGNVRLPKSKSISNRILLLSALAEGTTMVSNNLESDDTGRMLDALRLLGVAIV 65

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D R V GC GKFPV +A +LFLGNAG A R LTA + G+ Y L GVP
Sbjct: 66 RTDDGKYR--VAGCKGKFPVREA----ELFLGNAGTAFRPLTAVLALMQGH--YRLSGVP 117

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM ERPIGDLV L+Q+GA + C PP+ ++ PG + + G+ISSQ+LS LL
Sbjct: 118 RMHERPIGDLVDALRQIGAVITCLEHEGFPPLEIHPAVIRPG-NISIKGNISSQFLSGLL 176

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MA PL V I + LIS PYV +T+ M RFGV+ + +SW RF + Q Y+SP
Sbjct: 177 MALPLTGEPVTIVVSGTLISQPYVALTIAQMARFGVQVKQ-ESWQRFMLPENQTYRSPGK 235

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT----WTET 303
VEGDASSASYFLA AI GG V +EG G+ S QGD++F E LE MGA+++ W E+
Sbjct: 236 IAVEGDASSASYFLAAGAIAGGPVRIEGAGSDSCQGDIFVEALEAMGARISMGSDWIES 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G LKAID + N +PD AMTLA +ALFA G T +R++ASWRVKET+R
Sbjct: 296 GAPDGGG-----LKAIDFDCNHIPDAAMTLATMALFARGTTTLRNIAASWRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPE-KLNVT- IDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ EL KLGA VE G D+ ITPP+ L A IDTYDDHRMAM FSL + + VPV
Sbjct: 347 IAAMSAELRKLGARVEAGDDFLRITPPDGPLTADAVIDTYDDHRMAMCFSLVSL-VPVR 405

Query: 422 IRDPGCTRKTFPDYFD 437
I DPGC KTFPDYF+
Sbjct: 406 INDPGCVAKTFPDYFE 421

>ref|YP_088767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
succiniciproducens MBEL55E]
sp|Q65S78.1|AROAMANS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAU38182.1| AroA protein [Mannheimia succiniciproducens MBEL55E]
Length = 433

Score = 404 bits (1038), Expect = e-110, Method: Compositional matrix adjust.
Identities = 227/441 (51%), Positives = 289/441 (65%), Gaps = 19/441 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E++ L PI + GTV LPKSGKSLSNR LLLAAL++GTT V NLL+S+DV +ML AL+ LG
Sbjct: 2 EKLTLTPISHVEGTVNLPKSGKSLSNRALLAALAKGTTTRVTNLLSDSDVRHMLNALKQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN---ATY 121
++ + V G G F ++ + LFLGNAG AMR LTAA+ A + A
Sbjct: 62 VNYSLSSEDKSVCEVQGLGKAFWQNG---LALFLGNAGTAMRPLTAALCLANADSVPAEI 118

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+L G PRM+ERPI LV L Q GADV PP+ + G L GGVK+ GS+SSQ
Sbjct: 119 ILTGEPRMKERPIKHLVDALLQAGADVQYLEQEGYPLAIRNTG-LKGGKVKIDGSVSSQ 177

Query: 182 YLSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+L+ALLMAAP+A D EIEII +L+S PY+++TL +M+ F V ++ + + RF +KG Q+
Sbjct: 178 FLTALLMAAPMAERDTEIEIIGELVSKPYIDITLNMKIFAVDNDQN-YQRFVVKGNQQ 236

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA AI G V V G G S+QGD FAEVLE MGAK+TW
Sbjct: 237 YQSPNIFLVEGDASSASYFLAAGAIK-KVRVTGVGKNSIQGDRLFAEVLEKMGAKITWG 295

Query: 302 ETSVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E + R L ID++MN +PD AMT+A ALFA G T IR++ +WRVKET
Sbjct: 296 EDYIEAE-----RGELNGIDMDMNHIPDAAMTIATTALFAQGETVIRNIYNWRVKET 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TEL K+GA VEEG D+ I PP ++ I+TY+DHRMAM F+L A +
Sbjct: 348 DRLSAMATELRKVGAEVEEGEDFIRIQPPASDQFKHAEIETYNDRMAMCFALVALSNTA 407

Query: 420 VTIRDPGCTRKTFPDYFDVLS 440
VTI DP CT KTFP +FD S
Sbjct: 408 VTICDPKCTAKTFPTTFDEFS 428

>ref|ZP_08067507.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus ureae
ATCC 25976]
gb|EFX91698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus ureae
ATCC 25976]
Length = 432

Score = 404 bits (1038), Expect = e-110, Method: Compositional matrix adjust.
Identities = 227/435 (52%), Positives = 287/435 (65%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E+I L PI + G + LPKSGKSLSNR LLLAAL++GTT V NLL+S+D+ +ML ALR LG
Sbjct: 2 EKITLAPISRVEGEINLPKSGKSLSNRALLAALAKGTTKVTNLLSDSDIRHMLNALRALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123

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      ++      +      V G G G F  ++      + LFLGNAG AMR LTAA+      G      A      +L
Sbjct: 62 VNYLSSEDKTICTVEGIGGVFNWQNG---LSLFLGNAGTAMRPLTAALCLKGTAEAEVIL 118

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GA V      PPV +      GL GGKV++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDVLRQAGASVQYLENEGYPVAIRN-SGLKGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGV E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVNVENQN-YQTFVVKGNQSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE GAK+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIK-KVKVTGIGKNSIQGDRLFANVLEATGAKITWGDN 295

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      +      + LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QGELKGVMDMNHIPDAAMTIAATALFAEGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTIDTYDDHRMAMAFSLAACAEVPVT 421
      + A+ TEL K+GASVEEG D+ I P +      I TY+DHRMAM FSL A ++ PVT
Sbjct: 348 LAAMATELRKVGASVEEGEDFIRIQPLPLTQFQHAETATYNDHRMAMCFSLIALSDTPVT 407

Query: 422 IRDPGCTRKTTFPDYF 436
      I DP CT KTFP YF
Sbjct: 408 ILDPKCTAKTFTFYF 422

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>ref|YP_248938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
      influenzae 86-028NP]
ref|YP_001290862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
      influenzae PittEE]
sp|Q4QL19.1|AROAHAEI8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
sp|A5UCH8.1|AROAHAEIE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|AAx88278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
      influenzae 86-028NP]
gb|ABQ98479.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
      influenzae PittEE]
gb|ADO96461.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Haemophilus
      influenzae R2846]
      Length = 432

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Score = 404 bits (1037), Expect = e-110, Method: Compositional matrix adjust.
Identities = 223/435 (51%), Positives = 285/435 (65%), Gaps = 17/435 (3%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPGSKSLSNRALLLAALAKGTTKVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
      + +      V G G G F ++D      + LFLGNAG AMR LTAA+      G      + +L
Sbjct: 62 VRYQLSDDKTICEVEGLGGTFNIQD---NLSLFLGNAGTAMRPLTAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GAD+      PP+ +      G+ GGKVK+ GSISSQ+L
Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLM+APLA D EIEII +L+S PY+++TL +M FGVK E+      +F +KG Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNQSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIK-GVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      +      L ID++MN +PD AMT+A ALF++G T IR++ +WRVKET+R

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Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPDAAMTIATTALFSNGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHR+AM FSL A + PVT
Sbjct: 348 LTAMATELRKVGAEVEEGEDFIHIQPLPLNQFKHANIETYNDHRIAMCFSLIALSNTPTVT 407

Query: 422 IRDPGCTRKTFFPDYF 436
I DP CT KTFP +F
Sbjct: 408 ILDPKCTAKTFPTFF 422

>ref|YP_001354360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Janthinobacterium sp.
Marseille]
sp|A6T1G3.1|AROA_JANMA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR88781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Janthinobacterium sp.
Marseille]
Length = 441

Score = 404 bits (1037), Expect = e-110, Method: Compositional matrix adjust.
Identities = 222/443 (50%), Positives = 282/443 (63%), Gaps = 30/443 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+P G V+LPGSKS+SNR LLLAAL++GTT + +LL S+D H ML AL+ LG+ E
Sbjct: 10 LKPAMHAKGVRLPGSKSISNRTLLAALAQTTHIRDLLASDDTHVMLMALQKLGKWE 69

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ +V G G FPV A LF+GNAG A+R LTAA+ GG+ Y L GV R
Sbjct: 70 QIGESQDYIVHGVDSFPVHQA---DLFMGNAGTAIRPLTAALAVTGGD--YTLHGVS 123

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L +G ++ PP+ + G + ++ + G++SSQ+L+ALLM
Sbjct: 124 MHERPIGDLVDALNAIGTHIEYTGEPTYPLHIQR-GRIHAHEMSVRGNVSSQFLTALLM 182

Query: 189 AAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
AAPL DV I +I LIS PY+E+TL L++RFGV+ + + W F IK GQ+Y SP
Sbjct: 183 AAPLMTREQDVIINVGDLISKPYIEITLNLIRFGVEVQ-RNGWQSFTIKAGQRYISPG 241

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV---TWTE 302
N +VEGDASSASYFLA AI GG V VEG G S+QGDV+F E LE MGA V W E
Sbjct: 242 NIHVEGDASSASYFLAAGAIAGGPVRVEGVGRDSIQGDVRFVEALEQMGATVRMGDNWIE 301

Query: 303 TSVTVTGPPREPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
L+AD + N +PD AMT+AV AL+ADGP+ +R++ SWRVKET+
Sbjct: 302 AESNGV-----LRAIDADFNHIDPDAAMTIAAALYADGPSILRNIGSWRVKETD 350

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL-----AACAE 417
R+ A+ TEL KLGA VEEG DY +TTP ++ AIDTYDDHRMAM FSL AA
Sbjct: 351 RISAMATELRKLGAIVEEGEDYLKVTTPAEILSAAIDTYDDHRMAMCFSLATLDGAARRG 410

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLS 440
I DP C KTFP+YF+ +
Sbjct: 411 NKERINDPQCVAKTFPEYFEAFA 433

>ref|ZP_05989016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. BOVINE]
gb|EEY13025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. BOVINE]
Length = 432

Score = 404 bits (1037), Expect = e-110, Method: Compositional matrix adjust.
Identities = 226/439 (51%), Positives = 288/439 (65%), Gaps = 18/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L

Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGKV++ GSISQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGKVKQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y

Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 APQGNYLVEGDASSASYFLASGAIKG-KVKVTGIGKKSIGQDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V

Sbjct: 348 RLTMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTEV 407

Query: 421 TIRDPGCTRKTFPDYFDVL 439
TI DP CT KTFP YF L

Sbjct: 408 TILDPNCTAKTFPTYFREL 426

>ref|YP_001293174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittGG]
sp|A5UJ35.1|AROA_HAEIG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR00791.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae PittGG]
Length = 432

Score = 403 bits (1035), Expect = e-110, Method: Compositional matrix adjust.
Identities = 222/436 (50%), Positives = 285/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKITLAPISAVEGTINLPGSKSLSNRALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + G GG F +++ + LFLGNAG AMR LTAA+ G + +L

Sbjct: 62 VRYQLSDDKTICEIEGLGGAFFNIQN---NLSLFLGNAGTAMRPLAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGKVK+ GSISQ+L

Sbjct: 119 TGEPRMKERPIHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+ PLA D EIEII +L+S PY+++TL +M FGK E+ + +F +KG Q Y

Sbjct: 178 TALLMSTPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 SPKNYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----YAEINGIDMDMNHIPDAAMTIATTALFANGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM FSL A + PVT

Sbjct: 348 LTAMATELRKIGAEVEEGEDFIRIQPLPLNQFKHANIETYNDRMAMCFSLIALSNTPVT 407

Query: 422 IRDPGCTRKTFPDYFD 437
I DP CT KTFP +F+

Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|YP_003907846.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1003]
gb|ADN58555.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1003]
Length = 434

Score = 402 bits (1034), Expect = e-110, Method: Compositional matrix adjust.
Identities = 220/439 (50%), Positives = 286/439 (65%), Gaps = 20/439 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFSRASGTVRLPGSKSISNRVLLLAALAEGETTITNLLSDSDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ + VV G G F A LFLGNAG A+R LTAA++ GG+ Y +
Sbjct: 62 VRLK--REGDTCVVTGTRGAFTARTA---DLFLGNAGTAVRPLTAALSVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ +++ G +SSQ+L+
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGARIDYEENEGYPPLRIRPAQISAEAPIRVRGDVSSQFLT 173

Query: 185 ALLMAAPLAL---GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LLM PL G +++ +LIS PY+++T++LM RFG+ E + W +F + GQ+
Sbjct: 174 SLLMTPLVVRTSGVSTVQVDGELISKPYIDITIKLMARFGINVER-NGWHQFVVPAGQR 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+SP VEGDASSASYFLA + GG V VEG G S+QGDV FA+ L MGA +
Sbjct: 233 YQSPGTIMVEGDASSASYFLAAGVLGGGPVKVEGVGRASIQGDVGFDALIKMGANLQMG 292

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
E + V G G H L ID++ N +PD AMT+AV ALFADG T +R++ASWRVK
Sbjct: 293 EDWIEVRG----VGNDHGKLDPIDMDFNLIPDAAMTIAAALFADGTTTLRNIAVSRVK 347

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA V+EG D+ ++TPPEKL A IDTYDDHRMAM FSL + V
Sbjct: 348 ETDRIAAMATELRKVGAKVQEGDDFLMVTPEKLIIPNASIDTYDDHRMAMCFSLVSLGGV 407

Query: 419 PVTIRDPGCTRTKTFPDYFD 437
PV I DP C KTFPDYF+
Sbjct: 408 PVRINDPKCVAKTFPDYFE 426

>ref|ZP_06842784.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
Ch1-1]
gb|EFG69508.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia sp.
Ch1-1]
Length = 434

Score = 402 bits (1034), Expect = e-110, Method: Compositional matrix adjust.
Identities = 223/442 (50%), Positives = 287/442 (64%), Gaps = 26/442 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGT++LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFSRASGTIRLPKSGSKSISNRVLLLAALAEGETTITNLLSDSDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D VV G G F A LFLGNAG A+R LTAA+ GG+ Y +
Sbjct: 62 VRLKRD--GDTTCVVTGTRGAFTARTA---DLFLGNAGTAVRPLTAALAVNGGD--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPG-----GKVKLSGSI 179
GVPRM ERPIGDLV GL+QLGA +D PP+R+ PG + + G +S
Sbjct: 114 GVPRMHERPIGDLVDGLRQLGAKIDYEENEGYPPLRIR-----PGQINADAPITVRGDVS 168

Query: 180 SQYLSALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SQ+L++LLM PL G +++ +LIS PY+E+T++LMERFG+K E W +F +
Sbjct: 169 SQFLTSLMTPLLRRTGSGVSTVQVDGELISKPYIEITIKLMERFGIKVERH-GWHQFVV 227

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GQ+Y+SP VEGDASSASYFLA A+ GG + VEG G S+QGDV FA+ L MGA
Sbjct: 228 PAGQRYQSPGRIMVEGDASSASYFLAAGALGGGPLKVEGVGRASIQGDVGFDALIKMGA 287

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
+ + + V G + L+ ID++ N +PD AMT+AV ALFADG T +R++ASW
Sbjct: 288 NLQMGGDWIEVRGVGHD---SGKLEPIDMDCNLIPDAAMTIAVAALFADGATTLRNIASW 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAAC 415
RVKET+R+ A+ TEL K+GA V+EG D+ +I PPEKL AIDTYDDHRMAM FSL +
Sbjct: 345 RVKETDRLAAMATELRKVGAKVKEGEDFIVIEPPEKLIPNAIDTYDDHRMAMCFSLVSL 404

Query: 416 AEVPVTIRDPGCTRKTFFPDYFD 437
VPV I DP C KTFPDYF+
Sbjct: 405 GGVPVRINDPKCVGKTFPDYFE 426

>ref|ZP_07889958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
segnis ATCC 33393]
gb|EFU67370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
segnis ATCC 33393]
Length = 436

Score = 402 bits (1033), Expect = e-110, Method: Compositional matrix adjust.
Identities = 225/443 (50%), Positives = 288/443 (65%), Gaps = 20/443 (4%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A I L P I + GT+ LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL
Sbjct: 1 MQHATSITLNPPIHVEGTINLPGSKSLSNRALLAALAHGTTNVTNLLDSDDIRHMLNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
+ LG+ V G GG F D + LFLGNAG AMR L AA+ A A+
Sbjct: 61 KHLGVQYSLSDDKSICEVQGLGGAFQWHDG---LALFLGNAGTAMRPLAALCLAREGAS 117

Query: 121 ----YVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
+L G PRM+ERPI LV L Q GAD+ PP+ + G L GG +K+ G
Sbjct: 118 PQNEVILTGEPRMKERPIQHLVDALLQAGADIRYLENEGYPPIAIRNTG-LRGGTIKIDG 176

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SISSQ+L+ALLMAAPLA GD EIEII +L+S PY+++TL +M+ FGV+ E+ + + RF +
Sbjct: 177 SISSQFLTALLMAAPLAEGDSEIEIIGELVSKPYIDITLNMKIFGVEVENQN-YQRFLV 235

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
KG Q Y+SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA
Sbjct: 236 KGKQSYQSPGTLFVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQDRLFADVLEKMGA 294

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
K+TW E + P L +D++MN +PD AMT+A ALFA+G T IR++ +W
Sbjct: 295 KITWGEDFIEAEQAP-----LHGVMDMNHIPDAAMTIATTALFAEGETVIRNIYNW 346

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL K+GA VEEG D+ I P + + A I+TY+DHR+AM F+L A
Sbjct: 347 RVKETDRLTAMATELRKVGADVEEGEDFIRIQPLKLTDFKAAEIEITYNDHRIAMCFALVA 406

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFD 437
++ P+TI DP CT KTFP +F+
Sbjct: 407 LSDTPITILDPDCTAKTFPTFFE 429

>ref|YP_003466751.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Xenorhabdus bovienii
SS-2004]
emb|CBJ79957.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Xenorhabdus bovienii
SS-2004]
Length = 428

Score = 401 bits (1031), Expect = e-110, Method: Compositional matrix adjust.
Identities = 226/435 (51%), Positives = 288/435 (66%), Gaps = 16/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + L+PI I+GT+ LPGSKS+SNR LLLAA ++GTT + NLL+S+D+ +ML AL TL
Sbjct: 2 QSLTLKPISCINGTINLPGSKSVSNRALLLAFAKGTCLTNLLDSDDIRHMLNALTTLE 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + G K ++LFLGNAG AMR L AA+ N VL

Sbjct: 62 IPY---RLSDDRTCCEIDGIGGTITGKGALEFLGNAGTAMRPLAAALCLGDNNV--VLT 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+ + G G GGKV + GS+SSQ+L+

Sbjct: 117 GEPRMKERPIGHLVDALRQGGAKIDYLEQENYPLHIKG--GFSGGKVVVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D +I I L+S PY+++TL LME FGV E+ + F++KG Q+Y+S

Sbjct: 175 ALLMAAPLAANDTDIHIQGDVLSKPYIDITLALMESFGVTVENH-QYQVFHVKGQQYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDASSASYFLA AAI GGT V G G SLQGD KFA+VLE MGA + W

Sbjct: 234 PGHYLVEGDASSASYFLAAAAIKGGTVRVGTGIGKNSLQGDTKFADVLERMGATIRWGHDF 293

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V R L +D++MN +PD AMT+A ALFA G T IR++ +WRVKET+R+

Sbjct: 294 VECE-----RGTLIGVMDMNAIPDAAMTIATTALFAQGETVIRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
A+ EL K+GA VEEG DY + PP+KLN I+TY+DHRMAM FSL A ++ PVTI D

Sbjct: 346 NMAAELRKIGAEVEEGHDYIRVPPKQLNHAIEIETYNDHRMAMCFSLVALSDTPVTILD 405

Query: 425 PGCTRKTFFPDYFDVL 439
PGCT KTFPDYF+ L

Sbjct: 406 PGCTAKTFFPDYFNQL 420

>ref|ZP_04467199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 7P49H1]
gb|EEP45644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 7P49H1]
Length = 432

Score = 401 bits (1031), Expect = e-109, Method: Compositional matrix adjust.
Identities = 222/435 (51%), Positives = 284/435 (65%), Gaps = 17/435 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI I GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKITLAPISAIEGTINLPGSKSLSNRALLAALAKGTTKVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G G F ++D + LFLGNAG AMR LTAA+ G + +L

Sbjct: 62 VRYQLSDDKTICEIEGLDGTNIQD---NLSLFLGNAGTAMRPLTAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGKVK+ GSISQ+L

Sbjct: 119 TGEPRMKERPIHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +F +KG Q Y

Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALF++G T IR++ +WRVKET+R

Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPDAAMTIATTALFSNGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
+ A+ TEL K+GA VEEG D+ I P + I+TY+DHR+AM FSL A + PVT

Sbjct: 348 LTAMATELRKVGAEEVEGEDFIHIQPLNLFKQKHANIETYNDHRIAMCFSIALSNTPVT 407

Query: 422 IRDPGCTRKTFFPDYF 436
I DP CT KTFP +F

Sbjct: 408 ILDPKCTAKTFFPTFF 422

>ref|YP_004138971.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae F3047]

ref|YP_004135455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae F3031]
emb|CBY81129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae F3031]
emb|CBY87307.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae F3047]
Length = 432

Score = 401 bits (1030), Expect = e-109, Method: Compositional matrix adjust.
Identities = 221/436 (50%), Positives = 286/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVNDLNSQEDVHYMLGALRTLG 64
E+I L PI + GT+ LPKSKSLNRIILLAAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPKSKSLNRIILLAAALAKGTTKVTNLLDSDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + + G GG F +++ + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEIEGLGGAFNIQN---NLSLFLGNAGTAMRPLTAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GKKVK+ GSISQ+L
Sbjct: 119 TGEPRMKERPIHLVLDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGK E+ + +F +KG Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKIENH-HYQKFQVKGNSQYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIK-GKVKVTGIGKNSIQGDRFLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALF++G T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----QAEIENGIDMDMNHIPDAAMTIATATLFSNGETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDHRMAMAFSLAACAEPVPT 421
+ A+ TEL K+GA VE G D+ I P + I+TY+DHRMAM FSL A + PVT
Sbjct: 348 LTAMATELRKIGAEVEGGEDFIRIQPLPLNQFKHANIETYNDHRMAMCFSLIALSNTPVPT 407

Query: 422 IRDPGCTRKTFFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408 ILDPKCTAKTFPTFFN 423

>ref|YP_001100819.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Herminiimonas
arsenicoydans]
Length = 428

Score = 400 bits (1029), Expect = e-109, Method: Compositional matrix adjust.
Identities = 217/436 (49%), Positives = 280/436 (64%), Gaps = 22/436 (5%)

Query: 17 GTVKLPKSKSLNRIILLAAALSEGTTVVNDLNSQEDVHYMLGALRTLGLSVEADKAAKRA 76
G V+LPKSKS+SNR LLLAAL++GTT + +LL S+D H ML AL+ +G+ E ++
Sbjct: 5 GVVRLPKSKSISNRTLLAALADGTTQIRDLLASDDTHVMLMALQKIGVKWEQIGESQDY 64

Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
VV G G FPV A LF+GNAG A+R LTAA+ GG+ Y L GV RM ERPIGD
Sbjct: 65 VVHGUNGAFPVHQAD---LFMGNAGTAIRPLTAALAVTGGD--YTLHGVS RMHERPIGD 118

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL-- 194
LV L +G ++ PP+ + G + ++++ G++SSQ+L+ALLMAAPL
Sbjct: 119 LVDALNAIGTHIEYTGEPGYPLHIQR-GRIHAQRMQVRGNVSSQFLTALLMAAPLMARE 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
DV I+++ +LIS PY+E+TL LM RFGV+ + D W F I GQ+Y SP +VEGDA
Sbjct: 178 QDVTIDVVGELISKPYIEITLNMRRFGVEVQR-DGWQSFTIAAGQRYISPGIIHVEGDA 236

Query: 255 SSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SSASYFLA AI GG V VEG G S+QGDV+F E L+ MGA +T + + E
Sbjct: 237 SSASYFLAAGAIAGGPVRVEGVGKNSIQGDVRFVESLQQMGATITMGDNWI-----EA 289

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
L+ AID + N +PD AMT+AV AL+ADG + +R++ SWRVKET+R+ A+ EL KL
Sbjct: 290 KSNALRAIDADFNHIPPDAAMTIAYAALYADGTSTLRNIGSWRVKETDRISAMTIELRKL 349

Query: 375 GASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEV-----PVTIRDPGCTR 429
GASVEEG DY ITPP + AIDTYDDHRMAM FSLA + I DP C
Sbjct: 350 GASVEEGEDYLRIITPPAVIQPAIDTYDDHRMAMCFSLATLDGAIRKGSKIRINDPQCVA 409

Query: 430 KTFPDYFDVLSTFVKN 445
KTFPDYF + ++
Sbjct: 410 KTFPDYFTAFKVTED 425

>ref|NP_439734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae Rd KW20]
ref|ZP_05848197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae RdAW]
sp|Q03421.2|AROA_HAEIN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC23237.1| 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) [Haemophilus
influenzae Rd KW20]
gb|EEW76979.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae RdAW]
Length = 432

Score = 400 bits (1028), Expect = e-109, Method: Compositional matrix adjust.
Identities = 222/436 (50%), Positives = 284/436 (65%), Gaps = 17/436 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+I L PI + GT+ LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKITLAPISAVEGTINLPGSKSLSNRALLAALAKGTTKVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVL 123
+ + V G GG F ++D + LFLGNAG AMR LTAA+ G + +L
Sbjct: 62 VRYQLSDDKTICEVEGLGGTFNIQD---NLSLFLGNAGTAMRPLTAALCLKGKTESEIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGVK+ GSISQ+L
Sbjct: 119 TGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D EIEII +L+S PY+++TL +M FGV+ E+ + +F +KG Q Y
Sbjct: 178 TALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVQVENH-HYQKFQVKGNSYI 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
SP VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 SPNKYLVEGDASSASYFLAAGAIK-GKVKTGIGKNSIQGDRLFADVLEKMGAKITWGED 295

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ L ID++MN +PD AMT+A ALFA+ T IR++ +WRVKET+R
Sbjct: 296 FIQAE-----HAELNGIDMDMNHIPPDAAMTIATTALFANSETVIRNIYNWRVKETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ TEL K+GA VE G D+ I P + I+TY+DHRMAM FSL A + PVT
Sbjct: 348 LTAMATELRKVGAEEGGEDFIRIQPLPLNQFKHANIETYNDHRMAMCFSLIALSNTFPVT 407

Query: 422 IRDPGCTRKTTFPDYFD 437
I DP CT KTFP +F+
Sbjct: 408 ILDPKCTAKTFPTFFN 423

>dbj|BAE20404.1| 5-enolpyruvylshikimate-3-phosphate synthase [Lactuca sativa]
Length = 231

Score = 400 bits (1028), Expect = e-109, Method: Compositional matrix adjust.
Identities = 202/231 (87%), Positives = 218/231 (94%)

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
LSGSISSQ L+ALLMAAPLALGDVEIEIIDKLISIPYVEMTL+LMERFGV +HSD+WDR
Sbjct: 1 LSGSISSQXL TALLMAAPLALGDVEIEIIDKLISIPYVEMTLKLMERFGVSVQHSWTWDR 60

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEM 293
F+++GGQKYKSP NAYVEGDASSASYFLAGAAITGGT+TVEGCGT+SLQGDVKFAEVL
Sbjct: 61 FHVQGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTITVEGCGTSSLQGDVKFAEVLGQ 120

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDV 353
MGA+VTWTE SVTV GPPR+P GRKHL+ +DVNMNMPDVAMTLAVVAL+ADGPTAIRDV
Sbjct: 121 MGAQVWTENSVTVKGPPRDPSSGRKHLRPVDVNMNMPDVAMTLAVVALYADGPTAIRDV 180

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDH 404
ASWRVKETERM+AI TEL KLGA+VEEGPDYCIITPP KLNVTADITYDDH
Sbjct: 181 ASWRVKETERMIAICTELRKLGATVEEGPDYCIITPPKLNVTADITYDDH 231

>ref|ZP_08148670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
parainfluenzae ATCC 33392]
gb|EGC71936.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
parainfluenzae ATCC 33392]
Length = 432

Score = 400 bits (1027), Expect = e-109, Method: Compositional matrix adjust.
Identities = 222/434 (51%), Positives = 286/434 (65%), Gaps = 17/434 (3%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLS 66
I L+PI I G + LPGSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG +
Sbjct: 4 ITLEPISRIEGEINLPGSKSLSNRALLAALAKGTTTVTNLLDSDDIRHMLNALKALGGN 63

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NATYVLDG 125
+ + R V G GG F VE+ + LFLGNAG AMR LTAA+ G +L G
Sbjct: 64 YQLSEDKTRCEVEGLGAFQVENG---LSLFLGNAGTAMRPLTAALCLKGNTGEVILTG 120

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSA 185
PRM+ERPI LV L Q GADV PP+ + G+ GG V++ GSISSQ+L+A
Sbjct: 121 EPRMKERPIKHLVDALLQAGADVRYLENDGYPLAIRN-QGIKGGVVEIDGSISSQFLTA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLMAAPLA GD++I I+ L+S PY+++TL +M+ FG+ E+ + + F +KG Q Y SP
Sbjct: 180 LLMAAPLAEGDLDIHIVGDLVSKPYIDITLAMMKDFGISVENHN-YQVFKVKGNSYVSP 238

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA AAI G V V G G S+QGD FA+VLE MGAK+TW E +
Sbjct: 239 GKYMVEGDASSASYFLAAAAIK-GNVKVTGIGKHSIQGDRLFADVLEKMGAKITWGEDFI 297

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ L +D++MN +PD AMT+A +ALFA G T IR++ +WRVKET+R+
Sbjct: 298 QAE-----QAEHLGVMDMDNHIPDAAMTIATIALFAKGETVIRNIYNWRVKETDRLA 349

Query: 366 AIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM F+L A ++ PVTI
Sbjct: 350 AMATELRKVGAEVEEGEDFIRIQPLAISQFKHAEIETYNDHRMAMCFALIALSDTPVTIL 409

Query: 424 DPGCTRKTFPDYFD 437
DP CT KTFP +FD
Sbjct: 410 DPKCTAKTFPTFFD 423

>ref|YP_001344227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
succinogenes 130Z]
sp|A6VMU5.1|AROACTSZ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR74292.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinobacillus
succinogenes 130Z]
Length = 433

Score = 400 bits (1027), Expect = e-109, Method: Compositional matrix adjust.
Identities = 228/442 (51%), Positives = 292/442 (66%), Gaps = 20/442 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 64
E+I L PI + GTV LPGSKSLSNR LLLAAL++GTT V NLL+S+DV +ML AL+ LG
Sbjct: 2 EKITLNPRIARVEGTVNLPKSKSLSNRALLAALAKGTTKVTNLLDSDVVRHMLNALKRLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GN---AT 120
+S V G G F ++ + LFLGNAG AMR LTAA+ A GN A
Sbjct: 62 VSYTLSDDKTVCEVQGLGRAFEWQNG---LSLFLGNAGTAMRPLTAALCLANSNGESPAAE 118

Query: 121 YVLGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
VL G PRM+ERPI LV L Q GA+++ PP+ + GL GGVK+ GS+SS
Sbjct: 119 IVLTGEPRMKERPIKHLVDALLQAGAEIEYLEQDGYPLAIRN-KGLHGGKVKIDGSVSS 177

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+L+ALLMAAP++ D EIEII L+S PY+++TL +M+ FGV+ E+ + + RF +KG Q
Sbjct: 178 QFLTALLMAAPMSAADTEIEIIGDLVSKPYIDITLNMKIFGVEVENRN-YQRFTVKGCC 236

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTW 300
+Y+SPK VEGDASSASYFLA AI G V V G G S+QGD FA+VL MGAK+TW
Sbjct: 237 QYQSPKTFLEVGDAASSASYFLAAGAIGK-CVKVTGVGKNSIQGDRLEFADVLTAAMGAKITW 295

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E + + L +D++MN +PD AMT+A ALFA G T IR++ +WRVKE
Sbjct: 296 GEDFIRAE-----QGELSGVDMNMNIPDAAMTIATAALFAKGETVIRNIYNWRVKE 347

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEV 418
T+R+ A+ TEL K+GA+VEEG D+ I P + I+TY+DHRMAM F+L A ++
Sbjct: 348 TDRLAAMATELRKVGATVEEGEDFIRIQPLPLAEFKHAEIETYNDHRMAMCFALIALSDT 407

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
PVTI DP CT KTFP +FD S
Sbjct: 408 PVTILDPKCTAKTFPTFFDEFS 429

>ref|ZP_06573944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Providencia rettgeri
DSM 1131]
gb|EFE54886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Providencia rettgeri
DSM 1131]
Length = 392

Score = 399 bits (1026), Expect = e-109, Method: Compositional matrix adjust.
Identities = 206/404 (50%), Positives = 275/404 (68%), Gaps = 16/404 (3%)

Query: 37 LSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQL 96
+++GTT++ NLL+S+D+ +ML AL LG++ + + R V G GG D E ++
Sbjct: 1 MAKGTITLTLNLLSDDIRHMLNALSQGLVNYQLSEDKTRCRVEGLGGLNLSHPD---ETEI 57

Query: 97 FLGNAGIAMRSLTAAVTAAGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDC 156
FLGNAG AMR LTAA++ + N +L G PRM+ERPIG LV L++ GA+++ +
Sbjct: 58 FLGNAGTAMRPLTAALSLSRNNI--ILTGEPRMKERPIGHLVDALREGGAEIEYLEQENY 115

Query: 157 PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLR 216
PP+R+ G G GG++ + GS+SSQ+L+ALLMAAP A D I II +L+S PY+++TL
Sbjct: 116 PPLRLKG--GFIGGQISVDGSVSSQFLTALLMAAPRAEQDTTITIIGELVSKPYIDITLA 173

Query: 217 LMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC 276
LM+ FGV E+ ++ F IKG Q+Y+SP VEGDASSASYFLA AAI GG V V G
Sbjct: 174 LMKTFGVNVENH-QYEFVVIKQQQYQSPGEYLVGDASSASYFLAAAAIKGGVVRVTGI 232

Query: 277 GTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMT 336
G SLQGD KFA VLE MGA + W + V R+ L ID++MN +PD AMT
Sbjct: 233 GRNSLQGDTKFANVLEKMGATIRWGDDYVECE-----RRTLTGIDMDMNAIPDAAMT 284

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 396
+ VALFA+G T IR++ +WRVKET+R+ A+ TEL K+GA VEEG DY + PP+KL
Sbjct: 285 IGTVALFAEGETVIRNIYNWRVKETDRLYAMATELRKVGAEVEEGHDYIRVPPKKLQHA 344

Query: 397 AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
I+TY+DHR+AM FSL A ++ PVTI DPGCT KTFPDYF+ L+
Sbjct: 345 EIETYNDHRIAMCFSLVALSDTPVTILDPGCTAKTFPDYFEQLA 388

>ref|ZP_02412430.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei 14]
Length = 424

Score = 399 bits (1025), Expect = e-109, Method: Compositional matrix adjust.
Identities = 222/423 (52%), Positives = 275/423 (65%), Gaps = 20/423 (4%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
LPGSKS+SNR+LLLAAL+EG T V NLL+S+D ML AL LG+ + D VV G
Sbjct: 8 LPGSKSISNRVLLLAALAEGETTVTNLLDSDTRVMDALTKLGVKLSRDGGT--CVVGG 65

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
G F + A LFLGNAG A+R LTAA+ GG Y + GVPRM ERPIGDLV G
Sbjct: 66 TRGAFTAKTA----DLFLGNAGTAVRPLTAALAVNGGE--YRIHGVPRMHERPIGDLVDG 119

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL---GDV 197
L+Q+GA +D PP+R+ +++ G +SSQ+L+ALLM PL G
Sbjct: 120 LRQIGARIDYEGNEGFPPLRIRPATISVDAPIRVRGDVSSQFLTALLMTLPLVKAKDGAS 179

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+EI +LIS PY+E+T++LM RFGV E D W RF + G +Y+SP VEGDASSA
Sbjct: 180 VVEIDGELISKPYIEITIKLMARFGVTVER-DGWQRFTVPAGVRYRSPGTIMVEGDASSA 238

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA A+ GG + VEG G S+QGDV FA L MGA VT + + V G G
Sbjct: 239 SYFLAAGALGGGPLRVEGVGRASIQGDVGFANALMQGANVTMGDDWIEVRG----IGH 293

Query: 318 KH--LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
H L ID++ N +PD AMT+AV ALFADGP+ +R++ SWRVKET+R+ A+ TEL K+G
Sbjct: 294 DHGRLAPIDMDFNLIPDAAMTIAVAALFADGPSTLRNIGSWRVKETDRIAAMATELRKVG 353

Query: 376 ASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
A+VEEG DY ++TPP +L A IDTYDDHRMAM FSL + VPV I DP C KTFPD
Sbjct: 354 ATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFSLVSLGGVPVRINDPKCVGKTFPD 413

Query: 435 YFD 437
YFD
Sbjct: 414 YFD 416

>ref|ZP_05920862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pasteurella dagmatis
ATCC 43325]
gb|EEX49676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pasteurella dagmatis
ATCC 43325]
Length = 440

Score = 399 bits (1024), Expect = e-109, Method: Compositional matrix adjust.
Identities = 222/451 (49%), Positives = 285/451 (63%), Gaps = 20/451 (4%)

Query: 1 MAGAEIEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A I L P I I G ++LPGSKSLSNR LLLAAL+ GTT V NLL+S+DV +ML AL
Sbjct: 1 MQNATSITLNPITHIEGEIRLPGSKSLSNRALLLAALANGTTTVKNLLDSDDVHRMLNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---- 116
+ LG++ + G G F + + LFLGNAG AMR LTAA+ +
Sbjct: 61 KQLGVNYRLSDDKSVCTIEGLGRAFEWQGG---LALFLGNAGTAMRPLTAALCLSNAETE 117

Query: 117 GNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG 176
G +L G PRM+ERPI LV L Q GAD+ PP+ + G L GG +K+ G
Sbjct: 118 GQNEIILTGEPRMKERPIRHLVDALLQAGADIRYLEQEGYPPLVIRNTG-LQGGLIKIDG 176

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+SSQ+L+ALLMAAP+A D EIEII L+S PY+++TL +M+ FG+ E+ + + RF +
Sbjct: 177 SVSSQFLTALLMAAPMAKTDTEIEIIGDLVSKPYIDITLNMKIFGIHVENQN-YQRFIV 235

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGA 296
+G Q+Y+SP VEGDASSASYFLA AAI G V V G G S+QGD FA VLE MGA
Sbjct: 236 QGNQQYQSPNTFLVEGDASSASYFLAAAAIKG-KVKVTGVGKNSIQGDRLFANVLEKMGA 294

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
K+TW E + V + LK ID++MN +PD AMT+A ALFA G T IR++ +W
Sbjct: 295 KITWGEDFIEVE-----QGELKGIDMDMNHIPDAAMTIATTALFAQGETLIRNIYNW 346

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT- IDTYDDHRMAMAFSLAA 414

RVKET+R+ A+ EL K+GA VEEG D+ I P +K I+TY+DHRMAM F+L A
Sbjct: 347 RVKETDRLSAMAKELRKVGAEVEEGEDFIRIQPLALDKFQHAIEIETYNDRMAMCFALVA 406

Query: 415 CAEVPVTIRDPGCTRKTTFPDYFDVLSTFVKN 445
+ VTI DP CT KTFP +F+ + N
Sbjct: 407 LSNTAVTILDPNCTTKTFPTFFEEFAHLAHN 437

>ref|YP_003846937.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gallionella capsiferriiformans ES-2]
gb|ADL55173.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gallionella capsiferriiformans ES-2]
Length = 670

Score = 399 bits (1024), Expect = e-109, Method: Compositional matrix adjust.
Identities = 232/464 (50%), Positives = 290/464 (62%), Gaps = 48/464 (10%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M +E I L P+ G+V+LPGSKS+SNR+LLLAALS GTT+V +LL S+D ML L
Sbjct: 1 MNPSEFINLPPILLSARGSVRLPGSKSISNRVLLLAALSGGTTIVRDLLRSDDTDRMLEGL 60

Query: 61 RTLGLSVEA--DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+TLG++VE+ + A K V CGCG FVPV+AA +LFLGNAG A R LTAA+ +GG
Sbjct: 61 QTLGVTVESLGNAYK---VTGCGGDFPVKNA----ELFLGNAGTAFRPLTAALALSGG- 112

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI 178
+Y L GV RM ERPIGDLV L+ LGAD+ PP+++ V + G +
Sbjct: 113 -SYTSLSGVARMHERPIGDLVDALRGLGADIAYLANDGFPPQLIKPATLSGAASVSVRGDV 171

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQ+L+ALLMA PL V +E+I +LIS PY+E+TL +M RFG+ D W F +
Sbjct: 172 SSQFLTALLMALPLLGRVTVEVIGELISKPYIEITLAMMARFGIVVLR-DGWKSFTVAA 230

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
G +Y +P YVEGDASSASYFLA AI GG V VEG G S+QGDV+FA L MGA++
Sbjct: 231 GSRVYAPGEIYVEGDASSASYFLAAGAIGGPPVRVEGVGRGSIQGDVRFAGELAKMGAQI 290

Query: 299 ----TWETSVTVTGPPREPFGGRKHLKAIDVMNMKMPDVAMTLAVVALFADGPTAIRDVA 354
W E V G L+AID++ N +PD AMTLAV ALFA+G T +R++A
Sbjct: 291 EMGDNWIEARAPVNG-----KLQAIDLDCNHIPDAAMTLAVAALFANGTTTLRNIA 341

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT----- 396
SWRVKET+R+ A+ TEL K+GA VEEG DY IT E+L V+
Sbjct: 342 SWRVKETDRIHAMATELRKVGALVEEGADYIRITGLSSEELGVSENRSAAASILNPQSSIL 401

Query: 397 ----AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTTFPDYF 436
IDTYDDHRMAM FSLAA + I DP C KTFPDYF
Sbjct: 402 NPAAGIDTYDDHRMAMCFSLAAGNA-IRINDPRCVAKTFPDYF 444

>ref|YP_277892.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Blochmannia pennsylvanicus str. BPEN]
sp|Q492S6.1|AROA_BLOPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ41017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Blochmannia pennsylvanicus str. BPEN]
Length = 432

Score = 398 bits (1023), Expect = e-109, Method: Compositional matrix adjust.
Identities = 213/436 (48%), Positives = 287/436 (65%), Gaps = 14/436 (3%)

Query: 7 IVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L PIK+I GT+ LPGSKS+SNR LLLAA + GTT + NLL+S+DV ML ALR LG+S
Sbjct: 5 IKLAPIKKIQGTIHLPGSKSISNRALLAAQATGTTQLTNLLSDDDVRCMLDALRNLGVS 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
K + G GG ++ + + L LGNAG MR L AA++ N VL G
Sbjct: 65 YCLSNKRKTCEINGIGGPIQSKNNQLI-LSLGNAGTVMRPLIAALSQTQNI--VLTGH 121

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

PRM++RPI LV L+Q GA ++ PP+R+ GG GG++ + GSISSQ+LS++
Sbjct: 122 PRMKDRPIAHLVDALRQGGARIEYMERNGYPPIRL--YGGYYGGEIFIKGSISSQFLSSV 179

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM PLA D I++ L+S PY+++TL LM+ FG+ +H D++ FY KG Y+SP

Sbjct: 180 LMMTPLAYRDTLIKVDGALVSRPYIDITLSLMKIFGINIQH-DNYRVFYCKGNMAYQSPG 238

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYFLA +AI GGT V G G S QGD+ FA +LE MGAK+ W + +

Sbjct: 239 DYLVEGDASSASYFLAASAIRGGTVRVIGVGRNSKQGDIIYFANILESMGAKIAWGDNYIE 298

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFA-DGPTAIRDVASWRVKETERMV 365
T L A+D+++N +PD AMTLA+ ALF+ +GPT +R++ +WRVKE++R+

Sbjct: 299 CTRG-----ADLNAVLDLVNIPDAAMTLAITALFSINGPTILRNIYNWRVKESDRLA 351

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDP 425
A+ TEL K+GA + EG DY ITPP K+ I+TYDDHR+AM FSL A ++V + I +P

Sbjct: 352 AMATELRKIGAEIVEGYDYLQITPPFKIESAYINTYDDHRIAMCFSLVALSDVSIINNPN 411

Query: 426 GCTRKTFFPDYFDVLST 441
CT KTFPD+F LS+

Sbjct: 412 KCTDKTFFPDFFTLSS 427

>ref|YP_548624.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Polaromonas sp. JS666]
gb|ABE43726.1| 3-phosphoshikimate 1-carboxyvinyltransferase / cytidylate kinase
[Polaromonas sp. JS666]
Length = 668

Score = 398 bits (1023), Expect = e-109, Method: Compositional matrix adjust.
Identities = 219/447 (48%), Positives = 292/447 (65%), Gaps = 23/447 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + + P+ GTV+LPGSKS+SNR+LLLAALS G T V +LL S+D ML AL+ LG

Sbjct: 5 EYLDIPPLARAGGTVRLLPGSKSISNRVLLLAALSRRGQTTVHDLASDDTAVMLAALKQLG 64

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
SV + AV+ G GG+ + + LF+GNAG AMR LTAA+ GG + L

Sbjct: 65 CSVA--QHGTTAVIDGLGGQV---GQAKATLFMGNAGTAMRPLTAALALLGGE--FELS 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RM ERPIGDLV L+QLG ++ PP+R+ +++ G +SSQ+L+

Sbjct: 117 GVARMHERPIGDLVDALRQLGCSIEYLGNEGYPPLRLRPAQLKIEEPIRVRGDVSSQFLT 176

Query: 185 ALLMAAPLALG-DVEIEIIDKLISIPYVEMTLRLMERFGVKAH---SDSWDRFYIKGGQ 240
ALLMA PL G D+ IE++ +LIS PY+E+TL L++RFG+ + +D+W RF I G

Sbjct: 177 ALLMALPLVAGQDIHIEVVGELISRPIEITLNLKRFGIHVQRPLGADNWQRFTIPAGS 236

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-----GGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y+SP + +VEGDASSASYF+A AI+ + + G G S+QGD++F E MMG

Sbjct: 237 QYQSPGDIHVEGDASSASYFIALGAISEPAAGQNHIEILGVGADSIQGDIFIEAARMMG 296

Query: 296 AKVTWTETSVTVT-GPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
A++ T S+ ++ G P + + LKAID++ N +PD AMTLAV+AL+ADG T +R++A

Sbjct: 297 AQIESTPNSLRISRGKPGQGW---LKAIDLDCNHIPDAAMTLAVMALYADGTTTLRNIA 353

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
SWRVKET+R+ A+ EL KLGA+VEEG DY ITPP AI TYDDHR+AM FSLAA

Sbjct: 354 SWRVKETDRIAMACELQKLGA+VEEGADYKITPPLAWKSAAIHTYDDHRIAMCFSLAA 413

Query: 415 C--AEVPTIRDPGCTRKTFFPDYFDVL 439
A P+ I DP C KTFPDYF+ L

Sbjct: 414 FNPARQPIRILDPKCVAKTFFPDYFEAL 440

>ref|YP_004039563.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylovorus sp.
MP688]
gb|ADQ84327.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylovorus sp.
MP688]
Length = 432

Score = 397 bits (1021), Expect = e-108, Method: Compositional matrix adjust.
Identities = 223/430 (51%), Positives = 281/430 (65%), Gaps = 14/430 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L PI + G + LPGSKS+SNR LLLAAL++G T + +LL+S+D ML AL+TLG+ ++
Sbjct: 6 LAPIHQAHGDIVLPGSKSISNRCLLLAALADGVTDIRDLDSDDTARMLEALQTLGVEMK 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AA + GC GK+PV A LFLGNAG A R LTAA+ + G Y L GVPR
Sbjct: 66 -QLAAHDWRITGCRGKWPVRQAD----LFLGNAGTAFRPLTAALAFSQGE--YRLSGVPR 118

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L+Q GAD+ PP+++ +++ G+ISSQ+L+ALLM
Sbjct: 119 MHERPIGDLVDALRQAGADIQYEGNAGFPPLQIRPARITGQHTLQIRGNISSQFLTALLM 178

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A PL IE++ +LIS PY+E+TL LM +FGVK E + W F + +Y SP
Sbjct: 179 ALPLLKEQTRIEVVVELISKPYIEITLNLMAKFGVKVER-EGWQAFTVPAASQYSSPGEL 237

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
YVEGDASSASYFLA AI GG V V G G S+QGDV+F + L MGA + + ++ +
Sbjct: 238 YVEGDASSASYFLAAGAIAGGPVKVHGIGLDSIQGDVRFVDALREMGAVIEHGDNWSIAS 297

Query: 309 GPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LKA+D++ N +PD AMTLA ALFADG T +R++ASWRVKET+R+ A+
Sbjct: 298 APTS-----GKLKALDMDCNHIPDAAMTLATAALFADGTTTLRNIAASWRVKETDRLHAMA 352

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPTIIRDPGC 427
TEL K+GA VEEG DY ITPP L A IDTYDDHRMAM FSL A + PVTI DPGC
Sbjct: 353 TELRKVGAIVEEGQDYICITPPASLTNPATIDTYDDHRMAMCFSLVALGQTPVTINDPGC 412

Query: 428 TRKTFPDYFD 437
KTFPDYF+
Sbjct: 413 VAKTFPDYFE 422

>gb|AA45943.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia glucosida]
Length = 413

Score = 397 bits (1020), Expect = e-108, Method: Compositional matrix adjust.
Identities = 219/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E++ L PI + G + LPGSKSLSNR LLLAALS GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALSTGTTRVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
+ E + VV G GG F V++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKYELSEDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKAQIIL 118

Query: 124 DGVRPMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ + GL GGKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAITN-SGLQGGKVQIEGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLKKGQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNYLVEGDASSASYFLAAGAIK-GKVKVTGIGKKSIGQDRFLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQAP-----LKGVDMDMNHIPDAAMTIATLALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT-IDENTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHMMAM FSL A + V
Sbjct: 348 RLNAMATELRKIGAVVEEGDDFIRIQLALEHFQHAETIYNDHRMAMCFSLIALSNTTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDLP 412

>ref|YP_003050881.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylovorus sp.
SIP3-4]
gb|ACT50354.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylovorus sp.
SIP3-4]
Length = 432

Score = 397 bits (1019), Expect = e-108, Method: Compositional matrix adjust.
Identities = 221/430 (51%), Positives = 281/430 (65%), Gaps = 14/430 (3%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVE 68
L PI G + LPSKSKS+SNR LLLAAL++G T + +LL+S+D ML AL+TLG+ ++
Sbjct: 6 LAPIHHAHGDIVLPKSGKSLNRIALLAALADGVTDIRLLDSDDTARMLEALQTLGVEMK 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AA + GC G++PV A LFLGNAG A R LTAA+ + G Y L GVPR
Sbjct: 66 -QLAAHDWRITGCRQWPVRQAD---LFLGNAGTAFRPLTAALAFSQGE--YRLSGVPR 118

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L+Q GAD+ PP+ + +++ G++SSQ+L+ALLM
Sbjct: 119 MHERPIGDLVDALRQAGADIQYEGNAGFPPLHILPARVAGQHTLQIRGNVSSQFLTALLM 178

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A PL IE++ +LIS PY+E+TL LM +FGVK E + W F + +Y SP
Sbjct: 179 ALPLLNEQTRIEVVGELISKPYIEITLNLMAKFGVKVER-EGWQAFVPAASQYSSPGEL 237

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
YVEGDASSASYFLA AI GG V V G G S+QGDV+F + L MGA + + ++ +
Sbjct: 238 YVEGDASSASYFLAAGAIAGGPVKVHGIGLDSIQGDVRFVDALREMGAVIEHGDNWSIS 297

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LKA+D++ N +PD AMTLA ALFADG T +R++ASWRVKET+R+ A+
Sbjct: 298 AP-----ASGKLKALDMDCNHIPDAAMTLATAALFADGTTTLRNIAASWRVKETDRLHAMA 352

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTTIRDPGC 427
TEL K+GA+VEEG DY ITPP +L A IDTYDDHRMAM FSL A + PVTI DPGC
Sbjct: 353 TELRKVGATVEEGQDYICITPPARLTNPATIDTYDDHRMAMCFSLVALGQTPVTINDPGC 412

Query: 428 TRKTFPDYFD 437
KTTFPDYF+
Sbjct: 413 VAKTFPDYFE 422

>emb|CAA78480.1| aroA [Pasteurella multocida]
Length = 441

Score = 395 bits (1014), Expect = e-108, Method: Compositional matrix adjust.
Identities = 215/441 (48%), Positives = 286/441 (64%), Gaps = 25/441 (5%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 63
A I L PI I G V+LPSKSKS+SNR LLL+AL++G T + NLL+S+DV +ML AL+ L
Sbjct: 5 ATAITLNPISYIEGEVRLPGSKSLNRIALLAALAKGKTTLNLLDSDDVRHMLNALKEL 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---GNA 119
G++ + + + G G F + + LFLGNAG AMR LTAA+ + G
Sbjct: 65 GVTYQLSEDKSVCEIEGLGRAFEWQSG--LALFLGNAGTAMRPLTAALCLSTPNREGKN 121

Query: 120 TYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 179
VL G PRM+ERPI LV L Q GA++ PP+ + G L GG++++ GS+S
Sbjct: 122 EIVLTGEPRMKERPIQHLVDALCQAGAEIQYLEQEGYPPIAIRNTG-LKGGRIQIDGSVS 180

Query: 180 SQYLSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMAAP+A D EIEII +L+S PY+++TL++M+ FGV+ E+ ++ RF +KG
Sbjct: 181 SQFLTALLMAAPMAEADTEIEIIGELVSKPYIDITLKMMTQTFGVEVENQ-AYQRFLVKGH 239

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Q+Y+SP VEGDASSASYFLA AAI G V V G G S+QGD FA+VLE MGA +T

Sbjct: 240 QQYQSPHRFLVEGDASSASYFLAAAAIKG-KVKVTGVGKNSIQGDRLFADVLEKMGAHIT 298

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W + + V + +LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVK

Sbjct: 299 WGDDFIQVE-----KGNLKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVK 350

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAD----TYDDHRMAMAFSLAAC 415
ET+R+ A+ TEL K+GA VEEG D+ I P LN+ DHRMAM F+L A

Sbjct: 351 ETDRLTAMATELRKVGAEVEEGEDFIRIQP---LNLAQFQHAELNIHHRMAMCFALIAL 407

Query: 416 AEPVVTIRDPGCTRKTFFPDYF 436
++ VTI DP CT KTFP +

Sbjct: 408 SKTSVTILDPSCTAKTFPTFL 428

>ref|YP_002794869.1| AroA [Laribacter hongkongensis HLHK9]
sp|C1D543.1|AROA_LARHH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACO73860.1| AroA [Laribacter hongkongensis HLHK9]
Length = 428

Score = 394 bits (1012), Expect = e-107, Method: Compositional matrix adjust.
Identities = 220/443 (49%), Positives = 285/443 (64%), Gaps = 23/443 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
E + L P + GTV LPKSKS+SNR+LLLAAL+ G T V +L ++D ML AL+ LG

Sbjct: 2 EFLDLAPCATLRGTVALPGSKSISNRMLLLAALATGKTQVHGVLEADDTDRMLEALQQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + ++ + GC G++PV A LFLGNAG A R LTAA+ AGG+ Y L

Sbjct: 62 IRLAQQAHSRTFCIEGCDGRWPVRQA----DLFLGNAGTAFRPLTAALALAGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G+ RM ERPIGDLV L+ LGA ++ PP+ ++ PG ++ G++SSQ+LS

Sbjct: 116 GIARMHERPIGDLVEALQGLGAVIEYAGTPGYPLHIHPGHVTPGSTTRVKGNVSSQFLS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PLA G +E+ +LIS PYV++TLRL+ERFGV D + RF + G Y+S

Sbjct: 176 ALLMALPLAGGT-VEVEGELISKPYVDLTLRLIERFGVTVGR-DGYSRFTAEGASHYRS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT---W 300
P +VEGDASSASYFLA A+ GG V V G G S+QGD++FA+ L MGA + W

Sbjct: 234 PGAIHVEGDASSASYFLAAGALGGGPVRVTGVGRNSIQGDIRFADALAAMGAGIDMGDDW 293

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E +G L+A+ ++ N +PD AMTLAV ALFA+G T + ++ASWRVKE

Sbjct: 294 IEAQAPASG-----RLRAVTLDCNHIHPDAAMTLAVAALFANGTTTLTNIASWRVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVP 419
T+R+ A+ TEL KLGA VE G D+ ITPP++L AIDTYDDHRMAM FSLA+ A VP

Sbjct: 345 TDRIAAMATELGKLGALVETGHDFIRITPPDQLTPGAAIDTYDDHRMAMCFSLASLA-VP 403

Query: 420 VTIRDPGCTRKTFFPDYFDVLSTF 442
V I DP C KTFP YFD ++

Sbjct: 404 VRINDPRCVAKTFPGYFDFASL 426

>emb|CBW15902.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Haemophilus
parainfluenzae T3T1]
Length = 432

Score = 393 bits (1010), Expect = e-107, Method: Compositional matrix adjust.
Identities = 221/434 (50%), Positives = 283/434 (65%), Gaps = 17/434 (3%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I L+PI I G + LPKSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG++

Sbjct: 4 ITLEPISRIEGEINLPKSGKSLSNRALLLAALAKGTTTNTLLDSDDIRHMLNALKALGVN 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NATYVLDG 125
+ + V G GG F VE+ + LFLGNAG AMR LTAA+ G +L G

Sbjct: 64 YQLSEDKTCCEVEGLGGAFAQVENG---LSLFLGNAGTAMRPLTAALCLKGKIEGEVILTG 120

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
PRM+ERPI LV L Q GADV PP+ + G+ GG V++ GSISSQ+L+A

Sbjct: 121 EPRMKERPIKHLVDALLQAGADVRYLENDGYPLAIRN-QGIKGGVVEIDGSISSQFLTA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLMAAPLA GD++I I+ L+S PY+++TL +M+ FGV E+ + + F +KG Q Y SP

Sbjct: 180 LLMAAPLAEGDLDIHIVGDLVSKPYIDITLAMMKDFGVSVENHN-YQVFKVKNQSYVSP 238

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGDASSASYFLA AAI G V V G G S+QGD FA+VLE MGAK+TW E +

Sbjct: 239 GKYMVEGDASSASYFLAAAAIK-GNVKVTGIGKHSIQGDRLFADVLEKMGAKITWGEDFI 297

Query: 306 TVTGPPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ L ID++MN +PD AMT+A ALFA G T IR++ +WRVKET+R+

Sbjct: 298 QAE-----QAEHLGIDMDMNHIPDAAMTIATTALFAKGETVIRNIYNWRVKETDRLA 349

Query: 366 AIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ EL K+GA VEEG D+ I P + I+TY+DHRMAM F+L ++ PVTI

Sbjct: 350 AMAAELRKVGAEVEEGEDFIRIQPLALSQFKHAEIETYNDHRMAMCFALITLSDTPVTIL 409

Query: 424 DPGCTRKTFPDYFD 437
DP CT KTFP +FD

Sbjct: 410 DPKCTAKTFPTFFD 423

>ref|YP_412757.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosospora
multiformis ATCC 25196]
Length = 454

Score = 393 bits (1010), Expect = e-107, Method: Compositional matrix adjust.
Identities = 221/439 (50%), Positives = 290/439 (66%), Gaps = 21/439 (4%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I L ++ G+V+LPGSKS+SNRILLLAALSEG T V +LL S+D ML AL TLG+S

Sbjct: 4 IDLPVVERARGSVRLPGSKSISNRILLLAALSEGVTDCDLLASDDTARMLDALSTLGVS 63

Query: 67 V-EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + + R + G G +FP+ E LFLGNAG R LTA + A G+ Y L G

Sbjct: 64 ILQIGRDHYR--LQGVGDQFPLRLPTTEADLFLGNAGTVFRPLTAMLALAQGH--YRLSG 119

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
VPRM ERPIGDLV L+Q+GAD+ +LG + PP+++ G + G++ + G +SSQ+L+

Sbjct: 120 VPRMHERPIGDLVDALRQVGADI-TYLGKEGFPLQIKP-GRIHPGEITVRGEVSSQFLT 177

Query: 185 ALLMAAPLALGDVE----IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
ALLM P +++ I + +LIS PY+++T+ LM RFGV+ E + W RF + Q

Sbjct: 178 ALLMVLPLFLRAEMDELPIVITVAGELISRPYIDLTIALMARFGVQVEREE-WRRFTVPADQ 236

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y+SP +VEGDASSASYFLA AI G V VEG G S+QGD++FAE LE MGA + +

Sbjct: 237 RYRSPGQVFVEGDASSASYFLAAGATGRGPVRVEGLGRDSVQGDIFAEALERMGADIRF 296

Query: 301 TETSVTVTGPPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ + +GP G L+AID++ N +PD AMTLAV ALFA G T +R++ASWRVKE

Sbjct: 297 GDNWIEASGP-----GPGGLRAIDLDCNHIPDAAMTLAVTALFARGNTVLRNIASWRVKE 351

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEV 418
T+R+ A+ EL KLGA VE G D+ I+PP E + AIDTYDDHRMAM FSL +

Sbjct: 352 TDRIAAMAQELRKGAEEVAGSDFLQISPPRGELVANAAIDTYDDHRMAMCFSLVSFG-A 410

Query: 419 PVTIRDPGCTRKTFPDYFD 437
PV I DP C KTFPDYF+

Sbjct: 411 PVRINDPRCVSKTFPDYFE 429

>ref|YP_001565737.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Delftia acidovorans SPH-1]
gb|ABX37352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Delftia acidovorans
SPH-1]

Length = 675

Score = 393 bits (1010), Expect = e-107, Method: Compositional matrix adjust.
Identities = 218/443 (49%), Positives = 284/443 (64%), Gaps = 26/443 (5%)

```
Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P+ GTV LPSKKS+SNR+LLLAALS+GTTVV +LL+S+D ML AL+ LG +VE
Sbjct: 11 PLSRAQGTVSLPQSKSISNRVLLLAALSQGGTTVVHDLSDSDTRVMLRALQQLGCTVEPA 70

Query: 71 KAA--KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + G GG P + +LF+GNAG AMR LTAA++ GG+ + L GVPR
Sbjct: 71 TITLGPVRITGLGGVLP---SGASAEFLMGNAGTAMRPLTAALSVLGGD--FKLSGVPR 125

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCP--VRVNGIGGLPGGKVKLSGSISSQYLSAL 186
M ERPIGDLV L+QLG +D PP +R LP +++ G +SSQ+L++L
Sbjct: 126 MHERPIGDLVDAIRQLGCRIDYLGNEGFPPLHIRQPDFSQLPHSPIQVRGDIVSSQFLTSL 185

Query: 187 LMAAPLALG--DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LMA PL D+ IE++D+LIS PY+ +TL L+ RFG+ A H++W RF I G +Y S
Sbjct: 186 LMAPLPLANTRDITIEVVDELISKPYIHITLELLARFGI-AVHNENWQRFTIPAGSRYSS 244

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
P +VE DASSASYF+A AI + + G G S+QGD++F E MGA+V
Sbjct: 245 PGEIHVEADASSASYFIALGAIASDSAEGRILGVGLDSIQGDIRFVEAARAMGAEEVEGG 304

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + G LKAID++ N +PD AMTLAV+AL+ADG T +R++ASWRVKET
Sbjct: 305 PNWLRIRR-----GAWPLKAIDLDCNHPIDAAAMTLAVMALYADGTTTLRNIAASWRVKET 358

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAFSLAAC--A 416
+R+ A+ EL KLGA VEEG DY ITTP +I TYDDHR+AM FSLAA A
Sbjct: 359 DRIAAMTKELRLKLADVEEGADYIRITPPASTAAWRAASIHYYDDHRVAMCFSLAAFNPA 418

Query: 417 EVPVTIRDPGCTRKTFPDYFDVL 439
+PV I DP C KTFPDYF+ L
Sbjct: 419 ALPVRIEDPKCVAKTFPDYFEAL 441
```

>ref|ZP_06634730.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D7S-1]
gb|EFE01049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D7S-1]
Length = 443

Score = 393 bits (1010), Expect = e-107, Method: Compositional matrix adjust.
Identities = 223/442 (50%), Positives = 283/442 (64%), Gaps = 20/442 (4%)

```
Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A I L PI + G + LPSKKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL
Sbjct: 1 MQQAISITLNPRIARVEGAINLPKSGKSLSNRALLLAALAHGTTKVNTLLSDDIRHMLNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR--SLTAAVTAAGGN 118
+ LG+ + V G GG F D + LFLGNAG AMR + + AG +
Sbjct: 61 KQLGVQYTLSEDKSVCEVQGLGGAQWHDG---LALFLGNAGTAMRPLAALCLARAGDS 117

Query: 119 AT--YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
A +L G PRM+ERPI LV L Q GAD+ PP+ + G L GG +K+ G
Sbjct: 118 AQNEVILTGEPRMKRPIRHLVDALLQAGADIRYLENEGYPPIAIRNTG-LRGGLIKIDG 176

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SISSQ+L+ALLMAAPLA D EIEII +L+S PY+++TL +M+ FGV E+ + RF +
Sbjct: 177 SISSQFLTALLMAAPLAESDSEIEIIGELVSKPYIDITLNMKIFGVSVENQ-HYQRFIV 235

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
KG Q Y+SP + VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA
Sbjct: 236 KGKQSYQSPGSLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRFLFADVLEKMG 294

Query: 297 KVTWTETSVTGTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
+TW E + P L +D++MN +PD AMT+A ALFA+G T IR++ +W
Sbjct: 295 HITWGEDFIQAEQAP-----LHGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNW 346
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Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL K+GA VEEG D+ I P P + V I+TY+DHRMAM F+L A
Sbjct: 347 RVKETDRLTAMATELRKVGAEEVEGEDFIRIQPLKPTEFKVAEIEITYNDHRMAMCFALIA 406

Query: 415 CAEVPVTIRDPGCTRKTFFPDYF 436
++ PVTI DP CT KTFP +F
Sbjct: 407 LSDTPVTILDPNCTAKTFPTFF 428

>ref|ZP_02884875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia graminis
C4D1M]
gb|EDT09669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia graminis
C4D1M]
Length = 434

Score = 393 bits (1009), Expect = e-107, Method: Compositional matrix adjust.
Identities = 225/449 (50%), Positives = 290/449 (64%), Gaps = 30/449 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L P SGTV+LPGSKS+SNR+LLLAAL+EG T + NLL+S+D ML AL LG
Sbjct: 2 EFLDLGPFSSRASGTVRLPGSKSISNRVLLLAALAEGETTITNLLSDSDTRVMLDALEKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ + VV G G F A LFLGNAG A+R LTAA+ GGN Y +
Sbjct: 62 VRLK--REGDTCVVTGTRGAFTARTA---DLFLGNAGTAVRPLTAALAVNGGN--YRIH 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG----GKVKLSGSIS 179
GVPRM ERPIGDLV GL+Q+GA +D PP+R+ PG +++ G +S
Sbjct: 114 GVPRMHERPIGDLVDGLRQIGARIDYEENEGYPPLRIR----PGQISAEAPIRVRGDVS 168

Query: 180 SQYLSALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SQ+L++LLM PL A G +++ +LIS PY+E+T++LM RFG+ E + W +F +
Sbjct: 169 SQFLTSLMLTLPVLTASGVTTVQVDGELISKPYIEITIKLMARFGIDVER-NGWHQFVV 227

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GQ+Y+SP VEGDASSASY LA A+ GG V VEG G +S+QGDV FA+ L MGA
Sbjct: 228 PAGQRYQSPGTIMVEGDASSASYLLAAGALGGGPVKVEGVGRSSIQGDVGADALIRMG 287

Query: 297 KVTWTETSVTGTGPPREPFGRKH--LKAIDVMNMKMPDVAMTLAVVALFADGPTAIRDVA 354
+ + + V G G H L ID++ N +PD AMT+AV ALFADG T +R++A
Sbjct: 288 NLQMGGDWIEVRG----VGTDHGKLPIDMDFNLPDAAMTIAVAALFADGTTTLRNIA 342

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A-IDTYDDHRMAMAFSLA 413
SWRVKET+R+ A+ TEL K+GA VEEG D+ ++TPPEKL A IDTYDDHRMAM FSL
Sbjct: 343 SWRVKETDRIAMATELRKVGAKEVEGEDFLMVTPEKLI PNASIDTYDDHRMAMCFSLV 402

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
+ VPV I DP C KTFPDYF+ +
Sbjct: 403 SLGGVPVRINDPKCVAKTFPDYFERFTAL 431

>ref|YP_983018.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Polaromonas naphthalenivorans CJ2]
gb|ABM38097.1| 3-phosphoshikimate 1-carboxyvinyltransferase / cytidylate kinase
[Polaromonas naphthalenivorans CJ2]
Length = 667

Score = 392 bits (1008), Expect = e-107, Method: Compositional matrix adjust.
Identities = 222/456 (48%), Positives = 293/456 (64%), Gaps = 28/456 (6%)

Query: 1 MAGAEIIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E + + P+ + GTV LPGSKS+SNR+LLLAALS G T V +LL S+D ML AL
Sbjct: 1 MYDIEYLDIPPLTQAGGTVCPLPGSKSISNRVLLLAALSHGQTTVHDLASDPTAVMLTAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LG +V ++ AV+ G GG+ + + LF+GNAG AMR LTAA+ GG
Sbjct: 61 EQLGCTVV--QSGNTAVIGGLGGQL----VQRKAALFMGNAGTAMRPLTAALALLGGE-- 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVN-GIGGLPGGKVKLSGSIS 179
+ L GVPRM ERPIGDLV L+QLG +D PP+R+ G+ L +++ G +S
Sbjct: 113 FELSGVPRMHERPIGDLVDALRQLGCAIDYLGNEGFPPLRLRPGVLKLLDDA-IRVRGDVS 171

Query: 180 SQYLSALLMAAPL-ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
Sbjct: 172 SQFLTALLMALPLVAQQAIRIEVVGELISRPYIEITLNLKRFGIQUVER-EGWQRFITPA 230

Query: 239 GKQYKSPKNAYVEGDASSASYFLAGAAITG-----GTVTVEGCGTTSLQGDVKFAEVLEM 293
G +Y+SP +VE DASSASYF+A AI + + G G S+QGD++F E M
Sbjct: 231 GSQYQSPGEIHVEADASSASYFIALGAIAACAKGINDIKIMGVGADSIQGDIFIEAARM 290

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDV 353
MGAK+ T S+ ++ G LKAID++ N +PD AMTLAV+AL+ADG T +R++
Sbjct: 291 MGAKIDSTPNLSQISR-----GAWPLKAIDLDCNHIPDAAMTLAVMALYADGTTVLRNI 344

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---TAIDTYDDHRMAMAF 410
ASWRVKET+R+ A+ EL KLGA+VEEG DY ITTP + I TYDDHR+AM F
Sbjct: 345 ASWRVKETDRIAAMACELQKLGA+VEEGADYKITPPAQAGAWKPAVIHTYDDHRIAMCF 404

Query: 411 SLAAC--AEVPVTIRDPGCTRKTFPDYFDVLFSTFVK 444
SLAA AE+PV I DP C KTFPDYF+ L + +
Sbjct: 405 SLAAFNPAELPVRILDPKCVAKTFPDYFEALFSVAQ 440

>ref|YP_001798044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. necessarius STIR1]
gb|ACB44430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. necessarius STIR1]
Length = 442

Score = 392 bits (1007), Expect = e-107, Method: Compositional matrix adjust.
Identities = 226/445 (50%), Positives = 282/445 (63%), Gaps = 20/445 (4%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+G +I + P K+ G++ LPGSKS+SNR LLLAALS GTT + NLL+++D M AL
Sbjct: 1 MSGLPDIQIGPQKQAQGSIVLPGSKSISNRALLAALSTGTTTLKNLLDADDTQVMRNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LGLSV +K K +V GCGGK PV++A LF+GNAG A+R LTAA+ GGN
Sbjct: 61 RQLGLSV-INKENKACIVEGCGGKLPVQEA----DLFMGNAGTAIRPLTAALAMQGGN-- 113

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISS 180
Y L GV RMRERPI DLV GL+Q+GA + L PP+++ VK+ G +SS
Sbjct: 114 YRLSGVARMRERPIRDLVDGLRQVGAKIGYELQEGYPPKILAAIDIQIKDVVKVRGDVSS 173

Query: 181 QYLSALLMAAPLALGD-VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI--- 236
Q+L+ALLMA PL + V IE+I +LIS PY+++TL+LM RFGV D F I
Sbjct: 174 QFLTALLMALPLVANEPVRIEIVIGELISRPYIDITLKLMAFVGTVACPD-MQSFVIPAK 232

Query: 237 KGGQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G YKSP VEGDASSASYFLA AI GG V V G G S+QGDV FA+ L +MGA
Sbjct: 233 TSGAVYKSPGQLLVEGDASSASYFLALGAIGGPPVRVLGVGKESIQGDVAFADALALMGA 292

Query: 297 KVTWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASW 356
+T E + V G L I ++ ++PD AMTLAV ALFA+GPT + +ASW
Sbjct: 293 NITAGEDWIEVAGVKN---ANGKLNIGITIDCTEIPDAAMTLAVAALFAEGPTRLNSIASW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPP-----EKLNVTAIDTYDDHRMAMAFS 411
RVKET+R+ A+ EL K+GA+VEEG DY ++ P K +DTYDDHRMAM FS
Sbjct: 350 RVKETDRIAAMAKELKKVGANVEEGADYIVVQAPVLQSDWKSPSEGVDTYDDHRMAMCFS 409

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYF 436
LAA + I DP C KTFP YF
Sbjct: 410 LAAFGNLKINDPNCVAKTFPTYF 434

>gb|AAX45945.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Bibersteinia trehalosi]
Length = 413

Score = 392 bits (1006), Expect = e-107, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 284/425 (66%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

Sbjct: 2 E++ LQPI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
EKLTLQPIISLVLGEINLPGSKSLSNRALLLAALAHGTTTNTLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
+ + + V G GG F D + LFLGNAG AMR LTAA+ G A +L

Sbjct: 62 VQYDLSSEDKTVCTVQGVGGAFEWNDG---LSLFLGNAGTAMRPLTAALCLKGQSEAEVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA+V PP+ + G L GGK+++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIHLVDALRQAGANVQYLENEGYPPIAIRNTG-LKGGKIQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEI L+S PY+++TL +M+ FGV +++D + F+++G Q Y

Sbjct: 178 TALLMAAPLAEGDMEIEIKGDLVSKPYIDITLAMMQDFGVSVQNND-YKTFVQGNQHYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKAFAEVLEMMGAKVTWTE 302
+PKN Y VEGDASSASYFLA AI G V V G G S+QGD FAEVLE MGA+TW E

Sbjct: 237 APKNRYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLEFAEVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
V R L+ +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFVQSE-----RGLRGVDMNMNIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPE--KLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA+VEEG D+ + P + + I+TY+DHRMAM F+L A + PV

Sbjct: 348 RLTAMATELRKIGATVEEGEDFIRVQPLKLEFKHAEIETYNDHRMAMCFALVALSNTPV 407

Query: 421 TIRDP 425
TI DP

Sbjct: 408 TILDLP 412

>ref|YP_003256375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D11S-1]
gb|ACX83156.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D11S-1]
Length = 443

Score = 391 bits (1004), Expect = e-106, Method: Compositional matrix adjust.
Identities = 223/451 (49%), Positives = 283/451 (62%), Gaps = 20/451 (4%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A I L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL

Sbjct: 1 MQQAISITLNPRIARVEGAINLPGSKSLSNRALLLAALAHGTTKVNTLLDSDDIRHMLNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR--SLTAAVTAAGGN 118
+ LG + V G GG F D + LFLGNAG AMR + + AG +

Sbjct: 61 KQLGAQYTLSEDKSVCEVQGLGGAQFQWHDG---LALFLGNAGTAMRPLAALCLARAGDS 117

Query: 119 AT--YVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
A +L G PRM+ERPI LV L Q GAD+ PP+ + G L GG +K+ G

Sbjct: 118 AQNEVILTGEPRMKERPIRHLVDALLQAGADIRYLENEGYPPIAIRNTG-LRGGLIKIDG 176

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
SISSQ+L+ALLMAAPLA D EIEII +L+S PY+++TL +M+ FGV E+ + RF +

Sbjct: 177 SISSQFLTALLMAAPLAESDSEIEIIGELVSKPYIDITLNMKIFGVSVENQ-HYQRFIV 235

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKAFAEVLEMMGA 296
KG Q Y+SP + VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA

Sbjct: 236 KGKQSYQSPGSFLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLEFADVLEKMGA 294

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASW 356
+TW E + P L +D++MN +PD AMT+A ALFA+G T IR++ +W

Sbjct: 295 HITWGEDFIQAEQAP-----LHGVDMDNMNIPDAAMTIATTALFAEGETVIRNIYNW 346

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL K+GA VEEG D+ I P P + I+TY+DHRMAM F+L A

Sbjct: 347 RVKETDRLTAMATELRKVGAEEVEEGEDFIRIQPLKPTFKAAEIEIETYNDHRMAMCFALIA 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
++ PVTI DP CT KTFP +F T +

Sbjct: 407 LSDTPVTILDPNCTAKTFPTFFKEFLTIAQQ 437

>gb|AAx45947.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Bibersteinia trehalosi]
Length = 413

Score = 390 bits (1003), Expect = e-106, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 284/425 (66%), Gaps = 18/425 (4%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E++ LQPI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKLTLQPIISLVLGEINLPGSKSLSNRALLAALAHGTTTNTLLDSDDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
      + + + V G GG F D + LFLGNAG AMR LTAA+ G A +L
Sbjct: 62  VQYDLSSEDKTVCTVQGVGGAFEWNDG---LSLFLGNAGTAMRPLTAALCLKGQSEAEVIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GA V PP+ + G L GKG+++ GSISQ+L
Sbjct: 119  TGEPRMKERPILHLVDALRQAGASVQYLENEGYPPIAIRNTG-LKGGKIQIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLMAAPLA GD+EIEI L+S PY+++TL +M+ FGV +++D + F+++G Q+Y
Sbjct: 178  TALLMAAPLAEGDMEIEIKGDLVSKPYIDITLAMMQDFGVSVQNND-YKTFFVQGNQRYV 236

Query: 244  SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
      +PKN Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237  APKNRYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGE 295

Query: 303  TSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      V R L+ +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296  DFVQAE-----RGLRGVDMMDNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363  RMVAIRTELTKLGASVEEGPDYCIITPPE--KLNVTIAIDTYDHRMAMAFSLAACAEVPV 420
      R+ A+ TEL K+GA+VEEG D+ + P + + I+TY+DHMMAM F+L A + PV
Sbjct: 348  RLTAMATELRKIGATVEEGEDFIRVQPLKSEFKHAEIETYNDHRMAMCFALVALSNTPV 407

Query: 421  TIRDP 425
      TI DP
Sbjct: 408  TILDP 412

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>gb|AAx45944.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Bibersteinia trehalosi]
Length = 413

Score = 390 bits (1001), Expect = e-106, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 283/425 (66%), Gaps = 18/425 (4%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E++ LQPI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKLTLQPIISLVLGEINLPGSKSLSNRALLAALAHGTTTNTLLDSDDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
      + + + V G GG F D + LFLGNAG AMR LTAA+ G A +L
Sbjct: 62  VQYDLSSEDKTVCTVQGVGGAFEWNDG---LSLFLGNAGTAMRPLTAALCLKGQSEAEVIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GA V PP+ + G L GKG+++ GSISQ+L
Sbjct: 119  TGEPRMKERPILHLVDALRQAGASVQYLENEGYPPIAIRNTG-LKGGKIQIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLMAAPLA GD+EIEI L+S PY+++TL +M+ FGV +++D + F+++G Q Y
Sbjct: 178  TALLMAAPLAEGDMEIEIKGDLVSKPYIDITLAMMQDFGVSVQNND-YKTFFVQGNQHYV 236

Query: 244  SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
      +PKN Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237  APKNRYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGE 295

Query: 303  TSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      V R L+ +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296  DFVQAE-----RGLRGVDMMDNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

```

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPE--KLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA+VEEG D+ + P + + I+TY+DHRMAM F+L A + PV
Sbjct: 348 RLTAMATELRKIGATVEEGEDFIRVQPLKLSEFKHAEIETYNDRMAMCFALVALSNTPTV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDPT 412

>ref|YP_986705.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Acidovorax sp. JS42]
gb|ABM42629.1| cytidylate kinase / 3-phosphoshikimate 1-carboxyvinyltransferase
[Acidovorax sp. JS42]
Length = 673

Score = 389 bits (1000), Expect = e-106, Method: Compositional matrix adjust.
Identities = 226/452 (50%), Positives = 289/452 (63%), Gaps = 40/452 (8%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ + G+V+LPGSKS+SNR+LLLAALS+GTT V +LL S+D ML ALR LG +V
Sbjct: 9 LPPLASVQGSVQLPGSKSISNRVLLLAALSQGTTEVRDLLASDDTRVMDALRQLGCTV- 67

Query: 69 ADKAAKRAV-VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D+A V + G G P QLF+GNAG AMR LTAA+ GG Y L GVP
Sbjct: 68 -DEAGGTVRITGLGSSTP----PSPQLFMGNAGTAMRPLTAAALALLGGE--YELSGVP 120

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP----GGKVKLSGSISSQYL 183
RM ERPIGDLV L+QLG +D PP+R+ GGLP +++ G +SSQ+L
Sbjct: 121 RMHERPIGDLVDALRQLGCRIDYLGNGQGFPLRIAHAGGLPPLQLQAPIRVRGDVSSQFL 180

Query: 184 SALLMAAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+ALLMA PL DV IE++ +LIS PY+ +TL L+ RFG+ +H + W RF I G +
Sbjct: 181 TALLMALPLVARQDDVIEVVGELISKPYIHITLELLARFGIAVQH-EQWQRFITIPAGSR 239

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT----VTVEGCGTTSLQGDVKFAEVLEMMGA 296
Y+SP +VE DASSASYF+A AI G + + G G S+QGD++F E + MGA
Sbjct: 240 YQSPGLIHVEADASSASYFIAAGAIAGASGQKGIKILGVGLDSIQGDIFVEAAQAMGA 299

Query: 297 KVT---WTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+VT W E + T P LKAID++ N +PD AMTLAV+AL+A G T +R+
Sbjct: 300 RVTGGPNWLEVAR-TWP-----LKAIDLDCNHIPDAAMTLAVMALYARGTTVLRN 349

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMA 409
+ASWRVKET+R+ A+ EL KLGA+VEEG DY +TPP + +I TYDDHR+AM
Sbjct: 350 IASWRVKETDRIAAMTCELRLKLGATVEEGADYLCVTPPAQSGDWRAASIHTYDDHRVAMC 409

Query: 410 FSLAA--CAEVPVTIRDPGCTRKTFPDYFDVL 439
FSLAA A +PV I DP C KTFPDYF+ L
Sbjct: 410 FSLAAFNAAGLPVRIEDPKCVAKTFPDYFEAL 441

>ref|YP_004126485.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclophilus
denitrificans BC]
gb|ADU99597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclophilus
denitrificans BC]
Length = 674

Score = 389 bits (1000), Expect = e-106, Method: Compositional matrix adjust.
Identities = 220/451 (48%), Positives = 288/451 (63%), Gaps = 35/451 (7%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ GTV+LPGSKS+SNR+LLLAALS+GTT V +LL+S+D ML ALR +G +V+
Sbjct: 9 LPPLASAGGTVQLPGSKSISNRVLLLAALSQGTTEVHDLSSDDTRVMDALRAIGCTVD 68

Query: 69 ADKAAKRAVVVCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ R + G GG P + +LF+GNAG AMR LTAA+ GG + L G
Sbjct: 69 -EAGGVRITGLGGPDGTLP----RSPTKLFMGNAGTAMRPLTAAALALLGGE--FELSG 121

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGK----VKLSGSISS 180
VPRM ERPIGDLV L+QLG +D FLG + PP+ + GLP + +++ G +SS

Sbjct: 122 VPRMHERPIGDLVDALRQLGCRID-FLGNEGYPPLSIQHAAGLPALRLHEPIRVRGDVSS 180

Query: 181 QYLSALLMAAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
Q+L+ALLMA PL DV IE++ +LIS PY+ +TL L+ RFG+ H + W RF I

Sbjct: 181 QFLTALLMALPLVAKEQDVVIEVVGELISRPYIHITLELLARFGIAVRHEE-WQRFRTIPA 239

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEM 293
G +Y+SP +VE DASSASYF+A AI + + G G S+QGD++F E

Sbjct: 240 GSRYRSPGQIHVEADASSASYFIALGAIAESPKGQKGIKILGVGQDSIQGDIRFVEAARA 299

Query: 294 MGAKVTWTETSVTVTGPPEPFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
MGA++T + + G L+AID++ N +PD AMTLAV+AL+A G T +R++

Sbjct: 300 MGAQITGGPNWLQIER-----GSWPLRAIDLDCNHIPDAAMTLAVMALYAQGTTLRN 353

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAF 410
ASWRVKET+R+ A+ EL KLGASVEEG DY ITPP + +I TYDDHR+AM F

Sbjct: 354 ASWRVKETDRLAAMACELAKLGASVEEGADYLRIPTPARPADWKSASIRTYDDHRVAMCF 413

Query: 411 SLAAC--AEVPVTIRDPGCTRKTFPDYFDVL 439
SLAA A +PV I DP C KTFPDYF+ L

Sbjct: 414 SLAAFNPAAGLPVRIEDPKCVAKTFPDYFEAL 444

>ref|YP_003168109.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Candidatus Accumulibacter
phosphatis clade IIA str. UW-1]
gb|ACV36180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Accumulibacter phosphatis clade IIA str. UW-1]
Length = 655

Score = 389 bits (999), Expect = e-106, Method: Compositional matrix adjust.
Identities = 222/432 (51%), Positives = 280/432 (64%), Gaps = 32/432 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVE--ADKAAK 74
GT++LPGSKS+SNR+LLLAAL+ G T + +LL ++D ML ALR LG+ VE D +

Sbjct: 16 GTLRPLPGSKSISNRVLLLAALASGETELHDLVADDTARMLDALRALGVGVEPLGDTVFR 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G GG FPV A LFLGNAG A R LTA + AGG+ Y L GVPRM ERPI

Sbjct: 76 ---VTGVGVFPVRRA---DLFLGNAGTAFRPLTAVLALAGGD--YRLSGVPRMHERPI 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAP 191
GDLV GL+QLGAD+ PP+ ++ G G V + G +SSQ+LS LLMA P

Sbjct: 127 GDLVDGLRQLGADIRYLGEAGFPPLAISPPMPGRGEGRAVVVRGDVSSQFLSGLLMALP 186

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGQKYKSPKNAYVE 251
L + +E++ +LIS PYVE+TL M RFGV+ + D W RF + G Y+SP +VE

Sbjct: 187 LRGVETTVVEVVGELISKPYVEITLATMARFGVQIQR-DGWRRTVAAGSTYRSPGVHLHVE 245

Query: 252 GDASSASYFLAGAAITGGTTVTEGCGTTSLQGDVKFAEVLEMMGAKVT----WTETSVTV 307
GDASSASYFLA AI GG + VEG G S+QGDV+FA+ L +MGA++T W E S

Sbjct: 246 GDASSASYFLALGAIGGGLRVEGVGRDSMQGDVRFADALALMGARITCGANWLEASAPD 305

Query: 308 TGPPREPFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G L+ ID++ N +PD AMTLA VALFA+GPT++R++ASWRVKET+R+ A+

Sbjct: 306 AG-----SLQGIDLDCNHIPDAAMTLASVALFAEGPTSLRNIAASWRVKETDRIAAM 356

Query: 368 RTELTKLGASVEEGPDYCIITPP---EKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
TEL KLGA V+ G D+ ++PP L IDTYDDHR+AM FS+AA P+ I D

Sbjct: 357 ATELRLKGARVDVGEDFIRVSPPLAGRALQPAVIDTYDDHRIAMCFSSVAALG-TPLRIND 415

Query: 425 PGCTRKTFPDYF 436
P KTFPDYF

Sbjct: 416 PQTVAKTFPDYF 427

>ref|NP_777908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. Bp (Baizongia pistaciae)]
sp|P59416.1|AROA_BUCBP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|AA027013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. Bp (Baizongia pistaciae)]
Length = 427

Score = 389 bits (998), Expect = e-106, Method: Compositional matrix adjust.
Identities = 201/437 (45%), Positives = 273/437 (62%), Gaps = 16/437 (3%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E + L PI ++GT+ LPGSKS++NR LLL+A+S TT + N+L S+D YML L+ G
Sbjct: 3  ECLTLNPISLVNGTINLPGSKSITNRALLLSAMSNSTTHLKNILYSQDTQYMLNTLKICG 62

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + GC + + LFLGNAG A RSL A + N +L
Sbjct: 63  IKFNCSYTNLSCTIEGCNKPLNIS---HKTSLFLGNAGTAFRSLAAIFSLNNNNI--LLT 117

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G RM++RPI LV L+Q GA + PP+++ G G GG + +SG ISSQ+LS
Sbjct: 118  GNKRMRKQRIKHLVQALQQGGAQITYSEQDQYPPIKIKG--GFIGGNIFVSGKISSQFLS 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ALL+A PLA D I + +KL+S PY+++TL L+ +FG+K H D + +F ++G QKY S
Sbjct: 176  ALLIATPLAQLDSTITVTEKLVSKPYIDITLNLISKFGIKIHKD-YTKFNVQGRQKYIS 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      PK +EGDASSASYFLA AAI GG+V V G G S+QGDVKFA VL+ MGA +T+ +
Sbjct: 235  PKEYSIEGDASSASYFLAAAAIKGGSVKVTGIGLNSIQGDVKFANVLKMGAYITFGKDF 294

Query: 305  VTVTGPPEPFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      + +K L ID++MN +PD AMT+A+VALF+ G T IR++ +WRVKET+R+
Sbjct: 295  IVCK-----KKDLIGIDLMDNDIPDAAMTIAIVALFSKGKTVIRNIYNWRVKETDRL 346

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
      A+ EL K+GA V EG DY I PP I+TYDDHR+AM F+L A + + VT+ +
Sbjct: 347  SAMTNELKKIGAQVIEGNDYIEILPPINFVYAKINTYDDHRIAMCFALIALSGIKVTLN 406

Query: 425  PGCTRKTFFPDYFDVLST 441
      C KTFPDYF L +
Sbjct: 407  YKCVNKTFPDYFQKLKS 423
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>gb|AA45946.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Bibersteinia trehalosi]
Length = 413

Score = 387 bits (994), Expect = e-105, Method: Compositional matrix adjust.
Identities = 216/425 (50%), Positives = 282/425 (66%), Gaps = 18/425 (4%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E++ LQPI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKLTLQPISLVLGEINLPGSKSLSNRALLLAALAHGTTTNTNLLSDDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
      + + + V G GG F D + LFLGNAG AMR LTAA+ G A +L
Sbjct: 62  VQYDLSEDKTCTVQGVGGAFEWNDG---LSLFLGNAGTAMRPLTAALCLKGQSEAEVIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q GA V PP+ + L GGK+++ GSISSQ+L
Sbjct: 119  TGEPRMKERPIHLVLDALRQAGASVQYLENEGYPPIAIRNTD-LKGGKIQIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLMAAPLA GD+EIEI L+S PY+++TL +M+ FGV +++D + F+++G Q Y
Sbjct: 178  TALLMAAPLAEGDMEIEIKGDLVSKPYIDITLAMMQDFGVSVQNND-YKTFVQGNQHYV 236

Query: 244  SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +PKN Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237  APKNRYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFADVLEKMGAKITWGE 295

Query: 303  TSVTVTGPPEPFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      V R L+ +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296  DVFQAE-----RGLRGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363  RMVAIRTELTKLGASVEEGPDYCIITPPE--KLNVTADITYDDHRMAMAFSLAACAEVPV 420
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R+ A+ TEL K+GA+VEEG D+ + P + + I+TY+DHRMAM F+L A + PV
Sbjct: 348 RLTAMATELRKIGATVEEGEDFIRVQPLKLSEFKHAEIETYNDHRMAMCFALVALSNTPV 407

Query: 421 TIRDP 425
TI DP

Sbjct: 408 TILDP 412

>gb|AAV31127.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Yersinia ruckeri]
Length = 393

Score = 387 bits (993), Expect = e-105, Method: Compositional matrix adjust.
Identities = 214/408 (52%), Positives = 273/408 (66%), Gaps = 16/408 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI I+GTV LKSGKSLSNR LLLAAL+EGTT + NLL+S+D+ +ML AL++LG
Sbjct: 1 ESLTLQPIALINGTVNLPKSGKSVSNRALLAALAEGLTRLHNLDDDIRHMLNALKSLG 60

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ + V G GG A + ++LFLGNAG AMR L AA+ GN+ VL
Sbjct: 61 VNYRLSADRTQCDVDGLGGPLV--ADKTLELFLGNAGTAMRPLAALCL--GNSDIVLT 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPIG LV L+Q GA +D + PP+R+ G G GG++ + GS+SSQ+L+
Sbjct: 116 GEERMKERPIGHLVDALRQGGAQIDYLEQENYPPLRIRG--GFRGGELTVDGSVSSQFLT 173

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPLA D I I L+S PY+++TL LM FGV+ H + + F+I+GGQ Y S
Sbjct: 174 ALLMAAPLATQDTHIRIQGDLVSRPYIDITLHLMRSFGVEVTHQN-YQVFHIQGGQTYHS 232

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD KFA+VLE MGA + W +
Sbjct: 233 PGEYLVEGDASSASYFLAAAAIKGGTVRVTGIGKSVQGDTKFADVLEKMGAIHWDGDDY 292

Query: 305 VTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + R L ID++MN +PD AMT+A ALFA GPT IR++ +WRVKET+R+
Sbjct: 293 IECS-----RGELCGIDMDNMNHPDAAMTIATAALFAKGPTIIRNIYNWRVKETDRL 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSL 412
A+ TEL K+GA VEEG DY + PP L I TY+DHRMAM FSL
Sbjct: 345 SAMATELRKVGAEVEEGQDYIRVPPAHLIAAEIGTYNDHRMAMCFSL 392

>gb|AAx45928.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 386 bits (992), Expect = e-105, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 280/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LKSGKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPKSGKSLSNRALLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGVV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAEGDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237 APQGNLYVEGDASSASYFLASGAIKG-KVKVTGIGKSIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLTAMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTEV 407
Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>ref|YP_746641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosomonas eutropha
C91]
sp|Q0AIZ5.1|AROA_NITEC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI58676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosomonas eutropha
C91]
Length = 433

Score = 386 bits (992), Expect = e-105, Method: Compositional matrix adjust.
Identities = 220/443 (49%), Positives = 279/443 (62%), Gaps = 13/443 (2%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L ++ +G V+LPGSKS+SNR+LLL+AL+EGTT + NLL S+D ML AL+ LG
Sbjct: 2 EWLDLPLVRCAGKVRVLPGSKSISNRVLLLSALAEGTTTISNLLSDDTGRMLDALKMLG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++V + ++ GC G+F V++A LFLGNAG A R LTA ++ G+ Y L
Sbjct: 62 VAVTRTDE-DQYLITGCSGRFSVKEA----DLFLGNAGTAFRPLTAVLSLMHGH--YHLS 114
Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L+Q+GA + PP+ ++ P + ++G+ISSQ+LS
Sbjct: 115 GVPRMHERPIGDLVDALRQVGAVITYLEREHFPPLEIHPAAIHHPA-DILINGNISSQFSL 173
Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMA PLA I + LIS PYV +T+ M FGV+ E +SW RF + G Q Y S
Sbjct: 174 GLLMALPLAGEPATIIVNGTLISQPYVTLTIAQMAYFGVQVER-ESWLRFIVPGNQIYHS 232
Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AI GG V V+G G S QGD++F E LE MGA +
Sbjct: 233 PGKIVVEGDASSASYFLAAGAIAGGPVRVDGVRDSCQGDIFVEALEAMGACIKMGSDW 292
Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + P G K LKAID + N +PD AMTLA ALFA G T +R++ASWRVKET+R+
Sbjct: 293 IESSAPGCRSDG-KVLKAIDFDCNHIPDAAMTLATTALFAQGTTLTLRNIAASWRVKETDRI 351
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAACAEVPVTI 422
A+ TEL KLGA VE G D+ ITPP+ V T IDTYDDHRMAM FSL + PV I
Sbjct: 352 TAMSTELRKLGAQVESGDDFLRITPPDDPLVANTVIDTYDDHRMAMCFSLISLG-TPVRI 410
Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
DP C KTFPDYF+ +
Sbjct: 411 NDPHCVAKTFPDYFEKFTAITHQ 433

>ref|YP_003977767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Achromobacter
xylosoxidans A8]
gb|ADP15052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Achromobacter
xylosoxidans A8]
Length = 440

Score = 386 bits (991), Expect = e-105, Method: Compositional matrix adjust.
Identities = 229/442 (51%), Positives = 289/442 (65%), Gaps = 19/442 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L +++ G + LPGSKS+SNR+LLL+A++EG+TV+ LL+S+D MLGALR LG+ V
Sbjct: 9 LPRVRQARGVIALPGSKSISNRVLLLSAIAEGSTVITGLLSDSDTRVMLGALRQLGVQVS 68
Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A +V V +FPVE A LF+GNAG A+R LTAA+ GG+ Y L GVPR

Sbjct: 69 ELDAG--SVTVQGVRRFPVESA----DLFMGNAGTAIRPLTAALALMGDD--YRLSGVPR 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV-KLSGSISSQYLSALL 187
M ERPIGDLV LK LGA +D PP+R+ G G + V ++ GS+SSQ+L+ALL

Sbjct: 121 MHERPIGDLVDALKGLGASIDYLGQPGYPPLRI-GRGEIAADAVTRVQGSVSSQFLTALL 179

Query: 188 MAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
MAAPL G V IE++ +LIS PY+E+TL LM RFGV+ D W RF I GG Y+

Sbjct: 180 MAAPLQAGRSGKPVITIEVLGELISKPYIEITLNLMARFGVQVRR-DGWSRFVIDGGAAYR 238

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDAS+ASYFLA AI GG + V G G S+QGDV FA L MGA V++

Sbjct: 239 SPGQIAVEGDASTASYFLALGAIGGGLRVTGVGADSIQGDVAFATLADMGASVSYPGD 298

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V+G R G + LKA D + N +PD AMT A +AL+ADGP +R++ SWRVKET+R

Sbjct: 299 WIEVSGA-RVAQGER-LKAFDTDFNLIPDAAMTAALALYADGPCRLRNIGSWRVKETDR 356

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPVT 421
+ A++TEL KLGA VE GPD+ +TPP + I T+DDHRMAM FSLAA V

Sbjct: 357 IHAMQTELEKLGAQVESGPDWLRVTPPAQDAWRDAHIGTWDDHRMAMCFSLAAGPAAVR 416

Query: 422 IRDPGCTRKTFFPDYFDVLSTFV 443
I DPGC KTFP YFDV + V

Sbjct: 417 ILDPGCVSKTFPGYFDVYAGLV 438

>gb|AAx45938.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 386 bits (991), Expect = e-105, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G A +L

Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGAETAQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGV++ GSISQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQGAEVQYLENEGYPPLAISN-SGLQGKGVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y

Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 APQGNYLVEGDASSASYFLASGAIG-KVKVTGIGKKSIGDRLFADVLEKMGAKITWE 295

Query: 303 TSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V

Sbjct: 348 RLTAMATELRKVGAEEVEGEDFIRIQPLALENFQHAETIYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP

Sbjct: 408 TILDP 412

>ref|YP_002552856.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Acidovorax ebreus TPSY]
gb|ACM32856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidovorax ebreus
TPSY]
Length = 673

Score = 386 bits (991), Expect = e-105, Method: Compositional matrix adjust.
Identities = 225/452 (49%), Positives = 288/452 (63%), Gaps = 40/452 (8%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ + G+V+LPGSKS+SNR+LLLAALS+GTT V +LL S+D ML ALR LG +V
Sbjct: 9 LPPLASVQGSVQLPGSKSISNRVLLLAALSQGTTEVRDLLASDDTRVMDALRQLGCTV- 67

Query: 69 ADKAAKRAV-VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D+A V + G G P QLF+GNAG AMR LTAA+ GG Y L GVP
Sbjct: 68 -DEAGGTVRITGLGSSTP----PSPTQLFMGNAGTAMRPLTAALALLGGE--YELSGVP 120

Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLP----GGKVKLSGSISSQYL 183
RM ERPIGDLV L+QLG +D PP+R+ GGLP +++ G +SSQ+L
Sbjct: 121 RMHERPIGDLVDALRQLGCRIDYLGNGQGFPLRIAHAGGLPPLQLQAPIRVRGDVSSQFL 180

Query: 184 SALLMAAPLAL--GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+ALLMA PL DV IE++ +LIS PY+ +TL L+ RFG+ H + W RF I G +
Sbjct: 181 TALLMALPLVARQDDVIEVVGELISKPYIHITLELLARFGIAVRH-EQWQRFTIPAGSR 239

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT----VTVEGCGTTSLQGDVKFAEVLEMMGA 296
Y+SP +VE DASSASYF+A AI G + + G G S+QGD++F E + MGA
Sbjct: 240 YQSPGLIHVEADASSASYFIAAGAAIAGANGQNGIKILGVGLDSIQGDIRFVEAAQAMGA 299

Query: 297 KVT---WTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+VT W E + T P LK+ID++ N +PD AMTLAV+AL+A G T +R+
Sbjct: 300 RVTGGPNWLEVAR-DWP-----LKSIDLDCNHIPDAAMTLAVMALYARGTTVLRN 349

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMA 409
+ASWRVKET+R+ A+ EL KLGA+VEEG DY +TPP + +I TYDDHR+AM
Sbjct: 350 IASWRVKETDRIAAMTCELRLKLGATVEEGADYLCVTPPAQSGDWRAASIHTYDDHRVAMC 409

Query: 410 FSLAAC--AEVPVTIRDPGCTRKTFPDYFDVL 439
FSLAA A +PV I DP C KTFPDYF+ L
Sbjct: 410 FSLAAFNPAGLPVRIEDPKCVAKTFPDYFEAL 441

>gb|ABB75365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosospira
multiformis ATCC 25196]
Length = 437

Score = 385 bits (990), Expect = e-105, Method: Compositional matrix adjust.
Identities = 216/425 (50%), Positives = 282/425 (66%), Gaps = 21/425 (4%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVV 79
+PGSKS+SNRILLALLAALSEG T V +LL S+D ML AL TLG+S+ + + R +
Sbjct: 1 MPGSKSISNRILLALLAALSEGVDVCDLLASDDTARMLDALSTLGVSILQIGRDHYR--LQ 58

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G G +FP+ E LFLGNAG R LTA + A G+ Y L GVPRM ERPIGDLV
Sbjct: 59 GVGDDQFPLRLPTTEADLFLGNAGTVFRPLTAMLALAQQH--YRLSGVPRMHERPIGDLVD 116

Query: 140 GLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+Q+GAD+ +LG + PP+++ G + G++ + G +SSQ+L+ALLM P +++
Sbjct: 117 ALRQVGADI-TYLGKEGFPLQIKP-GRIHPGEITVRGEVSSQFLTALLMVLFPFLRAEMD 174

Query: 199 ----IEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
I + +LIS PY+++T+ LM RFGV+ E + W RF + Q+Y+SP +VEGDA
Sbjct: 175 ELPVITVAGELISRPIYIDLIALMARFGVQVEREE-WRRFTVPADQYRSPGQVFVEGDA 233

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SSASYFLA AI G V VEG G S+QGD++FAE LE MGA + + + +GP
Sbjct: 234 SSASYFLAAGATGRGPVRVEGLGRDSVQGDIRFAEALERMGADIRFGDNWIEASGP---- 289

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G L+AID++ N +PD AMTLAV ALFA G T +R++ASWRVKET+R+ A+ EL KL
Sbjct: 290 -GPGGLRAIDLDCNHIPDAAMTLAVTALFARGNTVLRNIAASWRVKETDRIAAMAQELRKL 348

Query: 375 GASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432
GA VE G D+ I+PP E + AIDTYDDHRMAM FSL + PV I DP C KTF
Sbjct: 349 GAEVEAGSDFLQISPPRGELVANAAIDTYDDHRMAMCFSLVSFQ-APVRINDPRCVSKTF 407

Query: 433 PDYFD 437
PDYF+
Sbjct: 408 PDYFE 412

>gb|ADX45885.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidovorax avenae
subsp. avenae ATCC 19860]
Length = 679

Score = 385 bits (989), Expect = e-105, Method: Compositional matrix adjust.
Identities = 220/451 (48%), Positives = 282/451 (62%), Gaps = 36/451 (7%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ G V+LPGSKS+SNR+LLLAALSEGTT V +LL S+D ML ALR +G V+
Sbjct: 9 LPPMDTAGVAVRLPGSKSISNRVLLLAALSEGTTVEVHDLASDDTRVMDLALREIGCGVD 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AA+ V + G P A+ +LFLGNAG AMR LTAA+ GG + L GVPR
Sbjct: 69 EGAAARGTVRITGLGTP---ARSPAKLFLGNAGTAMRPLTAAALALGGE--FELSGVPR 123

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLP----GGKVKLSGSISSQYLS 184
M ERPIGDLV L QLG + PP+R+ GG+P V++ G +SSQ+L+
Sbjct: 124 MHERPIGDLVEALLQLGCHISYLGNGFPPLRIAHAGGVPPPLALDAPVRVRGVDVSSQFLT 183

Query: 185 ALLMAAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKY 242
ALLMA PL DV IE++ +LIS PY+ +TL+L+ERFG+ H D W RF I G +Y
Sbjct: 184 ALLMALPLVTREQDVVIEVVGELISRPYIHITLQLLERFGIPVRHDD-WQRFITIPAGSRY 242

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVE-----GCGTSLQGDVVKFAEVLEMMGAK 297
+SP +VE DASSASYF+A A+ E G G S+QGD++FAE MGA+
Sbjct: 243 RSPGTIHVEADASSASYFIALGALAAPAPGQEPLRILGVGLDSIQGDIRFAEAARAMGAE 302

Query: 298 VT---WTETSVTVTGPPREPFGFRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDV 353
VT W E G L+A+D++ N +PD AMTLAV+AL+A G T +R++
Sbjct: 303 VTGGPNWLEVR-----RGAWPLRAVDLDCNHIPDAAMTLAVMALYAKGTTTLRNI 352

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAF 410
ASWRVKET+R+ A+ +LGA+VEEGPD+ +TPP +I TYDDHR+AM F
Sbjct: 353 ASWRVKETDRIAAMAQGCRRLGATVEEGPDFLRVTPPASPADWRAASIHTYDDHRIAMCF 412

Query: 411 SLAAC--AEVPVTIRDPGCTRKTFPDYFDVL 439
SLAA A++PV I DP C KTFPDYF+ L
Sbjct: 413 SLAAYNPAKLPVRIEDPKCVAKTFPDYFEAL 443

>ref|YP_802756.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. Cc (Cinara cedri)]
sp|Q057N6.1|AROA_BUCCC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ90663.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola
str. Cc (Cinara cedri)]
Length = 435

Score = 385 bits (989), Expect = e-105, Method: Compositional matrix adjust.
Identities = 189/432 (43%), Positives = 271/432 (62%), Gaps = 15/432 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+ + L+P+ I G + +PGSKS+SNR+LLL+ALS G T++ NLL S+D+ YML AL LG
Sbjct: 3 DSLTLKPVDYIQGKINIPGSKSISNRVLLLSALSNGKTILKNLLYSDDIKYMLKALKLKG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + DK + + G F V K +++LFLGNAG AMR L A ++ +L
Sbjct: 63 IFYKLDKKKSKCTIYGISDAFSV---KNKIKLFLGNAGTAMRPLLAILSLKKNKI--ILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPI LV L+Q GA++ PP+ + G G GKG+ + GSISSQ+LS
Sbjct: 118 GEKRMKERPIHHLVDSLRQGGANITYKNKKKFPPLYIKG--GFKGGKIFIDGSISSQFLS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKS 244

+LLMAAPLA D EI + ++L+S PY+ +T+ LME+FG+ + + FYIKG QKY S
Sbjct: 176 SLLMAAPLAELDTEIIVKNQLVSKPYINLTINLMEKFGISVSILNDYKHFYIKGNQKYIS 235

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
PK Y+E D SSA+YFLA AAI GG++ + G S+QGD+ F ++L+ MG + W + S
Sbjct: 236 PKKYIESDLSSATYFLAAAAIKGGSIQINGIQKKSQGDINFIKILKQMGVSIQWKNS 295

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V + L I V+ N +PD AMT+A++ +F+ I+++ +WRVKET+R+
Sbjct: 296 VICK-----KNKLLGITVDCNHIPDAAMTIAILGVFSKKKVIYIKNIYNWRVKETDRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V G DY + P + I+TY+DHR+AM FSL + + VT+ +
Sbjct: 348 YAMSTELKKIGARVITGKDYIKVYPVKNFHAKINTYNDHRIAMCFSLISLSTSVTLN 407

Query: 425 PGCTRKTFFPDYF 436
P C KTFP +F
Sbjct: 408 PKCVNKTFFPSFF 419

>gb|AAx45933.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
gb|AAx45934.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 385 bits (988), Expect = e-105, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LKSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTRVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E VV G GG F +++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFNIQNG--LSLFLGNAGTAMRPLAALCLKGAETAQIIL 118

Query: 124 DGVRPMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLKKGQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+TW E
Sbjct: 237 APQGNLYVEGDASSASYFLASGAIG-KVKVTGIGKKSQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIDPDAAMTIATLALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTIAIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLTAMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>ref|ZP_04762539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidovorax
delafieldii 2AN]
gb|EER60659.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidovorax
delafieldii 2AN]
Length = 676

Score = 385 bits (988), Expect = e-105, Method: Compositional matrix adjust.
Identities = 227/441 (51%), Positives = 294/441 (66%), Gaps = 33/441 (7%)

Query: 16 SGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+GTV LPGSKS+SNR+LLAALSEGTTVV +LL S+D ML ALR +G +V D+A

Sbjct: 16 AGTVDLPGSKSISNRVLLAALSEGTTVVHDLASDDTRVMLDALRQIGCTV--DEAGST 73

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ G GG P AK LF+GNAG AMR LTAA+ GG + L GVPRM ERPIG

Sbjct: 74 VRITGLGGHAPRSPAK---LFMGNAGTAMRPLTAALALLGGE--FELSGVPRMHERPIG 127

Query: 136 DLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPG---GKVKLSGSISSQYLSALLMAA 190
DLV L+QLG +D +LG D PP+R+ + G+P +++ G +SSQ+L+ALLMA

Sbjct: 128 DLVQALRQLGLCID-YLGNDGYPLRIAHVQGVPSLALTEPIRVRGDVSSQFLTALLMAL 186

Query: 191 PLALG--DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
PLA G + +E++ +LIS PY+ +TL+L+ERFG+ EH + W RF I G +Y+SP +

Sbjct: 187 PLAAGTQSIABVEVVGELISRPIAITLQLLERFGIVVEHQN-WQRFTIVAGSRYQSPGSV 245

Query: 249 YVEGDASSASYFLA-GAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+VE DASSASYF+A GA T T + ++G G S+QGD++F E MGA VT

Sbjct: 246 HVESDASSASYFIALGALTTSATGQKGIKIQVGLDSIQGDIRFVEAARAMGAVVTGGPN 305

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V G LKAID++ N +PD AMTLAV+AL+A+G T +R++ASWRVKET+R

Sbjct: 306 WLQVER-----GAWPLKAIDLDCNHIPDAAMTLAVMALYAEGTTTLRNIAASWRVKETDR 359

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAAC--AEV 418
+ A+ TEL KLGA+ EEG DY +TPP + +I TYDDHR+AM FSLAA A +

Sbjct: 360 IAAMATELRKLGATAEEGADYIRVTPPANVADWKAASIHTYDDHRVAMCFSLAAFNPAPL 419

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
PV I DP C KTFPDYF+ L

Sbjct: 420 PVRIEDPKCVAKTFPDYFEAL 440

>gb|AA45930.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 385 bits (988), Expect = e-105, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 280/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L

Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGV++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIKHLVDVLRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y

Sbjct: 178 TALLMSAPLAEGDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E

Sbjct: 237 APQGNLVEGDASSASYFLASGAIG-KVKVTGIGKKSIGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATATLFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V

Sbjct: 348 RLTAMATELRKVGAEEVEGEDFIRIQPLALENFQHAETIYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP

Sbjct: 408 TILDP 412

>gb|AA45941.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia glucosida]

Length = 413

Score = 385 bits (988), Expect = e-105, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 282/425 (66%), Gaps = 18/425 (4%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTVTNLLSDDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
      + E + VV G GG F V++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62  VKYELSEDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKAQVIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q+GA+V PP+ + GL GKKV++ GSISSQ+L
Sbjct: 119  TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLVITN-SGLQGGKVQIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLM+APLA D+EIEII L+S PY+++TL +M+ FG+ E+ D + F +KG Q Y
Sbjct: 178  TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMKDFGIMVENRD-YKTFVLVKGKQGYV 236

Query: 244  SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAKE+TW E
Sbjct: 237  APQGNLYVEGDASSASYFLAAGAIK-GNVKVTGIGKKSIGQDRLFADVLEKMGAKITWGE 295

Query: 303  TSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      + P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296  DFIQAEQAP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363  RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTIAIDTYDDHRMAMAFSLAACAEVPV 420
      R+ A+ TEL+K+GA +EEG D+ I P E+ I+TY+DHRMAM FSL A + V
Sbjct: 348  RLNAMATELSKIGAVIEEGEDFIRIQPLALEQFQHAEIETYNDRMAMCFSLIALSNTEV 407

Query: 421  TIRDP 425
      TI DP
Sbjct: 408  TILDP 412
```

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>gb|AAx45929.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
gb|AAx45932.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
gb|AAx45935.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
gb|AAx45937.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413
```

Score = 385 bits (988), Expect = e-104, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2  EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLSDDIRHMLNALKALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
      + E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L
Sbjct: 62  VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GKKV++ GSISSQ+L
Sbjct: 119  TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVQIDGSISSQFL 177

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178  TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244  SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAKE+TW E
Sbjct: 237  APQGNLYVEGDASSASYFLASGAIKG-KVKVTGIGKKSIGQDRLFADVLEKMGAKITWGE 295

Query: 303  TSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      + P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296  DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347
```

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLTAMATELRKVGAEEVEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>gb|AAx45936.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 384 bits (987), Expect = e-104, Method: Compositional matrix adjust.
Identities = 216/425 (50%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGA SKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGA SKSLSNRALLAALATGTRVTNLLDSDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
+ E VV G GG F +++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFNIQNG---LSLFLGNAGTAMRPLAALCLKGAETAQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GGV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SGLQGGKVVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNLYVEGDASSASYFLASGAIKG-KVKVTGIGKKSIIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 NFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ +EL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLTAMASELRKVGAEEVEGEDFIRIQPLALENFQHAETIETYNDRMAMCFSLIALSNTTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>gb|AAT45241.1| 5-enol-pyruvylshikimate-phosphate synthase [Nymphaea alba]
Length = 264

Score = 384 bits (987), Expect = e-104, Method: Compositional matrix adjust.
Identities = 198/255 (77%), Positives = 224/255 (87%), Gaps = 1/255 (0%)

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
LRTLGL V+ D+ KRA+V GC G+FPV +D+ +EV+LFLGNAG AMR LTA AV AAGGN
Sbjct: 1 LRTLGLRVDEDRDMKRAIVEGCSGQFPVAKDSAKEVELFLGNAGTAMRPLTAAVVAAGGN 60

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI 178
Y+LDGVPRMRERPIGDLV GL+QLGAD+ C LGT+CPPV +NG GGLPGGKVKLSGSI
Sbjct: 61 TRYILDGVPRMRERPIGDLVSLQLGADIGCTLGTCNPPVYINGKGLPGGKVKLSGSI 120

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQYL+ALLMAAPLALGDVE+E+ DKL+S+PYVEMTL+LMERFGV EH WDRF I+G
Sbjct: 121 SSQYLTALLMAAPLALGDVEVEMADKLVSVPYVEMTLKLMERFGVAVEHGGGWDRFLIRG 180

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKV 298
Q Y SP +AYVEGDASSASYFLAGAAITGGTVTVEGCGT+SLQGDVKFAEVLE MGAKV
Sbjct: 181 RQMYMSPGSAYVEGDASSASYFLAGAAITGGTVTVEGCGTSSLQGDVKFAEVLEKMGAKV 240

Query: 299 TWTETSVTVTGPPRE 313

TW++ SVTVTGPP++
Sbjct: 241 TWSQNSVTVTGPPKD 255

>ref|NP_660644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola str. Sg (Schizaphis graminum)]
sp|Q59178.2|AROA_BUCAP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC05428.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Buchnera aphidicola]
gb|AAM67855.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Buchnera aphidicola str. Sg (Schizaphis graminum)]
Length = 428

Score = 384 bits (986), Expect = e-104, Method: Compositional matrix adjust.
Identities = 212/429 (49%), Positives = 275/429 (64%), Gaps = 16/429 (3%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+P+ I+GT+ LPGSKS+SNR+LLL+A++ G T + NLL+S+D YML ALR +G+
Sbjct: 7 LKPVSyingtIYLPgSKSISNRVLLLSAMANGITCLTNLLDSQDTQYMLNLRKIGIKFF 66

Query: 69 ADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V G G F + + LFLGNAG AMR L AA++ N VL G R
Sbjct: 67 LSNNTTCHVHGIGKAFHLS---HPISLFLGNAGTAMRPLLAALSLYENNV--VLSGDDR 121

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPI LV LKQ GA ++ G PPV G G GG + L GSISQ+L++LLM
Sbjct: 122 MHERPIAHLVDALKQGATLEYKKGIGYPPVLTG--GFKGGSIMLDGSISSQFLTSLM 179

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
APLAL + I I L+S PY+++TL LM+ FGV +D + FYIKG QKY+SP N
Sbjct: 180 VAPLALQNTNIFIKGNLVSKPYIDITLNLMSKSGFVNIV-NDCYKSFYIKGNQKYESPGNY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGDASSASYFLA AAI GG+V V G G S+QGD+KFA+VLE MGA + W ++ +
Sbjct: 239 LVEGDASSASYFLAAAAIKGGSVKVVGVGKKSQGDIKFADVLEKMGAIIDWGD SFIVCR 298

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
L+ ID++MN +PD AMT+A+VALFA G + I+++ +WRVKET+R+ A+
Sbjct: 299 -----HNKLEKIDLDNMNHPDAAMTIAIVALFAKGTSLIKNIYNWRVKETDRLSAMS 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
EL K+GA ++EG D ITPP IDTY+DHRMAM FSL + + V I +P C
Sbjct: 351 KELKKVGAIIEGRDCLSITPPNFFKFAEIDTYNDHRMAMCFSLICLSGISVRILNPNCI 410

Query: 429 RKTFFPDYFD 437
KTFF YF+
Sbjct: 411 SKTFFPSYFE 419

>gb|AAx45940.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia glucosida]
Length = 413

Score = 384 bits (985), Expect = e-104, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 280/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPgSKSLSNRALLAALATGTTTRVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
+ E + VV G GG F V++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKYELSEDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKAQVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ + GL GKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLVITN-SGLQGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M+ FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMKDFGIMVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNYLVEGDASSASYFLAAGAIK-GNVKVTGIGKKSIIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQAP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLNAMATELRKIGAVVEEGDDFIRIQPLALEHFQHAIEIETYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>gb|AAx45942.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia glucosida]
Length = 413

Score = 383 bits (984), Expect = e-104, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 280/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NATYVL 123
+ E + VV G GG F +++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKCESEDKTVCVVEGIGGAFNIQNG---LSLFLGNAGTAMRPLAALCLKGEEKAQIIL 118

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ + GL GGKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLTITN-SGLQGGKVQIDGSISQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M+ FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMKDFGITVENRD-YKTFVLKKGQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNYLVEGDASSASYFLAAGAIK-GNVKVTGIGKKSIIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQAP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLNAMATELRKIGAVVEEGDDFIRIQPLALEHFQHAIEIETYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>gb|AAx45939.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia glucosida]
Length = 413

Score = 383 bits (983), Expect = e-104, Method: Compositional matrix adjust.
Identities = 218/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NATYVL 123
+ E + VV G GG F V++ + LFLGNAG AMR L AA+ G A +L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKAQVIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ + GL GGKV++ GSISQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAITN-SGLQGKQVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M+ FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMKDFGIMVENRD-YKTFLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGAK+TW E
Sbjct: 237 APQGNYLVEGDASSASYFLAAGAIKG-NVKVTGIGKKSIIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPREPFGRKHLKVIDNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQAP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLNAMATELRKIGAVVEEGDDFIRIQPLALEHFQHAETIYDHRMAMCFSLIALSNTTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILDP 412

>ref|YP_971618.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Acidovorax avenae subsp. citrulli
AAC00-1]
gb|ABM33844.1| cytidylate kinase / 3-phosphoshikimate 1-carboxyvinyltransferase
[Acidovorax citrulli AAC00-1]
Length = 679

Score = 383 bits (983), Expect = e-104, Method: Compositional matrix adjust.
Identities = 218/447 (48%), Positives = 282/447 (63%), Gaps = 28/447 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L P+ G V+LPGSKS+SNR+LLLAALSEGTT V +LL S+D ML ALR +G V+
Sbjct: 9 LPPLDTAGGAVRLPGSKSISNRVLLLAALSEGTTVEHDLASDDTRVMDLALREIGCGVD 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AA+ V + G P A+ +LFLGNAG AMR LTAA+ GG + L GVPR
Sbjct: 69 EGAAAQGTVRITGLGTSP---ARSPSKLFLGNAGTAMRPLTAALALLGGE--FELSGVPR 123

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP----GGKVKLSGSISSQYLS 184
M ERPIGDLV L QLG + PP+R+ GG+P V++ G +SSQ+L+
Sbjct: 124 MHERPIGDLVEALLQLGCHISYLGNGFPPLRIAHAGGVPLALDAPVRVRGDVSSQFLT 183

Query: 185 ALLMAAPLAL--GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
ALLMA PL DV IE++ +LIS PY+ +TL+L+ERFG++ H D W RF I G +Y
Sbjct: 184 ALLMALPLVAREKDVIEVVGELISRPIIHITLQLLERFGIRVRH-DEWQRFTIPAGSRY 242

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVE-----GCGTTSLQGDVVKFAEVLEMMGAK 297
+SP +VE DASSASYF+A A+ E G G S+QGD++FAE MGA+
Sbjct: 243 RSPGTIHVEADASSASYFIALGALAAPAPGQEPLRILGVGLDSIQGDIRFAEAARAMGAE 302

Query: 298 VTWTETSVTVTGPPREPFGRKHLKVIDNMNMKMPDVAMTLAVVALFADGPTAIRDVASWR 357
VT + V G L+A+D++ N +PD AMTLAV+AL+A G T +R++ASWR
Sbjct: 303 VTGGPNLVVRR-----GAWPLRAVDLDCNHIPDAAMTLAVMALYAQGTTLRNIAASWR 356

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAFSLAA 414
VKET+R+ A+ +LGA+VEEG D+ +TPP +I TYDDHR+AM FSLAA
Sbjct: 357 VKETDRIAMAQGCRRLGATVEEGSDFLRVTPPASPADWRAASIHTYDDHRIAMCFSLAA 416

Query: 415 C--AEVPVTIRDPGCTRKTFPDYFDVL 439
A++PV I DP C KTFPDYF+ L
Sbjct: 417 FNPAKLPVRIEDPKCVAKTFPDYFEAL 443

>gb|AAx45931.1| 5-enolpyruvylshikimate 3-phosphatesynthase [Mannheimia haemolytica]
Length = 413

Score = 382 bits (982), Expect = e-104, Method: Compositional matrix adjust.
Identities = 217/425 (51%), Positives = 279/425 (65%), Gaps = 18/425 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
Sbjct: 2 EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLDSDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-L 123
+ E VV G GG F V++ + LFLGNAG AMR L AA+ G + + L
Sbjct: 62 VKYELSDDKTVCVVEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GL GKV++ GSISSQ+L
Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLEYEGYPPLAISN-SGLQGKGVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYK 243
+ALLM+APLA D+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y
Sbjct: 178 TALLMSAPLAESDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G V V G G S+QGD FA+VLE MGA+K+TW E
Sbjct: 237 APQGNLYVEGDASSASYFLASGAIKG-KVKVTGIGKSIQGDRLFADVLEKMGAKITWGE 295

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+
Sbjct: 296 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TEL K+GA VEEG D+ I P E I+TY+DHRMAM FSL A + V
Sbjct: 348 RLTAMATELRKVGAEVEEGEDFIRIQPLALENFQHAETIYNDHRMAMCFSLIALSNTEV 407

Query: 421 TIRDP 425
TI DP
Sbjct: 408 TILD 412

>ref|ZP_07045860.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Comamonas testosteroni S44]
gb|EFI60520.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Comamonas testosteroni S44]
Length = 686

Score = 382 bits (982), Expect = e-104, Method: Compositional matrix adjust.
Identities = 219/468 (46%), Positives = 289/468 (61%), Gaps = 45/468 (9%)

Query: 1 MAGAEIIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E + L + +G+V LPGSKS+SNR+LLLAALS+GTT + +LL+S+D ML L
Sbjct: 1 MFTTEFLDLPALDSANGSVSLPGSKSISNRVLLAALSQGTTHDLSDSDTRVMLAGL 60

Query: 61 RTLGLSVEADKAAK-RAV-VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGN 118
+ LG S+ D +A+ V G GG+ P A LFLGNAG AMR LTAA++ GG+
Sbjct: 61 KQLGCSISPDVTPGQAIDVTGIGGQLP---AGTAATLFLGNAGTAMRPLTAALSVLGGD 117

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVN--GIGGLPGGKVKLSG 176
+ + GVPRM ERPIGDLV L+QLG +D PP+++ L +K+ G
Sbjct: 118 --FEMTGVPYERPIGDLVDALRQLGCKIDYKDEGFPPPLKIGQPDFSQLGSESIKVRG 175

Query: 177 SISSQYLSALLMAAPLALG--DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRF 234
+SSQ+L++LLMA PL D+ IE++ +LIS PY+ +TL L+ RFG+ A +D W RF
Sbjct: 176 DVSSQFLTSLMALPLLAKERDITIEVVGELISRPIHITLELLARFGI-AVKNDRWQRF 234

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTS 280
I G +Y+SP +VE DASSASYF+A AI GT + + G G S
Sbjct: 235 VIPSGSRYSQPGAIHVEADASSASYFIALGAIATGTTDDADADNVPQKNIRILVGQDS 294

Query: 281 LQGDVKFAEVLEMMGAKV---TWTETSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMT 336
+QGD++F E + MGA++ W + S G LKAID++ N +PD AMT
Sbjct: 295 IQGDIRFIEAAQAMGAQIESGPNWLQVSR-----GSWPLKAIDLDCNHIPDAAMT 344

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP---EKL 393
L +AL+ADG T +R++ASWRVKET+R+ A+ EL KLGASVEEG DY ITPP

Sbjct: 345 LGTMALYADGVTTLRNIASWRVKETDRIAAMAIELRKLGLASVEEGADYIRITPPAGKTAW 404

Query: 394 NVTADITYDDHRMAMAFSLAAC--AEVPVTIRDPGCTRKTFPDYFDVL 439

+I TYDDHR+AM FSLAA A++PV I DP C KTFPDYF+ L

Sbjct: 405 KAASIHTYDDHRVAMCFSLAAFNPAPKLPVRIEDPKCVAKTFPDYFEAL 452

>ref|YP_003277469.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Comamonas
testosteroni CNB-2]
gb|ACY32173.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Comamonas
testosteroni CNB-2]
Length = 690

Score = 382 bits (982), Expect = e-104, Method: Compositional matrix adjust.
Identities = 220/472 (46%), Positives = 290/472 (61%), Gaps = 49/472 (10%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGAL 60

M E + L + +G+V LPSKSK+SNR+LLLAALS+GTT + +LL+S+D ML L

Sbjct: 1 MFTTEFLDLPALDSANGSVSLPGSKSISNRVLLLAALSQGTTHDLDSDTRVMLAGL 60

Query: 61 RTGLSVEADKAAK-RAV-VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118

+ LG S+ D +A+ V G GG+ P A LFLGNAG AMR LTAA++ GG+

Sbjct: 61 KQLGCSISPDVTPGQAIDVTGIGGQLP---AGTAATLFLGNAGTAMRPLTAALSVLGGD 117

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVN--GIGGLPGGKVKLSG 176

+ + GVPRM ERPIGDLV L+QLG +D PP+++ L +K+ G

Sbjct: 118 --FEMTGVPYMERPIGDLVDALRQLGCKIDYKDEGFPLKIGQPDFSQLGSESIKVRG 175

Query: 177 SISSQYLSALLMAAPL-----ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230

+SSQ+L++LLMA PL A D+ IE++ +LIS PY+ +TL L+ RFG+ A +D

Sbjct: 176 DVSSQFLTSLMALPLLANVPGAQRDITIEVGELISRPYIHITLELLARFGI-AVKNDR 234

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGC 276

W RF I G +Y+SP +VE DASSASYF+A AI GT + + G

Sbjct: 235 WQRFVIPAGSRYPGAIHVEADASSASYFIALGAIATGTTDDADADNAPQPKSIRILGV 294

Query: 277 GTTSLQGDVKFAEVLEMMGAKV----TWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPD 332

G S+QGD++F E + MGA++ W + S G LKAID++ N +PD

Sbjct: 295 GQDSIQGDIRFIEAAQAMGAQIESGPNWLQVSR-----GSWPLKAIDLDCNHIPD 344

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-- 390

AMTL +AL+ADG T +R++ASWRVKET+R+ A+ EL KLGASVEEG DY ITPP

Sbjct: 345 AAMTLGTMALYADGVTTLRNIASWRVKETDRIAAMAIELRKLGLASVEEGADYIRITPPAG 404

Query: 391 -EKLNVTAIDITYDDHRMAMAFSLAAC--AEVPVTIRDPGCTRKTFPDYFDVL 439

+I TYDDHR+AM FSLAA A++PV I DP C KTFPDYF+ L

Sbjct: 405 KAAWKAASIHTYDDHRVAMCFSLAAFNPAPKLPVRIEDPKCVAKTFPDYFEAL 456

>ref|ZP_05909047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ4037]
gb|EFO44253.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ4037]
Length = 381

Score = 382 bits (982), Expect = e-104, Method: Compositional matrix adjust.
Identities = 204/391 (52%), Positives = 261/391 (66%), Gaps = 15/391 (3%)

Query: 49 NSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSL 108

+S+D+ +ML AL LG+ VV G G F V E V+LFLGNAG AMR L

Sbjct: 1 DSDDIRHMLNALTGLGVKYTSLADKTECVVEGLGRPFVS---SEPVELFLGNAGTAMRPL 57

Query: 109 TAAVTAAGGNATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLP 168

AA+ G YVL G PRM+ERPIG LV L++ GAD++ T+ PP+++ G G L

Sbjct: 58 AAALCV--GQGEYVLTGEPRMKERPIGHLVTALQKAGADIEYLENTNYPPLKIVGTG-LK 114

Query: 169 GGVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS 228

G V + GSISQ+L+A LM+APLA G+V I+I L+S PY+++TL +M++FGV+ ++

Sbjct: 115 AGTVSIDGSISSQFLTAFLMSAPLAEGEVRIKIEGDLVSKPYIDITLHIMKQFGVEVINN 174

Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFA 288

D + F I GQ Y +P + VEGDASSASYFLA AAI GG V V G G S+QGD++FA
Sbjct: 175 D-YQEFVIPAGQHYVAPGDFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFA 233

Query: 289 EVLEMMGAKVTTWTSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPT 348
+ LE MGA++ W + V G+ LK ID++ N +PD AMT+A ALFA+G T
Sbjct: 234 DALEKMGAEIEWGDDYVI-----SRVGK--LKIDMDYNHIPPDAAMTIATTALFAEGTT 285

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
AIR+V +WRVKET+R+ A+ TEL K+GA VEEG DY I+ P L AIDTYDDHRMAM
Sbjct: 286 AIRNVYNWRVKETDRLSAMATELRKVGAEVEEGEDYIIVKVPVPHLKHAADITYDDHRMAM 345

Query: 409 AFSLAACAEVPTIRDPGCTRKTFPDYFDVL 439
FSL A ++ PVTI DP CT KTFPDYFD L
Sbjct: 346 CFSLLALSDTPVTINDPKCTSKTFPDYFDKL 376

>ref|NP_760987.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio vulnificus
CMCP6]
Length = 376

Score = 382 bits (981), Expect = e-104, Method: Compositional matrix adjust.
Identities = 201/387 (51%), Positives = 257/387 (66%), Gaps = 15/387 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL LG+ E VV G G F +A+E LFLGNAG AMR L AA+
Sbjct: 1 MLNALTKLGVHYELSADKTVCVVEGLGRPFTATEAQE---LFLGNAGTAMRPLAALCL- 56

Query: 116 GGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
G +VL G PRM+ERPIG LV L++ GA ++ + PP+++N G L G V +
Sbjct: 57 -GKGEFVLTGEPKMRERPIGHLVDALEAGAQIEYLENENYPPLKINATG-LQAGTVNID 114

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
GSISSQ+L+A LMAAPLA G+V+I I+ +L+S PY+++TL +M++FGV ++++ F
Sbjct: 115 GSISSQPLTAFLMAAPLAQGEVKIHIIVGELVSKPYIDITLHIMKQFGVDVV-NNAYQEFI 173

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I GQ Y SP VEGDASSASYFLA AAI GG + V G G S+QGD+ FA+ LE MG
Sbjct: 174 IPAGQSYVSPGQFLVEGDASSASYFLAAAAIKGGEIKVTGIGKNSIQGDIHFADALEKMG 233

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
A++ W E V GR LK ID++ N +PD AMT+A ALFA G TAIR+V +
Sbjct: 234 AEIEWGEDYVI-----SRVGR--LKIDMDYNHIPPDAAMTIATTALFAQGTTAIRNVYN 285

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC 415
WRVKET+R+ A+ TEL K+GA VEEG DY I+ PP++L AIDTYDDHR+AM FSL A
Sbjct: 286 WRVKETDRLSAMATELRKVGAEVEEGEDYLIVNPPQQLRHAAIDTYDDHRIAMCFSLVAL 345

Query: 416 AEVPTIRDPGCTRKTFPDYFDVLSTF 442
++ PVTI DP CT KTFPDYFD L++
Sbjct: 346 SDTPVTINDPKCTSKTFPDYFDKLASL 372

>ref|ZP_03719717.1| hypothetical protein NEIFLAOT_01566 [Neisseria flavescens
NRL30031/H210]
gb|EEG33406.1| hypothetical protein NEIFLAOT_01566 [Neisseria flavescens
NRL30031/H210]
Length = 430

Score = 382 bits (981), Expect = e-104, Method: Compositional matrix adjust.
Identities = 214/433 (49%), Positives = 275/433 (63%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLAAALSEGTTVDNLLNSDEVHYMLGALRTLGLSVEADKAAKRAV 77
T+ LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E+ R
Sbjct: 16 TIALPGSKSISNRTLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIESLPEG-RLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP + A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHSGSGRFPNQTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
V L+ GADV + PP+++ NG +P + G++SSQ+L+ALLMA PL

Sbjct: 129 VDALRIAGADVQYLGNNYPPLQIGKRKDNNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV +++++ F I G KY +P++ YVEG

Sbjct: 184 TGQAFEIHMVGELISKPYIDITLKLMAQFGVDII-NENYRVFKIPAGAKYHAPHEHLYVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DASSASYFL I G + V G G S+QGDV FA LE +GA V W E V ++ P

Sbjct: 243 DASSASYFLGAGLIAGTPIRVTGIGAHSIQGDVAFARELEKIGADVIWGENFVEISRP-- 300

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ ++A D++ N +PD AMTLA+VAL P +R++ SWRVKET+R+ A+ TEL

Sbjct: 301 ---AERKIQAFDLNANHIPDAAMTLAIVALATKQPCTLRNIGSWRVKETDRIAAMATELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVTI-IDTYDDHRMAMAFSLAACAEVPTTIRDPGCTRKT 431
KLGA V E + ITPPE L A IDTYDDHRMAM FSLA+ VPV I DP CT KT

Sbjct: 358 KLGAEVVEEAIAIHITPPETLTSDAVIDTYDDHRMAMCFSLASLLGVPVIINDPKCTHKT 417

Query: 432 FPDYFDVLSTFVK 444
FPDYF V ++ K

Sbjct: 418 FPDYFQVFASLTK 430

>ref|ZP_03544339.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Comamonas
testosteroni KF-1]

gb|EED68625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Comamonas
testosteroni KF-1]

Length = 690

Score = 382 bits (980), Expect = e-104, Method: Compositional matrix adjust.
Identities = 221/472 (46%), Positives = 288/472 (61%), Gaps = 49/472 (10%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E + L + +GTV LPGSKS+SNR+LLLAALS+GTT + +LL+S+D ML L

Sbjct: 1 MFTTEFLDLPALDSANGTVSLPGSKSISNRVLLLAALSQGTTHDLSDSDTRVMLAGL 60

Query: 61 RTLGLSVEADKAAK-RAV-VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ LG S+ D RA+ V G GG+ P A LFLGNAG AMR LTAA++ GG+

Sbjct: 61 KQLGCSISPDVVTGPAIEVTGIGGQLP---AGTAATLFLGNAGTAMRPLTAALSVLGGD 117

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVN--GIGGLPGGKVKLSG 176
+ + GVPRM ERPIGDLV L+QLG +D PP+++ L +K+ G

Sbjct: 118 --FEMTGVPVPRMYERPIGDLVDALRQLGCKIDYLYKDEGFPPKIGQPDFSQLGTDSIKVRG 175

Query: 177 SISSQYLSALLMAAPL-----ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
+SSQ+L++LLMA PL A D+ IE++ +LIS PY+ +TL L+ RFG+ A +D

Sbjct: 176 DVSSQFLTSLMALPLLANVPGAQRDIVIEVVGELISRPYIHITLELLARFGI-AVKNDR 234

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGC 276
W RF I Y+SP +VE DASSASYF+A AI GT + + G

Sbjct: 235 WQRFVIPASSHYQSPGAIHVEADASSASYFIALGAIATGTTDDADADNAPQPKSIRILGV 294

Query: 277 GTTSLQGDVKFAEVLEMMGAKV---TWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPD 332
G S+QGD++F E + MGA++ W + S G LKAID++ N +PD

Sbjct: 295 GQDSIQGDIRFIEAAQAMGARIESGPNWLQVS-----RGSWPLKAIDLDCNHIPD 344

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-- 390
AMTL +AL+ADG T +R++ASWRVKET+R+ A+ EL KLGASVEEG DY ITPP

Sbjct: 345 AAMTLGTMALYADGVTTLRNIASWRVKETDRIAAMAIELRKLGAASVEEGADYIRITPPAG 404

Query: 391 -EKLNVTAIDTYDDHRMAMAFSLAAC--AEVPTTIRDPGCTRKTFFPDYFDVL 439
+I TYDDHR+AM FSLAA A++PV I DP C KTFPDYF+ L

Sbjct: 405 KAAWKAASIHTYDDHRVAMCFSLAFAFNPAKLPRIEDPKCVAKTFFPDYFEAL 456

>gb|EGB11856.1| hypothetical protein AURANDRAFT_19755 [Aureococcus anophagefferens]
Length = 486

Score = 381 bits (978), Expect = e-103, Method: Compositional matrix adjust.
Identities = 249/457 (54%), Positives = 295/457 (64%), Gaps = 41/457 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI ++ G V+LPGSKSLSNR LL+AAL EG T V+NLL S+D ML AL +G
Sbjct: 45 ESLSLSPIAKVGGVRLPGSKSLSNRALLIAALCEGETTVENLLASDDTERMLEALAAMG 104

Query: 65 LSVEADKAAKRAVVVCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA---GGNA 119
++V AD V G K P D LFLGNAG AMR L A + A GG+
Sbjct: 105 VAV-ADLGDAAVRVTSAGALKAPGAD-----LFLGNAGTAMRPLAAVLAAVAATDGGD- 156

Query: 120 TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTD---CPPVRVNGIGGLPGGKVKLSG 176
+VLDG PRMRERPI DLV GLKQLG DV+C D CPPV V + GG ++SG
Sbjct: 157 -FVLDTGTPMRERPIEDLVDGLKQLGCDVECTQNGDFGGCPPVVVKPGARVDGGVARVSG 215

Query: 177 SISSQYLSALLMAA-----PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD 229
SSQ+LSALL+A+ PL IEI D+LIS PYV++T+ LM +FGV +
Sbjct: 216 KTSSQFLSALLLASPLATTQPLV-----IEITDELISQPYVQLTVDLMAKFGVVVDIDG 270

Query: 230 SWDRFYIKGGQKYKS---PKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV 285
++ F + QKY + P Y VEGDASSASYFLA AA+TGG +TV GCG+ S QGDV
Sbjct: 271 AYRSFTVAPAKYTNAGLPDATYFVEGDASSASYFLAAAAMTGGDLTVVCGGSESTQGDV 330

Query: 286 KFAEVLEMMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFAD 345
+FAEVL MGA VT T++TV +LK IDV+ +PD AMTLA VAL A
Sbjct: 331 RFAEVLRLDMGAPVTLHPTNITVAA-----ATPNLKGIDVCLDIPDAAMTLAAVALVAA 384

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE-KLNVTI-IDTYDD 403
GPT IR+V SWRVKETERM AI E TKLGA V EG +C+ITPP K N A I+TYDD
Sbjct: 385 GPTTIRNVGSRVKETERMKAIVAETTKLGADVFEGDTHCVITPPAGKPNAGAEIETYDD 444

Query: 404 HRMAFSLAACAEPVPTIRDPGCTRKTFPDYFDVLS 440
HR+AM F+LAACA VPVTI DP CT KTFP YFD L+
Sbjct: 445 HRIAMTFALAACAGVPVTILDPKCTSKTFPTYFDELA 481

>ref|ZP_04758091.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria flavescens SK114]
gb|EER55877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria flavescens SK114]
Length = 430

Score = 381 bits (978), Expect = e-103, Method: Compositional matrix adjust.
Identities = 210/428 (49%), Positives = 271/428 (63%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + LL S+D ML AL LG+ +E+ R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNVCEIHSLLKSDDTDRMLEALDKLVHIES-LPEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP + A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNQTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV + PP++++ + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVQYLGNEYPPPLQISKRQDNGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV + D + F I G Y +P++ YVEGDASSA
Sbjct: 189 EIHMGVGLISKPYIDITLKLMAQFGVDIINED-YRVFKIPAGANYHAPEHLYVEGDASSA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 317
SYFL I G + V G G S+QGDV FA LE +GA V W E V ++ P
Sbjct: 248 SYFLGAGLIAGTPIRVTGIGAHSIQGDVAFARELEKIGADVIWGENFVEISRP-----AE 302

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ ++A D++ N +PD AMTLA+VAL P +R++ SWRVKET+R+ A+ TEL KLGA
Sbjct: 303 RKIQAFDLNANHIPDAAMTLAIVLATKQPCTLRNIGSWRVKETDRITAMATELRKLGAD 362

Query: 378 VEEGPDYCIITPPEKLNVTI-IDTYDDHRMAFSLAACAEPVPTIRDPGCTRKTFPDYF 436
V E + ITPPE L A IDTYDDHRMAM+FSLA+ +PV I DP CT KTFPDYF
Sbjct: 363 VIEEAEAIHITPPETLTSDAVIDTYDDHRMAMSFSLASLLGIPVIINDPKCTHKTFPDYF 422

Query: 437 DVLSTFVK 444

V ++
Sbjct: 423 QVFTSLTN 430

>ref|NP_878673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Blochmannia floridanus]
sp|Q7VR41.1|AROA_BLOFL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD83448.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Blochmannia floridanus]
Length = 433

Score = 380 bits (976), Expect = e-103, Method: Compositional matrix adjust.
Identities = 203/433 (46%), Positives = 276/433 (63%), Gaps = 15/433 (3%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L PIK+I+GT+ LPGSKS+SNR LLLAA S G T + NLL+S+D YML AL LG+
Sbjct: 5 ITLNPIKINGTIYLPGSKSISNRALLLAAQSVGATRLINLLSDDDTRYMLAALLQLGVK 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ K + G GG ++ + LFLGNAG A+R L AA++ N VL G
Sbjct: 65 YKLSTDHKICEIKGVGGS--LQSKNTQTTLFLGNAGTAIRPLIAALSISKSHNI--VLTGD 120

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM+ERPI LV L+Q G ++ PV++ GG GG + + G ISSQ+LSA+
Sbjct: 121 MRMKERPIFHLVDTLRQGGGRIEYIERDHHLPVKL--YGGYCGGNIVIKGDISSQFLSAV 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM PLA + IE+I L+S PY+++TL +M FG+ +H + FY +G + YK+P+
Sbjct: 179 LMMTPLASKNTYIEVIGSLVSKPYIDITLSVMRAFGICVQHDKDYKFFYCEGNRIYKAPQ 238

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+EGDASSASYFLA AAI GGT+ V G G S QGD+KFA +LE MG+ +TW + +
Sbjct: 239 EYVIEGDASSASYFLAAAAIKGGTIRLVGVGKNSKQGDIFANILERMGSIIITWGDNYIE 298

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG--PTAIRDVASWRVKETERM 364
+ LK+ID+++N +PD AMTLAV+ALF P +R++ +WRVKE++R+
Sbjct: 299 CSKGIM-----LKSIDIDVNDIPDAAMTLAVIALFTTNLPMILRNIYNWRVKESDRL 351

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL K+GA V EG DY I PP ++ I+TY+DHR+AM F+L A + V VTI +
Sbjct: 352 HAMATELRKVGAIVSEGYDYLHIVPPVQIQSAFINTYNDHRIAMCFALVALSNVSVTINN 411

Query: 425 PGCTRKTFFPDYFD 437
P C KTFPD+FD
Sbjct: 412 PKCVCKTFFPDFFD 424

>ref|NP_873807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus ducreyi
35000HP]
sp|Q7VLN9.1|AROA_HAEDU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAP96196.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus ducreyi
35000HP]
Length = 435

Score = 380 bits (976), Expect = e-103, Method: Compositional matrix adjust.
Identities = 214/439 (48%), Positives = 284/439 (64%), Gaps = 17/439 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E+I L PI I G + LPGSKSLSNR LLLAAL++GTT V NLL S+DV +ML AL
Sbjct: 1 MNTIEKIRLDPITRIEGEITLPGSKSLSNRALLLAALAKGTTRVTNLLVSDDVHMLNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-NA 119
+TLG+ + + +V G G ++ + LFLGNAG MR L A + G A
Sbjct: 61 QTLGIRYTLSDQKRECIVEGACGALAWQNG---LSLFLGNAGTVMRPLA AVLCLKGEVRA 117

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSIS 179
VL G RM++RPI LV L+Q GA+++ PP+ + G L GKG+++ GSIS

Sbjct: 118 EVVLTGEARMQQRPIQHLVDALRQAGANIEYLENQGYPLAIKNTG-LIGGKIQIDGSIS 176

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLM APLA D++IEI+ L+S PY++MTL +M FGV +++++ F+++

Sbjct: 177 SQFLTALLMVAPLAESDMQIEIVGDLVSKPYIDMTLAMMRDFGVVQNNN-YQSFFVQAQ 235

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Q Y SP +VEGDASSASYFLA AAI G V V G G S+QGD FA+VL MGA ++

Sbjct: 236 QCYLSPGQYVVEGDASSASYFLAAAAIKG-KVKVNGIGKNSIQGDRLFADVLAKMGANIS 294

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E + + L+ IDV++N +PD A+T+A+VALFA+ T IR+V +WRVK

Sbjct: 295 WGEDFIQAE-----KSVLRGIDVDLNIHIPDAAITIAIVALFAETETIIRNVYNWRVK 346

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAE 417
ET+R+ A+ TEL KLGA+VEEG D+ I P I+TY+DHR+AM FSL A +

Sbjct: 347 ETDRLSAMATELRKLGATVEEGQDFIRIQPLALTDFTAEIETYNDRHAMCFSLIALSN 406

Query: 418 VPVTIRDPGCTRKTTPDYF 436
VTI DP CTRKTTP+YF

Sbjct: 407 TAVTILDPQCTRKTTPNYF 425

>gb|EFV83522.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Achromobacter
xylosoxidans C54]
Length = 440

Score = 379 bits (974), Expect = e-103, Method: Compositional matrix adjust.
Identities = 227/443 (51%), Positives = 287/443 (64%), Gaps = 19/443 (4%)

Query: 9 LQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L ++ G + LPGSKS+SNR+LLLA++++G T + LL+S+D ML ALR LG++V

Sbjct: 9 LPRVRRAGQGMALPGSKSISNRVLLLAADIADGETAITGLLSDDDTRVMLAALRQLGVAV- 67

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ A R V G +FPV+ A LF+GNAG A+R LTAA+ GG+ Y L GVPR

Sbjct: 68 SELAEGRVTVRGVS-RFPVDSA----DLFMGNAGTAIRPLTAALALMGDD--YRLSGVPR 120

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV-KLSGSISSQYLSALL 187
M ERPIGDLV LK LGA +D PP+ + G G + V ++ GS+SSQ+L+ALL

Sbjct: 121 MHERPIGDLVDALKALGARIDYLGQPGYPPLHI-GRGAIATPAVTQVQGSVSSQFLTALL 179

Query: 188 MAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
MAAPL G V IE++ +LIS PY+E+TL LM RFGV + D W RF I GG +Y+

Sbjct: 180 MAAPLQAGQSGQPVVIEVLGELISKPYIEITLNLMARFGVTVQR-DGWGRFTIAGGARYR 238

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDAS+ASYFLA AI GG + V G G S+QGDVKFA+ L MGA V + +

Sbjct: 239 SPGQIAVEGDASTASYFLALGAIGGGPLRVTVGADSIQGDVKFADTLAAMGATVAYGDG 298

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ VTG GR LKA D + N +PD AMT A +AL+ADGP +R++ SWRVKET+R

Sbjct: 299 WIEVTGVRVAEGR--LKAFTDFNLIPDAAMTAAALALYADGPCRLRNIGSWRVKETDR 356

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAACAEVPVT 421
+ A++TEL KLGA VE G D+ +TPP I T+DDHRMAM FSLAA V

Sbjct: 357 IHAMQTELEKLGAEVSGLDWLRVTPADGAWRDAHIGTWDDHRMAMCFSLAAFGPAAVR 416

Query: 422 IRDPGCTRKTTPDYFDVLSTFVK 444
I DPGC KTFP YFDV + V

Sbjct: 417 ILDPGCVSKTFPGYFDVYAGLVS 439

>gb|AAA21529.1| 5-enolpyruvylshikimate 3-phosphate synthase [Mannheimia
haemolytica]
Length = 434

Score = 378 bits (971), Expect = e-103, Method: Compositional matrix adjust.
Identities = 220/439 (50%), Positives = 282/439 (64%), Gaps = 22/439 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64

Sbjct: 2 E++ L PI + G + LPGSKSLSNR LLLAAL+ GTT V NLL+S+D+ +ML AL+ LG
EKLTLTPISRVEGEINLPGSKSLSNRALLAALATGTTQVTNLLDSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATYVL 123
+ E V+ G GG F V++ + LFLGNAG AMR L AA+ G + +L

Sbjct: 62 VKYELSDDKTVCVLEGIGGAFKVQNG---LSLFLGNAGTAMRPLAALCLKGEEKSQIIL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q+GA+V PP+ ++ GSKV++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQVGAEVQYLENEGYPPLAISN-SVCRGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLM+APLA GD+EIEII L+S PY+++TL +M FG+ E+ D + F +KG Q Y

Sbjct: 178 TALLMSAPLAEGDMEIEIIGDLVSKPYIDITLSMMNDFGITVENRD-YKTFVLVKGKQGYV 236

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+P+ Y VEGDASSASYFLA AI G VT G G S+QGD FA+VLE MGA+TW E

Sbjct: 237 APQGNLYVEGDASSASYFLASGAIKAGKVT--GIGKKSIIQGDRLFADVLEKMGAKITWGE 294

Query: 303 TSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P LK +D++MN +PD AMT+A ALFA+G T IR++ +WRVKET+

Sbjct: 295 DFIQAEQSP-----LKGVDMDMNHIPDAAMTIATTALFAEGETVIRNIYNWRVKETD 346

Query: 363 RMVAIRTELTK---LGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAE 417
R+ A+ TEL K EEG D+ I P E I+TY+DHRMAM FSL A +

Sbjct: 347 RLTAMATELRKVGAEEVEEGEGDFIRIQPLALENFQHAIEIETYNDRMAMCFSLIALSN 406

Query: 418 VPVTIRDPGCTRKTFPDYF 436
VTI DP CT KTFP YF

Sbjct: 407 TEVTILDPNCTAKTFPTYF 425

>ref|YP_001155282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. asymbioticus QLW-P1DMWA-1]
gb|ABP33718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. asymbioticus QLW-P1DMWA-1]
Length = 442

Score = 376 bits (965), Expect = e-102, Method: Compositional matrix adjust.
Identities = 226/452 (50%), Positives = 285/452 (63%), Gaps = 20/452 (4%)

Query: 1 MAGAEIEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+G EI + P G++ LPGSKS+SNR LLLAAL+ GTT + NLL+++D M AL

Sbjct: 1 MSGIPEITIGPPTRAQGSIVLPGSKSISNRALLAALASGTTTLKNLLDADDTQVMRNAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LGLSV D+A VV GCGG+FPV +A LF+GNAG A+R LTAA+ GGN

Sbjct: 61 RQLGLSV-IDQANHVCVVKGCGGQFPVREA----DLFMGNAGTAIRPLTAALAMQGGN-- 113

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y L GV RM ERPI DLV GL+Q+GA +D L PP+++ VK+ G +SS

Sbjct: 114 YRLSGVARMHERPIRDLVDGLRQVGAKIDYELQEGYPPIKILAADIQIKDVVKVRGDVSS 173

Query: 181 QYLSALLMAAPLALGD-VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
Q+L+ALLMA PL + V IE+I +LIS PY+++TL+LM RFGV D+ F I

Sbjct: 174 QFLTALLMALPLVAQEAVRIEVIGELISRPYIDITLKLARFGVNVACPDQ-QSFVIPAK 232

Query: 240 QK---YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGA 296
YKSP N VEGDASSASYFLA A+ G V V G G S+QGDV FA+ L +MGA

Sbjct: 233 TSDAVYKSPGNLSVEGDASSASYFLALGALGAGPVRVLGVGKDSIQGDVAFADALALMGA 292

Query: 297 KVTWTETSVTVTGPPEPFRGRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASW 356
K+T E + V+G + G+ L I ++ ++PD AMTLAV ALFA+G T + ++ASW

Sbjct: 293 KITAGEDWIEVSGV-KNAGGK--LNGITLDCTEIPDAAMTLAVAALFAEGQTRLNNIASW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----VTAIDTYDDHRMAMAFS 411
RVKET+R+ A+ EL K+GA VEEG DY ++ P L IDTYDDHRMAM FS

Sbjct: 350 RVKETDRIAAMAKELKKIGAIVEEGADYIVVQAPALGDWKSPEGIDTYDDHRMAMCF 409

Query: 412 LAACAEPVTIRDPGCTRKTFPDYFDVLSTFV 443
LA + I DP C KTFP YF + V

Sbjct: 410 LATLGPNTLKLNDPNCVAKTFPTYFAEFAKIV 441

```
>ref|YP_588703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Baumannia
    cicadellinicola str. Hc (Homalodisca coagulata)]
sp|Q1LTL1.1|AROBA_BAUCH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
    AltName: Full=5-enolpyruvylshikimate-3-phosphate
    synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF14261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Baumannia
    cicadellinicola str. Hc (Homalodisca coagulata)]
    Length = 428
```

Score = 376 bits (965), Expect = e-102, Method: Compositional matrix adjust.
Identities = 203/436 (46%), Positives = 282/436 (64%), Gaps = 17/436 (3%)

```
Query: 5    EEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E + LQPI ++GT+ LKSKS+SNR LLLAA + G T + NLL+S DV YML AL LG
Sbjct: 3    ELLTLQPIVRVNGTIHLPGSKSISNRALLAALQALGKTCLINLLDSYDVRVYMLDALHKL 62

Query: 65   LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
          ++      +   + G G   V+ A E   L+LGN+GIA+RSL AA+   N   ++
Sbjct: 63   INYCLSIDRRSCEIDGIGRPLRVDTALE---LYLGNSGIALRSLVAALCLQ--NKNIIIT 117

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
          G RM+ RPIG LV L+Q A +   + PP+ + G G   G + + S+SSQ+L+
Sbjct: 118  GDKRMKNRPIGLVDALRQGSQIHYLEKDNYPPLLQ--GFYNGDITIDCSLSSQFLT 175

Query: 185  ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
          +LLM APLA D I +   +L+S PY++MTL +M+ FG+   +H D +   FYIKG   +Y+S
Sbjct: 176  SLLMMAPLASQDRCIFVKGRVSKPYIDMTLAMKSFQIVVQH-DQYKIFYIKGKSQYRS 234

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
          P +   VEGDA++ASYFLA AAI GGT V G G+ S+QGD++FA++L MGA + W
Sbjct: 235  PGHYLVEGDATNASYFLAAAAIRGGTVRVTVGVSNSIQGDIRFADILANMGAIIRWGVNY 294

Query: 305  VVTGTPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFA-DGPTAIRDVASWRVKETER 363
          + T           R L +ID++MN +PD AMT+A+VALF +G T +R++ +WR+KET R
Sbjct: 295  IECT-----RNSLCSIDIDMNALPDTAMTIAIVALFTYNGVTTLRNIYNWRIKETNR 346

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
          +VA+ TEL K+GA V EG +Y I PP   + I+TYDDHR+AM F+L A + V +TI
Sbjct: 347  LVAMATELRKVGAIIVVEGKEYLSIKPPNMFKIAKINTYDDHRIAMCFALVALSNVSITIV 406

Query: 424  DPGCTRKTFFPDYFDVL 439
          +P CT KTFPD+F +L
Sbjct: 407  NPKCTYKTFPDPFFKLL 422
```

```
>gb|AAF01290.1|AF182427_3 5-enolpyruvylshikimate-3-phosphate synthase [Bordetella
    bronchiseptica]
    Length = 442
```

Score = 371 bits (953), Expect = e-100, Method: Compositional matrix adjust.
Identities = 221/449 (49%), Positives = 278/449 (61%), Gaps = 17/449 (3%)

```
Query: 1    MAGAEIEVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
          M+G   + L   +   G V LKSKS+SNR+LLLAAL+EG+T +   LL+S+D   ML AL
Sbjct: 1    MSGLAYLDLPAARLARGEVALPGSKSISNRVLLAALAEGSTEITGLDSDDTRVMLAAL 60

Query: 61   RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
          R LG+SV   + A R   + G   +FP E A   +LFLGNAG A R LTAA+   GG+
Sbjct: 61   RQLGVSV-GEVADGRVTIEGVA-RFPTEQA----ELFLGNAGTAFRPLTAALALMGD-- 112

Query: 121  YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS 180
          Y L GVPRM ERPIGLV L+Q GA ++   PP+R+ G   G V++ GS+SS
Sbjct: 113  YRLSGVPRMHERPIGDLVDALRQFGAGIEYLGQAGYPLRIGGGSIRVDGPVRVEGVS 172

Query: 181  QYLSALLMAAPL----ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
          Q+L+ALLMAAP+   + D+ IE++ +LIS PY+E+TL LM RFGV   D W F I
Sbjct: 173  QFLTALLMAAPVLARRSGQDITIEVVGELISKPYIETLNLMARFGVSVRR-DGWRAFTI 231
```

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
Y+ P +EGDAS+ASYFLA AI GG V V G G S+QGDV FA L MGA
Sbjct: 232 ARDAAYRGPGRMAIEGDASTASYFLALGAIGGPPVRVTGVGEDSIQGDVAFATLAAMGA 291

Query: 297 KVTWTETSVTVTGPPREPFFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
V + + G GR LKA D + N +PD AMT A +AL+ADGP +R++ SW
Sbjct: 292 DVRYGPGWIETRGRVVAEGGR--LKAFDADFNLIPDAAMTAATLALYADGPCRLRNIGSW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL KLGA V+ G D+ + PP I T+DDHRMAM FSLAA
Sbjct: 350 RVKETDRIHAMHTELEKLGAGVQSGADWLEVAPPAPGGWRDAHIGTWDDHRMAMCFSLAA 409

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
V I DPGC KTFPDYFDV + +
Sbjct: 410 FGPAVRILDPGCVSKTFPDYFDVYAGLL 438

>ref|YP_003844455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
ref|ZP_07631702.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
gb|ADL52691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
Length = 428

Score = 371 bits (953), Expect = e-100, Method: Compositional matrix adjust.
Identities = 204/422 (48%), Positives = 274/422 (64%), Gaps = 22/422 (5%)

Query: 19 VKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ +PGSKS++NR L++AAL+EGTTV+ N+L S+D YM+ A+R LG +VE D+ KR V+
Sbjct: 18 IDVPGSKSVANRALIIAALAEGTTVLKNMFLSDDTRYMMEAIRKLGNTVEVDEQ-KRTVI 76

Query: 79 VGC GGK--FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
V + FP E +LF+GNAG AMR L ++A G + L G+ RM+ERPI D
Sbjct: 77 VKSAAEKVFP-----ETELFIGNAGTAMRFLPTYISAGKGKVS--LTGIERMKERPIKD 128

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
LV GL++LG +V PP ++ GLPGG++ + G SSQYL+++L++AP A D
Sbjct: 129 LVDGLRELGEVETYKEKDGFPFPEIDS-NGLPGGEISIRGDKSSQYLSILLSAPYAKED 187

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
V ++I KL+SIPYV++T+R+M+ FGV+ E+ D + F+IK GQKYKS + VEGD SS
Sbjct: 188 VTVKIQKGLVSIPIYVDITIRMMKDFGVEVENRD-YKEFFIKSGQKYKS-REYIVEGDCSS 245

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
ASYF AAIT + V ++QGD+K +VLE MG V++ E V V G +
Sbjct: 246 ASYFFGIAAITNSEIKVNNVCKNTMQGDIKLLDVLEKMGVSVSYGENHVLVKSGK---- 301

Query: 317 RKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L+ I V+M+ M DVA TL+VVALFADG T I +V + R+KET+R+ A+ EL KLGA
Sbjct: 302 ---LRGITVDMHMSDVAQTLSVVALFADGVTKIENVYNMRKETRIKAVYNELMKLGA 358

Query: 377 SVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
V E D II P K N IDTYDDHRMAM+FSLA V I+DP C KTFP Y
Sbjct: 359 KVTELEDGLIIEPAVKYNENVEIDTYDDHRMAMSFSLAGLRIPGVKIKDPDCVSKTFPSY 418

Query: 436 FD 437
F+
Sbjct: 419 FE 420

>ref|ZP_07342849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderiales
bacterium 1_1_47]
gb|EFL83403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderiales
bacterium 1_1_47]
Length = 431

Score = 371 bits (953), Expect = e-100, Method: Compositional matrix adjust.
Identities = 215/444 (48%), Positives = 276/444 (62%), Gaps = 17/444 (3%)

Query: 5 EEIV-LQPIKEISGTVKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 63

Sbjct: 2 EEI+ L PI ++ G+V LPGSKS+SNR LLLAALSEGTT ++NLL +ED M+GAL TL
EEILKLPIMKVGGSVDLPGSKSISNRALLLAALSEGTTTELNNLLVAEDTEMMIGALETL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ +E V GCGG FPV+ A LFLGNAG AMR L++++ +GG YVL

Sbjct: 62 GVKLEVSNDGTEVKVEGCGGNFPVKKAAAA--DLFLGNAGTAMRPLSSSLAFSGGE--YVL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DGV RMR+RPI LV L +G + PP+++ + V + G +SSQ++

Sbjct: 116 DGVARMRQRPIAHLVEALNSVGRLSYLGEPGFPPKIEPATRINSDIVHVRGVDVSSQFV 175

Query: 184 SALLMAAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
S LLMAAPL + + I I +LIS PYV +T RLMERFGV+ + S+ + ++

Sbjct: 176 SGLLMAAPLIAEPQGLRIRIDGELISSPYVSLTCLRLMERFGVEVKTSE---KDFLVPRTL 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
YK+P VE DASSASYFLA A+ G + + G G S+QGD F E L MGA VT

Sbjct: 233 YKAPSVFEVEADASSASYFLALGALVG-PLKINGIGADSVQGDAAFVEYLVKMGAAVTRG 291

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E + TGP R +G K L + ++ +PD AMT A +A +GPT +R ++SWRVKET

Sbjct: 292 ENWIK-TGPSR--YGHK-LHGLQADVRPIPDAAMTFAAMAPMCEGPTILRGISSWRVKET 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
+R+ A+ ELTK+G VE D ITPP KL DTY DHRMAM SL A VPV

Sbjct: 348 DRIAMHNETLKVGCVESTDDMIKITPPVKLRSVFDITYKDHRMAMCMSLIAAGGVPE 407

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 445
IRDP C RKTFPDYF+ L+ V+

Sbjct: 408 IRDPNCVRKTFPDYFERLAGVVEK 431

>ref|NP_879749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella pertussis
Tohama I]
sp|P12421.2|AROABORPE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE41250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella pertussis
Tohama I]
Length = 442

Score = 371 bits (952), Expect = e-100, Method: Compositional matrix adjust.
Identities = 221/449 (49%), Positives = 278/449 (61%), Gaps = 17/449 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+G + L + G V LPGSKS+SNR+LLLAAL+EG+T + LL+S+D ML AL

Sbjct: 1 MSGLAYLDLPAARLARGEVALPGSKSISNRVLLLAALAEGSTETGLDSDDTRVMLAAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LG+SV + A V + +FP E A +LFLGNAG A R LTAA+ GG+

Sbjct: 61 RQLGVSV--GEVADGCVTIEGVARFPEQA----ELFLGNAGTAFRPLTAALALMGGD-- 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y L GVPRM ERPIGDLV L+Q GA ++ PP+R+ G G V++ GS+SS

Sbjct: 113 YRLSGVPRMHERPIGDLVDALRQFGAGIEYLGQAGYPPLRIGGGSIRVDGPVRVEGSVSS 172

Query: 181 QYLSALLMAAPL----ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
Q+L+ALLMAAP+ + D+ IE++ +LIS PY+E+TL LM RFGV D W F I

Sbjct: 173 QFLTALMAAPVLARRSGQDITIEVVGELISKPYIETLNLMARFGVSVRR-DGWRAFTI 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
Y+ P +EGDAS+ASYFLA AI GG V V G G S+QGDV FA L MGA

Sbjct: 232 ARDAVYRGPRMAIEGDASTASYFLALGAIGGPVVRTGVGEDSIQGDVAFATLAAMGA 291

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
V + + G GR LKA D + N +PD AMT A +AL+ADGP +R++ SW

Sbjct: 292 DVRYGPGWIETRGVRVAEGGR--LKAFDADFNLPDAAMTATLALYADGPCRLRNIGSW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL KLGA V+ G D+ + PPE I T+DDHRMAM FSLAA

Sbjct: 350 RVKETDRIHAMHTELEKLGAGVQSGADWLEVAPPEGGWRDAHIGTWDDHRMAMCFSLAA 409

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
V I DPGC KTFPDYFDV + +
Sbjct: 410 FGPAAVRILDPGCVSKTFPDYFDVYAGLL 438

>ref|NP_885305.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella
parapertussis 12822]
sp|Q7W602.1|AROABORPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE38415.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella
parapertussis]
Length = 442

Score = 371 bits (952), Expect = e-100, Method: Compositional matrix adjust.
Identities = 220/449 (48%), Positives = 278/449 (61%), Gaps = 17/449 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+G + L + G V LPGSKS+SNR+LLLAAL+EG+T + LL+S+D ML AL
Sbjct: 1 MSGLAYLDLPAARLARGEVALPGSKSISNRVLLLAALAEGSTEITGLLDSDTRVMLAAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LG+SV + A V + +FP+E A +LFLGNAG A R LTAA+ GG+
Sbjct: 61 RQLGVSV--GEVADGCVTIEGVARFPFIEQA----ELFLGNAGTAFRPLTAALALMGGD-- 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y L GVPRM ERPIGDLV L+Q GA ++ PP+R+ G G V++ GS+SS
Sbjct: 113 YRLSGVPRMHERPIGDLVDALRQFGAGIEYLGQAGYPPLRIGGGSIRVDGPVRVEGSVSS 172

Query: 181 QYLSALLMAAPL----ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYI 236
Q+L+ALLMAAP+ + D+ IE++ +LIS PY+E+TL LM RFGV D W F I
Sbjct: 173 QFLTALLMAAPVLARRSGQDITIEVVGELISKPYIETLNLMARFGVSVRR-DGWRAFTI 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
Y+ P +EGDAS+ASYFLA AI GG V V G G S+QGDV FA L MGA
Sbjct: 232 ARDAAYRGPGRMAIEGDASTASYFLALGAIGGPPVRVTGVGEDSIQGDVAFATLAAMGA 291

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
V + + G GR LKA D + N +PD AMT A +AL+ADGP +R++ SW
Sbjct: 292 DVRYGPGWIETRGRVVAEGGR--LKAFDADFNLPDAAMTAATLALYADGPCRLRNIGSW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL KLGA V+ G D+ + PP I T+DDHRMAM FSLAA
Sbjct: 350 RVKETDRIHAMHTELEKLGAGVQSGADWLEVAPPAPGGWRDAHIGTWDDHRMAMCFSLAA 409

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
V I DPGC KTFPDYFDV + +
Sbjct: 410 FGPAAVRILDPGCVSKTFPDYFDVYAGLL 438

>ref|YP_002923575.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Candidatus
Hamiltonella defensa 5AT (Acyrtosiphon pisum)]
sp|C4K4D4.1|AROAHAMD5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACQ67427.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Candidatus
Hamiltonella defensa 5AT (Acyrtosiphon pisum)]
Length = 428

Score = 370 bits (951), Expect = e-100, Method: Compositional matrix adjust.
Identities = 208/437 (47%), Positives = 281/437 (64%), Gaps = 16/437 (3%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
++ + L+PI +I+GTV LPGSKS+SNR+LLL+AL+ G T + N L+S+D YML AL+ L
Sbjct: 2 SKSLNLEPIGKINGTVYLPKSKSISNRVLLLSALAAGKTRLTNFLDSDDTRYMLEALKAL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ K V G G + ++L GNAG MR LTA ++ G + VL
Sbjct: 62 GVRYTVSKNGTCCEVEGVNGPL--NTPHPIELMTGNAGTVMRFLTAVLSL--GQSDVVL 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RM+ERP+ LV L+Q A + + PP+R+ G G GG + L G+ISSQ+L
Sbjct: 117 TGGARMKERPMDFLVDALRQGNQAITYLEKKNSPPLRLRG--GFRGGNLTLRGNISSQFL 174

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALL+ APLA D IE+ L+S PYVEMTL LM FG+ H + F IK QK+K
Sbjct: 175 TALLIMAPLAEQDTAIEVQGFVSKPYVEMTLHLMRVFGISVTHKH-YRTFNIKAHQKFK 233

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP + +EGDA++ASYFLA AAI GG V V G G S+QGDV+FA+VL+ MGA + W E
Sbjct: 234 SPGHYRIEGDATAASYFLAAAAIKGGCVRVIGVGQKSIQGDVQFADVLQKMGAFIHWGED 293

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETER 363
+ P R LK ID++MN MPD AMTLA ALF++GPT I+++ +WR+KET+R
Sbjct: 294 YIECR-PGR-----LKGIDMDMNSMPDAAMTLATLALFSEGPTRIQNIYNWRLKETDR 345

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ EL KLGA ++EG DY I P+ L I TY+DHR+AM+FSL A +++P+ I
Sbjct: 346 LSAMSALRLKGAQIKEGQDYIEIISPKNLKAEEIQTYNDRHIAFSLMALSDMPIRIL 405

Query: 424 DPGCTRKTFPDYFDVLS 440
+P CT KTFPD+F L+
Sbjct: 406 NPRCTSKTFPDDFFQKLA 422

>sp|Q03321.4|AROA_AERSA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 427

Score = 370 bits (949), Expect = e-100, Method: Compositional matrix adjust.
Identities = 216/435 (49%), Positives = 278/435 (63%), Gaps = 20/435 (4%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+PI ++G V LPGSKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG+ +
Sbjct: 6 LEPISRVAGEVNLPKSKSVSNRALLAALARGTTTLNLDSDDIRHMLAALTQLGVKYK 65

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V G G F V V LFLGNAG AMR L AA+ G+ Y+L G PR
Sbjct: 66 LSADKTECTVHGLGRSFAVS---APVNLFLGNAGTAMRPLCAALCL--GSGEYMLGGEPR 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIG LV L GA + PP+ V+ GL GG V + GS+SSQ+L+A LM
Sbjct: 121 MEERPIGHLVDCLALKGAHIQYLKKGYPPLVVDA-KGLWGGDVHVDGSVSSQFLTAFLM 179

Query: 189 AAPLALGDV--EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
AAP A+ V I I +L+S PY+++TL +M GV EH D++ FYIKG Q SP
Sbjct: 180 AAP-AMAPVIPRIHIKELVSKPYIDITLHIMNSSGVVIEH-DNYKLFYIKGNQSIIVSPG 237

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYFLA AI G V V G G S+ GD+ FA+VLE MGA++TW + +
Sbjct: 238 DFLVEGDASSASYFLAAGAIG-KVRVTGIGKHSI-GDIHFADVLERMGARITWGDDFIE 295

Query: 307 VTGPPREPFGFRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVA 366
P L +D++MN +PD AMT+A VALFA+GPT+IR++ +WRVKET+R+ A
Sbjct: 296 AEQGP-----LHGVDMDMNHIPDXAMTIAXVALFAEGPTSIRNIYNWRVKETDRLHA 347

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ T++ KLG S E Y +TPP +L IDTY HR+AM FSL A +++ VTI DPG
Sbjct: 348 MATDVRKLGVSSEEDLHYITVTPPTQLKHAEIDTYKHHRIAMCFSLVALSDIAVTINDPG 407

Query: 427 CTRKTFPDYFDVLST 441
CT KTFPDYFD L++
Sbjct: 408 CTSKTFPDYFDKLA 422

>ref|NP_890002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella
bronchiseptica RB50]
sp|Q9RND7.2|AROA_BORBR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

emb|CAE33961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella
bronchiseptica RB50]
Length = 442

Score = 370 bits (949), Expect = e-100, Method: Compositional matrix adjust.
Identities = 220/449 (48%), Positives = 277/449 (61%), Gaps = 17/449 (3%)

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Query: 1  MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      M+G  + L  +   G V LPSKKS+SNR+LLLAAL+EG+T  +  LL+S+D  ML AL
Sbjct: 1  MSGLAYLDLPAARLARGEVALPGSKSISNRVLLLAALAEGSTEITGLLSDSDTRVMLAAL 60

Query: 61  RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
      R LG+SV  + A  V  +   +FP E A   +LFLGNAG A R LTAA+  GG+
Sbjct: 61  RQLGVSV--GEVADGCVTIEGVARFPTEQA----ELFLGNAGTAFRPLTAALALMGGD-- 112

Query: 121  YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
      Y L GVPRM ERPIGDLV  L+Q GA  ++      PP+R+ G      G V++ GS+SS
Sbjct: 113  YRLSGVPRMHERPIGDLVDALRQFGAGIEYLGQAGYPPLRIGGGSIRVDGPVRVEGSVSS 172

Query: 181  QYLSALLMAAPL----ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
      Q+L+ALLMAAP+  +  D+ IE++ +LIS PY+E+TL LM RFGV      D W F I
Sbjct: 173  QFLTALLMAAPVLARRSGQDITIEVVGELISKPYIEITLNLMARFGVSVRR-DGWRAFTI 231

Query: 237  KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
      Y+ P   +EGDAS+ASYFLA AI GG V V G G S+QGDV FA  L MGA
Sbjct: 232  ARDAAYRGPGRMAIEGDASTASYFLALGAIGGGPVRVTGVGEDSIQGDVAFATLAAMGA 291

Query: 297  KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
      V  +   +   G      GR  LKA D + N +PD AMT A +AL+ADGP +R++ SW
Sbjct: 292  DVRYGPGWIETRGVRVAEGGR--LKAFDADFNLIIPDAAMTAATLALYADGPCRLRNIGSW 349

Query: 357  RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
      RVKET+R+ A+ TEL KLGA V+ G D+  + PP      I T+DDHRMAM FSLAA
Sbjct: 350  RVKETDRIHAMHTELEKLGAGVQSGADWLEVAPPAPGGWRDAHIGTWDDHRMAMCFSLAA 409

Query: 415  CAEVPVTIRDPGCTRKTFFPDYFDVLSTFV 443
      V I DPGC  KTFPDYFDV  +  +
Sbjct: 410  FGPAAVRILDPGCVSKTFFPDYFDVYAGLL 438

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>ref|YP_785874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella avium
197N]
sp|Q2L2S7.1|AROABORAL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAJ48961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella avium
197N]
Length = 439

Score = 369 bits (947), Expect = e-100, Method: Compositional matrix adjust.
Identities = 220/442 (49%), Positives = 279/442 (63%), Gaps = 18/442 (4%)

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Query: 9  LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L I++ G  LPSKKS+SNR+LL+AAL+EG T  +  LL+S+D  ML ALR LG++V
Sbjct: 9  LPHIRQARGLAALPGSKSISNRVLLIAALAEGRTEISGLLSDSDTRVMLAALRQLGVAV- 67

Query: 69  ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
      D   R V G  +FP E A   +LFLGNAG A R LTAA+  GG+  Y L GVPR
Sbjct: 68  TDLGQGRVAVEGAR-RFPAEKA----ELFLGNAGTAFRPLTAALALMGGD--YRLSGVPR 120

Query: 129  MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      M ERPIGDLV  L+  GA +D      PP+ + G G  +   +V++ GS+SSQ+L+ALL+
Sbjct: 121  MHERPIGDLVDALRAWGARIDYLGQAGYPPLHI-GRGDIRADRVVRVQGSVSSQFLTALLL 179

Query: 189  AAPLALG----DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      AAP+  G   V IE+I +LIS PY+E+TL LM R+GV      D W F I+G  +Y+S
Sbjct: 180  AAPIEAGASGRPVTIEVIGELISKPYIEITLNLMARYGVNVVR-DGWRAFTIEGDARYRS 238

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P  +  VEGDAS+ASY LA  + GG V V G G S+QGD FA+ L MGA +T
Sbjct: 239  PGSIAVEGDASTASYLLALGLVGGGPVRVTGVGEQSIQGDATAFADTLAAMGANITKGSW 298

```


Query: 305 VVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ +G GR +KA D + N +PD AMT A +ALFADGP +R++ SWRVKET+R+
Sbjct: 299 IEASGQVAEGGR--IKAFDADFNLIIPDAAMTAATMALFADGPCRLRNIGSWRVKETDRI 356

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAACAEVPVTI 422
A+ TEL KLGA VE GPD+ +TPP + I T+DDHRMAM FSLAA V I
Sbjct: 357 HAMHTELAKLGAKEVSGPDWLSLTPPADSDWRDAHIGTWDDHRMAMCFSLAAFPAAVRI 416

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
DPGC KTFPDYFDV + V
Sbjct: 417 LDPGCVSKTFPDYFDVYAGLVS 438

>gb|AAA22968.1| 5-enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)
[Bordetella pertussis]
Length = 442

Score = 369 bits (946), Expect = e-100, Method: Compositional matrix adjust.
Identities = 220/449 (48%), Positives = 277/449 (61%), Gaps = 17/449 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+G + L + G V LPGSKS+SNR+LLLAAL+EG+T + LL+S+D ML AL
Sbjct: 1 MSGLAYLDLPAARLARGEVALPGSKSISNRVLLLAALAEGSTEITGLLSDSDTRVMLAAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LG+SV + A V + +FP E A +LFLGNAG A R LTAA+ GG+
Sbjct: 61 RQLGVSV--GEVADGCVTIEGVARFPTEQA----ELFLGNAGTAFRPLTAALALMGGD-- 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y L GVPRM ERPIGDLV L+Q GA ++ PP+R+ G G V++ GS+SS
Sbjct: 113 YRLSGVPRMHMERPIGDLVDALRQFGAGIEYLGQAGYPPLRIGGGSIRVDGPVRVEGVS 172

Query: 181 QYLSALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
Q+L+ALLMAAP+ + D+ IE++ +LIS PY+E+TL LM RFGV D W F I
Sbjct: 173 QFLTALLMAAPVLARRSGQDITIEVVGELISKPYIEITLNLMARFGVSVRR-DGWRAFTI 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGA 296
Y+ P +EGDAS+ASYFLA AI GG V V G G S+QGDV FA L MGA
Sbjct: 232 ARDAVYRGPGRMAIEGDASTASYFLALGAIGGPPVRVTGVGEDSIQGDVAFATLAAMGA 291

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASW 356
V + + G GR LKA D + N +PD AMT A +AL+ADGP +R++ SW
Sbjct: 292 DVRYGPGWIETRGRVVAEGGR--LKAFDADFNLIIPDAAMTAATLALYADGPCRLRNIGSW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL KLGA V+ G D+ + PPE I T+DDHRMAM F LAA
Sbjct: 350 RVKETDRIHAMHTELEKLGAGVQSGADWLEVAPPEPGGWRDAHIGTWDDHRMAMCFLLAA 409

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
V I DPGC KTFPDYFDV + +
Sbjct: 410 FGPAAVRILDPGCVSKTFPDYFDVYAGLL 438

>ref|YP_522830.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Rhodoferax ferrireducens T118]
gb|ABD69299.1| 3-phosphoshikimate 1-carboxyvinyltransferase / cytidylate kinase
[Rhodoferax ferrireducens T118]
Length = 669

Score = 369 bits (946), Expect = e-100, Method: Compositional matrix adjust.
Identities = 216/456 (47%), Positives = 287/456 (62%), Gaps = 45/456 (9%)

Query: 11 PIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P+ +SGTV LPGSKS+SNR+LL+ALS G T + +LL+S+D M ALR LG V
Sbjct: 11 PLTGVSGTVVLPGSKSISNRVLLLSALSAGRTTIDLLSDSDTRVMFEALRALGCGVR-- 68

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
++ + G GG+ + LF+GNAG A+R LTAA+ GG+ + L GVPRM
Sbjct: 69 QSGSTVEIEGLGGQL---GHRQAALFMGNAGTAIRPLTAALAVLGGD--FELRGVPRMH 122

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGK----VKLSGSISSQYLSA 185
ERPIGDLV L+Q+G +D +LG D PP+ + G P K +++ G +SSQ+L+A
Sbjct: 123 ERPIGDLVDALRQIGCHID-YLGQDGFPPPLHI----GRPSLKLDTPIRVRGDVSSQFLTA 177

Query: 186 LLMAAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
LLMA PL A D+ IE++ +LIS PY+E+TL L+ RF V+ D W RF I +++
Sbjct: 178 LLMALPLVAATRDIVIEVVGELISRPIEITLNLARFNVVRVVR-DGWQRFTIPAASQFR 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
SP +VE DASSASYF+A AI G + +EG G S+QGD++F E +MMGA+V
Sbjct: 237 SPGTLFVEADASSASYFIAAGAIATGAGGQKGLRIEYGVGADSIQGDIFIEAAQMMGAQV 296

Query: 299 ----TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
W E S G LKAID++ N +PD AMTLA++AL+A G T +R++A
Sbjct: 297 QSGPNWLEVS-----GCWPLKAIDLDCNHIPDAAMTLAMMALYAQGSTTLRNIA 346

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP---EKLNVTAIDTYDDHRMAMAFS 411
SWRVKET+R+ A+ EL KLGA+VEEG D+ +TPP +I TYDDHRMAM FS
Sbjct: 347 SWRVKETDRIAAMACELRKLKATVEEGADFIRVTPPAVAADWRAASIHTYDDHRMAMCFS 406

Query: 412 LAAC--AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
LAA A +PV I DP C KTFPDYF+ L + +
Sbjct: 407 LAAFNPAGLPVRIVDPKCVAKTFPDYFEALFSLAQT 442

>emb|CAX49833.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase; EPSP
synthase; EPSPS) [Neisseria meningitidis 8013]
Length = 433

Score = 368 bits (945), Expect = e-99, Method: Compositional matrix adjust.
Identities = 209/428 (48%), Positives = 267/428 (62%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ T + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNTCEIHSLLKSDDTDRMLEALDKLGVIEFY-LAEDRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALARAGADVEYLGKEHYPPPLHIGKRQDNGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I +Y +P++ +VEGDASSA
Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADARYHAPEHLHVEGDASSA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 317
SYFLA + I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 248 SYFLAASLIAATPVRTGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-----KE 302

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 303 RAVQAFDL DANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VAEEAEAIHTPPETPTDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
DV S+ +
Sbjct: 423 DVFSSLTE 430

>ref|ZP_06980072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria sp. oral
taxon 014 str. F0314]
gb|EFI24244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria sp. oral
taxon 014 str. F0314]
Length = 431

Score = 368 bits (944), Expect = 1e-99, Method: Compositional matrix adjust.
Identities = 217/437 (49%), Positives = 273/437 (62%), Gaps = 14/437 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E I L +K V LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG
Sbjct: 3 ESIRLPAVKTKPAVALPGSKSISNRSLLLAALSDNVCEIHSLLKSDDTDRMLDALAALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E R V G GG+FP A LFLGNAG A R LTA + GG +Y L
Sbjct: 63 VKIEFLDGG-RLKVYGTGGRFPNRS- - -DLFLGNAGTAFRPLTAVLAVLGG- -SYSLH 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L+ GADV + PP+ +N ++ + G +SSQ+L+
Sbjct: 116 GVPRMHERPIGDLVDALRIAGADVRYEGRENYPLHINERTDSGVREIPIRGDVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+LMA PL EI I+ +LIS PY+++TL+LM RFGV ++ + F I G +Y +
Sbjct: 176 AILMALPLTGQAFEIRIVGELISKPYIDITLKLMAFQVNV-NEGVRMFKIPAGARYHA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
P++ YVEGDASSASYFLA ITG V V G G S+QGDV FA LE +GA V W +
Sbjct: 235 PEHLYVEGDASSASYFLAAGLITGPVVRVTGIGRNSIQGDVAFARELEKIGADVWGGDF 294

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V+ P P ++A D++ N +PD AMTLAVVAL AD P +R++ SWRVKET+R+
Sbjct: 295 IEVSRPETRP- - - -VQAFDLNANHIPDAAMTLAVVALAADAPCTLRNIGSWRVKETDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ EL KLGA V E P+ ITPPE+L A IDTYDDHR+AM FSL + VPV I
Sbjct: 350 TAAAEELRKLGA VVVEPEAIRITPPEQLRTDAIIDTYDDHRIAMCFSLVSLMGVPVVIN 409

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT KTFP YFD +
Sbjct: 410 DPKCTHKTFPTYFDTF 426

>gb|ADO31856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis alpha710]
Length = 433

Score = 367 bits (943), Expect = 1e-99, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 266/428 (62%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ T + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNTCEIHSLLKSDDTDRMLEALNKLGVIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA- - -DLFLGNAGTAFRPLTAALAVLGGD- -YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGEHYPLHIGKRQDNGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ + + + F I Y +P++ +VEGDASSA
Sbjct: 189 EIRMVGEISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHAPEHLHVEGDASSA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPEPFGR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 248 SYFLAAGLIAATPVCVIGIGANSIQGDVAFARELEKIGADVWGFVEVSRP- - - -KE 302

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + + + D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 303 RAVQSFDLDANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
DV S+ +
Sbjct: 423 DVFSSLTE 430

>ref|YP_003083433.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis alpha14]
emb|CBA06624.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis alpha14]
Length = 433

Score = 367 bits (943), Expect = 1e-99, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 266/428 (62%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ GADV+ F PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVVEYFGKEHYPPHLHIGKRQDNGERVIPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++++ F I Y +P++ +VEGDASSA
Sbjct: 189 EIRMVGEIISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHAPEHLHVEGDASSA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDKVFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 248 SYFLAAGLIAATPVCVIGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-----KE 302

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ +++ D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 303 RAVQSFDLDANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKTFTPTF 422

Query: 437 DVLSTFVK 444
DV S+ +
Sbjct: 423 DVFSSLTE 430

>ref|ZP_03084951.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli O157:H7 str. EC4024]
Length = 375

Score = 367 bits (942), Expect = 2e-99, Method: Compositional matrix adjust.
Identities = 204/390 (52%), Positives = 261/390 (66%), Gaps = 16/390 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLSDSDVRHMLNALTALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSDRTRCEIIGGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGSGVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTKFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
++ T R L AID++MN +PD AMT+A ALFA G T +R++ +WRVKET+R+
Sbjct: 294 ISCT-----RGELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN 394
A+ TEL K+GA VEEG DY ITPPEKLN
Sbjct: 346 FAMATELRKVGAEVEEGHDYIRITPPEKLN 375

>ref|YP_004048828.1| 5-enolpyruvoylshikimate-3-phosphate synthase [Neisseria lactamica
ST-640]
emb|CBN87465.1| 5-enolpyruvoylshikimate-3-phosphate synthase [Neisseria lactamica
020-06]
Length = 432

Score = 367 bits (942), Expect = 2e-99, Method: Compositional matrix adjust.
Identities = 211/433 (48%), Positives = 269/433 (62%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNACEIHSLLKSDDTGRMLEALDKLGVGIEY-LAEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
V L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPPHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV+ ++++ F I Y++P++ YVEG
Sbjct: 184 TGQAFEIRMGVELISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYRAPEHLYVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS+VTVTGPPR 312
DAS ASYFLA I + V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 243 DASGASYFLAAGLIAATPIRVTGIGANSIQGDVAFARELEKIGADVWGFVEVSRPKE 302

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL
Sbjct: 303 -----RAVQAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
KLGA V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KT
Sbjct: 358 KLGAKVVEEAFAIRITPPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVVINDPKCTHKT 417

Query: 432 FPDYFDVLSTFK 444
FP YFDV S+ +
Sbjct: 418 FPTYFDVFSSLTE 430

>gb|ADZ03829.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis NZ-05/33]
Length = 433

Score = 367 bits (941), Expect = 2e-99, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 266/428 (62%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ T +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNTCEIHSLLKSDDTDRMLEALDKLGVIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197

L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGKEHYPLHIGKRQDNGERVIPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ +++++ F I Y +P++ +VEGDASSA

Sbjct: 189 EIRMVGEELISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHAPEHLHVEGDASSA 247

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P

Sbjct: 248 SYFLAAGLIAATPVCVIGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-----KE 302

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ +++ D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA

Sbjct: 303 RAVQSFDDLDAHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTTIRDPGCTRKTFPDYF 436
V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF

Sbjct: 363 VVEEAEAIHITPPETLTPDAVIDTYDDHRMAMCFSLVSLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
DV S+ +

Sbjct: 423 DVFSSLTE 430

>ref|NP_274444.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis MC58]
sp|Q9JYU1.1|AROA_NEIMB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAF41793.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis MC58]
gb|EFV63523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis H44/76]
gb|EGC63144.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis CU385]
gb|ADY95408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis H44/76]
Length = 433

Score = 367 bits (941), Expect = 3e-99, Method: Compositional matrix adjust.
Identities = 214/446 (47%), Positives = 273/446 (61%), Gaps = 25/446 (5%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG

Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRITLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L

Sbjct: 63 VQIEY-LAEDRLKVHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDPPVRV-----NGIGLPGGKVKLSGSIS 179
GVPRM ERPIGDLV L+ GADV+ PP+ + NG +P + G++S

Sbjct: 116 GVPRMHERPIGDLVDALRIAGADVEYLGKEHYPLHIGERQDNGERVIP-----IKGNVS 170

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I

Sbjct: 171 SQFLTALLMALPLTGQAFEIRMVGEELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPAD 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y +P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V

Sbjct: 230 AHYHAPEHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADV 289

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E V V+ P + +++ D++ N +PD AMTLA+VAL +R++ SWRVK

Sbjct: 290 WGENFVEVSRP-----KERAVQSFDDLDAHIPDAAMTLAIVALATGQTCTLRNIGSWRVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA V E + ITPPE L A IDTYDDHRMAM FSL + V

Sbjct: 345 ETDRIAAMANELRKLGAQVVEEAEAIHITPPETLTPDAVIDTYDDHRMAMCFSLVSLGV 404

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444

PV I DP CT KTFP YFDV S+ +
Sbjct: 405 PVVINDPKCTHKTFPTYFDVDFSSLTE 430

>ref|ZP_06393938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria mucosa ATCC 25996]
gb|EFC88796.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria mucosa ATCC 25996]
Length = 444

Score = 366 bits (940), Expect = 3e-99, Method: Compositional matrix adjust.
Identities = 209/428 (48%), Positives = 267/428 (62%), Gaps = 16/428 (3%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
TV LPGSKS+SNR LLLAALS+ T + +LL S+D ML AL LG+ +E A R
Sbjct: 27 ATVALPGSKSISNRTLALLAALSDNTCEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEGRL 85

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GV RM ERPIGD
Sbjct: 86 KVHGTGRFPNRTA----NLFLGNAGTAFRPLTAALAVLGGD--YHLHGVARMHMERPIGD 139

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
LV L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 140 LVDALRIAGTDVEYLGNEHYPLHIGERQDRGERVPIKGNVSSQFLTALLMALPLTGQA 199

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
EI ++ +LIS PY+++TL+LM +FGV+ + D + F I +Y +P++ +VEGDASS
Sbjct: 200 FEIRMGELISKPYIDITLKLMAQFGVQVANED-YRVFKIPADARYHAPEHLHVEGDASS 258

Query: 257 ASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
ASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 259 ASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVVGWGENFVEVSRP----- 312

Query: 317 RKH-LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
++H ++A D++ N +PD AMTLA+VAL + + ++ SWRVKET+R+ A+ EL KLG
Sbjct: 313 KEHTVQAFDLNANHIPDAAMTLAIVALASGQTCTLHNIGSWRVKETDRIAAMANELRKLK 372

Query: 376 ASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
A V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KTFP
Sbjct: 373 AKVVEEAEAIHTPPELTLPDAVIDTYDDHRMAMCFSLVSLGVPVVINDPKCTHKTFPT 432

Query: 435 YFDVLSTF 442
YF+V S+
Sbjct: 433 YFEVFSSL 440

>gb|EGC67044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis M01-240013]
Length = 433

Score = 366 bits (939), Expect = 4e-99, Method: Compositional matrix adjust.
Identities = 213/446 (47%), Positives = 273/446 (61%), Gaps = 25/446 (5%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG
Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRTLALLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L
Sbjct: 63 VQIEY-LAEDRLKVHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSIS 179
GVPRM ERPIGDLV L+ G DV+ PP+ + NG +P + G++S
Sbjct: 116 GVPRMHMERPIGDLVDALRIAGTDVEYLGNEHYPLHIGERQDNGEHVIP-----IKGNVS 170

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I
Sbjct: 171 SQFLTALLMALPLTGQAFEIRMGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPAD 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+Y +P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V

Sbjct: 230 ARYHAP EHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADV 289

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E V V+ P + ++A D++ N +PD AMTLA+VAL +R++ SWRVK

Sbjct: 290 WGENFVEVSRP-----KERAVQAFDL DANHIPDAAMTLAIVALATGQTCTLRNIGSWRVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A-IDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA V E + ITPP+ L A IDTYDDHRMAM FSL + V

Sbjct: 345 ETDRIAAMANELRKLGAQVVEAEAEIHITPPKTLTPDAVIDTYDDHRMAMCFSLVSLLG 404

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I DP CT KTFP YFDV S+ +

Sbjct: 405 PVVINDPKCTHKTFPTYFDVFSSLTE 430

>gb|EGC51388.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis N1568]
Length = 433

Score = 366 bits (939), Expect = 5e-99, Method: Compositional matrix adjust.
Identities = 211/441 (47%), Positives = 270/441 (61%), Gaps = 15/441 (3%)

Query: 6 EIVLQPIKEIS-GTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG

Sbjct: 3 ESVRLPVARLPSTVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L

Sbjct: 63 VEIEY-LAEDRLKVHGTGGRFPNRTA---DLFLGNAGTAFRPLTAAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L+ GADV+ PP+ + + + G++SSQ+L+

Sbjct: 116 GVPRMHERPIGDLVDALRIAGADVYLGEHYPLHIGKRQDNGERVIPIKGNVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHESDSWDRFYIKGGQKYKS 244
ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I +Y +

Sbjct: 176 ALLMALPLTGQAFEIRMVGELISKPYIDITLKLMAQFGVQVI-NEG YRVFKIPADARYHA 234

Query: 245 PKNAYVEGDASSASYFLAAGIAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V W E

Sbjct: 235 PEHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENF 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V+ P + ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+

Sbjct: 295 VEVSRP-----KERAVQAFDL DANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT A-IDTYDDHRMAMAFSLAACAEVPTIR 423
A+ EL KLGA V E + ITPPE A IDTYDDHRMAM FSL + VPV I

Sbjct: 350 AAMANELRKLGAQVVEAEAEIHITPPETPTPDAVIDTYDDHRMAMCFSLVSLLGVPVVIN 409

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
DP CT KTFP YFDV S+ +

Sbjct: 410 DPKCTHKTFPTYFDVFSSLTE 430

>ref|ZP_04727277.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae MS11]
ref|ZP_06133022.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae MS11]
gb|EEZ47662.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae MS11]
Length = 433

Score = 365 bits (937), Expect = 8e-99, Method: Compositional matrix adjust.
Identities = 209/428 (48%), Positives = 265/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R

Sbjct: 16 TVALPGSKSISNRTLLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137

Sbjct: 75 V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
VHGTGGRFPNRS-----DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ V + + + G++SSQ+L+ALLMA PL

Sbjct: 129 VDALARIAGADVEYLGNEHYPLHVVELQNGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A

Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR

Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS---RPKGR 303

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA

Sbjct: 304 A-VQAFDLANDHIPDAAMTLAIVALATRTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF

Sbjct: 363 VVEEAIAIHITPETPTDAVIDTYDDHRMAMCFSLISLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +

Sbjct: 423 EVFSSLTE 430

>ref|YP_975365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis FAM18]
sp|AlKUN6.1|AROAN_EIIMF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAM10584.1| 5-enolpyruvylshikimate-3-phosphate synthase [Neisseria
meningitidis FAM18]
gb|EGC55081.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis M6190]
gb|EGC60997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis ES14902]
gb|ADY94021.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis G2136]
gb|ADY97325.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis M01-240149]
Length = 433

Score = 365 bits (937), Expect = 8e-99, Method: Compositional matrix adjust.
Identities = 209/441 (47%), Positives = 270/441 (61%), Gaps = 15/441 (3%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG

Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRILLALLSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L

Sbjct: 63 VQIEY-LAEDRLKVHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDL L+ GADV+ PP+ + + + G++SSQ+L+

Sbjct: 116 GVPRMHERPIGDLADALRIAGADVEYLGKEHYPLHIGKRQDNGERVPIKGNVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ + + + F I Y +

Sbjct: 176 ALLMALPLTGQAFEIRMGELISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V W E

Sbjct: 235 PEHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENF 294

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V+ P + + + + D++ N +PD AMTLA+VAL +R++ SWRVKET+R+

Sbjct: 295 VEVSRP-----KRAVQSFDLANDHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIR 423
A+ EL KLGA V E + ITPP+ L A IDTYDDHRMAM FSL + VPV I
Sbjct: 350 AAMANELRKLGAKVVEEAEAIHITPPKTLTPDAVIDTYDDHRMAMCFSLVSLLGVPVVIN 409

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
DP CT KTFP YFDV S+ +
Sbjct: 410 DPKCTHKTFPTYFDVFSSLTE 430

>emb|CBA05487.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis alpha153]
Length = 433

Score = 365 bits (936), Expect = 1e-98, Method: Compositional matrix adjust.
Identities = 210/441 (47%), Positives = 269/441 (60%), Gaps = 15/441 (3%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG
Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L
Sbjct: 63 VEIEY-LAEDRLKVHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDL L+ GADV+ PP+ + + G++SSQ+L+
Sbjct: 116 GVPRMHERPIGLDALADRIAGADVEYLGEHYPLHIGKRQDNGERVIPIKGNVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +
Sbjct: 176 ALLMALPLTGQAFEIRMVGEISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V W E
Sbjct: 235 PEHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENF 294

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
V V+ P + +++ D++ N +PD AMTLA+VAL +R++ SWRVKET+R+
Sbjct: 295 VEVSRP-----KERAVQSFDLDANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIR 423
A+ EL KLGA V E + ITPPE L A IDTYDDHRMAM FSL + VPV I
Sbjct: 350 AAMANELRKLGAKVVEEAEAIHITPPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVVIN 409

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
DP CT KTFP YFDV S+ +
Sbjct: 410 DPKCTHKTFPTYFDVFSSLTE 430

>emb|CBX21677.1| unnamed protein product [Neisseria lactamica Y92-1009]
Length = 432

Score = 364 bits (935), Expect = 1e-98, Method: Compositional matrix adjust.
Identities = 209/433 (48%), Positives = 267/433 (61%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVGIEY-LAEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTA + GGN Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA----DLFLGNAGTAFRPLTAMLAVALGGN--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
V L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPLHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV+ ++++ F I Y +P++ +VEG
Sbjct: 184 TGQAFEIRMVGEISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHAPHLHVEG 242

Query: 253 DASSASYFLAGAAITGGTGTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS ASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 243 DASGASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVSRPKE 302

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL
Sbjct: 303 -----RAVRAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 431
KLGA V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KT
Sbjct: 358 KLGAKVVEEAIAIRITPPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKT 417

Query: 432 FPDYFDVLSTFVK 444
FP YF++ S+ +
Sbjct: 418 FPTYFEIFSSLTE 430

>emb|CBA07392.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis alpha275]
gb|ADZ01268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis M04-240196]
Length = 433

Score = 364 bits (934), Expect = 2e-98, Method: Compositional matrix adjust.
Identities = 207/428 (48%), Positives = 265/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ T + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNTCEIHSLLKSDDTDRMLEALDKLGEIEY-LAEDRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGKEHYPPHLHIGKRQDNGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ +++++ F I Y +P++ +VEGDASSA
Sbjct: 189 EIRMVGBELISKPYIDITLKLMAQFGVQVA-NENYRVFKIPADAHYHAPEHLHVEGDASSA 247

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 248 SYFLAAGLIAATPVCVIGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-----KE 302

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ +++ D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 303 RAVQSFDLDANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGAK 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPPETPTPDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKTFFPTYF 422

Query: 437 DVLSTFVK 444
DV S+ +
Sbjct: 423 DVFSSLTE 430

>ref|YP_002943532.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine monophosphate kinase [Variovorax paradoxus S110]
gb|ACS18266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Variovorax paradoxus S110]
Length = 670

Score = 363 bits (933), Expect = 2e-98, Method: Compositional matrix adjust.
Identities = 215/442 (48%), Positives = 290/442 (65%), Gaps = 26/442 (5%)

Query: 16 SGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SGTV+LPGSKS+SNR+LLLAAL+ GTT V +LL+S+D ML ALR LG ++A + R

Sbjct: 16 SGTVRLPGSKSISNRVLLLAALASGTTTVHDLSDSDTRVMLDALRALGCGIDAAGSTLR 75

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ G GG+ ++ + LFLGNAG AMR LTAA++ GG + L GVPRM ERPIG

Sbjct: 76 --ITGIGGQ--LKPGGPMLPLFLGNAGTAMRPLTAALSLLGGE--FELSGVPRMHERPIG 129

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGI--GGLP-GGKVKLSGSISSQYLSALLMAAPL 192
DLV L QLG +D PP+R+ + G L +++ G +SSQ+L+ALL+A PL

Sbjct: 130 DLVDALTQLGCRIDYLGNGPYPLRIRPVDHGALVLDAPIRVRGDVSSQFLTALLLALPL 189

Query: 193 AL-GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A D+ IE++ +LIS PY+E+TL L+ RFG+ A + W+RF I G +Y SP + +VE

Sbjct: 190 AARKDIVIEVVGELISKPYIEITLNLARFGI-AVQREGWERFTIPAGSRYSSPGDIHVE 248

Query: 252 GDASSASYFLAGAAITGG----TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
DASSASYF+A AI G ++ +EG G S+QGD++F E MGA+V +

Sbjct: 249 ADASSASYFIALGAIATGASGQDSIRIEGVGADSIQDIRFIEAARQMGAVDSGPNWLD 308

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPPVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V G LKAID++ N +PD AMTLAV+AL+ADGP+ +R++ASWRVKET+R+ A

Sbjct: 309 VR-----RGAWPLKAILDANHIPDAAMTLAVMALYADGPSTLRNIASWRVKETDRIDA 362

Query: 367 IRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAAC--AEVPVTI 422
+ EL KLGA+V+ GPD+ + P E+ +I TYDDHR+AM FSLAA A +PV I

Sbjct: 363 MANELRKLKATVDSGPDFIRVHPLERPGWQAASIRTYDDHRVAMCFSLAAFPAGLPVRI 422

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+P C KTFPDYF+ L + +

Sbjct: 423 LEPHCVAKTFPDYFETLFSVAQ 444

>ref|ZP_04718785.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
35/02]

ref|ZP_04721137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
DGI18]

ref|ZP_04723200.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
FA6140]

ref|ZP_04734749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID24-1]

ref|ZP_04736345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID332]

ref|ZP_06128871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
35/02]

ref|ZP_06148876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID332]

gb|EEZ43511.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
35/02]

gb|EEZ54698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID332]

gb|ADV07691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
TDCD-NG08107]

Length = 433

Score = 363 bits (932), Expect = 3e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSVDHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R

Sbjct: 16 TVALPGSKSISNRTLLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL

Sbjct: 75 VHGTGGRFPNRS----DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVP RMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL

Sbjct: 129 VDALRIAGADV EYLGNEHYPLHIGKRQDCGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A

Sbjct: 189 EIRMVGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAP EHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS----RPKGR 303

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDLNANHIPDAAMTLAIVALATRQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAEAIHITPPETPTDAVIDTYDDHRMAMCFSLISLLGVPVVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|ZP_06643322.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
F62]
gb|EFF39681.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
F62]
Length = 433

Score = 363 bits (932), Expect = 3e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- ---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPLHIGKRQDCGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMVGBELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS----RPKGR 303

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDLNANHIPDAAMTLAIVALATRQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAEAIHITPPETPTDAVIDTYDDHRMAMCFSLISLLGVPVVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|ZP_04738523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-92-679]
ref|ZP_05106820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
1291]
ref|ZP_06151087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-92-679]
gb|EEH62034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
1291]
gb|EEZ56909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-92-679]
Length = 433

Score = 363 bits (931), Expect = 3e-98, Method: Compositional matrix adjust.
Identities = 209/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

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Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
          TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
          V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- ---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
          V L+ GADV+ PP+ V + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPPPLHVGEREDCGERVIPKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
          EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
          SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS---RPKGR 303

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
          ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDL DANHIPDAAMTLAIVALATRQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTTIRDPGCTRKTFPDYF 436
          V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPPETPTDAVIDTYDDHRMAMCFSLISLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
          +V S+ +
Sbjct: 423 EVFSSLTE 430
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>ref|ZP_04725392.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
FA19]
ref|ZP_06131133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
FA19]
gb|EEZ45773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
FA19]
Length = 433
```

Score = 363 bits (931), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

```
Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
          TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
          V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- ---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
          V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPPPLHIGKREDCGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
          EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
          SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS---RPKGR 303

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
          ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDL DANHIPDAAMTLAIVALATRQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362
```

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAEAIHITPPETPTPDAVIDTYDDHRMAMCFSLISLLGVPVVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|ZP_04729600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID18]
ref|ZP_04731895.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID1]
ref|ZP_05794466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
DGI2]
ref|ZP_06135380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID18]
ref|ZP_06137701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID1]
ref|ZP_06569673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
DGI2]
gb|EEZ50020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID18]
gb|EEZ52341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
PID1]
gb|EFE04409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
DGI2]
Length = 433

Score = 363 bits (931), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTL LLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVQIE-HLAEGRLK 74

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGVPVRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- ---DLFLGNAGTAFRPLTAALAVLGDD--YHLHGVPRMHMERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPPHIGKREDGGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMVGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDKVFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS---RPKGR 303

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDL DANHIPDAAMTLAIVALATRTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAEAIHITPPETPTPDAVIDTYDDHRMAMCFSLISLLGVPVVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|ZP_08133171.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kingella
denitrificans ATCC 33394]
gb|EGC17572.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kingella
denitrificans ATCC 33394]
Length = 430

Score = 363 bits (931), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 207/441 (46%), Positives = 272/441 (61%), Gaps = 22/441 (4%)

Query: 5 EEIVLQP-IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+ I LQP + TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL L
Sbjct: 3 DAIRLQPRTLKPHNTVALPGSKSISNRTL LLLAALSDNECDIHSLLKSDDTDRMLEALTQL 62

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ +E + A VVG G+FP E LFLGNAG A R LTAA+ GG Y L
Sbjct: 63 GVPLE--QRAGSLHVVGQNGRFP----HTEADLFLGNAGTAFRPLTAALAVLGGE--YRL 114

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
GV RM ERPIGDLV L+ +GA +D PP+ ++ P + + G++SSQ+L
Sbjct: 115 HGVARMHMERPIGDLVDALRLVGAHIDYLGNEGYPLHIHARHNTPVLTIPKGNVSSQFL 174

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYK 243
+ALLMA PL +I++ +LIS PY+++TL LM++FGV E + + F++ +Y
Sbjct: 175 TALLMALPLTGDWQIQVEGELISKPYIDITLNLKQFGVNVE-NRQYRTFHLPAASRYH 233

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+P +VEGDASSASYFLA ++G V V G G ++QGDV FA LE +GA V W +
Sbjct: 234 APAQLHVEGDASSASYFLAAGLLSGKPVRVTGLGKHAIQGDVAFARELEKLGAIVLWGDD 293

Query: 304 SVTVTGPPRE---PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V+ + PF D++ N +PD AMTLAVVAL +IR++ SWRVKE
Sbjct: 294 FIEVSRAKNQAVLPF-----DLDAHIPDAAMTLAVVALATGQTCSIRNIGSWRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVP 419
T+R+ A+ EL K+GA+V E + ITPPE+L A IDTYDDHRMAM FSL + +VP
Sbjct: 346 TDRIAAMAAELRKVGATVVEEAEAIHITPPEQLIADAHIDTYDDHRMAMCFLVSLLDVP 405

Query: 420 VTIRDPGCTRKTFPDYFDVLS 440
V I DP CT KTFP YFDV +
Sbjct: 406 VIINDPQCTHKTFPTYFDVFA 426

>ref|ZP_04740753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-93-1035]
ref|ZP_06153343.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-93-1035]
gb|EEZ59165.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
SK-93-1035]
Length = 433

Score = 363 bits (931), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 264/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTL LLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGQIE-HLAEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- -DLFLGNAGTAFRPLTAALAVLGDD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPLHIGKREDCGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMVGEISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS----RPKGR 303

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDLDAHIPDAAMTLAIVALATRTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT-A-IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPPETPTDAVIDTYDDHRMAMCFSLISLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|YP_004154098.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Variovorax paradoxus
EPS]
gb|ADU35987.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Variovorax paradoxus
EPS]
Length = 688

Score = 362 bits (930), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 212/448 (47%), Positives = 286/448 (63%), Gaps = 34/448 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVNDLNLSEDVHYMLGALRTLGLSVE 68
L P+ +GTV+LPGSKS+SNR+LLLAAL+ GTT + +LL+S+D ML ALR LG ++
Sbjct: 27 LPPLVGAAGTVRLPGSKSISNRVLLLAALASGTTTTHDLLDSDDTRVMLDALRALGCGIQ 86

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + + G GG+ A + LFLGNAG AMR LTAA++ GG+ + L GVPR
Sbjct: 87 PSGSTLQ--ITGLGGQLKSSGAL--LPLFLGNAGTAMRPLTAALSLGGD--FELSGVPR 140

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG---LPGGKVKLSGSISSQYLSA 185
M ERPIGDLV L QLG ++D PP+R++ + +++ G +SSQ+L+A
Sbjct: 141 MHERPIGDLVDALTQLGCNIDYLGNGPYPLRIHPVDHDDLALDAPIRVRGDVSSQFLTA 200

Query: 186 LLMAAPLAL-GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LL+A P+A D+ IE++ +LIS PY+E+TL L+ RFG+ D W+RF I G Y S
Sbjct: 201 LLLALPIAARNDIVIEVVGELISKPYIEITLNLARFGITVRR-DGWERFTIPAGSSYSS 259

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKV- 298
P + +VE DASSASYF+A AI G + +EG G S+QGD++F + MGA+V
Sbjct: 260 PGDIHVEADASSASYFIALGAIATGVSGKTGIRIEGVGADSIQGDIFRIDAARQMGAEVD 319

Query: 299 ---TWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVAS 355
W E G LKAID++ N +PD AMTLAV+AL+ADGP+ +R++AS
Sbjct: 320 SGNWLEVR-----GAWPLKAIDLDAHNPDAAMTLAVMALYADGPSTLRNIAS 369

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLA 413
WRVKET+R+ A+ EL KLGA+VE GPD+ + P + +I TYDDHR+AM FSLA
Sbjct: 370 WRVKETDRIDAMANELQKLGAATVEAGPDFIRVHPLAQAGWQAASIRTYDDHRVAMCFSLA 429

Query: 414 AC--AEVPVTIRDPGCTRKTFPDYFDVL 439
A A VPV I +P C KTFPDYF+ L
Sbjct: 430 AFNPAGVPVRILEPHCVAKTFPDYFETL 457

>ref|YP_002001528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
NCCP11945]
sp|B4RL93.1|AROAN_EIG2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF29582.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
NCCP11945]
Length = 433

Score = 362 bits (929), Expect = 6e-98, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 263/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPKSGKSLNRILLALLAALSEGTTVVNDLNLSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLAALSNDVCEIHSLLKSDDTDRMLEALDKLGQIE-HLAEGRLK 74

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS-----DLFLGNAGTAFRPLTAALAVLGGG--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPLHIGKRQDCGERVPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMVGEELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS----RPKGR 303

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA
Sbjct: 304 A-VQAFDLNANHIPDAAMTLAIVALATGTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAEAIHITPETPTDAVIDTYDDHRMAMCFSLISLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>gb|ADY99871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis M01-240355]
Length = 433

Score = 361 bits (927), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 212/446 (47%), Positives = 271/446 (60%), Gaps = 25/446 (5%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG
Sbjct: 3 ESVRLPVARLKLSTVALPGSKSISNRITLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GGN Y L
Sbjct: 63 VEIEY-LAEDRLKVHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGN--YRLH 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRV----NGIGGLPGGKVKLSGSI 179
GV RM ERPIGDL L+ GA+V+ PP+ + NG +P + G++S
Sbjct: 116 GVARMHERPIGDLTDALRIAGANVEYLGKEHYPLHIGERQDNGERVIP-----IKGNVS 170

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I
Sbjct: 171 SQFLTALLMALPLTGQAFEIRMVGEELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPAD 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVT 299
+Y +P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V
Sbjct: 230 ARYHAPHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADV 289

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E V V+ P + ++A D++ N +PD AMTLA+VAL +R++ SWRVK
Sbjct: 290 WGENFVEVSRPK-----ERAVQAFDLNANHIPDAAMTLAIVALATGTCTLRNIGSWRVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA V E + ITPPE A IDTYDDHRMAM FSL + V
Sbjct: 345 ETDRIAAMANELRKLGAQVAEEAEAIHITPETPTDAVIDTYDDHRMAMCFSLVSLGV 404

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I DP CT KTFP YFDV S+ +
Sbjct: 405 PVVINDPKCTHKTFPTYFDVSSLTE 430

>ref|YP_208010.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria gonorrhoeae
FA 1090]
sp|Q5F889.1|AROAN_EIG1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|AAW89598.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Neisseria gonorrhoeae FA 1090]
Length = 433

Score = 361 bits (926), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 208/428 (48%), Positives = 263/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNVCEIHSLLKSDDTDRMLEALDKLGVIIE-HLAEGRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRS- ---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 VDALRIAGADVEYLGNEHYPLHIGKRQDCGERVIPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVA-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P GR
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVS----RPKGR 303

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++A D++ N +PD AMTLA+VAL +R++ SWRVKET R+ A+ EL KLGA
Sbjct: 304 A-VQAFDL DANHIPDAAMTLAIVALATRQTCTLRNIGSWRVKETGRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF
Sbjct: 363 VVEEAIAIHITPETPTDAVIDTYDDHRMAMCFSLISLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFK 444
+V S+ +
Sbjct: 423 EVFSSLTE 430

>ref|ZP_07369427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis ATCC 13091]
gb|EFM04862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis ATCC 13091]
Length = 433

Score = 361 bits (926), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 206/428 (48%), Positives = 262/428 (61%), Gaps = 14/428 (3%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA- ---DLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ GADV+ PP+ + + + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGKEHYPLHIGKRQDNGERVIPIKGNVSSQFLTALLMALPLTGQAF 188

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEGDAS A
Sbjct: 189 EIRMGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPEHLHVEGDASGA 247

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPREPFGFR 317
SYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 248 SYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-----KE 302

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA

Sbjct: 303 RAVQAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGA 362

Query: 378 VEEGPDYCIITPPEKLNVT-ADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V E + ITPPE A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF

Sbjct: 363 VAEAEAEIHITPPETPTDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKTFPTYF 422

Query: 437 DVLSTFVK 444

DV S+ +

Sbjct: 423 DVFSSLTE 430

>gb|EGC53282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis OX99.30304]
Length = 433

Score = 361 bits (926), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 210/433 (48%), Positives = 266/433 (61%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77

TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG+ +E A R

Sbjct: 16 TVALPGSKSISNRTLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137

V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GV RM ERPIGDL

Sbjct: 75 VHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGD--YRLHGVARMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192

L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL

Sbjct: 129 ADALRIAGADVEYLGKEHYPPHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252

EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEG

Sbjct: 184 TGQAFEIRMGVGLISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPEHLHVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLMMGAKVTWTETSVTVTGPPR 312

DASSASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P

Sbjct: 243 DASSASYFLAAGLIAATPVCVIGIGANSIQGDVAFARELEKIGADVWGENFVEVSRP-- 300

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372

+ ++A D++ N +PD AMTLAVVAL +R++ SWRVKET+R+ A+ EL

Sbjct: 301 ---KERAVQAFDLNANHIPDAAMTLAVVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT-ADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 431

KLGA V E + ITPPE A IDTYDDHRMAM FSL + +VPV I DP CT KT

Sbjct: 358 KLGAKVAEAEAEIHITPPETPTDAVIDTYDDHRMAMCFSLVSLLDVPVINDPKCTHK 417

Query: 432 FPDYFDVLSTFVK 444

FP YFDV S+ +

Sbjct: 418 FPTYFDVSSLTE 430

>ref|YP_003249697.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fibrobacter
succinogenes subsp. succinogenes S85]
gb|ACX75215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fibrobacter
succinogenes subsp. succinogenes S85]
gb|ADL26487.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fibrobacter
succinogenes subsp. succinogenes S85]
Length = 442

Score = 361 bits (926), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 207/440 (47%), Positives = 276/440 (62%), Gaps = 28/440 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68

L +G++++PGSKS++NR+LL++A++ GTT + NLL S+D YM AL+ LG+ V+

Sbjct: 13 LDAYHSFNFSIRVPGSKSITNRVLLISAANGTTRLHNLLRSDDTRYMGELKRLGVKVD 72

Query: 69 ADKAAKRAVVVGCG-----GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123

AVV G G G FPVE L+LGNAG AMRSLTAA++ G ++L

Sbjct: 73 FSDDYTDAVVEGHGKPFDAAGNFPVE-----LYLGNAGTAMRSLTAAALSLGWGK--FIL 123

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183

G RM ERPI DLV L LGAD+ PPVR+ GL GG V + G+ISSQYL
Sbjct: 124 RGEERMGERPILDLVDALSTLGADIKYLESEGYPPVRIKA-DGLKGGDVSVRGNISSQYL 182

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALL+ AP + I + KLIS PY+E+TL +M+ FGV H+D D FY+ G Y+

Sbjct: 183 TALLICAPYCKTPLHIHVEGKLISAPYIELTLDVMKCFGVNVVRHNDLTD-FYVPQGV-YQ 240

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-- 301
SP + YVEGDASSA+Y LA AAI+GG V V G S+QGD+ F +VL+ MG VT +

Sbjct: 241 SPGDYVVEGDASSATYPLAAAISGGEVVKVLGISEDSIQGDIAFIDVLKRMGVDVTPSVE 300

Query: 302 ---ETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
E + GP + L+++ D + ++PD AMTLAV+ALFAD PT IR + SWR

Sbjct: 301 PSGEKCIICKGPKD-----RRLRSLGDFSAVEIPDAAMTLAVLALFADAPTIRIGISWR 355

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
VKET+R+ A+ EL K+GA+V D I PP++L I+TY+DHRMAM FSL +

Sbjct: 356 VKETDRIAAMVAELRKVGATVSSDMDSITIEPPKELRPATITETYNDRMAMCFSLVSLGG 415

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
VP+ I DP C KT+P +F+

Sbjct: 416 VPIKILDPACVNKTYPHFFE 435

>ref|YP_003643565.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiomonas intermedia
K12]
gb|ADG31235.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiomonas intermedia
K12]
Length = 658

Score = 360 bits (924), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 212/445 (47%), Positives = 273/445 (61%), Gaps = 21/445 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ G VKLPGSKS+SNR+LLLAAL+EG T + LL+S+D ML AL+ LG++V

Sbjct: 8 LPPLIGAGGRVVKLPGSKSISNRVLLLAALAEQQTETGLLDSDDTRVMLAALQALGIAVR 67

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + A V G G+FP A LF+GNAG A+R LTAA+ GG+ Y L GVPR

Sbjct: 68 --REGETAHVQGGAGRFPAAQAD----LFMGNAGTAIRPLTAALALLGGD--YALHGVPR 119

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L+Q G D+ PP+ + G V + G +SSQ+L+ALL+

Sbjct: 120 MHERPIGDLVDALRQFGCDIRYTGQEGYPLHIGASHFRLNGDVAVRGDVSSQFLTALLL 179

Query: 189 AAPLALGDVEIEII--DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
A PL D +I I +LIS PY+E+TL L+ RFGV+ + + W+RF I G + +SP

Sbjct: 180 ALPLKASDHDAIAVQGELISKPYIEITLNLRRFGVQVQRT-GWERFVIPAGSRLRSPG 238

Query: 247 NAYVEGDASSASYFLAGAAI-----TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
VEGDASSASYFLA + G V VEG G S+QGDV FA VLE +GA+V W

Sbjct: 239 RIAVEGDASSASYFLAAGVLGQWHGKGAPVRVEGVGRDSIQGDVAFARVLEDLGAQVRWG 298

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + G G L+ D++ +PD AMTLA+ ALFAD PT + + SWRVKET

Sbjct: 299 DDFIETDG---LQAGLTALRGDIDCLAIPDAAMTLAMTALFADAPTTLTAIGSWRVKET 355

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAEVP 419
+R+ A+ TELTKLGA VE GPD+ + P + AI TYDDHRMAM FSLA+

Sbjct: 356 DRIHAMATELTKLGAQVESGPDWLRVHPLSAAQWRSAAIATYDDHRMAMCFSLASFGHAD 415

Query: 420 VTIRDPGCTRKTFPDYFDVLSFVK 444
+ I DPGC KT+P YFD + +

Sbjct: 416 IRILDPGCVAKTYPGYFDDFARIAR 440

>emb|CBY91058.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase; EPSP
synthase; EPSPS) [Neisseria meningitidis WUE 2594]
Length = 433

Score = 360 bits (924), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 210/433 (48%), Positives = 266/433 (61%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGEIEY-LAEDRLK 74

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GV RM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YRLHGVARMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGEHYPPHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEG
Sbjct: 184 TGQAFEIRMGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPHLHVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DASSASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 243 DASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFACELEKIGADVWGENFVEVSRP-- 300

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ ++A D++ N +PD AMTLAVVAL +R++ SWRVKET+R+ A+ EL
Sbjct: 301 ---KERAVQAFDLNANHIPDAAMTLAVVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
KLGA V E + ITPPE A IDTYDDHRMAM FSL + +VPV I DP CT KT
Sbjct: 358 KLGAKVAEEAEAIHITPPETPTDAVIDTYDDHRMAMCFSLVSLLDVPPVINDPKCTHKT 417

Query: 432 FPDYFDVLSTFK 444
FP YFDV S+ +
Sbjct: 418 FPTYFDVFSSLTE 430

>gb|EGC59129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis M0579]
Length = 433

Score = 360 bits (924), Expect = 3e-97, Method: Compositional matrix adjust.
Identities = 213/446 (47%), Positives = 271/446 (60%), Gaps = 25/446 (5%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG
Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L
Sbjct: 63 VQIEY-LAEDRLKVHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVLGGD--YRLH 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSISS 179
GV RM ERPIGDL L+ GADV+ PP+ + NG +P + G++S
Sbjct: 116 GVARMHERPIGDLADALRIAGADVEYLGEHYPPHIGERQDNGERVIP-----IKGNVS 170

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I
Sbjct: 171 SQFLTALLMALPLTGQAFEIRMGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPAD 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y +P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +GA V
Sbjct: 230 AHYHAPHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFACELEKIGADV 289

Query: 300 WTETSVTVTGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
W E V V+ P + ++A D++ N +PD AMTLAVVAL +R++ SWRVK
Sbjct: 290 WGENFVEVSRP----KERAVQAFDLNANHIPDAAMTLAVVALATGQTCTLRNIGSWRVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL KLGA V E + ITPPE A IDTYDDHRMAM FSL + +V
Sbjct: 345 ETDRIAAMANELRKLGAKEAEAEAIHITPPETPTDAVIDTYDDHRMAMCFSLVSLLDV 404

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I DP CT KTFP YFDV S+ +
Sbjct: 405 PVVINDPKCTHKTFPTYFDVFSSLTE 430

>ref|YP_002342947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis Z2491]
sp|Q9JTT3.1|AROA_NEIMA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAM08779.1| 5-enolpyruvylshikimate-3-phosphate synthase [Neisseria meningitidis Z2491]
Length = 433

Score = 360 bits (924), Expect = 3e-97, Method: Compositional matrix adjust.
Identities = 209/433 (48%), Positives = 266/433 (61%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GV RM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGDD--YRLHGVARMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGKEHYPLHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEG
Sbjct: 184 TGQAFEIRMGVGLISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPEHLHVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVGCGTSTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPR 312
DASSASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P
Sbjct: 243 DASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFACELEKIGADVWGENFVEVSRP-- 300

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL
Sbjct: 301 ---KRAVRAFDLDANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAIEVPVTIRDPGCTRK 431
KLGA V E + ITPPE A IDTYDDHRMAM FSL + +VPV I DP CT KT
Sbjct: 358 KLGAKVAEEAEAIHITPPETPTDAVIDTYDDHRMAMCFSLVSLDVPVINDPKCTHK 417

Query: 432 FPDYFDVLSTFVK 444
FP YFDV S+ +
Sbjct: 418 FPTYFDVFSSLTE 430

>gb|EGC65034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis 961-5945]
Length = 433

Score = 360 bits (923), Expect = 3e-97, Method: Compositional matrix adjust.
Identities = 210/433 (48%), Positives = 266/433 (61%), Gaps = 24/433 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS+SNR LLLAALS+ +LL S+D ML AL LG+ +E A R
Sbjct: 16 TVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLK 74

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L GV RM ERPIGDL
Sbjct: 75 VHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGDD--YRLHGVARMHERPIGDL 128

Query: 138 VVGLKQLGADVDCFLGTDCPPVRV-----NGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
L+ GADV+ PP+ + NG +P + G++SSQ+L+ALLMA PL
Sbjct: 129 ADALRIAGADVEYLGKEHYPLHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPL 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I Y +P++ +VEG

Sbjct: 184 TGQAFEIRMGVGLISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPEHLHVEG 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DASSASYFLA I V V G G S+QGDV FA LE +GA V W E V V+ P

Sbjct: 243 DASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFACELEKIGADVWGENFVEVSRPKE 302

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL

Sbjct: 303 -----RAVQAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELR 357

Query: 373 KLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
KLGA V E + ITPPE L A IDTYDDHRMAM FSL + VPV I DP CT KT

Sbjct: 358 KLGAKVVEEAIAIHITPPETLTPDAVIDTYDDHRMAMCFSLVSLLGVPVINDPKCTHKT 417

Query: 432 FPDYFDVLSTFVK 444
FP YFDV S+ +

Sbjct: 418 FPTYFDVFSSTE 430

>ref|YP_004124452.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Blochmannia vafer str. BVAf]

gb|ADV33778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Blochmannia vafer str. BVAf]
Length = 441

Score = 359 bits (922), Expect = 4e-97, Method: Compositional matrix adjust.
Identities = 198/437 (45%), Positives = 274/437 (62%), Gaps = 16/437 (3%)

Query: 7 IVLQPIKEISGTVKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I L PI +++GTV LPGSKS+SNR LLLAA S GTT + NLL+S+DV YML AL LG+

Sbjct: 5 IKLDPIYKVNVTSLPGSKSISNRALLAAQSVGTTTLINLLDSDVQYMLNLYKLGIQ 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKE---EVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ K + G GG ++ ++ LFLGNAG +R L AA++ +L

Sbjct: 65 YKLSSDRKICEIDGIGGPLQFQNKSSLHPQLTLFLGNAGTVVRPLIAALSIVTSQNI-ML 123

Query: 124 DGVRPMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RM+ERPI L+ L+Q G+ ++ PV +NG G GG + + G+ISSQ+L

Sbjct: 124 TGDVRMQERPIHHLIHALRQGSQINYLKKEYHVPVCLNG--GYRGGTIIIQGNISSQFL 181

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S++LM PLA + I++ KL+S PY+++TL +M+ FG+ +H D + FY +G + Y

Sbjct: 182 SSILMMIPLAPENTCIKVDGKLVSKPYIDLTLSIMKIFGITIQHQD-YKIFYCEGNRLYV 240

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SPK +EGDASSASYFLA +AI GGTV V G S QGDV F+++L MGA V+W +

Sbjct: 241 SPKEYIIEGDASSASYFLAASAIKGGTVKVLGIDKHSKQGDVYFSDILNRMGAFVSWGDN 300

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
+ T G +ID+++N MPD AMTLA++ALF P +R++ +WRVKE

Sbjct: 301 YIECTR-----GTTLNASIDIDVNMHPDAAMTLAIIALFTIEKKIPMILRNIYNWRVKE 354

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPV 420
++R+ A+ TEL K+GA V EG DY I P+K+ I+TY DHR+AM FSL A + V V

Sbjct: 355 SDRLYAMATELRKVGAKVIEGYDYLYIFAPQKIQSAYINTYDHRIAMCFSLIALSGVSV 414

Query: 421 TIRDPGCTRKTFFPDYFD 437
I +P C KTFPD+F+

Sbjct: 415 IIDNPQCICKTFPDFFN 431

>gb|EGC57232.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis M13399]
Length = 433

Score = 359 bits (922), Expect = 5e-97, Method: Compositional matrix adjust.
Identities = 208/441 (47%), Positives = 267/441 (60%), Gaps = 15/441 (3%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
E V P+ + TV LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG

Sbjct: 3 ESVRLPVARLKPSTVALPGSKSISNRTLLLAALSDNACEIHSLLKSDDTDRMLEALDKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E A R V G GG+FP A LFLGNAG A R LTAA+ GG+ Y L
Sbjct: 63 VQIEY-LAEDRLKVHGTGGRFPNRTA---DLFLGNAGTAFRPLTAALAVLGGD--YHLH 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDL L+ GADV+ PP+ + + + G++SSQ+L+
Sbjct: 116 GVPRMHERPIGDLADALRIAGADVEYLGEHYPLHIGKRQDNGERVIPIKGNVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++ + F I +Y +
Sbjct: 176 ALLMALPLTGQAFEIRMVGELISKPYIDITLKLMAQFGVQVI-NEGYRVFKIPADARYHA 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P++ +VEGDAS ASYFLA I V V G G S+QGDV FA LE +GA V W E
Sbjct: 235 PEHLHVGEDASASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENF 294

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V+ P + ++A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+
Sbjct: 295 VEVSRP-----KERAQAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ EL KLGA V E + IT PE A IDTYDDHRMAM FSL + VPV I
Sbjct: 350 AAMANELRKLGAKVAEEAEAIHITSPETPTDAVIDTYDDHRMAMCFSLVSLLGVPVVIN 409

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
DP CT KTFP YFDV S+ +
Sbjct: 410 DPKCTHKTFFPYFDVDFSSLTE 430

>ref|ZP_06686582.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Achromobacter
piechaudii ATCC 43553]
gb|EFF76472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Achromobacter
piechaudii ATCC 43553]
Length = 440

Score = 358 bits (919), Expect = 1e-96, Method: Compositional matrix adjust.
Identities = 222/443 (50%), Positives = 287/443 (64%), Gaps = 19/443 (4%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L +++ G + LPGSKS+SNR+LLL+A++EG+T++ LL+S+D ML ALR LG+ V
Sbjct: 9 LPRVRQAHGVMALPGSKSISNRVLLLSAIAEGSTLITGLLDSDDTVRMLAALRQLGVQV- 67

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+D A R V G +FPV+ A LF+GNAG A+R LTAA+ GG+ Y L GVPR
Sbjct: 68 SDLDAGRVTVEGVR-RFPVQSA---DLFMGNAGTAIRPLTAALALMGD--YRLSGVPR 120

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV-KLSGSISSQYLSALL 187
M ERPIGDL L LGA +D PP+ + G G + V ++ GS+SSQ+L+ALL
Sbjct: 121 MHERPIGDLADALNALGARIDYLGQPGYPPLHI-GQGQIADDAVTRVQGSVSSQFLTALL 179

Query: 188 MAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+AAPL G V IE++ +LIS PY+E+TL LM RFGV+ + W RF I+GG Y+
Sbjct: 180 LAAPLQAGRSGKPVTTIEVVGELISKPYIEITLNLMARFGVQVRR-EGWSRFVIEGGAGYR 238

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP VEGDAS+ASYFLA AI GG + V G G S+QGDV FA+ L MGA VT+
Sbjct: 239 SPGQIAVEGDASTASYFLALGAIGGGPLRVTVGVGANSIQGDVAFADTLAQMGANVTYGPD 298

Query: 304 SVTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V+G R LKA D + N +PD AMT A +AL+ADGP +R++ SWRVKET+R
Sbjct: 299 WIEVSGVHVADGAR--LKAFDTDFNLIPDAAMTAAALALYADGPCRLRNIGSWRVKETDR 356

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPVT 421
+ A++TEL KLGA VE GPD+ + PP + I T+DDHRMAM FSLAA V
Sbjct: 357 IHAMQTELEKLGALVESGPDWLRVIPPAQDAWRDAHIGTWDDHRMAMCFSLAAGPAAVR 416

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVK 444
I DPGC KTFP YFDV ++ V
Sbjct: 417 ILDPGCVSKTFPGYFDVYASLVS 439

>ref|YP_002474989.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus parasuis
SH0165]
gb|ACL32041.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus parasuis
SH0165]
Length = 385

Score = 358 bits (918), Expect = 1e-96, Method: Compositional matrix adjust.
Identities = 193/385 (50%), Positives = 248/385 (64%), Gaps = 17/385 (4%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL+ LG++ + V G GG F ++ + LFLGNAG AMR LTAA+
Sbjct: 1 MLNALKALGVNYQLSDDKTCTVEGVGGAFQWQNG---LSLFLGNAGTAMRPLTAALCLK 57

Query: 116 G-GNATYVLVDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
G A +L G PRM+ERPI LV L Q GA V PP+ + G+ GGK+++
Sbjct: 58 GEQEAIEVILTGEPRMKERPIKHLVDALLQAGASVQYLENEGYPPIAIRN-SGIQGGKIQI 116

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
GSISSQ+L+ALLM+APLA GD+EIEI+ +L+S PY+++TL +M+ FGV H++ + F
Sbjct: 117 DGSISSQFLTALLMSAPLASGDMEIEIVGELVSKPYIDITLAMMKDFGVTVSHNN-YQTF 175

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
++KG Q Y SP+ VEGDASSASYFLA AI G V V G G S+QGD FA+VLE M
Sbjct: 176 FVKGNQHYVSPQKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGDRLFADVLEKM 234

Query: 295 GAKVTWTETSVTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
GAK+TW E + LK ID++MN +PD AMT+A ALFA+G T IR++
Sbjct: 235 GAKITWGEDFIQAE-----QGELKGIDMDMNHIPDAAMTIATTALFAEGETVIRNIY 286

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSL 412
+WRVKET+R+ A+ TEL K+GA VEEG D+ I P +K I TY+DHRMAM FSL
Sbjct: 287 NWRVKETDRLTAMATELRKVGAEVEEGEDFIRIQPLALDKFQHAIEIATYNDHRMAMCFSL 346

Query: 413 AACAEVPTTIRDPGCTRKTFPDYFD 437
A + VTI DP CT KTFP YFD
Sbjct: 347 VALSNTSVTILDPKCTAKTFPTYFD 371

>ref|ZP_06753565.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Simonsiella muelleri
ATCC 29453]
gb|EFG31437.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Simonsiella muelleri
ATCC 29453]
Length = 431

Score = 357 bits (917), Expect = 2e-96, Method: Compositional matrix adjust.
Identities = 203/442 (45%), Positives = 270/442 (61%), Gaps = 22/442 (4%)

Query: 5 EEIVLQPIKEI--SGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRT 62
E + P +++ S TV LPGSKS+SNRILLLAALS+ + +LL S+D ML AL
Sbjct: 2 NEFIFLPPRQLKSSNTVALPGSKSISNRILLLAALSDNVCQIHSLLQSDDTDRMLEALEK 61

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
LG+ ++ + V G G GP + A LFLGNAG A R LTAA+ GGN Y
Sbjct: 62 LGIPLQKSLSGSLKVT-GQNGVFPNQHA---DLFLGNAGTAFRPLTAALAILGNN--YH 114

Query: 123 LDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L GV RM ERPIGDLV L+ +GA+V+ PP++++ K+ + G +SSQ+
Sbjct: 115 LYGVARMHERPIGDLVDALRIVGANVEYLGNEGYPPLQIHDFDTDKIRKIPKGDVSSQF 174

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+ALLMA PL EI + +LIS PY+ +TL LM++F + + + + F + Y
Sbjct: 175 LTALLMALPLTGKAYEIHVQGELISKPYINITLNLMKKFDIHVD-NQAHQIFRLPAKTHY 233

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTE 302
++P+ +VEGDASSASYFLA ++G V V G G ++QGDV F LE +GA VTW +
Sbjct: 234 RAPELIHVEGDASSASYFLAAGLLSGKPVVRTGLGKHAIQGDVAFVHELEKIGATVTWGD 293

Query: 303 TSVTVTGPPE---PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ V+ + PF D++ N +PD AMTLA+VAL P AIR++ SWRVK
Sbjct: 294 DFIEVSRVNSILPF-----DLNANHIPDAAMTLAIVALATGAPCAIRNIGSWRVK 345

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ TEL K+GA V E D ITPP++L N IDTYDDHRMAM FSL + V
Sbjct: 346 ETDRIATAMATELRKVGAIIVVEENDAIYITPPQLINNAKIDTYDDHRMAMCFSLSLLGV 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
VTI DP CT KTFP YF + +
Sbjct: 406 SVTINDPKCTHKTFPTYFQIFN 427

>ref|ZP_01786780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
ref|ZP_01797315.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
gb|EDJ90947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
gb|EDK13423.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae 22.4-21]
Length = 380

Score = 357 bits (916), Expect = 2e-96, Method: Compositional matrix adjust.
Identities = 192/385 (49%), Positives = 245/385 (63%), Gaps = 17/385 (4%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL+ LG+ + + G GG F +++ + LFLGNAG AMR LTAA+
Sbjct: 1 MLNALKALGVRYQLSDDKTICEIEGLGGAFNIQN---NLSLFLGNAGTAMRPLTAALCLK 57

Query: 116 GGNAT-YVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKL 174
G + +L G PRM+ERPI LV L+Q GAD+ PP+ + G+ GGKVK+
Sbjct: 58 GKTESEIILTGEPRMKERPIHLVDALRQAGADIRYLENEGYPPLAIRN-KGIKGGKVKI 116

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
GSISSQ+L+ALLM+APLA D EIEII +L+S PY+++TL +M FGVK E+ + +F
Sbjct: 117 DGSISSQFLTALLMSAPLAENDTEIEIIGELVSKPYIDITLAMMRDFGVKVENQ-HYQKF 175

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
YIKG Q Y SP VEGDASSASYFLA I G V V G G S+QGD FA+VLE M
Sbjct: 176 YIKGNQSYISPNKYLVEGDASSASYFLAAGTIKG-KVKVTGIGKNSIQGDRLFADVLEKM 234

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAK+TW E + L ID++MN +PD AMT+A ALFA+G T IR++
Sbjct: 235 GAKITWGEDFIQAE-----HAELNGIDMDMNHIDPAAMTIATTALFANGETVIRNIY 286

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSL 412
+WRVKET+R+ A+ TEL K+GA VEEG D+ I P + I+TY+DHRMAM FSL
Sbjct: 287 NWRVKETDRLTAMATELRKIGAEVEEGEDFIRIQPLVLNQFKHANIETYNDHRMAMCFSL 346

Query: 413 AACAEVPTVIRDPGCTRKTFPDYFD 437
A + PVTI DP CT KTFP +F+
Sbjct: 347 IALSNTPTVILDPKCTAKTFPTFFN 371

>ref|ZP_06735729.1| hypothetical protein NEIELOOT_02577 [Neisseria elongata subsp.
glycolytica ATCC 29315]
gb|EFE48603.1| hypothetical protein NEIELOOT_02577 [Neisseria elongata subsp.
glycolytica ATCC 29315]
Length = 429

Score = 355 bits (911), Expect = 7e-96, Method: Compositional matrix adjust.
Identities = 212/449 (47%), Positives = 279/449 (62%), Gaps = 35/449 (7%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I L+P + ++ LPGSKS+SNR LLLAALS+ + +LL S+D ML AL LG
Sbjct: 3 DSIRLEPRRLKPSSIALPGSKSISNRITLLAALSNDNGCTIRSLQSDDTDRMLDAL TALG 62

Query: 65 LSVE--ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ +E +D + + GCGG+FP + E LFLGNAG A R L AA+ GG+ Y
Sbjct: 63 VGIEPLSDGLIR---IRGCGGRFP---QREADLFLGNAGTAFRPLAAALAVLGGD--YR 113

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRV----NGIGGLPGGKVKLSGS 177
L GV RM ERPIGDLV L+ +GAD+ + PP+ + NGI +P + G+

Sbjct: 114 LHGVARMHERPIGDLVDALRIIGADIRYTGNNYPPLHIGKRQDNGIHSVP-----VKGN 168

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+SSQ+L+ALLMA PL EI++ +LIS PY+++TL LM RFGV E+ D + RF +

Sbjct: 169 VSSQFLTALLMALPLTGEVFEIQVEGELISKPYIDITLNLMMRRFGVNVEN-DGYRRFRLP 227

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+Y +P+ +VEGDASSASYFLA ++ + V G G ++QGD FA LE +GA

Sbjct: 228 AA-RYIAPETVHVEGDASSASYFLAAGLLSAVPIRVTLGKNAIQGDAFAFAELEKIGAA 286

Query: 298 VTWTETSVTVT---GPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVA 354
VTW + + V+ G PF D++ N +PD AMTLAVVAL A P +R++

Sbjct: 287 VTWGDDFIEVSRAEQAVLPF-----DLNANHIPDAAMTLAVVALAAGAPCTLRNIG 338

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVA-IDTYDDHRMAMAFSLA 413
SWRVKET+R+ A+ EL K+GA+V E + ITPP +L A IDTYDDHRMAM FSL

Sbjct: 339 SWRVKETDRIAAMAAELRKVGATVREEAEIHITPPARLTPNAVIDTYDDHRMAMCFSLV 398

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
A VPVTI DP CTRKTFFPDYF V +

Sbjct: 399 ALLGVPVTINDPQCTRKTFFPDYFAVFESL 427

>ref|YP_997872.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Verminephrobacter eiseniae EF01-2]
gb|ABM58854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Verminephrobacter
eiseniae EF01-2]
Length = 705

Score = 355 bits (910), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 221/471 (46%), Positives = 290/471 (61%), Gaps = 46/471 (9%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L + +G V+LPGSKS+SNR+LLLAALS GTT V LL S+D ML ALR +G +

Sbjct: 7 IDLPALDAAAGEVRLPGSKSISNRVLLLAALSNGTTTVHQLLASDDTRVMLDALRQIGCA 66

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V D+A + G GG+ P AK LFLGNAG AMR LTAA+ GG + L GV

Sbjct: 67 V--DEAGSSVHITGLGRAPRAPAK----LFLGNAGTAMRPLTAALALLGGE--FELSGV 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKV----- 172
RM +RPIGDLV L+QLG +D +LG D PP+R+ P V

Sbjct: 119 ARMHQRPIGDLVDALRQLGCRID-YLGNDDYPPPLRIAHAACAPADVPALVPGVPPPLALA 177

Query: 173 ---KLSGSISSQYLSALLMAAPLALG--DVEIEIIDKLISIPYVEMTLRLMERFGVKAH 227
++ G +SSQ+L+ALLMA PLA G + IE++ +LIS PY+ +TL L+ RFG+ E

Sbjct: 178 EPIRVRGDVSSQFLTALLMALPLAAGRQSIVIEVLGELISKPYIAITLELLARFGIVVER 237

Query: 228 SDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTT 279
W RF I G +Y+SP + +VE DASSASYF+A AI G + + G G

Sbjct: 238 Q-GWQRFTIAAGSRYQSPGSIHVEADASSASYFIALGAIASGAGGPNGAQGIRIAGLGLD 296

Query: 280 SLQGDVKFAEVLEMMGAKVTWTETSVTVT-GPPREPFGRKHLKAIDVNMNMKMPDVAMTLA 338
S+QGD++F E MGA VT + V G P + + LKAID++ N +PD AMTLA

Sbjct: 297 SIQGDIRFVEAARAMGAVVTGGPHWLHVQRGAPGQGW--PLKAIDIDCNHIPPDAAMTLA 353

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP---EKLNV 395
V+AL+A G + +R++ASWRVKET+R+ A+ L +LGASVEEG D+ ITPP E

Sbjct: 354 VMALYAQGSSRLRNIAASWRVKETDRIAAMAAGLRQLGASVEEGADFIRITPPPTEDWKA 413

Query: 396 TAIDTYDDHRMAMAFSLAAC--AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
+IDT+DDHR+AM F+LAA A +P+ I+DP C KTFPDYF+ L + +

Sbjct: 414 ASIDTHDDHRVAMCFALAAAFNPAGLPRIQDPKCVAKTFPDYFEALFSVAQ 464

>ref|YP_002521490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermomicrobium
roseum DSM 5159]
gb|ACM04612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermomicrobium
roseum DSM 5159]
Length = 434

Score = 355 bits (910), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 202/430 (46%), Positives = 267/430 (62%), Gaps = 20/430 (4%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP+ I V+LPGSKSL+NR L+LAAL++G +V++ L SED M+ +LR LG+ V+
Sbjct: 18 QPVDAI---VRLPGSKSLTNRALVLAALADGVSVLEGALLSEDSWVMVDSLRLGIPVDV 74

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
D+ A+R +V G GG P A +LF+GN+G R LTA A G+ Y++DGVPRM
Sbjct: 75 DEPAERMIVQKGKGTLPATRA---ELFVGNSGTTARFLTA--MTALGHGEYLIDGVPRM 128

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RERPI L+ L QLG + LGT CPPVRV GL GG ++L G ISSQYLSALLM
Sbjct: 129 RERPIQLLDALAQLGVQAESLLGTGCPPVRVRSY-GLAGGTIRLRGDISSQYLSALLMI 187

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P + IE+ L+S+PYVEMTL +M FG A H + F++ G Q+Y+S +
Sbjct: 188 GPCTRDGLRIELESPLVSPYVEMTLAVMADFGAIATHEHA-QVFHVPGNQRYRS-RTYA 245

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E DAS+ASYF A AA T G + V GT S QGDV+F ++LE MG V ++TV
Sbjct: 246 IEPDASAASYFFALAAATAGRIRVNLGTRSRQGDVQFVDLLERMGCTVIREPDALTV-- 303

Query: 310 PPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
G++ L+ I+ +MN + D TLA +A ADGP IR+V R KET+R+ A+
Sbjct: 304 -----IGKRPLRGIEADMNAISDTVPTLAALAPLADGPVIRNVQHIRYKETDRIAAVAN 358

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDGPCTR 429
EL +LG +VEE PD I P + I TY DHRMAM+F++ CA + I DPGC
Sbjct: 359 ELRRLGITVEEFPDGLRIE-PGPVQPAVIRTYGDHRMAMSFALLGCAVPGLEIDDPGCVA 417

Query: 430 KTFPDYFDVL 439
KTFPD+F+ L
Sbjct: 418 KTFPDDFFERL 427

>ref|ZP_01042651.1| 5-enolpyruvylshikimate-3-phosphate synthase [Idiomarina baltica
OS145]
gb|EAQ32395.1| 5-enolpyruvylshikimate-3-phosphate synthase [Idiomarina baltica
OS145]
Length = 441

Score = 354 bits (908), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 205/440 (46%), Positives = 276/440 (62%), Gaps = 18/440 (4%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P SGTV LPGSKS+SNR LL+AAL + N+L S+D M+ AL TLG+SV+
Sbjct: 17 LAPRSACSGTVTLPGSKSISNRALLMAALCGQPVTLNKLVESDDTARMIDALTTLGVSVK 76

Query: 69 -ADKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-LDGV 126
+D V GCGG++ + A E L+LGNAG A+R L A + A+ N + LDG
Sbjct: 77 RSDLDPSEYQVEGCGGRW--QPAHNE--LYLGNAGTAVRPLVAVLAASLSNTQVMRLDGN 132

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RMRERPI L+ L GA++ C P+ + G GG+V + GS SSQY+SAL
Sbjct: 133 ARMERPIAALIDSLTAAGANIQCHAEFGFLPTIES--GFKGGEVTIDGSASSQYISAL 190

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LMA PL D E+ +++++IS+PY+E+TL ++ FG++ + HSD + I G Q Y+SP
Sbjct: 191 LMALPLLADDSELLLVNEVISVPYIELTSLMLRDFGIQIDKHSDR--HYKIPGRQSYRSP 248

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ +VEGDAS ASY++ AAI+GG +T+ G G S+QGDV FAE+ + MGA V + ++
Sbjct: 249 GSYFVEGDASGASYWIGAAAISGGPITIYGVGKNSIQGDVHFAELAQQMGANVEMLDNAI 308

Query: 306 TVTGGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V+ LKAIDV+ N +PD AMTLA +ALFA G T IR+VASWRVKET+R+
Sbjct: 309 RVSR-----STELKAIDVDCNNLPDAAMTLAPMALFAQGTTVIRNVASWRVKETDRLA 361

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 425
A+ EL K+GA VEEG DY + P +DTYDDHRMAM +L A + V V+I DP

Sbjct: 362 AMAAELRKVGAQVEEGEDYLSVMAPAHWQHALLDITYDDHRMAMCSALIAFSPVGVSINDP 421

Query: 426 GCTRKTFPDYFDVLSTFVK 445

C KT+P +FD S +

Sbjct: 422 QCCSKTYPQFFDEFSLCHD 441

>emb|CAZ88944.1| 3-phosphoshikimate 1-carboxyvinyltransferase:Cytidylate kinase
[Thiomonas sp. 3As]
Length = 659

Score = 353 bits (905), Expect = 4e-95, Method: Compositional matrix adjust.
Identities = 212/453 (46%), Positives = 273/453 (60%), Gaps = 21/453 (4%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60

M +E L P+ G VKLPKSGK+SNR+LLLAAL+EG + LL+S+D ML AL

Sbjct: 1 MMKSEARDLPPLIGAGGRVKLPKSGKSLNRVLLLAALAEQAEITGLLSDSDTRVLAAL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120

+ LG++V + + A V G G+FP A LF+GNAG A+R LTAA+ GG+

Sbjct: 61 QALGIAVR--REGETAHVQGGAGRFPAAQA---DLFMGNAGTAIRPLTAALALLGGD-- 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180

Y L GVPRM ERPIGDLV L+Q G ++ PP+ + G V + G +SS

Sbjct: 113 YALHGVPRMHERPIGDLVDALRQFGCEIRYTGQEGYPLHIGASHFRLNGDVAVRGVDVSS 172

Query: 181 QYLSALLMAAPLALGDVEIEII--DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238

Q+L+ALL+A PL D +I I +LIS PY+E+TL L+ RFGV+ + W+RF I

Sbjct: 173 QFLTALLLALPLKASDHDAIAVQGEILSKPYIEITLNLRRFGVQVRRT-GWERFVIPA 231

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAI-----TGGTVTVEGCGTTSLQGDVKFAEVLEM 293

G +SP VEGDASSASYFLA + G V VEG G S+QGDV FA VLE

Sbjct: 232 GSGLRSPGRIAVEGDASSASYFLAAGVLGQWHGKGAPVRVEGVGRDSIQGDVAFARVLED 291

Query: 294 MGAKVTWTETSVTGTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353

+GA+V W + + G L+ D++ +PD AMTLA+ ALFAD PT + +

Sbjct: 292 LGAQVRWGDDFIETDG---LQAGLTALRGDIDCLAIPDAAMTLAMTALFADAPTTLTAI 348

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFS 411

SWRVKET+R+ A+ TELTKLGA VE GPD+ + P + AI TYDDHRMAM FS

Sbjct: 349 GSWRVKETDRIHAMATELTKLGAKVESGPDWLRVHPLPAVQWRSAAIATYDDHRMAMCFS 408

Query: 412 LAACAEVPTTIRDPGCTRKTFPDYFDVLSTFVK 444

LA+ + I DPGC KT+P YFD + +

Sbjct: 409 LASFGHADIRILDPGCVAKTYPGYFDDFARIAR 441

>ref|YP_003319237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphaerobacter
thermophilus DSM 20745]
gb|ACZ38415.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphaerobacter
thermophilus DSM 20745]
Length = 435

Score = 352 bits (902), Expect = 8e-95, Method: Compositional matrix adjust.
Identities = 201/437 (45%), Positives = 265/437 (60%), Gaps = 18/437 (4%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63

+EI +QP++ + V +PGSKS +NR L +AAL++GT+V+ L S D HYM AL L

Sbjct: 9 DEIEIQPVRAVPDVEVAVPGSKSDTNRALPIAALADGTSVIRGALFSDNTHYMAAALNAL 68

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123

G+ V A + + V G GG P A L +GN+G R LTA + A G YVL

Sbjct: 69 GIHVTASREDRTFTVAGAGGSIPARSAS---LVIGNSGTTARFLTALL--ALGRGEYVL 122

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183

DGV RMR+RPI L+ L+QLG D GT CPPVR+ GL GG +L G SSQ+L

Sbjct: 123 DGVERMRQRPIQLLNLQQLGVDVSIHGTGCPPVRIRA-NGLRGHTRLDGRESSQFL 181

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

SALLM P + I+I L+S PYV++T M FG + + + RF + G Q+Y+

Sbjct: 182 SALLMVGPCTPDGLTIDIEGLVSKPYVDLTASTMAAFGATLTN-ERYRRFVVPGEQRYR 240

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + VE DAS+ASYF A AA+TGG V V G G+ SLQGD++F EVLE MG V T
Sbjct: 241 ATEY-QVEPDASAASYFFALAAVTGGRVRVPGLSRSLQGDRLRFVEVLERMGCTVEMTAD 299

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V GP R L IDV+MN + D A TLA +A A GP AIR+VA R KET+R
Sbjct: 300 ATEVRGPER-----LAGIDVDMNAISDTAQTAAIAPLASGPVAIRNVAHIRAKETDR 352

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ TEL +LG VEE PD ++ P + ++TYDDHRMAM+F++ CA + I
Sbjct: 353 ISAVVTELRLRGVRVEEMPDGLVVY-PSPVRPGRVET YDDHRMAMSFALG CATPGIRIA 411

Query: 424 DPGCTRKTFPDYFDVLS 440
DPGC KTFP+++D L+
Sbjct: 412 DPGCVAKTFPEFWDTLA 428

>ref|ZP_04600796.1| hypothetical protein GCWU000324_00250 [Kingella oralis ATCC 51147]
gb|EEP68356.1| hypothetical protein GCWU000324_00250 [Kingella oralis ATCC 51147]
Length = 431

Score = 350 bits (898), Expect = 3e-94, Method: Compositional matrix adjust.
Identities = 210/443 (47%), Positives = 269/443 (60%), Gaps = 21/443 (4%)

Query: 5 EEIVLQPIK-EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
E + L P + + TV LPGSKS+SNR LLLAAL++ + +LL S+D ML AL L
Sbjct: 3 ESLTLAPRRLLKAHNTVALPGSKSISNRTLLAALADNACEIRSLLKSDDTDRMLEALAAL 62

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ +E + + G GG FPV+ A LFLGNAG A R LTAA+ GG+ Y L
Sbjct: 63 GIKLETTPSGSLKIQ-GSGGAFPVKHA---DLFLGNAGTAFRPLTAALALGGD--YHL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
GVPRM ERPIGDLV L+ GA VD PP+R++ ++ + G++SSQ+L
Sbjct: 116 HGVPRMHERPIGDLVDALRLAGARVDYLGNA GFPPLR IHERADNGMRQIPKGNVSSQFL 175

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALL+A PL EI + +LIS PY+++TL LM++FGV + S F + +Y
Sbjct: 176 TALLIALPLTGEAFEIRVAGELISKPYIDITLNLKQFGVSVANQ-SHQVFRLPENARYH 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+P+ VEGDASSASYFLA I+G V V G G ++QGDV FA LE +G V W +
Sbjct: 235 APQVVNVEGDASSASYFLAAGLISGCPVRVTGLGRNAIQGDVAFHAHELEKIGGTVQWGDD 294

Query: 304 SVTVT---GPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V+ G PF D++ N +PD AMTLAVVAL P IR++ASWRVKE
Sbjct: 295 FIEVSRAAGQAVLPF-----DL DANHIPDAAMTLAVVALATGAPCRIRNIASWRVKE 346

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVP 419
T+R+ A+ TEL KLGA+V E PD ITPP L AIDTYDDHRMAM FSL + VP
Sbjct: 347 TDRIAAMATELCKLGATVREDPDAIRITPPAALTPNAIDTYDDHRMAMCFLSVSLMGVP 406

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
+ I DP C KTFP YFDV +
Sbjct: 407 IIINDPKCVGKTFPPQYFDVFNAL 429

>ref|ZP_01552046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylophilales
bacterium HTCC2181]
gb|EAV47104.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylophilales
bacterium HTCC2181]
Length = 423

Score = 349 bits (895), Expect = 5e-94, Method: Compositional matrix adjust.
Identities = 194/433 (44%), Positives = 273/433 (63%), Gaps = 20/433 (4%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ +L+ E+ G + LPGSKS++NR++LLA+LS T++ N L S+D YML AL LG+
Sbjct: 3 QYILKGRSEVKGEIILPGSKSITNRVILLASLSNKKTLIRNYLQSDTRYMLEALEKLG 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E K V G G FP +D +LFLGNAG A R LTAA+ G+ Y L G
Sbjct: 63 MIE--KNGSEITVHGTNGSFPNKDC----ELFLGNAGTAFRPLTAALAMMDGH--YRLAG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
V RM ERPI DLV LK LGA ++ PP+ + K+ + G++SSQ+L++
Sbjct: 115 VQRMHERPIKDLVDSLKDLGARINYLENDGFPPLEIFPKTEKIIQKISIKGNVSSQFLTS 174

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL++ PL + I + +LIS PY+++TLRL+++FGV + + W++F + G ++SP
Sbjct: 175 LLISVPLLNQPLSINLDGELISKPYIDITLRLQLKFGVSFNNMN-WNQFNLNGITVFRSP 233

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ +VEGDASSASYF AAI G + V G S+QGD+KF +V+ MGAKVT+ E S+
Sbjct: 234 EEIWEVDASSASYFFGAAAI-AGKIEVHGINQESIQLDLKFLDVSSMGAKVTYLEKSI 292

Query: 306 TVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V E G L+A++V+ +PD AMTLA +ALF G T + ++ASW+VKET+R+
Sbjct: 293 IV-----EKSG--ELRALEVDCMKIPDAAMTLATMALFCKGTTKLINIASWKVKETDRIQ 345

Query: 366 AIRTELTKLGASVEEGPDYCIITPPE--KLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ EL KLGA+V + ITPP K NVT IDTYDDHR+AM FSL + +E V I
Sbjct: 346 AMSNELKKLGATVHSTNNTISITPPSIKDNVT-IDTYDDHRIAMCFSLISLERNVIIN 404

Query: 424 DPGCTRKTFPDYF 436
+P C KT+P++F
Sbjct: 405 NPECVNKTYPNFF 417

>ref|YP_155746.1| 5-enolpyruvylshikimate-3-phosphate synthase [Idiomarina loihiensis
L2TR]
sp|Q5QZ50.1|AROA_IDILO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAV82197.1| 5-enolpyruvylshikimate-3-phosphate synthase [Idiomarina loihiensis
L2TR]
Length = 429

Score = 347 bits (890), Expect = 2e-93, Method: Compositional matrix adjust.
Identities = 204/441 (46%), Positives = 276/441 (62%), Gaps = 18/441 (4%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L+P + GTV LPGSKS++NR LL+AAL + ++ NLL S+D M AL LG+S
Sbjct: 5 IHLEPRQHCRGTVTLPGSKSIANRALLMAALCQTPVILHNLVSDDTSRMREALNALGVS 64

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA--AVTAAGGNATYVLD 124
E DK R V G GG + K +L+LGNAG AMR L A A T + VL
Sbjct: 65 FEDDKLITR--VNLGGGW---NKPASELYLGNAGTAMRPLIAVLAATLKNEHQAVVLK 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM ERP+ L+ ++ GA V+ T PP+ + GL G ++ GS+SSQ++S
Sbjct: 119 GDARMHERPVKHLIDAIQPRGAGVNYLGETGFPPLEMTS--GLKPGDFEIDGSVSSQFIS 176

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMA PL GD + + ++S PY+E+TL+++ FG+ + DS + I GGQ Y+S
Sbjct: 177 ALLMALPLLPGDSTLTLLKGNVVSRYPIELTLQMLSDFGISIK-EDSPQCYAIPGGQCYQS 235

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 304
P +VEGDAS+ASY++A A + G V + G G S+QGD +FAEV+E MGA V++ + S
Sbjct: 236 PGEYWVEGDASAASYWMAAALLGKGVPVEIIGVGKNSIQGDKRFAEVIEAMGASVSYSRKNS 295

Query: 305 VVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TV+G ++ ID + N +PD AMT+A +ALFA+ PT IR+VA+WRVKET+R+
Sbjct: 296 MTSVSG-----TGSVQGIDQDFNDIPDAAMTVAPLALFANKPTTIRNVANWRVKETDRL 348

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TEL KLGA+V+EG D+ I P + AIDTYDDHRMAM FSL A + VTI D
Sbjct: 349 HAMATELRKLKLGATVDEGEDFLRIEPLKHWHRHIAIDTYDDHRMAMCFSLVAFSSAGVTIND 408

Query: 425 PGCTRKTFPDYFDVLSTFVKN 445
PGC KT+PDYF S +

Sbjct: 409 PGCCAKTYPDYFSEFSRLCHS 429

>ref|YP_004269980.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces
brasiliensis DSM 5305]
gb|ADY59958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces
brasiliensis DSM 5305]
Length = 430

Score = 347 bits (889), Expect = 3e-93, Method: Compositional matrix adjust.
Identities = 208/436 (47%), Positives = 276/436 (63%), Gaps = 23/436 (5%)

Query: 6 EIVLQPIK-EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EI + P+ + G ++ PGSKS++NR L++AAL++GT+ + L SED H ML +LR LG
Sbjct: 10 ETEMSPVSGPVQGAIQPPGSKSITNRALIIAALADGTSRLTGTASEDTHVMLESLRRLG 69

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
L D+ + GCGG P + A L+L N+G ++R LTAA + GN Y LD
Sbjct: 70 LEW-TDEGNGTISIQCNGNIPADKAD---LWLENSGTSIRFLTAACSL--GNGEYRLD 122

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RMRERPI DLV + Q G D+ C L +DCPPV +N G LPGG + + G++SSQYLS
Sbjct: 123 GNSRMRERPIRDLVQAISQFGVDIRCELDSDCPPVLINTTG-LPGGTITVPGNLSSQYLS 181

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM AP A VEI + +L+S+PYVEMTL++M+ FGV E RF I+ Q YK+
Sbjct: 182 ALLMVAPYAKEPVEIVVSGELVSVPYVEMTLQVMQSFQVNVV-VQQMQRFRIQ-PQTYKA 239

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ A +E DAS+ASYF A AA+TGG VTV G +LQGDV F E L MG V + + S
Sbjct: 240 REYA-IEPDASAASYFFAAAVTGGNVTVNLHRDALQGDVHFVEALRDMGCDVQYNDDS 298

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TV G P L +D++MN + D A TLA VA+FA+GPT +R+VA R+KET+R+
Sbjct: 299 ITVIGKP-----LNGVDIDMNAISDTAQTAAVAVFANGPTRVRNVAHMRIKETDRV 350

Query: 365 VAIRTELTKLGASVEEGPDYCIITP-PEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ EL +LG EE D I P P + + I+TY+DHRMAM+FSL V I
Sbjct: 351 SAVVNELRRLGIETEEHEDGFTIHPGTPQPAL--IETYNDHRMAMSFSLIGLRNAGVRIS 408

Query: 424 DPGCTRKTFPDYFDVL 439
+PGCT KT+P YF+ L
Sbjct: 409 NPGCTAKTYPHYFEDL 424

>ref|YP_001790000.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Leptothrix cholodnii SP-6]
gb|ACB33235.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptothrix cholodnii
SP-6]
Length = 699

Score = 343 bits (879), Expect = 4e-92, Method: Compositional matrix adjust.
Identities = 217/472 (45%), Positives = 277/472 (58%), Gaps = 56/472 (11%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P+ +GTV+LPKSGK+SNR+LLLA LS G T + +LL+S+D ML ALR LG +E
Sbjct: 9 LPPLGAAAGTVRLPGSKSISNRLLLLAGLSAGVTTLVDLLSDDDTRVMDALRGLGCRIE 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV----TAAGGNATYVLD 124
+ + + G GK A E FLGNAG AMR LTAA+ T GG Y L
Sbjct: 69 --QQRHTRITVAGK----PAVLEADFFLGNAGTAMRPLTAALAVISTQNGGR--YTLS 120

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GVPRM ERPIGDLV L+ LG V+C PP+R+ G L V++ G +SSQ+L+
Sbjct: 121 GVPRMHERPIGDLVDALRALGVAVECLGNEGYPPLRLAGGSLLLDAPVRVRGDVSSQFLT 180

Query: 185 ALL-----MAAPLALGDVEIEIIDKLISIPYVEMTL 215
ALL P A DV IE+I +LIS PY+E+TL
Sbjct: 181 ALLLALPLAAGPRAPTGLTDGSSLPPEGASPPWGGPAAGRVDVIEVIGELISKPYIEITL 240

Query: 216 RLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITG--GTVTV 273

L+ RFG+ A + W RF I G Y +P +VE DASSASYF+A A+ G V +
Sbjct: 241 NLLARFGI-AVRREGWQRFTIPAGSAYVTPGEVHVVEADASSASYFIALGALAGVDAPVRI 299
Query: 274 ECGGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDV 333
EG G S+QGD++F E + MGA+V ++ V G LKAI+++ N +PD
Sbjct: 300 EGVGAASIQGDIFRVEAAQAMGARVMAEPNALEVR-----RGAWPLKAIELDCNHIPDA 353
Query: 334 AMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
AMTLAV+AL+ADGP+ + ++ASWRVKET+R+ A+ TEL KLGA VEEG D+ + P +
Sbjct: 354 AMTLAVMALYADGPSTLTNIASWRVKETDRIAAMATELRKLGAQVEEGADHIRVWPLAQF 413
Query: 394 NVTADITYDDHRMAMAFSLAA-----CAEVPVTIRDPGCTRKTFPDYFDVL 439
AI TYDDHRMAM SLAA A VPV I DP C KT+PDYF+ L
Sbjct: 414 KPAAIHTYDDHRMAMCLSLAAFHTLKGAAFPVVRILDPKCVAKTYPDYFETL 465

>ref|YP_001021434.1| bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase/cytidine
monophosphate kinase [Methylibium petroleiphilum PM1]
gb|ABM95199.1| 3-phosphoshikimate 1-carboxyvinyltransferase / cytidylate kinase
[Methylibium petroleiphilum PM1]
Length = 674

Score = 342 bits (878), Expect = 6e-92, Method: Compositional matrix adjust.
Identities = 209/440 (47%), Positives = 271/440 (61%), Gaps = 24/440 (5%)

Query: 11 PIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P++ GTV+LPGSKS+SNR+LLLA L G T V +LL+S+D ML ALR LG +E D
Sbjct: 12 PLQAAGGTVRLPGSKSISNRVLLLAGLCAGRTRVLDLLSDDTQVMLDALRALGCDIETD 71
Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN--ATYVLDGVPR 128
AA+ VV G GG+ V +A+ LFLGNAG AMR L AA+ + + L GVPR
Sbjct: 72 GAAR--VVTGLGRLAVREAR----LFLGNAGTAMRPLAALALLAADQGGRFELSGVPR 125
Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPIGDLV L+ LG + C PP+R+ +++ G +SSQ+L+ALLM
Sbjct: 126 MHERPIGDLVDALRPLGCTITCLANEGYPPLRLERGTCLKLDAPIRVRGDVSSQFLTALLM 185
Query: 189 AAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPK 246
A PL A + IE+ +LIS PY+E+TL L+ RFG+ + + W RF I G Y+SP
Sbjct: 186 ALPLVAARQSITIEVDGELISKPYIEITLALLARFGISVQR-EGWQRFVIPQGSAYRSPG 244
Query: 247 NAYVEGDASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
VEGDASSASYF+A AI + +EG G+ S+QGD++F E MGA +T +
Sbjct: 245 EIAVEGDASSASYFIAAGAIAAADTPLRIEIGVGSASIQGDIFRVEAARAMGADITEEANA 304
Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ V G L AI ++ N +PD AMTLA +AL+A G T + ++ASWRVKET+R+
Sbjct: 305 LVVR-----RGAWPLTAITLDCNHIPDAAMTLAAMALYATGTTTLTNIASWRVKETDRI 358
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-----AEVP 419
A+ EL K GA+V EG D+ +TPP + AI TYDDHRMAM SLAA +VP
Sbjct: 359 AAMAIELRKFGATVLEGTDFIEVTPPARWQAAAIHTYDDHRMAMCASLAAFNPLAGGDVP 418
Query: 420 VTIRDPGCTRKTFPDYFDVL 439
V I DP C KTFP YFD L
Sbjct: 419 VRILDPKCVNKTFFPAYFDAL 438

>ref|YP_001630496.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella petrii DSM
12804]
sp|A9IJ17.1|ARO_A_BORPD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAP42227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bordetella petrii]
Length = 447

Score = 339 bits (870), Expect = 4e-91, Method: Compositional matrix adjust.
Identities = 224/451 (49%), Positives = 276/451 (61%), Gaps = 17/451 (3%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M G + L ++ G V LPGSKS+SNR+LLLAAL+ G T + LL+S+D ML AL

Sbjct: 1 MTGQPYLDLPRARQARGQVALPGSKSISNRVLLLAALAAGRTDISGLDSDDRVMLAAL 60

Query: 61 RTLGSLVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGNAT 120
R LG VE +A + V VG G+FPV+ A LFLGNAG A R LTAA+ GG

Sbjct: 61 RQLG--VELAEAGEGRVTVGGAGRFPVKQA---DLFLGNAGTAFRPLTAALALMGQ-- 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
Y L GVPRM ERPIGDLV L+Q GA +D PP+ V ++ G++SS

Sbjct: 113 YRLSGVPRMHERPIGDLVDALRQWGARIDYLGQAGYPPLAVGEGRIRADAPARVQGAUSS 172

Query: 181 QYLSALLMAAPLALGD---VEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYI 236
Q+L+ALL+AAP+ V IE+ +LIS PY+E+TL LM R+GV+ D W F I

Sbjct: 173 QFLTALLLAAPVLAQGS DRPVVIEVAGELISKPYIEITLNLMARYGVQVRR-DGWRTFTI 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+ G Y+SP VEGDASSASYFLA AI GG V V G G S+QGDV FA L MG

Sbjct: 232 EPGAAYRSPGAIAVEGDASSASYFLALGAIGGPPVRVTGVDGDSIQGDVAFARTLADMGV 291

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
++ + + G + GR LKA D + N +PD AMT A +AL+ADGP +R++ SW

Sbjct: 292 QIDYGPDWIEARGVRVDQGG--LKAFDTDFNLIPDAAMTAAALALYADGPCRLRNIGSW 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ TEL KLGA VE GPD+ ITPP I T+DDHRMAM FSLAA

Sbjct: 350 RVKETDRIHAMHTELAKLGAEVESGPDWLRITPPADGGWRDAHIGTWDDHRMAMCFSLAA 409

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
V I DPGC KTFPDYFDV + V

Sbjct: 410 FGPAAVRILDPGCVSKTFPDYFDVYAGLVSG 440

>ref|ZP_06390344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria subflava
NJ9703]
gb|EFC52172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria subflava
NJ9703]
Length = 377

Score = 339 bits (869), Expect = 6e-91, Method: Compositional matrix adjust.
Identities = 188/390 (48%), Positives = 241/390 (61%), Gaps = 14/390 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTA 115
ML AL LG+ +E+ R V G GG+FP + LFLGNAG A R LTAA+

Sbjct: 1 MLEALDKLGVQIES-LPEGRKLVHAGGRFP---NQSSDLFLGNAGTAFRPLTAALAVL 55

Query: 116 GGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
GG+ Y L GVPRM ERPIGDLV L+ GADV + PP+++ + +

Sbjct: 56 GGD--YHLHGVPVRMHERPIGDLVDALRIAGADVQYLGNNENYPLQIGKRQDNGERVIPIK 113

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFY 235
G+SSQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV + D + F

Sbjct: 114 GNVSSQFLTALLMALPLTGQAFEIHMVGELISKPYIDITLKLMAQFGVDIINED-YRVFK 172

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I G KY +P++ YVEGDASSASYFL I G + V G G S+QGDV FA LE +G

Sbjct: 173 IPAGAKYHAPEHLYVEGDASSASYFLGAGLIAGTPIRVTGIGAHSIQGDVAFARELEKIG 232

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
A V W E V ++ P + ++A D++ N +PD AMTLA+VAL P +R++ S

Sbjct: 233 ADVIWGENFVEISR--AERKIQAFLDANHIPDAAMTLAIVALATKQPCTLRNIGS 287

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAA 414
WRVKET+R+ A+ TEL KLGA V E + ITPPE L A IDTYDDHRMAM FSL +

Sbjct: 288 WRVKETDRIAMATELRKLGAADVIEEAEAIHTPPETLTPDAVIDTYDDHRMAMCFSLVS 347

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
VPV I DP CT KTFPDYF V ++

Sbjct: 348 LLGVPIIINDPKCTHKTFPDYFQVFASLTN 377

>emb|CAJ75373.1| strongly similar to 3-phosphoshikimate 1-carboxyvinyltransferase
[Candidatus Kuenenia stuttgartiensis]

Length = 424

Score = 335 bits (860), Expect = 6e-90, Method: Compositional matrix adjust.
Identities = 199/436 (45%), Positives = 269/436 (61%), Gaps = 23/436 (5%)

Query: 7 IVLQPIK-EISGTVKLPKSGKSLNRIILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
I ++P+ I+ +++PGSKS +NR L+ AL++G + ++N L S+D HYM L +LG+
Sbjct: 4 IEIKPVTGRINTIIRVPGSKSYTNRALITTALADGISSINNALFSDDTHYMASCLNSLGI 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE K +V G GG P E A LF+GNAG AMR LTA +T G Y + G
Sbjct: 64 PVEERKDTNTTFIVNGKGGCIPAEKA---NLFVGNAGTAMRFLTALTL--GYGVYEIGG 117

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
V RM +RPI DL+ GL QLGA+V L CPPV + G G G + ++G +SSQY SA
Sbjct: 118 VERMGQRPIQDLLEGLNQLGAEVKSKLDNGCPPVVIKKGKLGKGGKAI-VNGDLSSQYFSA 176

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLM +P A DV IE+ L+S YV+MT+ LM + GV E+ + R +K GQ+YK+
Sbjct: 177 LLMVSPYAENDVTIEVKDLVSKRYVDMTIDLMDKHGVTVENI-GYKRLLVKSGQRYKTI 235

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSV 305
+ VEGDAS+ASYF A AAITGG V VEG G SLQGDV+FA+VL+ MG V +
Sbjct: 236 -SYEVEGDASAASYFFAVAAITGGRVVEGVGKDSLQGDVQFADVLKMGCHVDGRDWI 294

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMV 365
V+G + L +DV+M MPDVA TLA VA++ G T +R+V + R+KET+R+
Sbjct: 295 EVSG-----RALHGVDVDMGDMPDVAQTLAAVAVYVKGKTRVRNVKNRIKETDRIA 346

Query: 366 AIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
A+ EL K+G SV E D I P P+ I+TYDDHRMAM+F+L + I+
Sbjct: 347 AVAKELRKMGISVTEYEDGFIEPSPMKP---AEIETYDDHRMAMSFALIGLKSDFGFIK 403

Query: 424 DPGCTRKTFFPDYFDVL 439
+P C KTFP+YF ++
Sbjct: 404 NPKCVSKTFPNYFQLI 419

>ref|ZP_03832181.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. carotovorum WPP14]
Length = 330

Score = 330 bits (847), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 176/337 (52%), Positives = 230/337 (68%), Gaps = 14/337 (4%)

Query: 105 MRSLTAAVTAAGGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGI 164
MR L AA+ G+ VL G PRM+ERPIG LV L+Q GA +D + PP+R++G
Sbjct: 1 MRPLAAALCLTDGDI--VLTGEPRMKERPIGHLVDALRQGGAKIDYLEQENYPPLRLHG- 57

Query: 165 GGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK 224
G GG++ + GS+SSQ+L+ALLM APLA D +I I L+S PY+++TL +M+ FG++
Sbjct: 58 -GFQGGEISVDGSVSSQFLTALLMTAPLATQDTQISIQGDLVSKPYIDITLHMMKAFGIE 116

Query: 225 AEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
H +++ RF++ G Q+Y+SP + VEGDASSASYFLA AAI GG V V G G S+QGD
Sbjct: 117 VRH-ENYQRFVAGRQQYRSPGDYLVVEGDASSASYFLAAAIKGGVVRVTGVGRNSVQGD 175

Query: 285 VKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVMATLAVVALFA 344
++FA+VLE MGA V W E + R L AID++MN +PD AMT+A ALFA
Sbjct: 176 IRFADVLEKMGATVRWGEDYIECE-----RGELHAIDMDMNHIDPDAAMTIATAALFA 227

Query: 345 DG-PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDD 403
G T +R++ +WRVKET+R+ A+ EL K+GA VEEG DY ITPP KL I TY+D
Sbjct: 228 QGGTTTLRNINWRVKETDRLAAMAIELRKVGAEEVEGNDYIRITPPTKLKAAEIGTYND 287

Query: 404 HRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFDVLS 440
HRMAM FSL A ++ PVTI DP CT KTFPDYF+ L+
Sbjct: 288 HRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLA 324

>ref|ZP_01852123.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces maris

DSM 8797]
gb|EDL62008.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces maris
DSM 8797]
Length = 428

Score = 330 bits (846), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 199/425 (46%), Positives = 261/425 (61%), Gaps = 18/425 (4%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I GTV+ PGSKS++NR L++AAL++GTT + +L+S+D M+ +L LG+ V+ D A
Sbjct: 14 IQGTVRPPGSKSITNRALIVAALAQGTTHLTGVLDSQDTQVMIESLNRLGIRVDHDPATC 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V GCGGK P E L+L N+G ++R LTA A G +VLDG RMR+RPI
Sbjct: 74 SIEVEGCGGKIP---SREATLWLENSGTSIRFLTA--LCAAGEGEFVLDGNARMRQRPI 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
DLV L QLG DV C T CPPV V GLPGG ++G++SSQYLSALLM AP A
Sbjct: 128 QDLVNSNLQLGIDVACAEDTGCPPVCVKA-HGLPGGDTSIAGNVSSQYLSALLMVAPAAQ 186

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ IEI +++S PY+++TL +M +FGV + + + Q Y+ P +E DA
Sbjct: 187 SPITIEIQGEMVSRPYLDITLGVMAQFGVTIDRIQ--ESVWRIQPQTYQRPVAYDIEPDA 244

Query: 255 SSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+ASYF A AAITGG VTV+G +LQGD+ F VLE MG ++ S+TV G P
Sbjct: 245 SAASYFFAAAAITGGRVTVDGLNQDALQGDINFIRVLEDMGCEIKRERNISITVQGP--- 301

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
L IDV+MN + D A TLA VALFA+G T IR+V R KET+R+ AI TE+ ++
Sbjct: 302 -----LHGIDVDMNDISDTAQTAAVALFAEGSTTIRNVGHIRHKETDRLYAIAIEIKRM 356

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFPD 434
G VEE D I P + I+TYDDHRMAM+F+L + I DP CT KT+P
Sbjct: 357 GIQVEETDDSVTIH-PGAIQPATIEYDDHRMAMSFALVGLKVPGIVADPDCTVKTYPR 415

Query: 435 YFDVL 439
+F L
Sbjct: 416 FFSDL 420

>ref|YP_004177275.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Isosphaera pallida
ATCC 43644]
gb|ADV60726.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Isosphaera pallida
ATCC 43644]
Length = 445

Score = 329 bits (843), Expect = 5e-88, Method: Compositional matrix adjust.
Identities = 198/433 (45%), Positives = 259/433 (59%), Gaps = 24/433 (5%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +++ ++PGSKSL+NR L+LAA++ G +V+ L+S+D M AL LG+SV A
Sbjct: 18 QPPRDLEA--RVPGSKSLTNRALILAAVARGRSVLTGALDSDDTRVMRRALDRLGVSVRA 75

Query: 70 DKAACKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
V GC G+FP +E +L GN+G ++R L AA+ AA G Y LDG PRM
Sbjct: 76 ADGGSTLTVDGCSGRFP----RETAELECGNSGTSRLFL-AAMLAAGRGPYRLDGNPRM 130

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPP--VRVNGIGGLPGGKVKLSGSISSQYLSALL 187
R+RP DL+ L LGA LGT PP +RV GL GG + G +SSQ+LSALL
Sbjct: 131 RQRPAADLIQALNGLGAFASSELGTGYPLLIRVEE-PGLDGGFAFVKGDVSSQFLSALL 189

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MA PLA G IE+ L+S PYV MT+++ME FGV + D + RF I+ + +
Sbjct: 190 MALPLAKGPSSIEVEGLVSKPYVTMTMKMMEHFGVIIISNRD-FKRFNIR--PSAYTAAH 246

Query: 248 AYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E DAS+ASYF A AAI+GG+V V G S+QGDV F +VLE MG +V + V
Sbjct: 247 CAIEPDASAASYFWALAAISGGSVRVVGLDASVQGDVAFVQVLEHMGCRVDRNARGIQV 306

Query: 308 TGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367

G P L+ +DV+MN + D MTLAVVALFA+GPT IR V R KET+R+ A+
Sbjct: 307 AGGP-----LRGVDVDMNAISDVTMTLAVVALFAEGPTRIRRVGHIRHKETDRIAL 358
Query: 368 RTELTKLGASVEEGPDYCIITPPE---KLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
TEL K GA PD I PP +L + TYDDHRMAMAF+L + V I D
Sbjct: 359 ATELRFKGAEIAHPDGLTILPPSDPAQLVLPARVSTYDDHRMAMAFALTSARLEGVIID 418
Query: 425 PGCTRKTFPDYFD 437
PGC KT+P +++
Sbjct: 419 PGCVAKTYPGFW 431

>ref|YP_003629142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces
limnophilus DSM 3776]
gb|ADG66943.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planctomyces
limnophilus DSM 3776]
Length = 441

Score = 328 bits (841), Expect = 9e-88, Method: Compositional matrix adjust.
Identities = 194/452 (42%), Positives = 259/452 (57%), Gaps = 24/452 (5%)

Query: 1 MAGAEEIVLQPI-KEISGTVKLP GSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGA 59
M+ +QP+ + ISG ++ PGSKSL+NR L+ AAL+ GT+ + +L+S D M+ +
Sbjct: 1 MSANSTYAMQPVGRAISGVMRPPGSKSLTNRALVTAALAAGTSELTGVLHSRDTEVMIDS 60
Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA AVTAAGGNA 119
LR LG+S+E R VV GCGG+ P L+L N+G ++R L A G+
Sbjct: 61 LRRLGISIEEYTD EHRVVVQCGGQIP---NARADLWLENSGTSIRFLAAMCALGPGDG 116
Query: 120 ---TYVL DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
Y LDG RMRERPI DL+ L +G C L + CPPV + G L KV +
Sbjct: 117 QPGNYRLDGNRMRERPIDDLISALGAMGCQARCELNSGCPPVVIESTG-LSASKVAIRA 175
Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSDWDRFYI 236
SSQ+LSALL+A+P ++IE I ++S PYVEMT +M FGV E YI
Sbjct: 176 EKSSQFLSALLASPYNQQT LQIETIGTMVSEPYVEMTSGVMAAFGVTV ECPQPGT--YI 233
Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTV EGGTTS LQGDV KF AEVLEMMGA 296
Y+ + +E DAS+ASYF A AAITGG VTV+G +LQGDV F + LE MG
Sbjct: 234 VKPATYQGIRYD-IEPDASAASYFFAVAAITGGEVTV DGLNANALQGDVMFVKALEQMGC 292
Query: 297 KVTWTETSVTVTGPPREPFG RKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDVASW 356
+V W E +TV G P LK I+++MN + D A TLAVVA FA PT IR++A
Sbjct: 293 EVHWGERQITVKGHP-----LKGIEIDMNAISDTAQT LAVVATFAQSPTTIRNIAHV 344
Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP---PEKLNVT AIDTYDDHRMAMAFSL 412
R KET+R+ A+ TEL+KLG E D I P + +DTYDDHRMAM+F+L
Sbjct: 345 RHKETDRIQAVVTELSKLG I HAVEFEDGMTIHPGTPRCSESKPALVD TYDDHRMAMSFAL 404
Query: 413 AACAEVPTIRDPGCTRKTFPDYFDVLSTFVK 444
+ I +PGCT KT+PD+F L+ +
Sbjct: 405 LGLVHSGIVIDNPGCTSKTYPDFFADLARLCE 436

>ref|YP_001599470.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
meningitidis 053442]
gb|ABX73513.1| 5-enolpyruvylshikimate-3-phosphate synthase [Neisseria
meningitidis 053442]
Length = 399

Score = 327 bits (838), Expect = 2e-87, Method: Compositional matrix adjust.
Identities = 193/414 (46%), Positives = 248/414 (59%), Gaps = 24/414 (5%)

Query: 37 LSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQL 96
+S+ + +LL S+D ML AL LG+ +E A R V G GG+FP A L
Sbjct: 1 MSDNACEIHSLLKSDDTDRMLEALDKLGVEIEY-LAEDRLKVHGTGGRFPNRTA---DL 55
Query: 97 FLGNAGIAMRSLTA AVTAAGGNATYVL DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDC 156
FLGNAG A R LTAA+ GG+ Y L GV RM ERPIGDL L+ GADV+
Sbjct: 56 FLGNAGTAFRPLTAALAVLGGD--YRLHGVARMHERPIGDLADALRIAGADVEYLGKEHY 113

Query: 157 PPVRV-----NGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV 211
PP+ + NG +P + G++SSQ+L+ALLMA PL EI ++ +LIS PY+
Sbjct: 114 PPLHIGERQDNGERVIP-----IKGNVSSQFLTALLMALPLTGQAFEIRMVGELISKPYI 168

Query: 212 EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
++TL+LM +FGV+ ++ + F I Y +P++ +VEGDASSASYFLA I V
Sbjct: 169 DITLKLMAQFGVQVI-NEGYRVFKIPADAHYHAPEHLHVEGDASSASYFLAAGLIAATPV 227

Query: 272 TVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKP 331
V G G S+QGDV FA LE +GA V W E V V+ P + ++A D++ N +P
Sbjct: 228 RVTGIGANSIQGDVAFACELEKIGADVWGENFVEVSRPKE-----RAVQAFDLNANHIP 282

Query: 332 DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE 391
D AMTLAVVAL +R++ SWRVKET+R+ A+ EL KLGA V E + ITPPE
Sbjct: 283 DAAMTLAVVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGAKEVAEEAEAIHITPPE 342

Query: 392 KLNVT-A-IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
A IDTYDDHRMAM FSL + VPV I DP CT KTFP YFDV S+ +
Sbjct: 343 TPTPDAVIDTYDDHRMAMCFSLVSLGVPVVINDPKCTHKTFPTYFDVFSSLTE 396

>ref|ZP_06158732.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria lactamica
ATCC 23970]
gb|EEZ75798.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria lactamica
ATCC 23970]
Length = 379

Score = 326 bits (835), Expect = 5e-87, Method: Compositional matrix adjust.
Identities = 184/390 (47%), Positives = 239/390 (61%), Gaps = 14/390 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL LG+ +E A R V G GG+FP A LFLGNAG A R LTAA+
Sbjct: 1 MLEALDKLGVGIE-HLAEGRLKVHGTGGRFPNRTA----DLFLGNAGTAFRPLTAALAVL 55

Query: 116 GGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
GG+ Y L GVPRM ERPIGDLV L+ GADV+ PP+ ++ + +
Sbjct: 56 GGD--YHLHGVPVRMHERPIGDLVDALRIAGADVEYLGNEHYPLHISERQDNGERLIPIK 113

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
G++SSQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++++ F
Sbjct: 114 GNVSSQFLTALLMALPLTGQAFEIRMVGELISKPYIDITLKLMAQFGVQVA-NENYRVFK 172

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMG 295
I Y +P++ +VEGDAS ASYFLA I V V G G S+QGDV FA LE +G
Sbjct: 173 IPADAHYHAPEHLHVEGDASGASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIG 232

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVAS 355
A V W E V V+ P + ++A D++ N +PD AMTLA+VAL +R++ S
Sbjct: 233 ADVVWGENFVEVSRPKE-----RAVQAFDLNANHIPDAAMTLAIVALATGQTCTLRNIGS 287

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-A-IDTYDDHRMAMAFSLAA 414
WRVKET+R+ A+ EL KLGA V E + ITPPE L A IDTYDDHRMAM FSL +
Sbjct: 288 WRVKETDRIAAMANELRKLGAKEVEAEAIRITPPELTPTDAVIDTYDDHRMAMCFSLVS 347

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
VPV I DP CT KTFP YF++ S+ +
Sbjct: 348 LLGVPVVINDPKCTHKTFPTYFEIFSSLTE 377

>ref|ZP_05317708.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria sicca ATCC
29256]
gb|EET45228.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria sicca ATCC
29256]
Length = 379

Score = 325 bits (834), Expect = 6e-87, Method: Compositional matrix adjust.
Identities = 186/388 (47%), Positives = 237/388 (61%), Gaps = 14/388 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL LG+ +E A R V G GG+FP A LFLGNAG A R LTAA+
Sbjct: 1 MLEALDKLGVGIEY-LAEGRLKVHGTGGQFPNRTA----DLFLGNAGTAFRPLTAALAVL 55

Query: 116 GGNATYVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS 175
GG+ Y L GV RM ERPIGDLV L+ GADV+ PP+ + + +
Sbjct: 56 GGD--YHLHGVARMH ERPIDLV DALRIAGADVEYLGNEHYPLHIGERQDRGERVIPIK 113

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
G++SSQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ + D + F
Sbjct: 114 GNVSSQFLTALMALPLTGQAFEIRMVVELISKPYIDITLKLMAQFGVQVANED-YRVFK 172

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I +Y +P++ +VEGDASSASYFLA I V V G G S+QGDV FA LE +G
Sbjct: 173 IPADTRYHAPEHLHVEGDASSASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIG 232

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
A V W E V V+ P + ++A D++ N +PD AMTLA+VAL +R++ S
Sbjct: 233 ADVVWGENFVEVSRPKE-----RAVQAFDL DANHIPDAAMTLAIVALATGQTCTLRNIGS 287

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A-IDTYDDHRMAMAFSLAA 414
WRVKET+R+ A+ EL KLGA V E + ITPPE L A IDTYDDHRMAM FSL +
Sbjct: 288 WRVKETDRIAMANELRKLGAQVVEEAIAIHITPPETLTPDAVIDTYDDHRMAMCFSLVS 347

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
VPV I DP CT KTFP YF+V S+
Sbjct: 348 LLGVPVINDPKCTHKTFTYFEVFFSSL 375

>ref|YP_003603071.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Riesia
pediculicola USDA]
gb|ADD79630.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Riesia
pediculicola USDA]
Length = 427

Score = 325 bits (833), Expect = 8e-87, Method: Compositional matrix adjust.
Identities = 177/433 (40%), Positives = 254/433 (58%), Gaps = 13/433 (3%)

Query: 7 IVLQPIKEISGTVKLP GSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I + PI + G V++PGSKS+SNRILL+ALS G T + NL + +D ML L+ +G+
Sbjct: 2 ITIPPISYLKGNVEVPGSKSISNRILLLSALSRGKTKIVNLSDCQDTEIMLSVLKKIGIK 61

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ K ++ G F + +L GN+GI++R LTA ++ + N VL G
Sbjct: 62 FDLFKRNNFCIIYGNPNCFINCGKTDPTRLSFGNSGISIRFLTAILSISNNNV--VLTGT 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM+ERPI LV LKQ A + P++V IGG GG++ L ISSQ+LSAL
Sbjct: 120 KRMQERPIKQLVSSLKQGNAKIFYEKRYGFVPLKV--IGGFHGGEIVLDSHISSQFLSAL 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+AAPLA I + +++S PY++MTL ++ F V E+ + F + QKY SPK
Sbjct: 178 LIAAPLAPNSTRILVKKRIVSKPYIDMTLSMIRLKFVHIENYH-YRLFQVNPQNQKYVSPK 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VE D +SASYFLA +AI G + + G S+QGD KF +++ MGA + W E V
Sbjct: 237 FYCVEPDMTSASYFLAASAIKGFIRINGIKKDSIQGDSKFIDIIRKMGANILWKEDYVE 296

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ L I+++ N +PD AMT+A++ALFA G T I+++ WR KE+ R+++
Sbjct: 297 CR-----KGELCGINIDANDVPDSAMTIAIALFARGKTIKMNHWRFKESNRIIS 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
++ L + GA VEE + II PPEK + I TY+DHR+AM FSL + + V I PG
Sbjct: 349 MKDGLIRAGAYVEEKNRIIIPPEKFQQSKIRTYNDHRIAMCFSLLSLSNRTVIIDHPG 408

Query: 427 CTRKTFPDYFDVL 439
C KTFP++F L
Sbjct: 409 CVNKTFPNFFQKL 421

>ref|YP_322772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anabaena variabilis
ATCC 29413]
sp|Q3MAV9.1|AROANAVT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABA21877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anabaena variabilis
ATCC 29413]
Length = 426

Score = 325 bits (832), Expect = 1e-86, Method: Compositional matrix adjust.
Identities = 188/424 (44%), Positives = 252/424 (59%), Gaps = 17/424 (4%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKS++NR LL+AAL++G + ++N L SED Y + LG+ + +
Sbjct: 11 RPVDATVEIPGSKSITNRALLVAALAQGDSTLENALFSEDSEYFAKCEVQLGIPITLNPH 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G GG P + A LF+G AG A R +TA V A GN Y LDGVPRMRER
Sbjct: 71 LAQIQVSGKGGDIPAKQAD----LFVGLAGTAARFITALV--ALNGEYRLDGVPRMRER 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+GDLV L+ G ++ + P + G GG +L + +SQ LSALLM AP
Sbjct: 125 PMGDLVTVLQNSGIKINFEGSGFMPYTIYG-QQFAGGHFRLKANQTSQQLSALLMIAPY 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D IE+ L+S YV+MT RLM FGV +D ++F+IK GQ+Y++ ++ +E
Sbjct: 184 AQQDTTIEVEGLTVSQSYVKMTCRLMADFGVDVTQTDD-NQFHIKAGQRYQA-RHYTIEP 241

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TGG V V S QGD+ + VLE MG +V E V GP
Sbjct: 242 DASNASYFFAAAVTGGRRVRVNHLLTKQSCQGDILWLVLEQMGCQVLEGEDYTEVIGP-- 299

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
+ L+ IDV+MN M D+ TL +A +A+ P IR+V R KETER+ A+ TEL
Sbjct: 300 -----EQLQGIDVDMNDMSDLVQTLGAIAPYANSPVIIRNVEHIRYKETERIRAVVTELR 354

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTF 432
+LG VEE D I P +N AI+TY DHRMAMAF++ + I+DPGCT KTF
Sbjct: 355 RLGKVEEFADGMKIE-PTPINPAIETYHDMAMAFVAVTGLKTPGIVIQDPGCTAKTF 413

Query: 433 PDYF 436
PDYF
Sbjct: 414 PDYF 417

>ref|YP_003704460.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Truepera radiovictrix
DSM 17093]
gb|ADI13917.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Truepera radiovictrix
DSM 17093]
Length = 428

Score = 322 bits (826), Expect = 5e-86, Method: Compositional matrix adjust.
Identities = 205/441 (46%), Positives = 268/441 (60%), Gaps = 27/441 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ ++P++ + V +PGSKSL+NR L+ AAL+EG + + L +ED M+ ALR LG++
Sbjct: 7 LAIRPLRRVDARVSVPGSKSLTNRALITAALAEGDSTLSGCLVAEDSEVMVRALRALGIA 66

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V + V G GG+ P A+ +++L +G ++R LTA V A G +VLDG
Sbjct: 67 VAI--SGTTMTVSGQGRVPAARAELDLKL---SGTSIRFLTALV--ALGRGRFVLDGN 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RMRERPI DL+ L LG L T CPPV V GLPGG+ L+G SSQYLSAL
Sbjct: 119 ARMRERPIQDLLDAL TALGVKATSQLTGCPVVEA-AGLPGEAVLAGGSSSQYLSAL 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAAP A V + + +L S P+V+MTL+LM FGV+ D + RF + G +Y +
Sbjct: 178 LMAAPYAQTPVTLTVSGELPSKPFVDMTLKLMADFGVEVAR-DGYRRFEVPG-RYAA-- 233

Query: 247 NAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSV 305
AY VEGDA +A Y A AA+TGG V V G +S+QGD + AEVL MG VTW+ETS
Sbjct: 234 RAYAVEGDAMAAGYLWAAAALTGGRVEVTNVGASSVQGDKRLAEVLAEMGCAVTWSETSC 293

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G R L+ ++N M D A TLAVVALFAD P I ++ + R+KET+R+
Sbjct: 294 TVRGTTGR-----LRGGTFDLNDMSDQAQTLAVVALFADAPVTITNIWNLRIKETDRLS 346

Query: 366 AIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
A+R EL+KLGA VEEG D+ + PPE I TY DHRMAMAF+LA V
Sbjct: 347 ALRAELSKLGRARVEEGDWITVHPLTAPPE--GAVEIATYGDHRMAMAFALAGRLPLPGVV 404

Query: 422 IRDPGCTRKTFPDYFDVLS 442
IRDP C KTFP +F+VL+
Sbjct: 405 IRDPACVGKTFPTFFFEVLAAL 425

>ref|ZP_08079252.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Succinatimonas hippei
YIT 12066]
gb|EFY06312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Succinatimonas hippei
YIT 12066]
Length = 424

Score = 320 bits (819), Expect = 3e-85, Method: Compositional matrix adjust.
Identities = 195/437 (44%), Positives = 264/437 (60%), Gaps = 19/437 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L +ISG++ LPSKSKLSNR LLL+A+++GTT + NLL S+D M+ AL+ LG
Sbjct: 2 ETLHLNKKSKISGSITLPSKSKLSNRALLLSAVAKGTRRLHNLRSDDTARMIDALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D VV G G F A++ + L LGNAG AMR L A ++ + G + L
Sbjct: 62 VKLYED--GDVMVVEGIGSAFKCS-AEKRIVLDLGNAGTAMRPLCAMLISISEG--CFELT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM ERPIG L LK LG ++ PP+ + G G + +V + GS SSQ++S
Sbjct: 117 GEVRMMERPIGLSESLKTLGLSIEYLNPNPGFPPLLIRG-GMVNTHVHVDGSTSSQFIS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM+APL G + I++ LIS PVV++T+ L+E+FG K + F + G Y S
Sbjct: 176 ALLMSAPLC-GGLTIKVDGDLISKPYVDLTIALIEKFGAKVTRQ-GYRSFTVAAGD-YVS 232

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + VEGDAS A+YF A AAI G +TV G G S QGD+ F +VLE MGA+V ++
Sbjct: 233 PSDYLVEGDASGATYFCAAAAI-AGEITVNGIGEESTQGDINFLKVLEKMGARVERFKSC 291

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V P L ID++MN MPD AMTL +AL+ G I ++ASWRVKET+R+
Sbjct: 292 VKVYKAP-----ELLGIDIDMNMMPDAAMTLVPMALYTKGKVRITNIASWRVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPP-EKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
A+ E++KLG +V G D+ I + DTY+DHRMAM+ SLAA + + I
Sbjct: 345 AAMVKEMSKLGVNNSGEDFIEIDASVRNHDEVTFDYNDRMAMSMSSLAALF-DRDININ 403

Query: 424 DPGCTRKTFPDYFDVLS 440
DP CT+KTFPDYF + S
Sbjct: 404 DPECTKTKTFPDYFGLFS 420

>ref|NP_489059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nostoc sp. PCC 7120]
sp|Q8YMB5.1|AROANASAP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB76718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nostoc sp. PCC 7120]
Length = 425

Score = 317 bits (813), Expect = 2e-84, Method: Compositional matrix adjust.
Identities = 185/424 (43%), Positives = 248/424 (58%), Gaps = 17/424 (4%)

Query: 13 KEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKS++NR LL+AAL++G + ++N L SED Y + LG+ +
Sbjct: 11 RPVDATVEIPGSKSITNRALLVAALAQGDSTLENALFSEDSEYFAKCVLQIGIPITLHPH 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G GG P + A LF+G AG A R +TA V A GN Y LDGVPRMRER

Sbjct: 71 LAQIQVSGKGGDIPAKQAD----LFVGLAGTAARFITALV--ALGNGEYRLDGVPRMRER 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+GDLV L+ G ++ + P + G GG +L + +SQ LSALLM AP

Sbjct: 125 PMGDLTVTLQNSGITINFEGNSGFMPYTIYG-QQFAGGHFRLKANQTSQQLSALLMIAPY 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D IE+ L+S YV+MT RLM FGV +D ++F+IK GQ+Y++ ++ +E

Sbjct: 184 AQQDTTIEVEGTLVSQSYVKMTCRLMADFGVDVTQTDD-NQFHIKAGQRYQA-RHYTIEP 241

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TGG V V S QGD+ + VLE MG +V V GP

Sbjct: 242 DASNASYFFAAAAVTGGRRVRVNHCLKQSCQGDILWLVLEQMGCVIEGADYTEVIGP-- 299

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ L+ ID++MN M D+ TL +A +A P IR+V R KETER+ A+ TEL

Sbjct: 300 -----EQLQGIDIDMNDMSDLVQTLGAIAPYASSPVIIRNVEHIRYKETERIRAVVTELR 354

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 432
+LG VEE D I P + AI+TY DHRMAMAF++ + I+DPGCT KTF

Sbjct: 355 RLGKVKVEEFADGMKIE-PTPITPAAIETYHDMAMAFVAVTGLKTPGIVIQDPGCTAKTF 413

Query: 433 PDYF 436
PDYF

Sbjct: 414 PDYF 417

>gb|AAV52048.1| AroA [Actinobacillus ureae ATCC 25976]
Length = 338

Score = 317 bits (812), Expect = 2e-84, Method: Compositional matrix adjust.
Identities = 173/345 (50%), Positives = 226/345 (65%), Gaps = 15/345 (4%)

Query: 46 NLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAM 105
NLL+S+D+ +ML AL+ LG++ + V G GG F ++ + LFLGNAG AM

Sbjct: 2 NLLDSDDIRHMLNALKALGVNYSLSSEDKTVCTVEGIGGAFNWQNG---LSLFLGNAGTAM 58

Query: 106 RSLTAAVTAAGG-NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI 164
R LTAA+ G A +L G PRM+ERPI LV L+Q GA V PPV +

Sbjct: 59 RPLTAALCLKGATEAEVILTGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVPAIRN- 117

Query: 165 GGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK 224
GL GGV++ GSISSQ+L+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGV

Sbjct: 118 SGLKGGKVQIDGSISSQFLTALLMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVN 177

Query: 225 AEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
E+ + + F +KG Q Y SP+ VEGDASSASYFLA AI G V V G G S+QGD

Sbjct: 178 VENQN-YQTFVVGKNQSYISPEKYLVEGDASSASYFLAAGAIKG-KVKVTGIGKNSIQGD 235

Query: 285 VKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA 344
FA VLE MGAK+TW + + + LK +D++MN +PD AMT+A ALFA

Sbjct: 236 RLFANVLEAMGAKITWGDDFIQAE-----QGELKGVMDMNMHIPPDAAMTIATTALFA 287

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITP 389
+G T IR++ +WRVKET+R+ A+ TEL K+GA+VEEG D+ I P

Sbjct: 288 EGETVIRNIYNWRVKETDRLAAMATELRKVGATVEEGEDFIRIQP 332

>ref|ZP_06157994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria cinerea
ATCC 14685]
gb|EEZ72611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria cinerea
ATCC 14685]
Length = 359

Score = 317 bits (811), Expect = 3e-84, Method: Compositional matrix adjust.
Identities = 175/364 (48%), Positives = 223/364 (61%), Gaps = 13/364 (3%)

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G GG+FP LFLGNAG A R LTAA+ GG+ Y L GVPRM ERPIGDLV

Sbjct: 3 GTGGRFP----NRTTDLFLGNAGTAFRPLTAALAVLGGD--YHLHGVPRMHERPIGDLVD 56

Query: 140 GLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ GADV+ PP+ + + G++SSQ+L+ALLMA PL EI
Sbjct: 57 ALRIAGADVEYLGNEHYPLHIGKRQDRGERVPIKGNVSSQFLTALLMALPLTGQAFEI 116

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
++ +LIS PY+++TL+LM +FGV+ + D + F I Y +P++ +VEGDASSASY
Sbjct: 117 RMVGELISKPYIDITLKLMAQFGVQVANED-YRVFKIPADAHYHAPEHLHVEGDASSASY 175

Query: 260 FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKH 319
FLA I V V G G S+QGDV FA LE +GA V W E V V+ P +
Sbjct: 176 FLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVWGENFVEVSRPK-----ERA 230

Query: 320 LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
+ A D++ N +PD AMTLA+VAL +R++ SWRVKET+R+ A+ EL KLGA V
Sbjct: 231 VLAFLDLNANHIPDAAMTLAIVALATGQTCTLRNIGSWRVKETDRIAAMANELRKLGAQVV 290

Query: 380 EGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDV 438
E + ITPP+ L A IDTYDDHRMAM FSL + VPV I DP CT KTFP YF+V
Sbjct: 291 EEAEAIHITPPKMLTPDAVIDTYDDHRMAMCFLVSLGLGVPVINDPKCTHKTFTPTYPEV 350

Query: 439 LSTF 442
S+
Sbjct: 351 FSSL 354

>ref|ZP_01093993.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blastopirellula
marina DSM 3645]
gb|EAQ77334.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blastopirellula
marina DSM 3645]
Length = 427

Score = 317 bits (811), Expect = 3e-84, Method: Compositional matrix adjust.
Identities = 203/437 (46%), Positives = 259/437 (59%), Gaps = 19/437 (4%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
I + P I G++ PGSKSL+NR L++AAL++G + + L SED H M+ +LR LG+
Sbjct: 4 RIEIAPSPPIILSGSILPPGSKSLTNRALVIAALAQKSSLTGALESEDTHVMIDSLRRLGI 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V+ D+ AK V GC G P DA LF+ N+G +R LTA V A G Y LDG
Sbjct: 64 DVQHDDRRAKVIDVTGCDGVIPSSDA----DLFVANS GTTIRFLTAMV--AAGKGRYRLDG 117

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
V RMRERPI DL+ L LG CPPV V GL GG +++G ISSQYLS
Sbjct: 118 VQRMREPIRDLLETLSALGVTCRSEAENGCPPVVVE-TSGLVGGVAQIAGDISSQYLSG 176

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLMAAP A V +E++ +L+S PYV MT +M FGV + D + I G KY
Sbjct: 177 LLMAAPYAAQGVSLVGVGELVSKPYVHMTTAVMRDFGVNVDAGD-LTKLVIPHG-KYVGR 234

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ A +E DAS+ASYF A AAITGG+VTVEG +LQGDV F E LE MG +V + S+
Sbjct: 235 QYA-IEPDASAASYFWAAAAITGGSVTVEGLSRDALQGDVAFCECLEQMGCVVEYGPNSI 293

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G ++ I V+MN + D TLA VALFADGPT + VA R KET+R+
Sbjct: 294 KVVG-----SRMRGICVDMNAISDTVQTLAVALFADGPTTVTGVAHNRHKTDRIG 345

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
+ EL KLGA VEE D I P +L I+TY+DHRMAM+ +L + V I +P
Sbjct: 346 DLACELRLKGA VVEELEDGLTIV-PSRLQPAEIEIYNDHRMAMSLALVGLRQPGVVILNP 404

Query: 426 GCTRKTFPDYFDVLSTF 442
CT KT+P+YF+ LS
Sbjct: 405 ACTGKTYPNYFEDLSRL 421

>ref|YP_001864974.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nostoc punctiforme
PCC 73102]
sp|B2IYE4.1|AROA_NOSP7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|ACC80031.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nostoc punctiforme
PCC 73102]
Length = 426

Score = 315 bits (808), Expect = 7e-84, Method: Compositional matrix adjust.
Identities = 183/424 (43%), Positives = 253/424 (59%), Gaps = 17/424 (4%)

Query: 13 KEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKSL+NR LL+AAL++G ++++N L SED Y L LG+ + +
Sbjct: 11 RPYDATVEIPGSKSLTNRALLVAALAQGDSILENALFSEDSEYFAKCLEQLGIPITLNP 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G GG+ P + A LF+G +G R ++A V A GN Y LDGVPRMRER
Sbjct: 71 LAQIQLAGRGGEIPAKQAD---LFVGLSGTTARFISALV--ALNGEYRLDGVPRMRER 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+GD++ L+ GA V+ + P V G GG L + +SQ LSALLM AP
Sbjct: 125 PMGDMLTVLETTGGATVNFEGNSGFMPYTVYS-QGFAGGNFCLKANQTSQQLSALLMIAPY 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D E+ L+S+ Y++MT RLM FGV+ ++F IK GQ+Y++ ++ VE
Sbjct: 184 AQQDTIFEVEGTLVSLSYIKMTCRLMADFGVEVIQIGD-NQFQIKAGQRYQA-QHYTVEP 241

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TGG V V+ S QGD+ + VLE MG ++ ++ VTGP
Sbjct: 242 DASNASYFFAAAAVTGGRRVVKHLTKQSCQGDILWLVLEQMGCQIKDSDDYTEVTGP-- 299

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
K L+ ID++MN + D+ TLA +A FA P IR+V R KET+R+ A+ TEL
Sbjct: 300 -----KQLQGIDIDMNDISDLVQTLAAIAPFASSPITIRNVEHIRYKETDRIKAVVTEL 354

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432
+LG VEE PD I P + I+TY DHRMAMAF++ + I+DPGCT KTF
Sbjct: 355 RLGQVQVEEFPDLRKIE-PGPITPAEIEITYHDMAMAFVAVTGLKVPVGIKDPGCTAKTF 413

Query: 433 PDYF 436
PDYF
Sbjct: 414 PDYF 417

>ref|XP_002505432.1| predicted protein [Micromonas sp. RCC299]
gb|AC066690.1| predicted protein [Micromonas sp. RCC299]
Length = 229

Score = 311 bits (797), Expect = 1e-82, Method: Compositional matrix adjust.
Identities = 160/232 (68%), Positives = 179/232 (77%), Gaps = 9/232 (3%)

Query: 213 MTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVT 272
MT++LMERFGV+ + D RF +KGGQ Y+SP A+VEGDASSASYFLAGAAITGG V
Sbjct: 1 MTVKLMERFGVEVQVFDMDQRFVVKGGQTYQSPGEAFVEGDASSASYFLAGAAITGGKVK 60

Query: 273 VEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPD 332
V GCGT SLQGD KFA+ + +MGAKV W + VVTGTP G K LKAIDVNMN MPD
Sbjct: 61 VIGCGTDSLQGDTKFADTMGLMGAKVEWGKNDVTVTGPF-----GGK-LKAIDVNMNAMPD 114

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-- 390
AMTLAV AL+ADG T IRDV SWRVKETERM+AI TE+ KLG V EG DYC+ITPP
Sbjct: 115 AAMTLAVAALYADGVTTIRDVGSWRVKETERMIAICTEMRKLGCDEVYEGADYCVITPPGS 174

Query: 391 EKLNV-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLST 441
K+N +IDTYDDHRMAMAFSLAAC V VTI DP CT+KTFP YFD L+T
Sbjct: 175 GKINEGVSIDTYDDHRMAMAFSLAACGGVGTIMDPTCTKKTFPTYFDALAT 226

>ref|YP_003370952.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pirellula staleyi DSM
6068]
gb|ADB17092.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pirellula staleyi DSM
6068]
Length = 431

Score = 310 bits (794), Expect = 3e-82, Method: Compositional matrix adjust.
Identities = 192/433 (44%), Positives = 258/433 (59%), Gaps = 20/433 (4%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALLSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
I G+++ PGSKS++NR L+ AAL+ G +++ L+SED M+ +L LG+ VEA +
Sbjct: 13 IVGSIQPPGSKSITNRLVCAALAHGNSILRGALDSEDTQVMIDSLDRLGIVVEASDEKQ 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V GCGG+ P K LF+GN+G +R LTA + A G + LDGVPRMRERPI
Sbjct: 73 TLAVTGCGRLP----KPTGDLFVGNSGTTIRFLTAMLAACEGE--FRLDGVPRMRERPI 126

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
GDL+ L +LG+D + PPV++ GL GG V++ G +SSQ+LS LLMAAP+A
Sbjct: 127 GDLMDALNRLGSDCQGEIKPGFPPVKLKA-RGLGGGDVEVRGDVSSQFLSGLLLMAAPVAK 185

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGV---KAEHSDSWDRFYIKGGQKYKSPKNAYVE 251
V + + L+S PYV MTL +M+ FG+ + DS + QKY + +E
Sbjct: 186 NPVRVHVTGDLVSKPYVHMTLAVMKSFGIDVGQTRSEDSLSLIELAAPQKYTG-IDYQIE 244

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
DAS+ASYF A AAITGG+VTV+ G +LQGDV + LE MG +V +TV+G
Sbjct: 245 PDASAASYFWAAAAITGGSVTVKNLGPDALQGDVGIVDCLEQMGCRCRVERQPHQITVSG-- 302

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
K L+ I+V+MN + D TLA VALF DGPT I V R KET+R+ + EL
Sbjct: 303 -----KALRGIEVDMNAISDTVQTLAAVALFVDGPTIIHGVGHIRHKETDRIGDLAREL 356

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 431
KLGA+VEE D + P L I+TY DHRMAM+ +L V I DPGCT KT
Sbjct: 357 RKLGAATVEE-RDEGLTIIPGPKAATITETYRDHRMAMSLALPGLLVPGVILDPGCTAKT 415

Query: 432 FPDYFDVLSTFVK 444
+P YF+ L+ +
Sbjct: 416 YPHYFEDLAALCR 428

>ref|ZP_05716512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio mimicus VM573]
gb|EEW11581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio mimicus VM573]
Length = 296

Score = 309 bits (791), Expect = 7e-82, Method: Compositional matrix adjust.
Identities = 152/269 (56%), Positives = 192/269 (71%), Gaps = 9/269 (3%)

Query: 169 GKGKVLKSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHES 228
G V + GSISSQ+L+A LM+APLA G V I+I+ +L+S PY+++TL +ME+FGV+ +
Sbjct: 30 AGTVTIDGSISSQFLTAFLMSAPLAQGVKVTIKIVGELVSKPYIDITLHIMEQFGVQVINH 89

Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA 288
D + F I GQ Y SP N VEGDASSASYFLA AAI GG V V G G S+QGD++FA
Sbjct: 90 D-YQEFVIPTGQSYVSPGNFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFA 148

Query: 289 EVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPT 348
+ LE MGA++ W + V R L A+D++ N +PD AMT+A ALFA G T
Sbjct: 149 DALEKMQAQIEWGDDYVISR-----RGELNAVDLDFNHIPDAAMTIATTALFAKGT 200

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
AIR+V +WRVKET+R+ A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM
Sbjct: 201 AIRNVYNWRVKETDRLAAMATELRKVGATVEEGEDFVITPPAKLTHAAIDTYDDHRMAM 260

Query: 409 AFSLAACAEVPTIRDPGCTRKTFFPDYFD 437
FSL A ++ PVTI DP CT KTFPDYF+
Sbjct: 261 CFSLVALSDTPVTINDPKCTSKTFFPDYFE 289

>gb|AAV52046.1| AroA [Haemophilus parasuis]
Length = 329

Score = 307 bits (787), Expect = 2e-81, Method: Compositional matrix adjust.
Identities = 171/338 (50%), Positives = 221/338 (65%), Gaps = 15/338 (4%)

Query: 53 WHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV 112

Sbjct: 1 + +ML AL+ LG++ + V G GG F + K + LFLGNAG AMR LTAA+
IRHMLNALKALGVNYSLSSEDKTVCTVEGVGGAF---NWKNGLALFLGNAGTAMRPLTAAL 57

Query: 113 TAAGGN-ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK 171
G + A VL G PRM+ERPI LV L+Q GA V PPV + GL GGK

Sbjct: 58 CLKGSSEAEVLTGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGK 116

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
V++ GSISSQ+L+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGVK E+ + +

Sbjct: 117 VQIDGSISSQFLTALLMAAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVKVENRN-Y 175

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 291
F +KG Q Y SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VL

Sbjct: 176 QTFVVKGNQSYLSPEKYLVEGDASSASYFLAAGAIG-KVKVTGIGKNSIQGDRLFANVL 234

Query: 292 EMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIR 351
E MGAK+TW + + + LK +D++MN +PD AMT+A ALFA+G T IR

Sbjct: 235 EAMGAKITWGDDFIQAE-----QGKLGVDMDMNHIPDAAMTIATAALFAEGETVIR 286

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITP 389
++ +WRVKET+R+ A+ TEL K+GA+VEEG D+ I P

Sbjct: 287 NIYNWRVKETDRLTAMATELRKVGATVEEGDFIRIQP 324

>emb|CBY95002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Weltevreden str. 2007-60-3289-1]
Length = 288

Score = 303 bits (777), Expect = 3e-80, Method: Compositional matrix adjust.
Identities = 152/276 (55%), Positives = 194/276 (70%), Gaps = 11/276 (3%)

Query: 166 GLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK- 224
G GG +++ GS+SSQ+L+ALLM APLA D I + +L+S PY+++TL LM+ FGV+

Sbjct: 17 GFTGGDIEVDGVSQQFLTALLMTAPLAPEDTTIRVKGELVSKPYIDITLNLMTKTFGVEI 76

Query: 225 AEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
A H + +F +KGGQ+Y SP VEGDASSASYFLA AI GGTV V G G S+QGD

Sbjct: 77 ANHH--YQQFVVKGGQYHSPGRYLVVEGDASSASYFLAAGAIGGTVKVTGIGRKSQGD 134

Query: 285 VKFAEVLMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA 344
++FA+VLE MGA +TW + + T R L AID++MN +PD AMT+A ALFA

Sbjct: 135 IRFADVLEKMGATITWGDDFIAC-----RGEHAIMDMDMNHIPDAAMTIATTALFA 186

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDH 404
G T +R++ +WRVKET+R+ A+ TEL K+GA VEEG DY ITPP KL I TY+DH

Sbjct: 187 KGTTTTLRNIYNWRVKETDRLFAMATELRKVGAEVEEGHDYIRITPPAKLQHADIGTYNDH 246

Query: 405 RMAMAFSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
RMAM FSL A ++ PVTI DP CT KTFPDYF+ L+

Sbjct: 247 RMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLA 282

>emb|CAA10164.1| 5-enolpyruvylshikimate 3-phosphate synthase [Actinobacillus
pleuropneumoniae]
Length = 332

Score = 300 bits (769), Expect = 3e-79, Method: Compositional matrix adjust.
Identities = 178/343 (51%), Positives = 225/343 (65%), Gaps = 15/343 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+I L PI + G + LKPSKSLSNR LLLAAL++GTT V NLL+S+D+ +ML AL+ LG

Sbjct: 2 EKITLAPISRVEGEINLPKSGKSLSNRALLAALAKGTTKVTNLLSDDIRHMLNALKALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN-ATYVL 123
++ + V G GG F + K + LFLGNAG AMR LTAA+ G + A VL

Sbjct: 62 VNYLSSEDKTVCTVEGVGGAF---NWKNGLALFLGNAGTAMRPLTAALCLKGSSEAEVVL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G PRM+ERPI LV L+Q GA V PPV + GL GGK++ GSISSQ+L

Sbjct: 119 TGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGKVQIDGSISSQFL 177

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGVK E+ + + F +KG Q Y
Sbjct: 178 TALLMAAPLAEGDMEIEIIGELVSKPYIDITLAMMKDFGVKVENRN-YQTFVVKGNSYL 236

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MGAK+TW +
Sbjct: 237 SPEKYLVEGDASSASYFLAAGAIK-GKVKVTGIGKNSIQGDRLFANVLEAMGAKITWGDD 295

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG 346
+ + LK D++MN +PD AMT+A ALFA+G
Sbjct: 296 FIQAE-----QGKLGKGDMDMNHIPDAAMTIATAALFAEG 330

>ref|ZP_02737777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gemmata obscuriglobus
UQM 2246]
Length = 436

Score = 297 bits (760), Expect = 2e-78, Method: Compositional matrix adjust.
Identities = 189/447 (42%), Positives = 263/447 (58%), Gaps = 26/447 (5%)

Query: 6 EIVLQPI-KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVD--NLLNSEDVHYMLGALRT 62
E+ +QP+ + +S TV +PGSKS++NR L+LAAL++G + +L SED MLGAL
Sbjct: 8 ELEIQPLARSVSATVTVPGSKSITNRALVLAALAKGDAPCELRGVLRSEDTEVMLGALAQ 67

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
LG SV D A V P + LF+ N+G +MR L A V+ G Y
Sbjct: 68 LGYSVHEDWATN---TVRVTNPTPTIPADRADLFVANSGMTSMRFLAAMVSLGAGR--YR 122

Query: 123 LDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
LDG+PRMRERPI DL+ L+ LG + G CPPV + GL G V + + SSQ+
Sbjct: 123 LDGIPRMRERPIEDLLSALRALGVNATSESGNCCPPVIEA-NGLRTGPVHIKVAKSSQF 181

Query: 183 LSALLMAAPLALGDVE----IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
LSAL+MA P A E + + ++S PY+EMT+R++E + + + + + I+
Sbjct: 182 LSALMMAVPFARASSEHPATIVHLDGTVVSEPYIEMTVRMLESWAIRVDRV-APNAYRIE 240

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ ++ + +E DAS+ASYF A AA+ GG+VTV G SLQGDV+F +VL MG +
Sbjct: 241 PQRGHRERYD--IEPDASAASYFWAAAALVGGSVTVRGLNRASLQGDVRFVDVLGQMCCR 298

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
+ + +TV G P L+ +DV+MN + D MTL VALFADGPT +R+VA R
Sbjct: 299 IEENDGGITVHGGP-----LRGVDVMDNDISDTVMTLGAVALFADGPTTVRNVAHIR 350

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
KET+R+ A+ EL KLGA VEE D IT P L AIDTY+DHRMAM+ +L
Sbjct: 351 HKETDRIAALAIELRKLGAEVEEREDGLTIT-PRPLKGCAIDTYNDHRMAMSLALVGLKV 409

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVK 444
V IR+PGC KT+P +++ L K
Sbjct: 410 PGVVIRNPGCAKTYPGFWEDLEVLRLK 436

>ref|XP_001746575.1| hypothetical protein [Monosiga brevicollis MX1]
gb|EDQ88471.1| predicted protein [Monosiga brevicollis MX1]
Length = 1520

Score = 295 bits (756), Expect = 8e-78, Method: Compositional matrix adjust.
Identities = 190/454 (41%), Positives = 260/454 (57%), Gaps = 40/454 (8%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
MA A E+V P I+GT+++PGSKS+SNR+LL+AAL G + LL+S+D M+ AL
Sbjct: 359 MAPAVEVV--PHGPIAGTIRVPGSKSISNRVLLMAALGRGVCRRLGLLHSDTKVMIAAL 416

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R LG+ +E + ++ GC GK A + LFL NAG A R LT+A A +
Sbjct: 417 RKLGVRIEFEDNGHVLLIQGCDGKL---QAAGDNALFLANAGTASRFLTSACCLASSGHS 473

Query: 121 YVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
V GV RM ERPIGDLV L+ + +D PP+RV+G G LPGG ++L+ ++SS
Sbjct: 474 LV-TGVKRMHERPIGDLVEALRAVDCAIDYLDQEGYPPLRVHGTG-LPGGTIQLAATVSS 531

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSWDRFYIKGG 239
QY+S++L+AAP A V +E++ ++S PY++MT+ LM++FGV E HS S Y+
Sbjct: 532 QYVSSILLAAPYAQAPVTLELVGEVVSQPYIDMTVALMKQFGVDVEAHSGSR---YVIPN 588

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y+ P VE DASSASY LA AAI+GG VTV G+ SLQGD F VLE MG +V
Sbjct: 589 TGYQLPDTDFVEDSASSASYPLAMAAISGGRVTVAAMGSGSLQGDAAFCRVLERMGCEVE 648

Query: 300 WTETSVTVTG--PPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGP----TAIRDV 353
T + TV G P L+ +DV+M + D MT AV L A P + I ++
Sbjct: 649 QTSDATTVVGCVP-----GTLQPVVDVMDGIDITDTFMTAAV--LMATCPKGSRSSTITNI 699

Query: 354 ASWRVKETERMVAIRTELTKLGASVEE-----GPDYCIITPPEKLNVTADITYDD 403
A+ RVKE R+ A+ TEL K G EE G D +P ++ Y D
Sbjct: 700 ANQVRVKECNRITAMLTGKCGVHCEELETGLAIFGQGAD----SPASLKRGVVPECYRD 755

Query: 404 HRMAFAFLAACAEPVPTIRDPGCTRKTFPDYFD 437
HR+AM+F + C V I D CT KT+P ++D
Sbjct: 756 HRIAMSFVGLGCLWPNVQITDKDCTDKTYPSEFWD 789

>ref|NP_630891.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
coelicolor A3(2)]
sp|Q9L213.1|AROAl_STRCO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 1;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase 1; Short=EPSP synthase 1; Short=EPSPS 1
emb|CAB71266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
coelicolor A3(2)]
Length = 440

Score = 294 bits (752), Expect = 2e-77, Method: Compositional matrix adjust.
Identities = 183/442 (41%), Positives = 249/442 (56%), Gaps = 23/442 (5%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE + ++ + TV++ GSKS +NR L +A+LS TV+DN L S+D Y A+ T
Sbjct: 11 AETLTIRTTLTGFDVTVRLGSKSYTNRYLAIASLSGQETVIDNALLSDDTVYFSRAIETF 70

Query: 64 G-LSVEADKAAKRAVVVGCGG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
G ++ + D A R V G + P ED +F+G AG +R L + A G T
Sbjct: 71 GHVTCIDHATARIRVPTGRPMRASED-----IFVGAGTPLRFLISMAGHADG--T 122

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
++ G RM+ERP+GDL+ L LG D G PPVRV G G GG +SG++SS
Sbjct: 123 TIITGNARMQERPMGDLKALPALGVDATAVRNGSPPVRVVG-GSFKGGATSISGAVSS 181

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QY+ S+L++ A A D EI I D L+S PYVEMTL + GV + D + RF + GQ
Sbjct: 182 QFTSSLIINALRAQTDTEITISDDLVSQPYVEMTLAGLAEMGVSVDR-DGYRRFTVPSGQ 240

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + VE DAS SYFLA AAI V + G G S QGDV + LE MG +
Sbjct: 241 QARGGQ-VTVEPDASMSYFLAAAAILQSRVVIPGIGAGSHQGDVHLVQALERMGCRTVEV 299

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ S+TVTG P L+ ID++M MPDV +LA+VA +A+G T I ++AS RVKE
Sbjct: 300 GDDSIITVTGGP-----LRGIDIDMEAMPDVVPSLAIVAAYAEGTTRITNIASLRVKE 351

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEPV 420
+R+ A+ TEL K+G VEE D IT + IDTYDDHR+AM F++ V
Sbjct: 352 CDRIAAVTTELKMGIDVEEHSADAMYITGGTP-HGAVIDTYDDHRIAMTFAIGGLRTEGV 410

Query: 421 TIRDPGCTRKTFPDYFDVLSF 442
I+DPGC K+FP ++ L T
Sbjct: 411 VIKDPGCVAKSFPAFWQTLDTL 432

>ref|ZP_07198687.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
NaphS2]
gb|EFK12016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
NaphS2]

Length = 421

Score = 294 bits (752), Expect = 2e-77, Method: Compositional matrix adjust.
Identities = 181/428 (42%), Positives = 250/428 (58%), Gaps = 19/428 (4%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV +PGSKS+++R L+ AL++GTT++ N L SED + AL +G+ ++ + +
Sbjct: 9 TVTIPGSKSITHRALITGALAKGTTILGNLISEDTLHTARALAAIGVGMK--RRDDHLI 66

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G G D E ++LGN+G + R L + A G +++ G PRMRERP+G L
Sbjct: 67 VEGIGQT--ACDQPWEKAIYLGNSGTSFRLLLPVLALARGR--FLVTGTPRMRERPVGPL 122

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+QLG + C PPVR+ G+ GG V L G SSQ+LSALL+A P A V
Sbjct: 123 VDALRQLGVRIICTGRDGFPPVRLLS-DGIKGGAVNLPGDASSQFLSALLLAGPYAEQGV 181

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+I + L+S PYV++T+ +M FGV E + + RF + GGQ+Y +P V GDASSA
Sbjct: 182 DITVKGDLVSKPYVDVTVDVMNSFGVSIER-EGFSRFRVFGGQY-NPMEYTVSGDASSA 239

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SYF AGAAITG TVT QGD++ EVLE MG V VTV+G
Sbjct: 240 SYFWAGAAITGKTVTTRNINPQGRQGDIRLLEVLQMGCVVQRDTRVTVSG----- 291

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
L +DV+M MPD+ TLA VALFA G T IR+V R KE++R+ A+ E +LG
Sbjct: 292 GKLSGVDVDMGAMPDMVPTLAAVALFAPGKTTIRNVGHLRFKESDRLSAVTREWRRLGGR 351

Query: 378 VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP-VTIRDPGCTRKTFPDYF 436
VEE D +I L+ +DTYDDHR+AM+ ++ EVP V I++P C K+FP ++
Sbjct: 352 VEELEDALVIRGGASLHGCDVDTYDDHRIAMSLAVIGL-EVPGVRIQNPDCVNKSFRFW 410

Query: 437 DVLSTFVK 444
D+ V+
Sbjct: 411 DLWEDLVR 418

>gb|EFW98669.1| dehydroquinase class 1 [Grosmanina clavigera kwl407]
Length = 1584

Score = 293 bits (751), Expect = 3e-77, Method: Compositional matrix adjust.
Identities = 196/438 (44%), Positives = 259/438 (59%), Gaps = 19/438 (4%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADK 71
K++ TV PGSKS+SNR L+LAAL G+ + NLL S+D YML A+ L G S ++
Sbjct: 412 KDLHVTVPVPGSKSVSNRALVLAALGTGSCRLRLNLLRSDDTEYMLSAIAQLQGASYSWEE 471

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRM 129
+ + V G GG+F A E L+LGNAG A R LT+ V +A + VL G RM
Sbjct: 472 SGEVLAVQGNNGR---TASSE-PLYLGNAGTASRFLTSVVALCSPSAVSSTVLTGNERM 527

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+ RPIG LV L+ G V+ PV+V+ GGL GG ++L+ ++SSQY+S++LMA
Sbjct: 528 KVRPIGLVDALRSNGVKVEYLGNGKSLPVQVDAAGGLEGGVIELAATVSSQYVSSILMA 587

Query: 190 APLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AP A V + ++ K IS PY++MTL +ME FG+ AE S+S Y Y++P
Sbjct: 588 APYAKKPVVLRVLVGKPISQPYIDMTLSMMEAFGIHAERSESEPNTYHIPTGTYNPAEY 647

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTV 307
VE DASSA+Y LA AAITG T T+ G+ SLQGD FA VL MG VT TS TV
Sbjct: 648 VVESDASSATYPLAIAAITGTTCTIPNIGSASLQGDADFAVSVLRPMGCSVTQAITSTTV 707

Query: 308 TGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
TGPP LKAI V+M M D +T +V+A ADG T I +A+ RVKE R++A+
Sbjct: 708 TGPP-----PGSLKAISVDMPEMTDAFLTASVLAADGTTTRITGIANQVRKECNILAM 762

Query: 368 RTELTKLGASVEEGPDYCIIT--PPEKLN--TAIDTYDDHRMAMAFS-LAACAEVPVTI 422
+ EL K G E D +T P +L+ ID YDDHR+AM+FS L+ A PV I
Sbjct: 763 KDELAKFGVQCTELDDGLEMTGRPIGQLSTPEDGIDCYDDHRVAMSFVLSVAAPQPVLI 822

Query: 423 RDPGCTRKTFPDYFDVLS 440
+ C KT+P ++D LS
Sbjct: 823 LERECVGKTWPGWWDTLS 840

>gb|AAL65914.1|AF440390_1 5-enolpyruvylshikimate-3-phosphate synthase [Orychophragmus violaceus]
gb|AAL65915.1|AF440391_1 5-enolpyruvylshikimate-3-phosphate synthase [Orychophragmus violaceus]
Length = 170

Score = 291 bits (745), Expect = 1e-76, Method: Compositional matrix adjust.
Identities = 153/170 (90%), Positives = 161/170 (94%)

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
VVGLKQLGADV+C LGT+CPPVRVN GGLPGGKVKLSGSISSQYL+ALLMAAPLALGDV
Sbjct: 1 VVGLKQLGADVCTLTGNCPPVRVNANGGLPGGKVKLSGSISSQYLTALLMAAPLALGDV 60

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EIEIIDKLIS+PYVEMTL+LMERFGV AEHSDSWDRF++KGGQKYKSP NAYVEGDASSA
Sbjct: 61 EIEIIDKLISVPYVEMTLKLMERFGVSAHSDSWDRFFVKGQKYKSPGNAYVEGDASSA 120

Query: 258 SYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
SYFLAGAAITG TVTVEGCGTSLQGDVKFAEVLE MG KV+WTE SVTV
Sbjct: 121 SYFLAGAAITGETVTVEGCGTSLQGDVKFAEVLEKMGCKVSWTENSVTV 170

>ref|YP_004193764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfobulbus propionicus DSM 2032]
gb|ADW16473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfobulbus propionicus DSM 2032]
Length = 425

Score = 290 bits (742), Expect = 3e-76, Method: Compositional matrix adjust.
Identities = 187/441 (42%), Positives = 259/441 (58%), Gaps = 20/441 (4%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLNSEDVHYMLGALRTLGLS 66
I +QP+ I V +PGSKSL+ R L+ AAL+EG++ + L SED H+ + ALR +G++
Sbjct: 2 ITIQPVATIDAVVTVPGSKSLTQRALIAAALAEGLSLLGLPLASEDTHFTMNALRAMGIA 61

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D+ R V G GG+ E +FLGN G A R LT+ AA G + + G
Sbjct: 62 CD-DRDPNRWQVEGSGGRV----LAPEGDIFLGNNGTATRFLTS--VAALGQGRFHITGS 114

Query: 127 PRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM ERPI L+ L+ +D GT CPP+ + GL GG+ L SSQYLS+L
Sbjct: 115 ERMAERPILPLMEALRGWQVSDAGTGCPPLTIMA-KGLAGGRTVLPEGKSSQYLSL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+ AP A E+E++ +++S PYVEMTL +M FGV+ E + + + F I G Y+ +
Sbjct: 174 LLVAPYANAPAELEVLGEILSKPYVEMTLAVMADFGVRVEAAPTINFFRIPRG-SYQG-R 231

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+EGDAS ASYF A AA+TGG VTV SLQGD K L MG ++ TE +T
Sbjct: 232 TYAIEGDASGASYFWAAAATGGRVTVANVPVPSLQDALLPYLARMGCRIEQTEAGIT 291

Query: 307 VTGPPREFFGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ GP R L+ I+V+M MPDVA TLAVVA FA+G T I ++A R+KE +R+ A
Sbjct: 292 LIGPDR-----LEGIEVDMGDMPDVAPTLAVVAFAEGTTIINNIAHLRIKECDRLSA 344

Query: 367 IRTELTKLGASVEEGPDYCIITPPE---KLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ EL KLGA VEE P II + L+ +I TY+DHRMAM+F++A V I
Sbjct: 345 VVNELRLKGAEEVEEPARMIIHGKQGRTLHGASIAATYNDHRMAMSAVAGLRIPGVYIG 404

Query: 424 DPGCTRKTFPDYFDVLSFVK 444
+P C K+FPD+++ + +
Sbjct: 405 NPQCVKSFPPDFWERFARLAE 425

>ref|XP_003007290.1| pentafunctional AROM polypeptide [Verticillium albo-atrum VaMs.102]

gb|EEY17320.1| pentafunctional AROM polypeptide [Verticillium albo-atrum VaMs.102]
Length = 1574

Score = 289 bits (739), Expect = 7e-76, Method: Compositional matrix adjust.
Identities = 189/438 (43%), Positives = 260/438 (59%), Gaps = 20/438 (4%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++ TV PGSKS+SNR L+LAAL EGT + NLL+S+DV +ML A+ LG S + A
Sbjct: 404 KLATTVTTPGSKSISNRALILAALGEGTCRIKLLHSDDEFLMTAITRLGGASYAWEDA 463

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTA--AVTAAGGNATYVLDGVPRMR 130
+ V+ G GG+ L+LGNAG A R LT A+ + ++ VL G RM+
Sbjct: 464 GEVLVLTKGGQLRASSDP----LYLGNAGTASRFLTTVVALCSPADVSSTVLTGNARMQ 519

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPIG LV L+ G +D P+R++ GG GG ++L+ ++SSQY+S++LMAA
Sbjct: 520 VRPIGPLVDALRSNGVSIDYLGPGKSLPLRIDAAGGFAGGVIELAATVSSQYVSSILMAA 579

Query: 191 PLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P A V + ++ K IS PY++MTL +M+ FGV+ E S S Y YK+P
Sbjct: 580 PYAKEPVTLRVLGGKPISQPYIDMTLAMMKTFGVQVERSSSDPNTYHIAKGTYNPAEYT 639

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
+E DASSA+Y LA AAITG T TV G++SLQGD +FA +VL+ MG V T +S TVT
Sbjct: 640 IESDASSATYPLAIAAITGTTCTVPNIGSSSLQGDARFAIDVLQPMGCTVQQTASSTTVT 699

Query: 309 GP-PREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GP P G H V+M M D +T +V+A A G T I +A+ RVKE R+ A+
Sbjct: 700 GPAPGGLGLPH----VDMEPMTDAFLTASVLAAVAAGTTKISGIANQRVKECNRIAAM 754

Query: 368 RTELTKLGASVEEGPDYCIIT--PPEKLVN--TAIDTYDDHRMAMAFS-LAACAEVPVTI 422
R +L K G + +E D I+T P + L + YDDHR+AM+FS L+ A PVTI
Sbjct: 755 REQLGKFGIATDEFDDGIIVTGQPLDTLTKTPDAGVFCYDDHRVAMSFVSLSTVANAPVTI 814

Query: 423 RDPGCTRKTFPDYFDVLS 440
+ CT KT+P ++D LS
Sbjct: 815 LERECTGKTWPGWWDTLS 832

>gb|ABA54838.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nostoc commune DRH1]
Length = 403

Score = 288 bits (736), Expect = 2e-75, Method: Compositional matrix adjust.
Identities = 174/400 (43%), Positives = 238/400 (59%), Gaps = 17/400 (4%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKSL+NR LL+AAL++G ++++N L SED Y + LG+ + +
Sbjct: 11 RPVDATVEIPGSKSLTNRRALLVAALAQGDSLEENALFSEDSEYFAKCVLQIPITLNP 70

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTA--AVTAAGGNATYVLDGVPRMR 132
+ V G GG P + A LF+G AG A R ++A V A GN Y LDGVPRMR
Sbjct: 71 LAQIRVAGRGDIPAKQAD----LFVGLAGTAARFISALV--ALNGEYRLDGVPRMR 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+GDL+ L+ GA V+ + P V G GG +L + +SQ LSALLM AP
Sbjct: 125 PMGDLTLVLQTGGATVNFEGNSGFMPYTVYS-QGFTGGNFRLKANQTSQQLSALLMIAPY 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D IE+ L+S YV+MT RLM FGV+ ++F IK GQ+Y++ ++ VE
Sbjct: 184 AQQDTNIEVEGLTVLSQSYVKMTCRLMADFGVEVIQIGD-NQFQIKAGQRYQA-RHYTVEP 241

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TGG V V+ S QGD+ + VLE MG ++ ++ VTGP
Sbjct: 242 DASNASYFFAAAAVTGGRVRVKHLTKQSCQGDILWLVLEQMGCCQIKDSDDYTEVTGP-- 299

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
K L+ ID++MN + D+ TL +A FA IR+V R KET+R+ A+ TEL
Sbjct: 300 -----KQLQGIDIDMNDISDLVQTLGAIAPFASSTITIRNVEHIRYKETDRIKAVVTELR 354

Query: 373 KLGASVEEGPDYCIITPPEKLVNTAIDTYDDHRMAMAFSL 412
+LG VEE PD I P + AI+TY DHRMAMAF++

Sbjct: 355 RLGTVQVEEFPDQLKIEPG-PVTPAAIETYHHRMAMAFV 393

>ref|ZP_05082175.1| 3-phosphoshikimate 1-carboxyvinyltransferase [beta proteobacterium
KB13]
gb|EDZ64862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [beta proteobacterium
KB13]
Length = 432

Score = 287 bits (734), Expect = 3e-75, Method: Compositional matrix adjust.
Identities = 181/433 (41%), Positives = 248/433 (57%), Gaps = 20/433 (4%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P +I G +K PGSKS++NR+LLL++L + + N L S+D YM+ AL LG+S+
Sbjct: 9 LAPRSKIDGVKPPGSKSITNRLLLSSLCNQSISLTNHLISDDSKYMIKALEDLGVSIS 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+D K + G KF LFLGNAG A R L A ++ GGN Y LDGV R
Sbjct: 69 SDTKDK-ITIFGDPKKF-----NNSADLFLGNAGTAYRPLCALLSILGGN--YRLDGVPR 120

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERPI DLV L +GAD+ PPV+V+ + + G+ISSQ+L++LLM
Sbjct: 121 MHERPIKDLVDSLSSIGADIKYLNIGFPPVQVSDFKFNGKTDISIKGNISSQFLTSLM 180

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKN 247
A PL D ++ I +LIS PY+ +T++L++ F V H+ S F K S +
Sbjct: 181 AVPLIGQDFKLNIDGELISKPYINITIKLLKLFNVNYINHNYSSEFNCNDNPKVYSLDS 240

Query: 248 AYV--EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ E DASSASYF A AAI+G V VEG S+QGD++F EVLE MGA +T+ S+
Sbjct: 241 GLIDIEPDASSASYFFAAAAISGN-VRVEGLNKESIQGDIQFLEVLEKMGADITYNNDISI 299

Query: 306 TVTGGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G+ AI PD AMTLA + LF P + ++ SW+VKET+R+V
Sbjct: 300 DVRKANTLVGGQFDCIAI-----PDAAMTLAAMGLFTSSPVELFNINSWKVKETDRIV 352

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ EL K GA+V + + PP + + ++ TYDDHR+AM FSL A V I+D
Sbjct: 353 AMENELRKFGATVTSTDNSLKVIPPTNISDNVSVHTYDDHRIAMCFSLTCLANKSVEIQD 412

Query: 425 PGCTRKTFFPDYFD 437
P C KT+P+YF+
Sbjct: 413 PECVNKTYPNYFN 425

>ref|XP_956000.1| pentafunctional AROM polypeptide [Neurospora crassa OR74A]
emb|CAD21207.1| probable PENTAFUNCTIONAL AROM POLYPEPTIDE [Neurospora crassa]
gb|EAA26764.1| pentafunctional AROM polypeptide [Neurospora crassa OR74A]
Length = 1563

Score = 286 bits (732), Expect = 4e-75, Method: Compositional matrix adjust.
Identities = 195/443 (44%), Positives = 264/443 (59%), Gaps = 21/443 (4%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K+++ +V PGSKS+SNR L+LAAL EGTT + NLL+S+D ML A+ L + + +
Sbjct: 401 KDLNVSVTPPGSKSISNRALILAALGEGTTRIHNLLHSDDTQVMLNAVAQLQGASFSWEE 460

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYVLDGVPRMR 130
VV G GSK L+LGNAG A R LT AA+ + VL G RM+
Sbjct: 461 GDVLVVGKNGGKL---QATSTPLYLGNAGTASRFLTSVAALCNPSDVNSTVLTGNARMK 516

Query: 131 ERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RPIG LV L+ G V PV+V+ GGL GG ++L+ +ISSQY+S+LLMAA
Sbjct: 517 QRPICALVDALRANGVGKYLEKEHSLPVQVDAAGGLAGGVMELAAATISSQYVSSLLMAA 576

Query: 191 PLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNA 248
P A V + ++ K IS PY++MT+ +M FGV+ + S + + +YI G YK+P+
Sbjct: 577 PYAREPVTLRVLGGKPISQPYIDMTIAMMASFGVQVQRSADPNTYYIPQG-TYKNPETY 635

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTV 307
VE DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL MG V T+ S TV

Sbjct: 636 VVESDASSATYPLAIAAITGTTCTVPNIGSKSLQGDARFAIEVLRLPMGCTVEQTDVSTTV 695

Query: 308 TGPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
TGP P G LKAI V+M M D +T +V+A A G T I +A+ RVKE R++A

Sbjct: 696 TGP---PIGT---LKAIPHVDMEPMTDAFLTASVLAASGTTQITGIANQRVKECNRILA 750

Query: 367 IRTELTKLGAS---VEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFS-LAACAEVPVT 421
++ +L K G +E+G + I E N T I YDDHR+AM+FS L+ + PV

Sbjct: 751 MKDQLAKFGVHCNELEDGIEVIGIPYTELKNPTEGIYCYDDHRVAMSFSVLSSTISHPVL 810

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + CT KT+P ++D +S + K

Sbjct: 811 ILERECTGKTWPGWWDTMSNYFK 833

>ref|NP_864842.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopirellula
baltica SH 1]
emb|CAD72526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopirellula
baltica SH 1]
Length = 501

Score = 286 bits (731), Expect = 6e-75, Method: Compositional matrix adjust.
Identities = 188/446 (42%), Positives = 264/446 (59%), Gaps = 23/446 (5%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G+++ PGSKSL+NR LL+AA GT+ ++ L SED H M +LR +G+ +E+

Sbjct: 57 PGGPVCGSIRPPGSKSLTNRALLMAAFGRGTSQLEGALVSEDTHVMTDSLRIKIGVEIESH 116

Query: 71 KAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A + VV G P D+ + L++ N+G +R LTAA++A GGN YVL GVPRM

Sbjct: 117 DAGRTLVTGVQSA-PESDSPYD--LYIANS GTTVRFLTAALSALGNN--YVLSGVPRMH 171

Query: 131 ERPIGDLVVGLKQL-GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
ERPIGDLV L + ++ CPPV + G ++ ++GS+SSQYLS L+MA

Sbjct: 172 ERPIGDLVDALSPVVDGRIEAVSEGGCPPVHIQ-TAGWAKHELVSAGSVSSQYLSGLMMA 230

Query: 190 APLAL----GDVEIEIIDKLISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGGQKY 242
APLA V I ++ +L+S PYVEMT M+ FG E + + D ++ Y

Sbjct: 231 APLASRRSNQPVTIRVVGELVSRPYVEMTADAMQVFGASVELQWPAAQDDVLVQISGDY 290

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ +E DAS+ASYF A AAI+GG VTV G + QGDV F +VLEMMG ++ E

Sbjct: 291 DA-IGWSIEPDASAASYFWAAAISGGDVTVNGLSRAATQGDVAFVDVLEMMGCQIEEGE 349

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
S+ V P G+ L+ +DV+MN + D TLA+VALFA+ PT +R VA R KET+

Sbjct: 350 DSIRVIAT-NLPGGQ--LRGVDVDMNAISDTVQTLAMVALFANSPTVRVGVVHNRFKETD 406

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----AIDTYDDHRMAMAFSLAACAE 417
R+ + +EL KLGAAA+E D I P + V+ +DTY DHRMAM+FSLA

Sbjct: 407 RIGDLASELRKLGATIQEHDDGMTIHLSEPAVSDESPPVRLDTYHDMAMSFSLAGLRL 466

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFV 443
+ I +P CT KT+P+Y+ L +

Sbjct: 467 GGIEIENPACTGKTYPNYWSDLLEQLI 492

>ref|XP_002896252.1| pentafunctional AROM polypeptide, putative [Phytophthora infestans
T30-4]
gb|EEY67699.1| pentafunctional AROM polypeptide, putative [Phytophthora infestans
T30-4]
Length = 1548

Score = 284 bits (727), Expect = 2e-74, Method: Compositional matrix adjust.
Identities = 179/440 (40%), Positives = 261/440 (59%), Gaps = 16/440 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+++ + P + +GT+++PGSKS+SNR+LL+AAL EG+ + LL+S+D M+ AL+ +G

Sbjct: 373 KQVRMLPGAKANGTIRVPGSKSISNRVLLMAALGEGSCRITGLLHSDDTQVMMNALQKVG 432

Query: 65 LSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT--AAGGNATYV 122

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+      VV G  GKF      EE+ +L NAG A R LT+A+T  +  + T V
Sbjct: 433 AKFSWEDNGAVLVVEGTAGKFATVADGEEI--YLSNAGTAARFLTSAmtLVPSendGTvv 490

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ G RM+ERPI LV L+ G D+      CPP+ + G GL GG V+L+ +SSQY
Sbjct: 491 VTGNYRMKERPIASLVDALRGNGCDISYLENEGCPPLAIRG-SGLRGGAVRLAAKVSSQY 549

Query: 183 LSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+S++L++AP A  + +E+ +K S+PY+ MT +LM++FG+ E + + +R+ + G
Sbjct: 550 VSSVLISAPYAKEPLVLELEEKEPTSLPYILMTTQLMKQFGIPVE-TLAPNRYRVPCG-V 607

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y++PK VE DASSA+Y LA AAITGG VTVE G TSLQGD F +L MG T
Sbjct: 608 YQNPKVESVEVDASSATYPLAFAAITGGQVTVEALGNTSLQGDAAFHTLLRSMGCTTTQD 667

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
TS TVTGP      LKA++++M M D MT  +A ADG T I  +A+ RVKE
Sbjct: 668 ATSTTVTGPQ----DGTPLKAVEIDMETMTDAFMTAVALAAVADGTKITGIANQRVKEC 723

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIIT----PPEKLNVTaidTYDDHRMAMAFSLAACAE 417
R+ + TEL+K+G E PD I      E L  +I ++DHR+AM+F++
Sbjct: 724 NRIEVMVTELSKIGVEGELPDGIWIKGTAGKTEHLKKVSIACHNDHRIAMSFVAVLGSVV 783

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
+ I D CT KT+P+++D
Sbjct: 784 DNIIITKECTDKTYPEFWD 803

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>ref|ZP_05881560.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio metschnikovii
CIP 69.14]
gb|EEX36986.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio metschnikovii
CIP 69.14]
Length = 248

```

Score = 281 bits (719), Expect = 1e-73, Method: Compositional matrix adjust.
Identities = 141/250 (56%), Positives = 173/250 (69%), Gaps = 9/250 (3%)

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Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
M+APLA G V I+I +L+S PY+++TL LM++FGV+ + + + +F I GQ Y SP +
Sbjct: 1 MSAPLAEGTVTIDIEGELVSKPYIDITLHLMQQFGVQVINHN-YQQFVIPAGQSYVSPGD 59

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VEGDASSASYFLA AAI GG V V G G S+QGDV+FA LE MGA++ W + V
Sbjct: 60 FLVEGDASSASYFLAAAIAKGGQVKVGTIGKNSIQGDVQFAYALEKMGAIQIEWGDDYVIA 119

Query: 308 TGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
R L A+D++ N +PD AMT+A ALFA G TAIR+V +WRVKET+R+ A+
Sbjct: 120 R-----RGELTAVDLDFNAIPDAAMTIATTALFAKGSTAIRNVYNWRVKETDRLTAM 171

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTaidTYDDHRMAMAFSLAACAEVPTIRDPGC 427
TEL K+GA VEEG DY IITPP L IDTYDDHRMAM FSL A E PVTI DP C
Sbjct: 172 ATELRKVGAVQVEEGEDYIIITPPSHLQHATIDTYDDHRMAMCFSLVALGETPVTINDPKC 231

Query: 428 TRKTFPDYFD 437
T KTFPDYF+
Sbjct: 232 TSKTFPDYFE 241

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>ref|ZP_01287548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
ref|ZP_01289809.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
gb|EAT03771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
gb|EAT06004.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
Length = 427

```

Score = 281 bits (719), Expect = 2e-73, Method: Compositional matrix adjust.
Identities = 176/445 (39%), Positives = 253/445 (56%), Gaps = 22/445 (4%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M +EI P + I TV++PGSKS++ R L+ AAL++G +V+ L SED Y AL
Sbjct: 1 MQQWQEITPFPGR-IEQTVRVPGSKSITQRALIAAALADGASVLRGPLASEDTEYTSAL 59

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R +GL V D ++ + G GG+ A ++FLGN G A R LT+ AA G+
Sbjct: 60 RAMGLVV--DHLGEQWRIFGQGGRI----APPATEIFLGNNGTATRFLTS--VAALGHGI 111

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISS 180
++++G RM ERPIG L+ L GAD+ CPP+ + GL GG L SS
Sbjct: 112 FLINGDERMGERPIGPLLSALAGWGADIRSLRNNGCPPLEIQA-AGLKGGATVLPAGKSS 170

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
QYLS+LL+ AP ++ + +++S PYV MT+ +M FG++ E ++ + F I G
Sbjct: 171 QYLSLLLVAPYTAQPAQLRVEGEVLSKPYVRMTAMVMRAFGIEVEANEQLNHFRIPQGS 230

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + VEGDASSASYF A AA+TGGTVTVE SLQGD ++LE MG +V+
Sbjct: 231 YQR--REYAVEGDASSASYFWAAA+VGGTVTVENVPAVSLQGDALVDILEKMGCRVSR 288

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+TV+ P + L+ ++V M PDV TLAVVA A G T I ++A R+KE
Sbjct: 289 GADGITVSAP-----EELRGVEVEMADCPDVVPTLAVVAALARGRTTISNIAHLRIKE 341

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVTIDTYDDHRMAMAFSLAACAE 417
+R+ + EL +LG EEGPDY +I + AI T++DHR+AM F++A
Sbjct: 342 CDR LAVMARELARLGV RTEEGPDYLVIEGRGRAHDYHGAAIATHNDHRIAMCFVAVGLVI 401

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLSTF 442
+ I +P C +K+FPD++ +T
Sbjct: 402 PGIRIENPDCVKKSFPDFWQRFATL 426

>emb|CBI53120.1| unnamed protein product [Sordaria macrospora]
Length = 1563

Score = 280 bits (715), Expect = 4e-73, Method: Compositional matrix adjust.
Identities = 193/445 (43%), Positives = 263/445 (59%), Gaps = 23/445 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ +V PGSKS+SNR L LAAL EGTT + NLL+S+D ML A+ L + + +
Sbjct: 401 KDLKVSVPKSGKSLSNRALTALALGEGTTIRYNLLHSDDTQVMLNAVAQLQGASFSWED 460

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG---NATYVLDGVPRM 129
+ VV G GG+ L+LGNAG A R LT+ V N+T VL G RM
Sbjct: 461 SDVLVVKNGNGRL---QATSTPLYLGNAGTASRFLTSVVALCNPTDVNST-VLTGNARM 515

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
++RPIG LV L+ G V PV+V+ GGL GG ++L+ +ISSQY+S+LLMA
Sbjct: 516 KQRPICALVDALRANGVGKYLEKEHSLPVQVDAAGGLAGGVMELAAATISSQYVSSLLMA 575

Query: 190 APLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AP A V + ++ K IS PY++MT+ +M FGV+ + S + + ++I G YK+P+
Sbjct: 576 APYAREPVTLRLVGGKPISQPYIDMTIAMMASFGVQVQVQSAEDPNTYHIPQG-TYKNPET 634

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVT 306
VE DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL MG V T+ S T
Sbjct: 635 YIVESDASSATYPLAVAAITGTTCTVTPNIGSKSLQGDARFAIEVLRPMGCTVEQTDASTT 694

Query: 307 VTGPPREPFGKHLKAI-DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
VTGPP LKAI V+M M D +T +V+A A G T I +A+ RVKE R+
Sbjct: 695 VTGPP-----VGT LKAIPHVDMEPMTDAFLTASVLAASVAGTTQITGIANQRVKECNRIK 749

Query: 366 AIRTELTKLGAS---VEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFS-LAACAEVPV 420
A++ EL K G + +E+G + I E N T I YDHR+AM+F L+ + PV
Sbjct: 750 AMKDELAKFGVTCNELEDGIEVTGIPYTELKNPTEGIYCYDDHRVAMSFGVLSTISPHPV 809

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFVKN 445
I + CT KT+P ++D +S + K+
Sbjct: 810 LILIRECTGKTWPGWWDMSNYFKS 834

>ref|YP_001529830.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfococcus
oleovorans Hxd3]
gb|ABW67753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfococcus
oleovorans Hxd3]
Length = 423

Score = 279 bits (714), Expect = 5e-73, Method: Compositional matrix adjust.
Identities = 193/436 (44%), Positives = 259/436 (59%), Gaps = 24/436 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
+EI QP++ S V +PGSKS ++R+L+ AALS+G + N L SED H AL +G
Sbjct: 2 KEIQQQPVQ--SCEVSVPGSKSYTHRVLIAAALSDGVCRLGNCLESEDTHTREALVKMG 59

Query: 65 LSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E KA R VV G GG+ P D +FLGN+G +MR LT AA G TY+L
Sbjct: 60 VRIE--KAEDRLVVHGTGGRLLPCGDP-----IFLGNSGTSMLRLTG--VAAIGQGTLYL 110

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RM +RP+ DL+ GL Q+G CPP+ + G GG V+L ISSQYL
Sbjct: 111 IGTDRMAQRPVADLLEGLDQIGVPPARSVNNNGCPPLEIVA-GKAQGGHVRRLRCGISSQYL 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S+LL+AAP G + IE+ + +S PY++MTL +M+RFGV E D + RF + GGQ Y+
Sbjct: 170 SSLLLAAPYIDGGLNIEVTEGPVSKPYIDMTLDIMDRFGVTVER-DGYTRFRVAGGQCYR 228

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
A VE DAS ASYF A AA+TG TV V G S QGDV+F EVLE MG KV
Sbjct: 229 KGDYA-VEPDASQASYFWAAAVTGATVKVMGMTPESRQGDVRFVEVLEAMGCKVNREID 287

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETER 363
+ VTG P L A+DV+M MPD+ TL+VVA F G T IR+VA + KE++R
Sbjct: 288 GIAVTGGP-----LSAVDVMGMDPDLVPTLSVVAFTQGKITVIRNVAHLKEKESDR 339

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ EL+K+G +V D + + + I+TY+DHRMAM+F++A VTI
Sbjct: 340 LAAVAALSKMGITVVR-TDTGLEITGGRPHGAVIETYNDRMAMSAFVAGLVTPGVTIA 398

Query: 424 DPGCTRKTFFPDYFDVL 439
+ GC K+FP ++ V
Sbjct: 399 NEGCVAKSFPFGWFQVF 414

>ref|YP_002430927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfatibacillum
alkenivorans AK-01]
gb|ACL03459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfatibacillum
alkenivorans AK-01]
Length = 419

Score = 279 bits (713), Expect = 6e-73, Method: Compositional matrix adjust.
Identities = 171/432 (39%), Positives = 251/432 (58%), Gaps = 22/432 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 65
+I ++P+ + T +PGSKS ++R+L+ AAL++G + V N L SED + AL +G+
Sbjct: 4 QITIRPMGKTELTA M VPGSKSYTHRLICAALADGLSQVKNGLVSEDTLLTMNALNKMVG 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
SV ++ + V G GG + E + LGN+G +R + A AA G TY L G
Sbjct: 64 SVRKERGS--FWVNGTGGSL---GRYEDPIHLGNSGTTLRMLCA--VAAMGVGTYYTLTG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
RM++RPI DL L+QLG V+ G CPP+++ G + GGKV ++ +SSQYLSA
Sbjct: 116 TERMQQRPIDLAQAQLGVPVETNNG--CPPIKIQGTA-IKGGKVSINCGVSSQYLSA 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+ AP +EI + + +S PY++MT+ +M+ GV+ + D F + G +Y++
Sbjct: 173 LLLIAPYTQDGMETVTEGPVSKPYIDMTVSMKAMGVEIKR-DGHTWFSVPQSQYQAG 231

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ VE DAS ASYF AAITG T+ V G + S QGD +FA +L+ MG ++ T+ +
Sbjct: 232 EY-MVEADASGASYFWGAAAITGATIRVAGTHSASCQGDSRFAYILKSMGCRLDETDEGL 290

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G + LK I V+M MPDVA TLAVVA FA G T I +V + KE++R+
Sbjct: 291 AVAG-----RDLKGITVDMGNMPDVAPTLAVVAFAKGETRIENVGHLKAKESDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ TEL K+G D I K IDTYDDHR+AM+F++A V I +P
Sbjct: 343 AVITELKKMGVQASCTDDSMTIIGG-KPKGAVIDTYDDHRIAMSFAVAGLLAPGVIINNP 401

Query: 426 GCTRKTFPDYFD 437
C K+FP++++
Sbjct: 402 SCVDKSFPNFW 413

>emb|CCA26166.1| unnamed protein product [Albugo laibachii Nc14]
Length = 1594

Score = 279 bits (713), Expect = 7e-73, Method: Compositional matrix adjust.
Identities = 180/449 (40%), Positives = 258/449 (57%), Gaps = 22/449 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ + +G +++PGSKS+SNR+LL+AAL GT + LL+SED M+ AL +G
Sbjct: 391 KQVVVKNGTQANGNIRVPGSKSVSNRVLLMAALGNGTCRISGLLHSEDTQVMMAALTKIG 450

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT--AAGGNAT-- 120
++ VV G GKKF D EE+ +L NAG A R LT +T A N
Sbjct: 451 AKFSWEEKDVTVVVEGTGGKFKALDDGEEI--YLSNAGTAARFLTTMTLVQAPKNENEL 508

Query: 121 --YVLDGVPRMRERPIGDLVVLGLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVKLSGS 177
+L G RM+ERPIG LV L+Q G + C + CPP+ + G GG ++L+
Sbjct: 509 GRIILGTNHRMQERPIGLVESLRQNGCRIQCTGVHEGCPPLAIQ-YTGFKGGDIRLAAK 567

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+SSQY+S++L+ AP A V +E+ ++ I S+PY+ MT+ LM FG+ E + +RF I
Sbjct: 568 VSSQYVSSILINAPYAENSVVLELEEEIITSLPYIHMTIELMRAFGIHVER-EGKNRFRI 626

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G Y++P VE DASSASY LA AITGG V VE G++S+QGD F VL MG
Sbjct: 627 PKG-AYQNPSMFQVEVDASSASYPLALGAITGGQVVVEALGSSSVQGDAAFHSVLRAMGC 685

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAID-VNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
+ + T TS TV GPP LKAI+ ++M M D MT AV+A A G T I +A+
Sbjct: 686 ETSQTPSTTVRGPP----SGVRLKAIEYLDMETMTDAFMTAAVLAAVAQGTTKIVGIAN 741

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE----KLNVTATIDTYDDHRMAMAFS 411
RVKE R+ + TEL+K+G E D + +L I ++DHR+AM+F+
Sbjct: 742 QRVKECNRIEVMITELSKIGVECELEDGMWVKANGDIGQLRKAIEIACHNDHRIAMSFA 801

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ ++I D CT KT+P+++D L
Sbjct: 802 VLGAYVPDISITDKKCKTEKTYPEFWDHLQ 830

>gb|EFW44924.1| pentafunctional AROM polypeptide [Capsaspora owczarzaki ATCC 30864]
Length = 1811

Score = 278 bits (712), Expect = 9e-73, Method: Compositional matrix adjust.
Identities = 185/450 (41%), Positives = 254/450 (56%), Gaps = 41/450 (9%)

Query: 19 VKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V++PGSKS+SNR+LLAAL GT + LL+S+D ML AL++LG+ E + V
Sbjct: 456 VQVPGSKSISNRVLLAALGTGTCRIRGLLHSDTRVMLQALKSLGVHSEFENEGTVLAV 515

Query: 79 VCGGKGF--PVEDAKEEVQLFLGNAGIAMRSLTA-----AVTAAGGNAT---YVLDGV 126
G G P +D ++LG NAG A R LT+ + GG +T VL G
Sbjct: 516 RGAEGLLTAPQDD-----IYLG NAGTAARFLTSVAALVCSAAPTGGTSTARSHVLTGK 569

Query: 127 PRMRERPIGDLVVLGLKQLGADVDCFLGTDCPPVRVN-----GIGGLPGGKVKLSGSISSQ 181
PRM+ER P G L+ L GA ++C C P+RV G G L GG V+L+ +ISSQ
Sbjct: 570 PRMKERPNGPLISALVANGASIECLEKPGCLPIRVACAPSAGSGTLRGGDVELAANISSQ 629

Query: 182 YLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHEH---SDSWDRFYIK 237
Y+S+LL++AP V + ++ ++S Y++MTL LM+ FGV D Y
Sbjct: 630 YVSSLLISAPYTTQQPVRLRLVGGEVVSQLYIDMTLALMKDFGVPVAAFPVAGSGADPVYQI 689

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
KY +P VEGDASSA+Y LA AA+TG VTV G SLQGD +F +L MG
Sbjct: 690 PTAKYANPPEYAVEGDASSATYPLAIAAVTGKKVTVANVGKLSLQGDAQFCHLLARMGCT 749

Query: 298 VTWTETSVTVTGP----PREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
V T+ + TVTGP PR L+A+ V+M M D MTLA V ADG T+IR+
Sbjct: 750 VEQTDMTTTVTGPSGIAPR-----LRALGTVDMDGMDTDAFMTLAAVCAIADGVTSIRN 802

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADTYDDHRMAMAF 410
+A+ RVKE R++ + ELTK+G V E D I P +L+ I +DDHR+AM+F
Sbjct: 803 IANQVRKECNRLVLMQLTKMGIHVVELEDGLEIHGRPASELHGATIVCHDDHRIAMSF 862

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
++ C V I + C KT+P+++D L+
Sbjct: 863 AVLGCVPVNVIIISERACVEKTYPEFWDDL 892

>ref|NP_986731.2| AGR066Wp [Ashbya gossypii ATCC 10895]
gb|AAS54555.2| AGR066Wp [Ashbya gossypii ATCC 10895]
Length = 1577

Score = 277 bits (709), Expect = 2e-72, Method: Compositional matrix adjust.
Identities = 187/467 (40%), Positives = 267/467 (57%), Gaps = 38/467 (8%)

Query: 5 EEIVLQPIKEISG----TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P ++ T+ PGSKS+SNR L+LAAL +G + NLL+S+D +ML A+
Sbjct: 401 DEALVYPFTDVRSSSTGHTIVPPGSKSISNRALILAAALGKGKCRIRNLLHSDDTKHMLEAV 460

Query: 61 RTLGL-SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
+ L ++ + V+ G GG+ ++ L+LGNAG A R S+ + V G
Sbjct: 461 QQLNAATISWEDNGDTVVIDGHGGR---TLTASDLPLYLGNAGTASRFLASVASLVCPEG 517

Query: 117 GNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
+ +L G RM+ERPIG LV L+ G VD P++V+ GG++ L
Sbjct: 518 NRDSVILTGARMQERPIGPLVESLRLNGVRVDYLNREGSLPIKVHAESKFRGGRINLEA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS-DSWDRFY 235
SISSQY+S++LM AP A V + + K IS Y+EMT+R+ME+FG+K E S D ++
Sbjct: 578 SISSQYVSSILMCAPYAEPTLSLDGKPISELYIEMTIRMMEKFGIKVEKSNDLYTYH 637

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMM 294
I GQ Y +P +E DASSA+Y LA AA+TG TVT+ G SLQGD +FA +VL+ M
Sbjct: 638 IPRGQ-VYNPAEYVIESDASSATYPLAFAALTGTTVTIPNIGHDSLQGDSRFACDVLKPM 696

Query: 295 GAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTA----- 349
G V T TS TVTGP EP K L+ +D M M D +T VVA A P +
Sbjct: 697 GCTVQQTATSTTVTGP--EPGTLKPLEHVD--MEPMTDAFLTACVVAAAHSPECKCKNI 752

Query: 350 --IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDD 403
I +A+ RVKE R++A+ T+L+K G + EE PD + E+L+ A++TYDD
Sbjct: 753 ITITGIANQVRKECNRLAMVTQLSKFGVTAEEELPDGIQVHGVEQLSQLKVPDAVETYDD 812

Query: 404 HRMAMAFSL-----AACAEVPVTIRDPGCTRKTFPDYFDVLST 441
HR+AM+FSL A + P+ I + CT KT+P ++DVL +
Sbjct: 813 HRVAMSFSLLAGMVNYGQAPSSCRPIKILERRCTGKTWPGWWDVLHS 859

>ref|XP_003048265.1| predicted protein [Nectria haematococca mpVI 77-13-4]
gb|EEU42552.1| predicted protein [Nectria haematococca mpVI 77-13-4]
Length = 1569

Score = 277 bits (709), Expect = 2e-72, Method: Compositional matrix adjust.
Identities = 185/446 (41%), Positives = 257/446 (57%), Gaps = 34/446 (7%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
TV PGSKS+SNR L+LAAL G+ + NLL+S+D YML A+ LG S A +
Sbjct: 406 TVTPPGSKSISNRALVLAALGLGSCRINKNLLHSDTEYMLSAIHQLGGASYSWQDAGEVL 465

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV---TAAGGNATYVLDGVPRMRERP 133
VV G GG + +KE L+LGNAG A R LT V + + ++ +L G RM+ RP
Sbjct: 466 VVDGKGGNL--QASKE--ALYLG NAGTASRFLTTVVALCSPSESASSTILTGNARMKVRP 521

Query: 134 IGD LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV L+ G +++ + P+RV+ GGL GG ++L+ ++SSQY+S++LMAAP A
Sbjct: 522 IGPLVDALRSNGVEIEYQCKENSLPLRVDAAGGLKGGVIELAATVSSQYVSSILMAAPYA 581

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYVE 251
V + ++ K IS PY++MT+ +M FGV SD + ++I GQ Y++P +E
Sbjct: 582 KNPVTLRLVGKPISQPYIDMTISMASFVHVTASSDEPNYHIPQGQ-YQNPSEYIIE 640

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGP 310
DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL+ MG V ++ S TVTGP
Sbjct: 641 SDASSATYPLAAITGTTCTIPNIGSKSLQGDARFAVDVLQPMGCTVNQSDYSTTVTGP 700

Query: 311 -PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P E G H V+M M D +T +V+A A G T I +A+ RVKE R+ A++
Sbjct: 701 APGELKGLPH-----VDMEPMTDAFLTASVLA AVASGKTQITGIANQRVKECNRIAMKD 755

Query: 370 ELTKLGASVEE-----GPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEV 418
+L K G E G D I P I YDDHR+AM+FS LA +
Sbjct: 756 QLAKFGVQCNELEDGIEVLGKGQDGGISAP-----TVGIHCYDDHRVAMSFVSLAVASPS 810

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV + + C KT+P ++D+LS K
Sbjct: 811 PVIVTERECVGKTPGWWWDILSQAFK 836

>ref|XP_001910024.1| hypothetical protein [Podospora anserina S mat+]
emb|CAP71158.1| unnamed protein product [Podospora anserina S mat+]
Length = 1567

Score = 277 bits (708), Expect = 2e-72, Method: Compositional matrix adjust.
Identities = 192/440 (43%), Positives = 264/440 (60%), Gaps = 22/440 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADK 71
K ++ +V PGSKS+SNR L+LAA+ EGTT + LL+S+D HYML A+ L G + ++
Sbjct: 403 KGLNVSVTPPGSKSISNRALVLAAMGEGTTRIKGLLHSDDTHYMLTAIAQLQGATYTWE 462

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV---TAAGGNATYVLDGVPR 128
A + VV G GKK + L+LGNAG A R LT+ V + + VL G R
Sbjct: 463 AGEVLVVGKRGKLLASNEP----LYLG NAGTASRFLTSVVALCSPTDTTSTVLGTGNAR 518

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M+ RPIG LV L+ G V + PV+V+ + G GG ++L+ +ISSQY+S++LM
Sbjct: 519 MKVRPIGPLVDALRSNGVAVKYLEKENS L PVQVDAVSGFAGGVIELAATISSQYVSSILM 578

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKA EH-SDSWDRFYIKGGQKYKSPK 246
AAP A V ++++ K IS Y++MT+ +M FGVK E ++ + ++I G YK+P+
Sbjct: 579 AAPYARQPVVLKLVGGKPISQFYIDMTIAMMASFGVKVERDAEDPNYHIPQGS-YKNPE 637

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
VE DASSA+Y LA AAITG T T+ G TSLQGD +FA +VL MG V T+TS
Sbjct: 638 EYVVESDASSATYPLAVAAITGTTCTIPNIGRTSLQGDARFAVDVLRPMGCTVEQTDST 697

Query: 306 TVTGPPPREPFGRKHLKAI-DVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
TVTGPP LKAI V+M M D +T +V+A A G T I +A+ RVKE R+
Sbjct: 698 TVTGPP-----VGALKAIPHVDMEPMTDAFLTASVLA AVASGTTQITGIANQRVKECNRI 752

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKL-NVTAIDTYDDHRMAMAFS-LAACAEVPV 420
A++ EL K G E D +T P ++L N I YDDHR+AM+FS L+ A V
Sbjct: 753 KAMKDELAKFVGHCELEDGIEVTGKPYKELANPEPIYCYDDHRVAMSFVSLVSLAPHKV 812

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
I + CT KT+P ++D+LS
Sbjct: 813 LILERECTAKTWPWWWDILS 832

>ref|YP_001613674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sorangium cellulosum]

'So ce 56']
emb|CAN93194.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sorangium cellulosum
'So ce 56']
Length = 428

Score = 277 bits (708), Expect = 3e-72, Method: Compositional matrix adjust.
Identities = 169/418 (40%), Positives = 246/418 (58%), Gaps = 21/418 (5%)

Query: 20 KLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
++PGSKS++NR L+LAAL++G + ++ +L+S+D +M AL LG+ +E A +VV
Sbjct: 21 RVPGSKSITNRALVLAALADGESTLEGVLHSDDRHMRSALEALGIGIE--DAGPHTLVV 78

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G + +E LF+GN+G +R L A G VL G M +RPI DLV
Sbjct: 79 KGGRRRLRAPGRE--LFIGNSGTTVRFLAALACLVPEV--VLVGDEHMAKRPIADLVD 133

Query: 140 GLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
GL+QLGADV+C T CPP+R+ G G L GG + + G SSQY SA++MA P A +++
Sbjct: 134 GLRQLGADVEC--ATGCPPLRIRG-GRLKGGTLTMRGRSSQYFSAVMMAGPFADAAIDL 190

Query: 200 EIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
+ +L+S PYVE+T R++ FG + + + F + Y+ P+ +E DASSASY
Sbjct: 191 RVAGELVSRPYVEITRRMVADFGRIDEAAG--FTVHPAAGYR-PRAYPIEPDASSASY 247

Query: 260 FLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKRKH 319
A AA GG +TV G +LQGD +F E+LE GA+V+ + TV R
Sbjct: 248 PFALAAAAGGAI TVPGLSEGALQGDYRFVLELQAGARVSRQADATTVRSDGR----- 300

Query: 320 LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
L+ IDV+M+ + D MTLA +A +GPT IR+VA+ R+KET+R+ A EL +LG V
Sbjct: 301 LRGIDVDMHHISDTVMTLAAIAPLLEGGPTTIRNVANIRIKETDRLAATVAELRRLQGEVT 360

Query: 380 EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFTPDYFD 437
G D+ I P L + +Y DHRMAM+F++ +TI DP C KT+P +++
Sbjct: 361 HGDDWLRIE-PRPLTPALVRSYSYDHRMAMSFALLGLCRPGITIEDPACVAKTYPTFWE 417

>ref|ZP_03493643.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclobacillus
acidocaldarius LAA1]
gb|EED07696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclobacillus
acidocaldarius LAA1]
Length = 450

Score = 276 bits (706), Expect = 5e-72, Method: Compositional matrix adjust.
Identities = 168/426 (39%), Positives = 244/426 (57%), Gaps = 20/426 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ V++PGSKS++NR L++AAL+EG +V+ +L S+D ++ + ALRTLGL+ VE D
Sbjct: 33 VDADVVRVPGSKSVTNRALVIAALAEESVLSGILRSDDAYWCIEALRTLGPVEVD--GD 90

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + GCGG+FP DA+ ++ G G R LTAA+ A+ G Y + G RM ERP+
Sbjct: 91 RVRMTGCGGQFPRSDAR----VYTGAGGTTARFLTAAALASRGE--YEIRGSRRMNERPM 144

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G+L L+ LGA+++ D P+R+ GL GG+V +SG+ SSQ++S +L+AAP A
Sbjct: 145 GELFRALRVLGAEIEPLERPDTLPIRLKA-RGLAGGEVAMSGAQSSQFVSGVLIAAPYAK 203

Query: 195 GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
++++I+D ++ YV +TL +M FG K E ++ Y+ AY +E D
Sbjct: 204 APLQVKIVDHIVQHAYVHITLDMRAFKAESDLAVISVE-PSGYRG--RAYDIEAD 260

Query: 254 ASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
AS+A YF A AA+TGG V V + Q DV F +VL MG +V ++ + V GP
Sbjct: 261 ASTACYFFAAAAVTGGRRVANLTRDTRQPDVHFVDVLAKMGCEVESSDAGIEVRGP--- 317

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K V+M +M D +TLA +A FADGP I V R E++R+ I L +
Sbjct: 318 ---EKLRRGGFSVSMKEMSDQTLTLAFLAPFADGPIETGVGHIRHHESDRIRVIVETLAR 374

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFT 433

+G EE D II P +A+ +YDDHR+AMA S+ A V I DPGC KT P
Sbjct: 375 VGVRAEEREDGVIIYPGAP-RPSALASYDDHRVAMALSVLALRAEGVEIEDPGCVSKTCP 433

Query: 434 DYFDVL 439
+F+ L
Sbjct: 434 TFFNHL 439

>gb|EFQ95851.1| hypothetical protein PTT_04545 [Pyrenophora teres f. teres 0-1]
Length = 1591

Score = 275 bits (704), Expect = 8e-72, Method: Compositional matrix adjust.
Identities = 183/448 (40%), Positives = 257/448 (57%), Gaps = 39/448 (8%)

Query: 22 PGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR+L+LAAL G+ + NLL+S+D ML AL + G S + K VV G
Sbjct: 417 PGSKSISNRVLVLAALGTGSCRITNLLHSDDTQVMLDALAKMQGASFAWENDGKELVVTG 476

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
GG +L+LGNAG A R S+TA G + V+ G RM+ERPIG L
Sbjct: 477 NGGNLKAASSN---ELYLGNAGTAARFLTSVTALCQPVDTTSTVVTGNARMKERPIGPL 532

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG---GKVKLSGSISSQYLSALLMAAPLA 193
V L+ +G ++D P+R++ GG G+++L+ ++SSQY+S++L++AP +
Sbjct: 533 VKSLRTMGVEIDYQEKEGSLPLRISACGGFGSDSFTGEIELTANVSSQYVSSILLSAPYS 592

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V + ++ K+IS PY++MT+ +M FGV+ E S+S Y + Y +P VE
Sbjct: 593 KKPVTTLRLVGGKVISQPYIDMTIAMMAAFGVQVERSESDPNTYHIPNKPYPNPSEYEVE 652

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPP 311
DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL+ MG KV ++TS TVTGPP
Sbjct: 653 DASSATYPLAIAAITGTTCTVPNIGSGSLQGDARFAVEVLKPMGCKVEQSKTSTTVTGPP 712

Query: 312 REPFGRKHLKAID-VNMNKMPPDVAMTLAVVALFA--DGPTA---IRDVASWRVKETERMV 365
R LKA++ +M M D +T +V+A A +G T+ + +A+ RVKE R+
Sbjct: 713 -----RGELKAVNEIDMEPMTDAFLTASVLAAVASSNGSTSTTRVYGIANQRVKECNRIQ 767

Query: 366 AIRTELTKLGASVEE-----GPDYCIITPPEKLNVTADTYDDHRMAMAFS-LAACA 416
A+ EL K G + + G Y I P I YDDHR+AM+F+ LA A
Sbjct: 768 AMEDELAKFGVTCRQFDDGIEVDGRGYQIDAPK-----VGIHCYDDHRVAMSFVLAALVA 822

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
PV I + CT KT+P Y+D LS K
Sbjct: 823 PAPVLILEKECTGKTWPGYWDSLSQIFK 850

>gb|AAV52047.1| AroA [Actinobacillus equuli]
Length = 297

Score = 275 bits (704), Expect = 9e-72, Method: Compositional matrix adjust.
Identities = 153/311 (49%), Positives = 201/311 (64%), Gaps = 15/311 (4%)

Query: 57 LGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
L AL+ LG++ + V G GG F ++ + LFLGNAG AMR LTAA+ G
Sbjct: 1 LNALKALGVNYSLEDKTVCTVEGIGGAFNWQNG---LSLFLGNAGTAMRPLTAALCLKG 57

Query: 117 GN-ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
+ A +L G PRM+ERPI LV L+Q+GA V PP+ + GL GGKV++
Sbjct: 58 ASEAEVILTGEPRMKERPIKHLVDALRQVGASVQYLENEGYPPLAIRN-SGLKGGKVQID 116

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
GSISSQ+L+ALMAAPLA GD+EIEII +L+S PY+++TL +M+ FGV E+ + + F
Sbjct: 117 GSISSQFLTALMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVNVENQN-YQTFV 175

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+KG Q Y SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MG
Sbjct: 176 VKGNQSYISPEKYLVEGDASSASYFLAAGAIK-GKVKVTGIGKNSIQGDRLFANVLEAMG 234

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
AK+TW + + + LK +D++MN +PD AMT+A ALFA+G T IR++ +

Sbjct: 235 AKITWGDDFIQAE-----QGELKGVDMMDNHIPDAAMTIATTALFAEGETIIRNIYN 286

Query: 356 WRVKETERMVA 366

WRVKET+R+ A

Sbjct: 287 WRVKETDRLAA 297

>dbj|BAH89270.1| putative 5-enolpyruvylshikimate 3-phosphite synthase [Diospyros
kaki]
Length = 164

Score = 275 bits (703), Expect = 1e-71, Method: Compositional matrix adjust.
Identities = 142/164 (86%), Positives = 155/164 (94%)

Query: 171 KVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230

KVKLSGSISSQYL+ALLMAAPLALGDVEIEIIDKLIS+PYVEMTL+LM+RFGV E++D+

Sbjct: 1 KVKLSGSISSQYLTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLMKRFVGDVEYTDN 60

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290

W RF I+GGQKYKSP NAYVEGDASSASYFLAGAA+TGGT+TVEGCGTTSLQGDVKFAEV

Sbjct: 61 WYRFLIRGGQKYKSPGNAYVEGDASSASYFLAGAAVTGGTITVEGCGTTSLQGDVKFAEV 120

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVA 334

LE MGA VTWT+ SVTVTGPPR PFGRKHL+AI+VNMNKMMPDVA

Sbjct: 121 LEKMGATVTWTDNSVTVTGPPRNPFGRKHLRAIEVNMNKMMPDVA 164

>gb|AAA21937.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Aeromonas
salmonicida]
Length = 426

Score = 275 bits (702), Expect = 1e-71, Method: Compositional matrix adjust.
Identities = 190/443 (42%), Positives = 245/443 (55%), Gaps = 36/443 (8%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68

L+PI ++G V LPSKKS+SNR LLLAAL+ GTT + NLL+S+D+ +ML AL LG+ +

Sbjct: 5 LEPISRIVAGEVNLPGSKSVSNRALLAALARGTTRLTNLLSDDIRHMLAALTQLGVKYK 64

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

V G G F V V LFLGNAG AMR L AA+ G+ Y+L G PR

Sbjct: 65 LSADKTECTVHGLGRSFAVS---APVNLFLGNAGTAMRPLCAALCL--GSGEYMLGGEPR 119

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLM 188

M ERPIG LV L GA + PP+ V+ GL GG V + GS+SSQ+L+A LM

Sbjct: 120 MEERPIGHLVDCALKGAHIQYLKKGYPPLVDA-KGLWGGDVHVDGSVSSQFLTAFLM 178

Query: 189 AAPLALGDV--EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

AAP A+ V I I +L+S PY+++TL +M GV EH D++ FYIKG Q SP

Sbjct: 179 AAP-AMAPVIPRIHIKELVSKPYIDITLHIMNSSGVVIEH-DNYKLFYIKGNQSIIVSPG 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306

+ VEGDASSASYFLA AI G V V G G S+ GD+ FA+VLE MGA++TW + +

Sbjct: 237 DFLVEGDASSASYFLAAGAIK-GKVRVTGIGKHSI-GDIHFADVLERMGARITWGDDFIE 294

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMMPDV-----AMTLAVVALFADG-PTAIRDVASWRV 358

P L +D++MN +PDV + L V + A+RD

Sbjct: 295 AEQGP-----LHGVDMDNHIPDVGHDSGQSHCLPRVPPHSHQLQLAVRDDRCTPC 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418

R + G S EEG + + R+AM FSL A +++

Sbjct: 347 THGHRR-----AQAGVS-EEGTTFITRDAADPAQARRDRHLQRSRIAMCFSLVALSDI 398

Query: 419 PVTIRDPGCTRKTFPDYFDVLST 441

VTI DPGCT KTFPDYFD L++

Sbjct: 399 AVTINDPGCTSKTFPDYFDKLAS 421

>ref|YP_003184077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclobacillus
acidocaldarius subsp. acidocaldarius DSM 446]

gb|ACV57688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alicyclobacillus
acidocaldarius subsp. acidocaldarius DSM 446]

Length = 450

Score = 275 bits (702), Expect = 1e-71, Method: Compositional matrix adjust.
Identities = 166/426 (38%), Positives = 242/426 (56%), Gaps = 20/426 (4%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ V++PGSKS++NR L++AAL+EG +V+ +L S+D ++ + ALR LG+ VE D
Sbjct: 33 VDADVVRVPGSKSVTNRALVIAALAEGESVLSGILQSDDAYWCIEALRALGVPVEVD--GD 90

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + GCGG+FP DA+ ++ G G R LTAA+ A+ G Y + G RM ERP+
Sbjct: 91 RVRMTGCGGQFPRSDAR----VYTGAGGTTARFLTAAALASRGE--YEIRGSRMRNERPM 144

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G+L L+ LGA+++ D P+R+ GL GG+V +SG+ SSQ++S +L+AAP A
Sbjct: 145 GELFRALRVLGAEIEPLERPDTPRLRLA-RGLAGGEVAMSGAQSSQFVSGVLIAAPYAR 203

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
V + I+D ++ YV +TL +M+ FG K E + ++ G Y+ AY +E D
Sbjct: 204 APVSVRIVDHVQHAYVHITLDMMQAFGAKCEAAGDLAVISVEPG-GYRG--RAYDIEAD 260

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
AS+A YF A AA+TGG V V + Q DV F +VL MG +V ++ + V GP
Sbjct: 261 ASTACYFFAAAVTGGVRVANLTRDTRQPDVHFVDVLAKMGCEVASSDAGIEVRGP--- 317

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K V+M +M D +TLA +A FADGP I V R E++R+ I L +
Sbjct: 318 ---EKLRRGGFSVSMKMSDQTLTLAFLAPFADGPIETGVGHIRHHESDRIRVIVETLAR 374

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
+G EE D ++ P A+ +YDDHR+AMA S+ A + I DPGC KT P
Sbjct: 375 VGVRAEEREDGVVYPGAP-RPAALPSYDDHRVAMALSVLALRAEGIEIEDPGCVSKTCP 433

Query: 434 DYFDVL 439
+F L
Sbjct: 434 TFFHHL 439

>ref|YP_002603512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfobacterium
autotrophicum HRM2]
gb|ACN15348.1| AroA [Desulfobacterium autotrophicum HRM2]
Length = 439

Score = 275 bits (702), Expect = 1e-71, Method: Compositional matrix adjust.
Identities = 176/445 (39%), Positives = 251/445 (56%), Gaps = 39/445 (8%)

Query: 18 TVKLPKSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
+V +PGSKS+S+R+++ AAL+ G + VDNLLNSED+ + AL +G S E +K
Sbjct: 13 SVVVPKSKSISHRMVICAALASGESTVDNLLNSEDIRLTMDALACMGASFE-NKGENIYS 71

Query: 78 VVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G GG P D ++LGN+G +MR L A + AA G++ Y L G RM +RP+
Sbjct: 72 IQGFGMPGPFADP-----IYLGNSGTSMR-LIAGI-AALGDSPTYHLCDRMSQRPMEA 124

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ LK +G D G CPPV + G G GG V L S SSQYLS+L+M P
Sbjct: 125 LLSSLKMIGIDAAAALHGKGCPPVVIK-GNRRGGAVTLDCSTSSQYLSLLMMIGPFFKDG 183

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
++I + +S PY+++TL +M +F VK + + RF + GGQ Y P + VE D S+
Sbjct: 184 LDITLTSLPVSSPYIDLTLVMSKFQVKQRL-APTFRKVNNGQVY-VPGHFSVEPDLSN 241

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
ASYF A A++G VTV G TS QGD+ F +LE MG KV T+ +TV G
Sbjct: 242 ASYFWAAGAVSGAPVTVMGATQTSSQGDALFVHILERMGCCKVDTTDRGITVQG----- 294

Query: 317 RKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L+ I+V+M PDVA TLAVVA FA+G T I +VA R KE +R+ A+ ++L ++G
Sbjct: 295 -NGLRGIEVDMGDCPDVAPTLAVVAFAAEGTTRIVNVHLRAKECDRIDAVVSQLGRMGV 353

Query: 377 SVEEGPDYCIITPE-----KLNVTADITYDDHRMAMAFSLAACAE 417


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      ++G D+  IT                      ++  +IDT++DHR+AMAFS+A
Sbjct: 354 HADQGADWLSITGTAAGHGTGGMGSGQDDFNHGLSIHGASIDTFNDHRIAMAFSVAGLMV 413

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
      V I +  C K+FP +++V  T
Sbjct: 414 DNVIENESCVGKSFPPTFWFVETL 438

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>ref|XP_002545280.1| pentafunctional polypeptide AROM [Candida tropicalis MYA-3404]
gb|EER35322.1| pentafunctional polypeptide AROM [Candida tropicalis MYA-3404]
Length = 1551

Score = 274 bits (701), Expect = 2e-71, Method: Compositional matrix adjust.
Identities = 185/459 (40%), Positives = 261/459 (56%), Gaps = 34/459 (7%)

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Query: 5  EEIVLQPIKE--ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
      +E+++ P K+      + PGSKS+SNR L+LAAL GT + NLL+S+D +ML A+
Sbjct: 388 DEVLVHPFKQPQENVITPPGSKSISNRALILAALGTGTVRIKNLLHSDDTKHMLAAVAA 447

Query: 63  L-GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---GN 118
      L G + + + V+ G GG      D      +L+LGNAG A R LT + G N
Sbjct: 448 LKGAEITTEDNGETIVLKGNGGDLVTCDE----ELYLGNAGTASRFLTTVASLVGKSES 503

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      VL G RM+ERPIG LV L+ G++V      P+++      GL GG+++L+ +I
Sbjct: 504 DHVVLVTGNARMQERPIGPLVDALRSNGSEVQYLNKEGSLPLKITAGNGLKGGRIELAATI 563

Query: 179 SSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      SSQY+S++LM AP A V + ++ K IS Y++MT +M+ FG++ S + D Y
Sbjct: 564 SSQYVSSILMCAPYAKEPVTALVGGKPISQLYIDMTCAMMKSFGIEVTKSTEDYTYHI 623

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFA-EVLEMMGA 296
      YK+P      +E DASSA+Y LA AA+TG + TV G++SLQGD +FA +VL+ MG
Sbjct: 624 PKGTYKNPAEYVIESDASSATYPLAFAAMTGTCTVPNIGSSSLQGDARFAVDVLKPMGC 683

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFA--DGPTAIRDV 353
      KV T TS TVTGPP      R LK + V+M M D +T +VVA A D T I +
Sbjct: 684 KVEQTATSTTVTGPP-----RGQLKPLPHVDMPEPMTDAFLTASVVAAVAQGDSSTTITGI 738

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT AIDTYDDH 404
      A+ RVKE R+ A+ TEL K G +E PD I      TP + + +YDDH
Sbjct: 739 ANQVRVKECNRIEAMITELAKFGVKADELPGDIEIHGIDIADLKTP--SIEKRGVCSYDDH 796

Query: 405 RMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLST 441
      R+AM+FSL + C E PV I + T KT+P ++D+L +
Sbjct: 797 RVAMSFSLLSGLCKE-PVLILERSTTGKTPGWWDILHS 834

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>gb|EDK39572.2| hypothetical protein PGUG_03670 [Pichia guilliermondii ATCC 6260]
Length = 1210

Score = 273 bits (699), Expect = 3e-71, Method: Compositional matrix adjust.
Identities = 187/458 (40%), Positives = 259/458 (56%), Gaps = 31/458 (6%)

```

Query: 5  EEIVLQPIKEISGT----VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      +E+ + P E T V PGSKS+SNR L+LAAL GT + NLL+S+D +ML A+
Sbjct: 42  DEVFVHPFPESKSTESTVVVPPGSKSISNRALILAALGTGTVRIKNLLHSDDTKHMLDAV 101

Query: 61  RTL-GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV---TAA 115
      L G + + + VV G GK      +      +L+LGNAG A R LT      ++
Sbjct: 102 SALQGAQISTEDGGETIVVTGNGGKLLSTNN----ELYLGNAGTASRFLTTVAALVEVSS 157

Query: 116 GGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
      G      VL G RM+ERPIG LV L G+ +      P+++      GG+++L+
Sbjct: 158 NGPKHVVLVTGNARMQERPIGPLVDALTANGSSIQYLNREGSLPLKIEAGKRFNGGRIELA 217

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
      +ISSQY+S++LM AP A V + ++ K IS Y++MT+ +M+ FG+ S + +
Sbjct: 218 ATISSQYVSSILMGAPYAQEPVTLVGGKPISQLYIDMTIAMMKNFGVEVVKSTTEEHT 277

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFA-EVLEM 293

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Y YK+P+ +E DASSA+Y LA AA+TG + TV G TSLQGD KFA +VL
Sbjct: 278 YHIPKATYKNPEEYVIESDASSATYPLAFAAMTGTSTVNPNGFTSLQGD KFAVDVLRP 337

Query: 294 MGAKVTWTETSTVTVTGPPREPFGKRLKAI-DVNMNKMPPDVAMTLAVVALFADG--PTAI 350
MG V TETS TV GPP R LK + V+M M D +T +VVA A+ T+I
Sbjct: 338 MGCTVEQTETSTTVVGPP-----RGQLKPLATVDMPEMTDAFLTASVVAIAIANSSQSTSI 392

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLVN---TAIDTYDDHR 405
+A+ RVKE R+ A+ T+L K G E PD I KL + + TYDDHR
Sbjct: 393 TGIANQVRVKECNRIEAMVTQLAKFGVLANELPDGIEIHGIDYRKLKIPQGRGVGTYYDDHR 452

Query: 406 MAMAFSLAA--CAEVPVTIRDPGCTRTFPDYFDVLST 441
+AM+FSL A C++ PV I++ CT KT+P ++DVL T
Sbjct: 453 VAMSFSLLAGMCSQ-PVLIQERSCTGKTWPGWWDVLHT 489

>ref|XP_001484289.1| hypothetical protein PGUG_03670 [Meyerozyma guilliermondii ATCC 6260]
Length = 1210

Score = 273 bits (698), Expect = 4e-71, Method: Compositional matrix adjust.
Identities = 187/458 (40%), Positives = 259/458 (56%), Gaps = 31/458 (6%)

Query: 5 EEIVLQPIKEISGT----VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E+ + P E T V PGSKS+SNR L+LAAL GT + NLL+S+D +ML A+
Sbjct: 42 DEVFVHPFPESKSTESTVVPVPGSKSISNRALILAAALGTGTVRIKLLHSDDTKHMLDAV 101

Query: 61 RTL-GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV----TAA 115
L G + + + VV G G G K + +L+LGNAG A R LT ++
Sbjct: 102 SALQGAQISTEDGGETIVVTGNGGKLLSTNN----ELYLGNAGTASRFLTVAALVEVSS 157

Query: 116 GGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLS 175
G VL G RM+ERPIG LV L G+ + P+++ GG+++L+
Sbjct: 158 NGPKHVLTGNARMQERPIGPLVDALTANGSSIQYLNREGSLPLKIEAGKRFNGGRIELA 217

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
+ISSQY+S++LM AP A V + ++ K IS Y++MT+ +M+ FGV+ S + +
Sbjct: 218 ATISSQVSSILMGAPYAQEPVTLSLVGGKPISQLYIDMTIAMMKNFGVEVVKSTTEEHT 277

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
Y YK+P+ +E DASSA+Y LA AA+TG + TV G TSLQGD KFA +VL
Sbjct: 278 YHIPKATYKNPEEYVIESDASSATYPLAFAAMTGTSTVNPNGFTSLQGD KFAVDVLRP 337

Query: 294 MGAKVTWTETSTVTVTGPPREPFGKRLKAI-DVNMNKMPPDVAMTLAVVALFADG--PTAI 350
MG V TETS TV GPP R LK + V+M M D +T +VVA A+ T+I
Sbjct: 338 MGCTVEQTETSTTVVGPP-----RGQLKPLATVDMPEMTDAFLTASVVAIAIANSSQSTSI 392

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLVN---TAIDTYDDHR 405
+A+ RVKE R+ A+ T+L K G E PD I KL + + TYDDHR
Sbjct: 393 TGIANQVRVKECNRIEAMVTQLAKFGVLANELPDGIEIHGIDYRKLKIPQGRGVGTYYDDHR 452

Query: 406 MAMAFSLAA--CAEVPVTIRDPGCTRTFPDYFDVLST 441
+AM+FSL A C++ PV I++ CT KT+P ++DVL T
Sbjct: 453 VAMSFSLLAGMCSQ-PVLIQERSCTGKTWPGWWDVLHT 489

>ref|XP_002492733.1| Pentafunctional arom protein [Pichia pastoris GS115]
emb|CAY70554.1| Pentafunctional arom protein [Pichia pastoris GS115]
Length = 1545

Score = 273 bits (697), Expect = 5e-71, Method: Compositional matrix adjust.
Identities = 179/438 (40%), Positives = 255/438 (58%), Gaps = 30/438 (6%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL +G + NLL+S+D +ML A+ L G + D + VV G
Sbjct: 411 PGSKSISNRALILAAALGKGECKIKNLLHSDDEHMLNAVAALKGADISFDDNGETVTVTG 470

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYV-LDGVPRMRERPIGDL 137
GG F DA +++LGNAG A R LT A++ N T+V L G RM+ERPIG L
Sbjct: 471 NGGNFTATDA----EIYLGNAGTASRFLTSVASIVKPSNTTHVILTGNARMQERPIGPL 526

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G+D++ P+++ GL GG+++L+ +ISSQY+S++LM AP A V
Sbjct: 527 VDALRTNGSDIEYLNREGSLPLKIKSGNGLKGGRIELAATISSQYVSSVLMCAPYASEPV 586

Query: 198 EIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS+ YV+MT+ +M+ FG++ S + Y Y +P +E DASS
Sbjct: 587 TSLVGGKPIISLLYVDMTIAMKSFIEVTKSTTEPYTYHVPQGHYVNPAYEVIESDASS 646

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREP 315
A+Y LA AA+ G VT+ G++SLQGD +FA +VL+ MG KV T TS TV GP +
Sbjct: 647 ATYPLAFAAMNGTQVTIPNIGSSSLQGDARFAVDVLKPMGCKVEQTATSTTVQGPTKGT 706

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADG---PTAIRDVASWRVKETERMVAIRTELT 372
K L +D M M D +T +VVA A+ T+I +++ RVKE R+ A+ T+L
Sbjct: 707 --KPLPLVD--MEPMTDAFLTASVVAIAANDTNQSTSIVGISNQRVKECNRIEAMITQLA 762

Query: 373 KLGASVEE-----GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEVPTIR 423
K G +E G DY + P + TYDDHR+AM+ S LA AE PV I+
Sbjct: 763 KFGVRAKELEDGIEVFGIDYHHLKTPSD---GVYTYDDHRVAMSLSLLAGLAESPVL 818

Query: 424 DPGCTRKTFFPDYFDVLST 441
+ CT KT+P ++D+L T
Sbjct: 819 ERHCTGKTWPGWWDILHT 836

>gb|AAW33954.1| AROM pentafunctional enzyme [Pichia pastoris]
Length = 1539

Score = 273 bits (697), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 179/438 (40%), Positives = 255/438 (58%), Gaps = 30/438 (6%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL +G + NLL+S+D +ML A+ L G + D + VV G
Sbjct: 405 PGSKSISNRALILAAALGKGECKIKNLLHSDDEHMLNAVAALKGADISFDDNGETVVTG 464

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYV-LDGVPRMRERPIGDL 137
GG F DA +++LGNA G A R LT A++ N T+V L G RM+ERPIG L
Sbjct: 465 NGGNFTATDA---EIYLGNA GTASRFLTSVASIVKPSNTTHVILTGNARMQERPIGPL 520

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G+D++ P+++ GL GG+++L+ +ISSQY+S++LM AP A V
Sbjct: 521 VDALRTNGSDIEYLNREGSLPLKIKSGNGLKGGRIELAATISSQYVSSVLMCAPYASEPV 580

Query: 198 EIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS+ YV+MT+ +M+ FG++ S + Y Y +P +E DASS
Sbjct: 581 TSLVGGKPIISLLYVDMTIAMKSFIEVTKSTTEPYTYHVPQGHYVNPAYEVIESDASS 640

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREP 315
A+Y LA AA+ G VT+ G++SLQGD +FA +VL+ MG KV T TS TV GP +
Sbjct: 641 ATYPLAFAAMNGTQVTIPNIGSSSLQGDARFAVDVLKPMGCKVEQTATSTTVQGPTKGT 700

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADG---PTAIRDVASWRVKETERMVAIRTELT 372
K L +D M M D +T +VVA A+ T+I +++ RVKE R+ A+ T+L
Sbjct: 701 --KPLPLVD--MEPMTDAFLTASVVAIAANDTNQSTSIVGISNQRVKECNRIEAMITQLA 756

Query: 373 KLGASVEE-----GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEVPTIR 423
K G +E G DY + P + TYDDHR+AM+ S LA AE PV I+
Sbjct: 757 KFGVRAKELEDGIEVFGIDYHHLKTPSD---GVYTYDDHRVAMSLSLLAGLAESPVL 812

Query: 424 DPGCTRKTFFPDYFDVLST 441
+ CT KT+P ++D+L T
Sbjct: 813 ERHCTGKTWPGWWDILHT 830

>ref|ZP_06935856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
OP50]
Length = 303

Score = 272 bits (696), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 156/304 (51%), Positives = 201/304 (66%), Gaps = 8/304 (2%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + GT+ LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGTINLPGSKSVSNRALLAALAHGKTVLTNLLDSDVHRHMLNALTGL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S R ++G GG E A ++LFLGNAG AMR L AA+ G+ VL
Sbjct: 62 VSYTLSADTRCEIIGNGGPLHAEGA---LELFLGNAGTAMRPLAALCL--GSNDIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+ GA + + PP+R+ G G GG V + GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQG--GFTGGNVVDGSSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I L+S PY+++TL LM+ FGV+ E+ + +F +KGGQ Y+S
Sbjct: 175 ALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMTFGVEIENQ-HYQQFVVKGGQSYQS 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P VEGDASSASYFLA AAI GGT V G G S+QGD++FA+VLE MGA + W +
Sbjct: 234 PGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDY 293

Query: 305 VTVT 308
++ T
Sbjct: 294 ISCT 297

>ref|ZP_05060087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Verrucomicrobiae
bacterium DG1235]
gb|EDY85227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Verrucomicrobiae
bacterium DG1235]
Length = 446

Score = 272 bits (696), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 163/434 (37%), Positives = 252/434 (58%), Gaps = 24/434 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G+V +PGSKS++NR L++AAL+ G T+++N L SED M+ AL+ LG ++ D+ AK
Sbjct: 14 VNGSVTVPGSKSITNRALIIAALANGETLLENCLFSEDEIMVKALQDLGFEIQPDRDAK 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G G+ P ++ +F+GN+G + R LTA + + G Y LDGVP+MR+RPI
Sbjct: 74 TIRVSGLSGQIP---NKQANIFVGNSGTSARFLTAFLCLSEG-GDYTLGVPQMRKRPI 128

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
DL L QLGA+++ G P+R+ GL GG+ + S SSQ++SAL+MAAP A
Sbjct: 129 ADLAETLNQLGAEIETNG--FAPLRIKS-RGLRGRASIDASSSSQFVSALVMAAPYAT 185

Query: 195 GDVEIEIIDKLISIPYEMTLRLMERFGV-KAEHSDSWDRFYIKGGQKYKS-PKNAYVEG 252
VEI + D + Y++MTL ++++FGV K+ + S + I+ Y++ P+ VEG
Sbjct: 186 EGVEIVLADTSVRRGYIDMTLEMLKQFGVPKSALASSEGSYSIQRHPTYQAKPEGYLVEG 245

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-SVTVTGPP 311
DAS+ASYF A G + + G SLQGD+ F+ +E GA + W +T +V P
Sbjct: 246 DASAASYFFALPVAVTGQLEIHGVTKSLQGDIAFSTRMEEAGAYIEWHDTYAVCHYEPG 305

Query: 312 REPFGRKHLKAIDVNMKNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P +++ + D +T A +A +GPT I ++ R +E +R+ A+ L
Sbjct: 306 AQP-----ESLQGSFYPSYSDTFLTAIAIAPLLNGPTTIEEIGHTRHQECDRIAAMADGL 359

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-----P-VTIRDP 425
+LG V AE IT P+ L +++ TY DHR+AM+F + C + P + I +P
Sbjct: 360 QRLGQIVAETEGSLTIT-PQPLQPSSVATYHHRVAMSFGLGICYDALGNGQPWLQIENP 418

Query: 426 GCTRKTFPDYFDVL 439
C +KTFPD+F VL
Sbjct: 419 TCCKKTFPDFFQVL 432

>ref|XP_002419765.1| pentafunctional AROM polypeptide, putative [Candida dubliniensis
CD36]
emb|CAX41980.1| pentafunctional AROM polypeptide, putative [Candida dubliniensis
CD36]

Length = 1550

Score = 272 bits (696), Expect = 7e-71, Method: Compositional matrix adjust.
Identities = 184/442 (41%), Positives = 260/442 (58%), Gaps = 31/442 (7%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
Sbjct: 407 PGSKSISNRALILAAALGNGTVRVKNLLHSDDTKHMLDAVASLKGAESTEDNGETIVVKG 466

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT---YVLDGVPRMRERPIGDL 137
GG EE L+LGNA G A R LT + G + +L G RM+ERPIG L
Sbjct: 467 NGGNLVT--CGEE--LYLGNAGTASRFLTTVASLVGKSPASDDVILTGNARMQERPIGPL 522

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G++++ P++++ GL GG+++L+ +ISSQY+S++LM AP A V
Sbjct: 523 PGALRSNGSEIEYLNKQGSPLKISAGNGLKGGRIELAATISSQYVSSILMCAPYAKEPV 582

Query: 198 EIEIII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT +M+ FG++ S + + Y YK+P +E DASS
Sbjct: 583 TLALVGGKPLISQLYIDMTCAMMKSFEGIEVTKSTTEEYTYHIPKGIYKNPTEYVIESDASS 642

Query: 257 ASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPPREPF 315
A+Y LA AA+TG + T+ G++SLQGD +FA +VL+ MG KV T TS TVTGPP
Sbjct: 643 ATYPLAFAAMTGTSTIPNIGSSSLQGDARFAVDVLKPMGCKVEQTATSTTVTGPP---- 698

Query: 316 GRKHLKAI-DVNMNKMPPDVAMTLAVVALFAD-GPTAIRDVASWRVKETERMVAIRTELTK 373
R HLK + V+M M D +T +VVA A G T+I +A+ RVKE R+ A+ TEL K
Sbjct: 699 -RGHLKPLPHVDMPEMTDAFLTASVVAVAAGGSGTSITGIANQRVKECNRIEAMVTELAK 757

Query: 374 LGASVEEGPDYCI-----TPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTI 422
G S E PD I TP +++ + +YDDHR+AM+FSL A C E PV I
Sbjct: 758 FGVSANELPDGIEIHGIDIKDLKTP--EISDRGVCSYDDHRVAMSFSLLAGLCKE-PVLI 814

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ T KT+P ++D+L + K
Sbjct: 815 LERSTTGKTWPGWWDILHSEFK 836

>ref|XP_505337.1| YALIOF12639p [Yarrowia lipolytica]
emb|CAG78144.1| YALIOF12639p [Yarrowia lipolytica]
Length = 1556

Score = 272 bits (695), Expect = 9e-71, Method: Compositional matrix adjust.
Identities = 180/436 (41%), Positives = 253/436 (58%), Gaps = 24/436 (5%)

Query: 16 SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-LSVEADKAAK 74
S TV PGSKS+SNR +L AL +G + NLL+S+D +ML A+ LG S E + +
Sbjct: 410 SYTVTPPGSKSISNRAFVLTAALGKGPCKLRNLLHSDDTQHMLEAIELLGGASFWEADGE 469

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVT--AAGGNATYVLDGVPRMR 130
+V G GKG P + +L+LGNA G A R LT A T G +L G RM+
Sbjct: 470 TLLVTGNGGKLTAPAQ-----ELYLGNAGTASRFLTTAATLVQKGDKDHVILTGNKRMQ 523

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
ERPIG LV L+ GAD+ P+++ GL GG +++++ ++SSQY+S+LLM A
Sbjct: 524 ERPIGPLVDALRSNGADIAFQNAEGLPLKIEAGVGLKGGLEVAATVSSQYVSSLLMCA 583

Query: 191 PLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P A V + ++ K IS Y++MT+ +M FGV ++ + Y Y +P+
Sbjct: 584 PYAQTPTVLSLVGGKPLISQFYIDMTIAMMADFGVVVTKDETKEHTYHIPQGVYTNPEEYV 643

Query: 250 VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
VE DASSA+Y LA AA+TG TVTV G+ SLQGD +FA +VL+ MG V T TS TVT
Sbjct: 644 VESDASSATYPLAYAAMTGTHTVTVPNIGSKSLQGDARFAIDVLKAMGCTVEQTATSTTVT 703

Query: 309 GPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G P +LKAI V+M M D +T VVA ++G T I +A+ RVKE R+ A+R
Sbjct: 704 GVP-----NLKAIAMDPEMTDAFLTACVVAASEGTTVITGIANQRVKECNRIEAMR 756

Query: 369 TELTKLGA---SVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEVPVTIRD 424
+L K G +E+G + I+ + ++ +YDDHR+AM+FS L++ PV I +

Sbjct: 757 VQLAKYGVVCRELEDGIEVDGISRSDLKTPVSVHSYDDHRVAMSFSLLSSIMAAPVAIEE 816

Query: 425 PGCTRKTFPDYFDVLS 440

C KT+P ++DVLS

Sbjct: 817 RRCVEKTWPGWWDVLS 832

>gb|EFQ33466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Glomerella
graminicola M1.001]
Length = 1579

Score = 271 bits (694), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 192/461 (41%), Positives = 258/461 (55%), Gaps = 28/461 (6%)

Query: 3 GAEEIVLQPI-----KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVH 54
GA +VL P K + TV PGSKS+SNR L+LAAL +GT + NLL+S+D
Sbjct: 386 GAIRVVLSPATQVIPGVKSLHTTVTPPGSKSISNRALVLAALGQGTCCITNLLHSDDE 445

Query: 55 YMLGALRTLGLSVEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA--A 111
YML A+ LG + A + A + V G GG+ + + L+LGNAG A R LT A
Sbjct: 446 YMLSAIAQLGGATYAWEDAGEVLAVQKGGRL---SASKKALYLGNAGTASRFLTTVVA 501

Query: 112 VTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK 171
+ A ++ VL G RM+ RPIG LV L+ G + P++V+ G GG
Sbjct: 502 LCAPSDVSSTVLTGNARMKVRPIGPLVDALRANGLGIKYLQGEKSLPLQVDAADGFEGGV 561

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDS 230
++L+ +ISSQY+S++LMAAP A V + ++ K IS Y++MT+ +M FGV S
Sbjct: 562 IELAATISSQYVSSILMAAPYAKNPVTLRLVGGKPISQFYIDMTIAMMRTFGVNVTKSAE 621

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-E 289
Y Y++P VE DASSA+Y LA AAITG T TV G+ SLQGD +FA +
Sbjct: 622 EPNTYHVPKAVYQNPPEYVVEDASSATYPLAIAAITGTTCTVPNIGSDSLQGDSRFAVD 681

Query: 290 VLEMMGAKVWTETSVTVTGPPREPFRGKHLKAID-VNMNMPDVAMTLAVVALFADGPT 348
VL MG V T TS TVTGP P G LKAI+ V+M M D +T +V+A A G T
Sbjct: 682 VLRPMGTQVEQTGTSTTVTGP---PIG--SLKAIHVDMPEMTDAFLTASVLAAVASGTT 736

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDH 404
I +A+ RVKE R+ +R +L K G +E D I+ ++ I YDDH
Sbjct: 737 RISGIANQRVKECNRIGVMREQLAKFGVETDEFDDGIIVNGRSVQSLQGPTEGIFCYDDH 796

Query: 405 RMAMAFS-LAACAEVPTIRDPGCTRKTFPDYFDVLSTFVK 444
R+AM+FS L+ A PVTI + CT KT+P ++D LS K
Sbjct: 797 RVAMFSVLSVVPKPVTLERECTGKTWPGWWDTLQSFK 837

>ref|XP_002615931.1| hypothetical protein CLUG_04813 [Clavispora lusitaniae ATCC 42720]
gb|EEQ40685.1| hypothetical protein CLUG_04813 [Clavispora lusitaniae ATCC 42720]
Length = 1568

Score = 271 bits (694), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 186/460 (40%), Positives = 258/460 (56%), Gaps = 33/460 (7%)

Query: 5 EEIVLQPIKEIS----GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P +E + V PGSKS+SNR L+LAAL +GT + NLL+S+D +ML A+
Sbjct: 389 DETLVHPFQEETTPKENNVIPPGSKSISNRALILAALGKGTVRIKNNLHSDDTKHMLAAV 448

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG--- 116
L G + + VV G GG F D QL+LGNAG A R LT +
Sbjct: 449 AALKGAIEISTEDNGDTIVVKNGGNFITCDE----QLYLGNAGTASRFLTTVASLVNVNE 504

Query: 117 -GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
N VL G RM+ERP+G LV L+ G++++ P+++ GL GG+V+L+
Sbjct: 505 QSNDYTVLTGNARMQERPVGPLVNALRANGSEIEYLNNEGSLPLKIKAGKGLKGGRVELA 564

Query: 176 GSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
+ISSQY+S++LM AP A +V + ++ K IS Y++MT+ +M+ FG+ +
Sbjct: 565 ATISSQYVSSILMCAPYAEKEVTLALVGGKPISQLYIDMTIAMMKDFGISVTRDPHEEHT 624

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293

Y Y + P VE DASSA+Y LA AA+TG + TV G++SLQGD +FA +VL+
Sbjct: 625 YHIPKGVYSNPGVYEVESDASSATYPLAFAAMTGTSTVTPNIGSSSLQGDARFAVDVLKP 684

Query: 294 MGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADG--PTAIR 351
MG V T TS TV GP + K L +D M M D +T +VVA A+ PT I
Sbjct: 685 MGCTVEQTSTSTTVRGPSKGS--KPLTHVD--MEPMTDAFLTASVVAIANSSVPTQIT 740

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGP-----DYCIITPPEKLNVTATIDTYDD 403
+A+ RVKE R++A+ EL K G EE P DY + P L + TYDD
Sbjct: 741 GIANQRVKECNRLAMVDELAKFGVRAEELPDGIEIYGIDYKNLKVPSLENRGVCTYDD 799

Query: 404 HRMAAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLST 441
HR+AM+FSL A C E PV I + CT KT+P ++DVL T
Sbjct: 800 HRVAMSFSLLAGMCPE-PVLITERSCTGKTWPGWWDVLHT 838

>ref|XP_384463.1| hypothetical protein FG04287.1 [Gibberella zeae PH-1]
Length = 1568

Score = 271 bits (693), Expect = 1e-70, Method: Compositional matrix adjust.
Identities = 185/450 (41%), Positives = 255/450 (56%), Gaps = 32/450 (7%)

Query: 13 KEISGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
K+++ TV PGSKS+SNR L+LAAL GT + NLL+S+D YML A+ LG S
Sbjct: 401 KD LAVTVAPPGSKSISNRALVLAALGSGTCRIKNLLHSDDTQYMLSAIHQLGGASYSQWD 460

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNAT-YVLDGVPR 128
A + VV G GG ++ +KE L+LGNAG A R LT V A G +AT VL G R
Sbjct: 461 AGEVLVVEGKGN--LQASKEP--LYLGNAGTASRFLTTVVALASPGQDATTNVLTGNAR 516

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLM 188
M+ RPIG LV L+ G +++ + P+R++ GG GG ++L+ +ISSQY+S++LM
Sbjct: 517 MKVRPIGALVDALRSNGLEIEYLGKENSPLRLIDAAGGFKGGDIELAATISSQYVSSILM 576

Query: 189 AAPALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AAP A V + ++ K IS Y++MT+ +M FG+ E S Y YK+P
Sbjct: 577 AAPYAKNPVTLRLVGGKPISQYIDMTIAMMASFGIDVEVSSKEPNTYHIPKGAYKNPPE 636

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVT 306
+E DASSA+Y LA AAITG T+ G+ SLQGD +FA +VL MG V ++ S T
Sbjct: 637 YTIESDASSATYPLAVAAITGKCTIPNIGSKSLQGDARFAVDVLRPMGCSVEQSDYSTT 696

Query: 307 VTGPPREPFGKRHLKAI-DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
VTGP LKA+ V+M M D +T +V+A A G T I +A+ RVKE R+
Sbjct: 697 VTGP-----APGQLKALAHVDMEPMTDAFLTASVLAAVASGTTQITGIANQRVKECNRIA 751

Query: 366 AIRTELTKLGASVEE-----GPDYCIITPPEKLNVTATIDTYDDHRMAMAFS-LAA 414
A++ +L K G E G D + TP +I YDDHR+AM+FS LA
Sbjct: 752 AMKDQLAKFGVQCNELEDGIEVIGKQDGGVSTPE-----ASIHCYDDHRVAMSFSVLAV 806

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ PV + + C KT+P ++D+L K
Sbjct: 807 ASPGPVIVTERECVGKTWPGWWDILFQVFK 836

>ref|XP_368116.2| hypothetical protein MGG_01128 [Magnaporthe oryzae 70-15]
gb|EDK02180.1| hypothetical protein MGG_01128 [Magnaporthe grisea 70-15]
Length = 1575

Score = 271 bits (692), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 185/433 (42%), Positives = 255/433 (58%), Gaps = 23/433 (5%)

Query: 22 PGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL +G + NLL+S+D +ML A+ L G S + + VV G
Sbjct: 428 PGSKSISNRALILALGKGPCRIKNLLHSDDEHMLNAIGKLRGASFSEWEDDGEILVVEG 487

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT----AAGGNATY-VLDGVPRMRERPIG 135
GG+ A E +L+LGNAG A R LT ++ G+AT VL G RM+ RPIG
Sbjct: 488 RGGQL---FAPSEGELYLGNAGTASRFLTTVAALCSPSSDGDATSTVLTGNARMKLRPIG 544

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLALG 195

LV L+ G +++ P+RV+ GG GG ++L+ ++SSQY+S+LLMAAP A
Sbjct: 545 ALVDALRSNGINIEYMGKESLPIRVDAAGFGGGVIELAATVSSQYVSSLLMAAPYAKE 604

Query: 196 DVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYVEGD 253
V + ++ K IS PY++MT+ +M FG+ + S + D ++I G Y +P VE D
Sbjct: 605 PVTLRVLGGKPISQPYIDMTIAMMRSFGIDVQRSTTEADTYHIPQG-IYTNPAEYTVESD 663

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPR 312
ASSA+Y LA AAITG T T+ G+ SLQGD +FA EVL MG V + +S TVTGP
Sbjct: 664 ASSATYPLAVAAITGTTCTIPNIGSASLQGDARFAVEVLRPMGCTVEQSASSTTVTGTP-- 721

Query: 313 EPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
P G+ LK I V+M M D +T +V+A A G T I +A+ RVKE R+ A++ +L
Sbjct: 722 -PLGQ--LKGIPHVDMEPMTDAFLTASVLAASVSGTTQITGIANQVRKECNRIKAMKDQL 778

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPTIIRDPGC 427
K G E D +T +T I YDDHR+AM+FS L+ + PV I + C
Sbjct: 779 AKFGVHCNELDDGIEVTGNSWTELTEPREIYCYDDHRVAMSFSVLSVISPHVLILEREC 838

Query: 428 TRKTFPDYFDVLS 440
T KT+P ++DVLS
Sbjct: 839 TGKTWPGWWDVLS 851

>ref|YP_066747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotalea
psychrophila LSv54]
emb|CAG37740.1| related to 3-phosphoshikimate 1-carboxyvinyltransferase
[Desulfotalea psychrophila LSv54]
Length = 451

Score = 270 bits (691), Expect = 2e-70, Method: Compositional matrix adjust.
Identities = 179/433 (41%), Positives = 251/433 (57%), Gaps = 21/433 (4%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLNSEDVHYMLGALRTLGLS 66
I +Q + + +V +PGSKSL+ R L+ AAL+EG + + L SED Y ALR +G++
Sbjct: 32 IEIQTVGSDVSVAVPGSKSLTQRALIAAALAEGESTLHGPLVSEDTFYSSAALRQVGVT 91

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ +++ + V G G+ A +FLGN G A R LT+ ++ GN+ +VLDG
Sbjct: 92 IDHEESWR---VQGNAGRI----APCAEPIFLGNNGTATRFLTSVLSL--GNSRFVLDGD 142

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM ERPI L+ L+ G DV T CPP+ +N G L GG L SSQYLS+L
Sbjct: 143 KRMAERPIEPLMTALQGWGVDVSSMHDTCPPPLVINSTG-LAGGMTVLPEGKSSQYLSL 201

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+ AP A E+ + ++ S PY+ MTL +M RFG+ E+S + F I G Y+ +
Sbjct: 202 LLVAPYAREVAELRVEGEVFSKPYITMTLDVMSRFGIHVEYSSDYKYFKIPRG-IYRG-Q 259

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGDASSASYF A AA+TGG V VE +SLQGDVK +L MG ++ +T
Sbjct: 260 DYSVEGDASSASYFWAAAATGGRVRVENSVSSLQGDVKLVPLLGRMGCGLSIEGGGIT 319

Query: 307 VTGPPPREFFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ L+ I V+M MPDV TLAVVA FA+G T I+++ R+KE +R+ A
Sbjct: 320 LAST-----GMLEGISVDMADMPDVPTLAVVAAFAEGKTHIQNIGHLRIKCDRLHA 372

Query: 367 IRTTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIIRD 424
+ TELT++GA VEE D +I L+ I+TYDDHRMAM+ ++A V I
Sbjct: 373 VVTELTRMGAEVEEHSDSMVIHGKGGRD LHGATIETIYDDHRMAMSMAGLVKVPGEISG 432

Query: 425 PGCTRKTFPDYFD 437
GC K+FPD++
Sbjct: 433 EGCVAKSFPDFWQ 445

>ref|XP_001528832.1| pentafunctional AROM polypeptide [Lodderomyces elongisporus NRRL
YB-4239]
gb|EDK47592.1| pentafunctional AROM polypeptide [Lodderomyces elongisporus NRRL
YB-4239]
Length = 1551

Score = 270 bits (691), Expect = 3e-70, Method: Compositional matrix adjust.
Identities = 179/434 (41%), Positives = 255/434 (58%), Gaps = 24/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL EGT + NLL+S+D +ML A+ + G +V + + VV G
Sbjct: 408 PGSKSISNRALILAALGEGTTRIKNLLHSDDTKHM L DAVVLMKGATVSFEDSGDTVVVQG 467

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA--VTAAGGNATYVLDGVPRMRERPIGDL 137
GGK KEE+ +LGNAG A R LTA V + + L G RM+ERPI L
Sbjct: 468 HGGKLFA--CKEEI--YLGNAGTASRFLTAVAALVNSTQDEKSVTLTG NARMQERPIAAL 523

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L G+ VD P+++ G GG+++L+ + SSQY+SA+LM AP A +V
Sbjct: 524 VDALTNGSKVDYLNKQGSPLKIEAGNGFKGGRIELAAATSSQYVSAILMCAPYAEKEV 583

Query: 198 EIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT+ +M+ FGV S++ + Y Y++P+ VE DASS
Sbjct: 584 TSLVGGKPIISQLYIDMTIAMMKDFGVDVTKSETEEYTYHIPKSVYQNPQEYVVESDASS 643

Query: 257 ASYFLAGAAITGGTVTVEGCGTTS LQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREP 315
A+Y LA AA+T + T+ G++SLQGD +FA +VL+ MG V T S TVTGP P
Sbjct: 644 ATYPLAFAALTNSSCTIPNIGSSSLQGDARFAVDVLKPMGCTVEQTSKSTTVTGP---PI 700

Query: 316 GRKHLKAI-DVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G LKA+ +++M M D +T +VVA + G T I +A+ RVKE R+ A+ EL K
Sbjct: 701 GT--LKALPEIDMEPMTDAFLTASVVAASVQGT T TISGIANQRVKECNRIKAMVDELAKF 758

Query: 375 GASVEEGPDYCIITPPEKLNVT A-----IDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
G S +E D I + ++ + TYDDHR+AM+FSL A C + PV I++
Sbjct: 759 GVSADETEDGIRIHGVQLRDLKTPGGRGVKTYDDHRVAMSFLLAGLCKD-PVLIQERST 817

Query: 428 TRKTFPDYFDVLST 441
T KT+P ++DVL +
Sbjct: 818 TGKTWPGWWDVLHS 831

>ref|YP_644215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rubrobacter
xylanophilus DSM 9941]
gb|ABG04403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rubrobacter
xylanophilus DSM 9941]
Length = 447

Score = 270 bits (691), Expect = 3e-70, Method: Compositional matrix adjust.
Identities = 189/437 (43%), Positives = 260/437 (59%), Gaps = 21/437 (4%)

Query: 5 EEIVLQPI-KEISGTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
EE+ + P+ + TV+LPGSKS++NR LL+AAAL+ GT+ ++N L ++D +++ AL L
Sbjct: 23 EEMEVALPERPPDATVRLPGSKSITNRALLVAALAGGTSRIENPLLADDPFWMNALVGL 82

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G V + V G GG P A +F+GNAG R L A+ A G+ Y +
Sbjct: 83 GFGVRVGEEGA-VEVAGGGGGIPAPSA----DVFVGNAGTVARFLPPAL--ALGSGPYRV 135

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG PRMRER+ +LV L+ LGA V+C P+ V G GG++ +SG SSQ+L
Sbjct: 136 DGTPRMRERPVAELVEALRALGARVECEEREHGLPLVVRGGARG-GGEISVSGERSSQFL 194

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S LL++AP G + + L+S PYV++T+R+M FG E S F + G Y+
Sbjct: 195 SGLLISAPCLPGGLTVRPRGALVSRPYVDITVRVMRSFGASVEEESGAAFRVAPG-AYR 253

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTE 302
+ AY VE DAS+ASYFLA AA+T G V + G G +SLQGDV FA +L MG +V+ +E
Sbjct: 254 A--TAYRVEPDASAASYFLAAALTAGRVVIPGLGRSSLQGDVAFAGILRRMGCRVSLSE 311

Query: 303 TSVTVTGPPREPFPGRKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + GPPR L+ ++ +MN + D MTLA +A FA PT I++VA R++ET+
Sbjct: 312 DRIELAGPPR-----LRGVEADMNAISDTMMTLAAIAPFASPTLIK NVAHTRLQETD 364

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI 422

R+ A+ EL++LG V E PD I P K+ AI TY DHRMAMAFSL V I
Sbjct: 365 RLAAVAELSLRGLVRVHETPDSLRILII-PGKVRPAAIRTYGDHRMAMAFSLVGLRVGRVRI 423
Query: 423 RDPGCTRKTFPDYFDVL 439
DPGC KT P YF +L
Sbjct: 424 LDPGCVTKTLPGYFRL 440

>ref|XP_001792082.1| hypothetical protein SNOG_01444 [Phaeosphaeria nodorum SN15]
gb|EAT91093.2| hypothetical protein SNOG_01444 [Phaeosphaeria nodorum SN15]
Length = 1661

Score = 270 bits (690), Expect = 3e-70, Method: Compositional matrix adjust.
Identities = 182/456 (39%), Positives = 256/456 (56%), Gaps = 39/456 (8%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL-RTLGLSVEADKA 72
+++ T PGSKS+SNR+L+LAAL G+ + NLL+S+D ML AL + G S +
Sbjct: 408 DLNVTCTPPGSKSVSNRVLVLAALGTGSCRITNLLHSDDTQVMDALAKMQGASFSWEND 467

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAGGNATYVLDGVPRM 129
K VV G GG+ +L+LGNAG A R S+TA A G + V+ G RM
Sbjct: 468 GKELVVTGNGGQLKASSN---ELYLGNAGTAARFLTSVTALCQAQEGVTSVTVTGNARM 523

Query: 130 RERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG---GKVKLSGSISSQYLSA 185
+ERPIG LV L+ +G DVD P+R++ GG G+++L+ ++SSQY+S+
Sbjct: 524 KERPIGLVVKSLRTMGIDVDYQEKEGSLPLRISACGGFGSEAFSGEIELTANVSSQYVSS 583

Query: 186 LLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L++AP + V + ++ K+IS PY++MT+ +M FGV+ + S Y + Y +
Sbjct: 584 ILLSAPYSKPKPVTLRVLVGGKVISQPYIDMTIAMMASFGVQVKRDQSDPNTYRIPNKPYN 643

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTET 303
P VE DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL+ MG KV T+T
Sbjct: 644 PAEYVVESDASSATYPLAIAAITGTTCTVPNIGSGSLQGDARFAIEVLKPMGCKVEQTKT 703

Query: 304 SVTVTGPPREPFGKHLKAI-DVNMMKMPDVAMTLAVVALFADG-----PTAIRDVASWR 357
S TVTGPP R LKA+ +++M M D +T +V+A T I +A+ R
Sbjct: 704 STTVTGPP-----RGLKAVKEIDMEPMTDAFLTASVLAAVCSSNGTSTTTIRYIGIANQR 758

Query: 358 VKETERMVAIRTELTKLGASVEE-----GPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
VKE R+ A+ EL K G + + G Y + P I YDDHR+AM+
Sbjct: 759 VKECNRIQAMEDELAKFGITCRQFDDGIEVDGRGYQLDAPK-----VGHCYDDHRVAMS 813

Query: 410 FS-LAACAEVPTIRDPGCTRKTFPDYFDVLSTFVK 444
F L A PV I + CT KT+P Y+D+L+ K
Sbjct: 814 FGVGLVAPEPVLILEKDCGTGKTWPGYWDILNQFK 849

>gb|EFY99234.1| pentafunctional AROM polypeptide [Metarhizium anisopliae ARSEF 23]
Length = 1570

Score = 270 bits (690), Expect = 3e-70, Method: Compositional matrix adjust.
Identities = 180/441 (40%), Positives = 253/441 (57%), Gaps = 25/441 (5%)

Query: 18 TVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
TV PGSKS+SNR L+LAAL G + NLL+S+D +ML A++ LG S A +
Sbjct: 406 TVTPPGSKSISNRALILAALGSGPCKIKNLLHSDDTFMLSIAIKQLGGASYSWHDAGEIL 465

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT---AAGGNATYVLDGVPRMRER 132
V G GKG ++E+ L++GNAG A R LT +T G N+T VL G RM+ R
Sbjct: 466 EVTGNGGKLSA--SRED--LYIGNAGTASRFLTTVTLCSSTQGSNST-VLTGNARMKVR 520

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+Q GA ++ P+RV+ GG GG ++L+ ++SSQY+S++LMAAP
Sbjct: 521 PIGPLVLRLQNGAQIEYLEQEKSPLIRVHSTGGFQGGMIELAATVSSQYVSSILMAAPY 580

Query: 193 ALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYV 250
A V + ++ K IS PY++MT+ +M FG+ S + D ++I G YK+P + +
Sbjct: 581 AKSPVTLRLVGGKPISQPYIDMTISMSSFGISVTKSTTEMDTYHIPLG-AYKNPSDYII 639

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTG 309

Sbjct: 640 E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL MG V E S TVTG
ESDASSATYPLAVAAITGTTCTIPNIGSASLQGDARFAIDVLRPMGCSVQQDEHSTTVTG 699

Query: 310 PPREFPGRKHLKAI-DVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LK + V+M M D +T +V+A A+G T I +A+ RVKE R+ A++

Sbjct: 700 PI-----TGQLKPLPQVDMPEMTDAFLTASVLA AVANGETQITGIANQRVKECNRIAAMK 754

Query: 369 TELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFS-LAACAEVPVTIR 423
+L K G + E D I+ ++ I YDDHR+AM+ S L+ A I

Sbjct: 755 EQLAKFGITCTELDDGIQISGKSLSDIQTNPVGIHCYDDHRVAMSLSVLSVAVPGSTIIT 814

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
+ C KT+P ++D L+ K

Sbjct: 815 ERECVGKTWPGWWDTLAQSK 835

>sp|Q12659.1|ARO1_PNECA RecName: Full=Pentafunctional AROM polypeptide; Includes: RecName:
Full=3-dehydroquinase synthase; Includes: RecName:
Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS; Includes:
RecName: Full=Shikimate kinase; Includes: RecName:
Full=3-dehydroquinase dehydratase;
Short=3-dehydroquinase; Includes: RecName:
Full=Shikimate dehydrogenase

gb|AAA17839.1| pentafunctional enzyme [Pneumocystis carinii]
Length = 1581

Score = 270 bits (689), Expect = 4e-70, Method: Composition-based stats.
Identities = 173/444 (38%), Positives = 251/444 (56%), Gaps = 28/444 (6%)

Query: 18 TVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLS-VEADKAAKRA 76
T+ LPGSKS+SNR L+LA+LS G + N L+S+D +YML AL L + + ++

Sbjct: 409 TITLPGSKSISNRALILASLSNGICYLKNFLSHDDTYMLSALEKLNAAEFKWEQDGDVL 468

Query: 77 VVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT---YVLDGVPRMRERP 133
VV G G +++L+LGN+G R LT+ T N+ +L G RM++RP

Sbjct: 469 VVGKSGSYL----ENPQMELYLGNSGTTARFLTSICTLVQPNSRENHLILTGSNRMKQRP 524

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG-GLPGGKVKLSGSISSQYLSALLMAAPL 192
IG LV LK G ++ +C P+ + GL GG + LS ++SSQY+S++LM +P

Sbjct: 525 IGPLVDALKNNGCCIEYLELENCLPLLIKPEIGLYGGNINLSATVSSQYVSSILMCSPY 584

Query: 193 ALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A V + +I K IS PY++MT+ +M FG+K S S + Y Y P +E

Sbjct: 585 AKTQVTLSLIGGKPISQPYIDMTISMSSFGIKVTRSHSKENTYYIPKGCYTCPSEYIIE 644

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAE-VLEMMGAKVTWTETSVTVTGP 310
GDA+SA+Y LA AAITGG+ T+ G+ SLQGD KF+E +L+ MG +V + T+ + GP

Sbjct: 645 GDATSATYPLAIAAITGGCTISNVGSASLQGDSKFSEYILKPMGCEVVQSPTTTYIKGP 704

Query: 311 PREPFGRKHLKAI-DVNMNMPDVMATLAVVALFA---DGP--TAIRDVASWRVKETERM 364
P + LK++ +NM M D +T AV+A A P T I +++ R+KE R+

Sbjct: 705 P-----KGKLSLGSINMESMTDTFLTA AVLASVAYEESKPYVTKITGISNQRKECNRI 759

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN-----VTAIDTYDDHRMAMAFSLAAC-AEVP 419
A+ EL K G E PD + N V I+ Y+DHR+AM+FS+ AC + P

Sbjct: 760 NAMVCELKKFGIEAGELPDGIYVKALNTSNLPYSVEGINCYNDHRIAMSFSVLACISSKP 819

Query: 420 VTIRDPGCTRKTFFPDYFDVL-STF 442
TI D C KT+P ++D+L STF

Sbjct: 820 TTILDKACVNKTWPYWWDILNSTF 843

>ref|XP_001528849.1| pentafunctional AROM polypeptide [Lodderomyces elongisporus NRRL
YB-4239]
gb|EDK47578.1| pentafunctional AROM polypeptide [Lodderomyces elongisporus NRRL
YB-4239]
Length = 1551

Score = 270 bits (689), Expect = 4e-70, Method: Compositional matrix adjust.

Identities = 179/434 (41%), Positives = 255/434 (58%), Gaps = 24/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL EGT + NLL+S+D +ML A+ + G +V + + VV G
Sbjct: 408 PGSKSISNRALILAALGEGTTRIKNLLHSDTKHMLDAVVLKMGATVSFEDSGDTVVVQG 467

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA--VTAAGGNATYVLDGVPRMRERPIGDL 137
GGK KEE+ +LGNAG A R LTA V + + L G RM+ERPI L
Sbjct: 468 HGGKLFA--CKEEI--YLGNAGTASRFLTAVAALVNSTQDEKSVTLTGNARMQERPIAAL 523

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L G+ VD P+++ G GG+++L+ + SSQY+SA+LM AP A +V
Sbjct: 524 VDALTNGSKVDYLNKQGSPLKIEAGNGFKGGRIELAATTSSQYVSAILMCAPYAEKEV 583

Query: 198 EIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT+ +M+ FGV S++ + Y Y++P+ VE DASS
Sbjct: 584 TSLVGGKPIQQLYIDMTIAMMKDFGVDVTKSETEEYTYHIPKAVYQNPQEYVVEDASS 643

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPF 315
A+Y LA AA+T + T+ G++SLQGD +FA +VL+ MG V T S TVTGP P
Sbjct: 644 ATYPLAFAALTNSSCTIPNIGSSSLQGDARFAVDVLKPMGCTVEQTSKSTTVTGP---PI 700

Query: 316 GRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G LKA+ +++M M D +T +VVA + G T I +A+ RVKE R+ A+ EL K
Sbjct: 701 GT--LKALPEIDMEPMTDAFLTASVVAASVQGTTTISGIANQRVKECNRIKAMVDELAKF 758

Query: 375 GASVEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
G S +E D I + ++ + TYDDHR+AM+FSL A C + PV I++
Sbjct: 759 GVSADETEDGISIHGVQLKDLKTPGGRGVKTYDDHRVAMSFLLAGLCKD-PVLIQERST 817

Query: 428 TRKTFPDYFDVLST 441
T KT+P ++DVL +
Sbjct: 818 TGKTWPGWWDVLHS 831

>gb|ABB04469.1| 5-enolpyruvylshikimate 3-phosphate synthase [Yersinia kristensenii]
Length = 235

Score = 270 bits (689), Expect = 5e-70, Method: Compositional matrix adjust.
Identities = 133/237 (56%), Positives = 169/237 (71%), Gaps = 9/237 (3%)

Query: 204 KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAG 263
+L+S PY+++TL LM+ FGV+ H +++ F+IKGGQ Y SP VEGDASSASYFLA
Sbjct: 2 ELVSKPYIDITLHLMKTFGVEVVH-ENYQVFHIKGGQTYHSPGTYLVEGDASSASYFLAA 60

Query: 264 AAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAI 323
AAI GGTV V G G S+QGD KFA+VLE MGAKV+W + + + R L+ I
Sbjct: 61 AAIKGGTVRVVTGIGKKSVDGDKFADVLEKMGAKVSWGDDYIECS-----RGTLQGI 112

Query: 324 DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD 383
D++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+ A+ TEL K+GA VEEG D
Sbjct: 113 DMDMNHIPDAAMTIATTALFADGPTTIRNIYNWRVKETDRLSAMATELRKVGAEVEEGQD 172

Query: 384 YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
Y + PP +L I TY+DHRMAM FSL A ++ VTI DP CT KTFPDYF+ L+
Sbjct: 173 YIRVVPPTQLIAAEIGTYNDHRMAMCFSLVALSDTQVTILDPKCTAKTFPDYFEQLA 229

>ref|ZP_03367581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E98-0664]
Length = 243

Score = 269 bits (687), Expect = 7e-70, Method: Compositional matrix adjust.
Identities = 135/246 (54%), Positives = 171/246 (69%), Gaps = 11/246 (4%)

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D I + +L+S PY+++TL LM+ FGV+ A H + +F +KGGQ+Y SP VEGDA
Sbjct: 2 DTIIRVKGELVSKPYIDITLNLKMTFGVEIANHH--YQQFVVKGGQYHSPGRYLVEGDA 59

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA +TW + + T

Query: 9 LQPIKEISGTVKLPGSKSLSNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P I+ V++PGSKS++ R L+ AAL++G +++ L SED Y AL +G+ ++
Sbjct: 10 ITPCGPITAAAEVPGSKSITQRALIAAALAKGESILRGPLASEDTDYTTKALLAMGMVID 69

Query: 69 ADKAAKRAVVVCGGGKFVEDAKEEVQLFLGNAGIAMRSLTAATAVTAAGGNATYVLDGVP 128
+ R + G GG+ A +++LGN G A R L T+ AA G +++++G R

Sbjct: 70 TGRDKWR--IFGQGGRV---APPATEIYLGNNGTATRFLTS--VAALGRGIFLINGDER 121

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI L+ L+ G + GT CPP+ + GL GG L SSQYLS+LL+

Sbjct: 122 MQQRPIEFLLQALRGWGVQIRSIQGTGCPPELIIQA-DGLAGGATVLPPEGKSSQYLSLLL 180

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+P A E+++ ++S PYV MTL +M FG++AE + + F I G Y+ +

Sbjct: 181 VSPYARQPAELKVEGEVLSKPYVAMTLAVMRDFGIEAEEAPELNHFKIPQG-IYQG-REY 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGDASSASYF A AA+TGG VTV + SLQGD ++LE MG +V + ++V

Sbjct: 239 RVEGDASSASYFWAAAATGGKVTVTNVPSPSLQGDVAVLDILEQMGCRVERDQAGISVA 298

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P L+ ++V+M PDV TLAVVA A G T I ++A R+KE +R+ +

Sbjct: 299 AP-----DELRGVEVDMGDCPDVPTLAVVAALAQGRTRINNIAHLRIKECDRLGVMA 351

Query: 369 TELTKLGASVEEGPDYCIIT---PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
EL KLG EEGPDY ++ I T++DHR+AM+F++A+ A + I +P

Sbjct: 352 AELAKLGVKTEEGPDYLVVEGRGRQHDYQGAETIATHNDHRIAMSFVASLAIPGIRIENP 411

Query: 426 GCTRKTFFDYFDVLSTFV 443
GC +K+FPD++ L + +

Sbjct: 412 GCVKKSFPDFWQRLSIL 429

>ref|XP_003169854.1| pentafunctional AROM polypeptide [Arthroderma gypseum CBS 118893]
gb|EFR05019.1| pentafunctional AROM polypeptide [Arthroderma gypseum CBS 118893]
Length = 1571

Score = 268 bits (686), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 184/450 (40%), Positives = 259/450 (57%), Gaps = 28/450 (6%)

Query: 13 KEISGTVKLPGSKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K + T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + + ++

Sbjct: 402 KSLQVCTTPPGSKSISNRALVLAALSGTCRIRNLLHSDDETEVMLNALEALGAATFSWEE 461

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATY-VLDGVPR 128
+ VV G GKK A +L+LGNAG A R LT A ++ A G+ ++ +L G R

Sbjct: 462 EGEVLVVGKGGKL---AASAHELYLGNAGTASRFLTTVATLSNAKGDVSHNLTGNAR 517

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPIGDLV LK G V+ P++V GG GG ++L+ +SSQY+S+LLM

Sbjct: 518 MKQRPIGDLVDALKANGVSVEYLEQQGSLPLKVPACGGFKGGAIELAAKVSSQYVSSLLM 577

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPK 246
AP A V +++ K IS Y+ MT +M+ FG+ E S S + ++I+ GQ YK+P

Sbjct: 578 CAPYAKEKVTLKLVGGKPISEYTIAMTAAAMKSFGINVEKSTSEEYTHIQGGQ-YKNPP 636

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA++G T T+ G+ SLQGD +FA +VL MG V T+TS

Sbjct: 637 EYVIESDASSATYPLAIAAMSGTTCTIPNIGSKSLQGDARFAVDVLRPMGCNVKQTDST 696

Query: 306 TVTGPPREPFGKRHLKAI-DVNMNMPDVAMTLAVVALFAD---GPTAIRDVASWRVKE 360
TVTGP LK I +V+M M D +T +V+A A T I +A+ RVKE

Sbjct: 697 TVTGPVNGA-----LKPIVNVDMPEMTDAFLTASVLAASVADKSGNTTRIYGIANQRVKE 751

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPE----KLNVTADITYDDHRMAMAFSL--AA 414
R+ A++ EL K G + E D I + K+ V + YDDHR+AM+FS+ AA

Sbjct: 752 CNRIKAMKDELAKEFGVTCREHDDGIEDGIDRSALKVPVNGVHCYDDHRVAMSFVLA 811

Query: 415 CAEVPVTIRDPGCTRKTFFDYFDVLSTFVK 444
+ P I + C KT+P ++D L+ K

Sbjct: 812 ASSQPTLILEKECVGKTWPAWWDALAQTFK 841

>ref|XP_001228231.1| hypothetical protein CHGG_10304 [Chaetomium globosum CBS 148.51]
gb|EAQ83900.1| hypothetical protein CHGG_10304 [Chaetomium globosum CBS 148.51]
Length = 1464

Score = 268 bits (685), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 190/442 (42%), Positives = 259/442 (58%), Gaps = 22/442 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAA 73
+S +V PGSKS+SNR L+LAAL +GTT + LL+S+D +ML A+ L G + + A
Sbjct: 310 LSVSVTPPGSKSVSNRALILAAALGQGTTRIHLHSDDTQFMLAAIAQLQGATYSWEDAG 369

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA--AVTAAGGNATYVLDGVPRMRE 131
+ VV G G G K A E L+LGNAG A R LT+ A+ + ++ VL G RM+
Sbjct: 370 EVLVVKGRGGKL---QASGE-SLYLGNAGTASRFLTSVVALCSPTTASSTVLTGNARMKV 425

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPIG LV L+ G V+ PVRV+ G GG ++L+ ++SSQY+S++LMAAP
Sbjct: 426 RPIGPLVDALRANGVAVEYLEKEKSLPVRVDANAGFAGGVIELAATVSSQYVSSILMAAP 485

Query: 192 LALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNAY 249
A V + ++ K IS Y +MT+ +M FG+K E S + + ++I G Y++P
Sbjct: 486 YAHKPVTLRLVGGKPISSQYTDMTIAMMASFGIKVERSTEDPNTYHIPQG-VYQNPAEYV 544

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
+E DASSA+Y LA AAITG T T+ G+ SLQGD +FA EVL MG V TETS TVT
Sbjct: 545 IESDASSATYPLAVAAITGTTCTIPNIGSASLQGDARFAVEVLRPMGCTVEQTETSTTVT 604

Query: 309 GPPREPFGKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GPP LKAI V+M M D +T +A A G T I +A+ RVKE R+ A+
Sbjct: 605 GPP-----VGTLKAIKHVDMEPMTDAFLTATALAAVASGTTQITGIANQVRKECNRIAAM 659

Query: 368 RTELTKLGASVEEGPD--YCIITPPEKLNVT--IDYDDHRMAMAFS-LAACAEVPVTI 422
+ +L K G E D I P ++L A I YDDHR+AM+FS L+ + PV I
Sbjct: 660 KDQLAKFGVVCNELEDGIEVIGKPYQELQNPAGEIYCYDDHRVAMSFVSLSTVSPHPVLI 719

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ CT KT+P ++D+LS K
Sbjct: 720 LERECTAKTWPGWWDILSQAFK 741

>ref|XP_002790866.1| pentafunctional AROM polypeptide [Paracoccidioides brasiliensis
Pb01]
gb|EEH36684.1| pentafunctional AROM polypeptide [Paracoccidioides brasiliensis
Pb01]
Length = 1523

Score = 268 bits (684), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 184/452 (40%), Positives = 252/452 (55%), Gaps = 33/452 (7%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + + +
Sbjct: 403 KSLNVCTTPPGSKSISNRALVLAALGSGTCRIKNLLHSDDETEVMTALERLGAATFSWEN 462

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVLDGVPRMR 130
+VV G V KE L+LGNAG A R LT T A G A+ VL G RM+
Sbjct: 463 QGEVLVVGNGGRMVASPK---LYLGNAGTASRFLTTVATLAQNGSVASSVLTGNARMK 519

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RPIGDLV LK GAD++ P+++ GG GG+++LS +SSQY+S+LLM A
Sbjct: 520 QRPIGDLVDALKANGADIEYLENPKSLPLKITASGGFAGGEIRLSAKVSSQYVSSLLMCA 579

Query: 191 PLALGDVEIEIIE-DKLISIPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNAY 249
P A V + ++ +S Y++MT +M FG+ + S++ + Y YK+P
Sbjct: 580 PYAKEPVTLRLVGGNPVSQLYIDMTTAMMRSFGIDVKKSETEHTYHIPRGVYKNPAEYV 639

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
VE DASSA+Y LA AA+TG + TV G+ SLQGD +FA +VL MG V T+ S +VT
Sbjct: 640 VESDASSATYPLAIAAMTGTCTVPNIGSKSLQGDARFAIDVLRPMGCTVNQTDFTSVT 699

Query: 309 GPPREPFGKHLKAI-DVNMNKMPPDVAMTLAVVALFADGP-----TAIRDVASWRVKETE 362
GP G K LK+I ++M M D +T +V+A A G T I +A+ RVKE
Sbjct: 700 GPA----GGK-LKSIPTIDMEPMTDAFLTASVLAAVARGQGSNHTTRICGIANQVRKECN 754

Query: 363 RMVAIRTELTKLGASVEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFS-L 412
R+ A++ EL K G + E D + PPE + YDDHR+AM+FS L

Sbjct: 755 RIKAMKDELAKEFGVTCREHDDGLEIDGIDRSTLCHPPE-----GVFCYDDHRVAMSFSIL 809

Query: 413 AACAEVPTVIRDPGCTRKTFPDYFDVLSTFVK 444

A AE P I + C KT+P ++D L+ K

Sbjct: 810 ALAAEQPTLILEKECEVGKTPGWWDTLAQTFK 841

>ref|YP_461861.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Syntrophus aciditrophicus SB]

gb|ABC77693.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Syntrophus aciditrophicus SB]

Length = 446

Score = 268 bits (684), Expect = 2e-69, Method: Compositional matrix adjust.

Identities = 155/421 (36%), Positives = 244/421 (57%), Gaps = 18/421 (4%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78

+++PGSKS++ R L +AAL+ G +++ N L +ED Y++ AL LG ++ + + R +

Sbjct: 40 LQVPGSKSITQRALTI AALANGESLLRNALIAEDTRYLMKALELLGAFIQVEGSEIR--I 97

Query: 79 VGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138

G GG+ V D + ++LGN G A+R LT V G +VLDG PR+RERP+ L+

Sbjct: 98 TGTGGRLQVPDQR---IYLGNGGTALRFLTLVCL--GEGGFVLDGSPRLRERPVEPLL 151

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198

L+ +G +D CPP+ + GLPGG+ + SSQY+S+LL+++P A +V+

Sbjct: 152 QVLRGCMGVFIDTPENPGCPPIHIT-TRGLPGGRAFFADLDSSQYISSLLISSPYAARNVK 210

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258

I + + +S PY+EMTL++ME FG+ F++ GQ Y + ++ +EGD SSAS

Sbjct: 211 IMLAGRTVSEPIYEMTLKVMHFHGISVGR-QYGKAFFVAAGQSYVA-QSFDIEGDFSSAS 268

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPEPFGRK 318

YF AA+ G V V G S QGD +F ++L+ +G V+W E V V +

Sbjct: 269 YFFLAALGLGRVQVPLTAESSQGDARFLKILQNLGCAVSWNEKGVEVACE-----KL 322

Query: 319 HLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378

H + + M +PD+ +LAV+A F G T I + A R+KE+ R+ A+ EL+++G +

Sbjct: 323 HAGDLILPMGDIPDMVPSLAVLAAFRSGRTVITEAAHLRIKESNRLAALARELSRIGIAA 382

Query: 379 EEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFPDYFDV 438

+E D II + I+TY+DHR+AM+F++A + I D C RK+FP ++D

Sbjct: 383 QETLDGLIIDGGHP-HGGDIETYNDHRIAMSFVAGLVVPEINIADRDCVRKSFPGFWD 441

Query: 439 L 439

L

Sbjct: 442 L 442

>ref|XP_002496718.1| ZYR00D06578p [Zygosaccharomyces rouxii]

emb|CAR27785.1| ZYR00D06578p [Zygosaccharomyces rouxii]

Length = 1589

Score = 266 bits (681), Expect = 3e-69, Method: Compositional matrix adjust.

Identities = 187/464 (40%), Positives = 260/464 (56%), Gaps = 43/464 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADK 71

+E + T+ PGSKS+SNR L+LAAL +GT + NLL+S+D +ML A++ L G S+ +

Sbjct: 413 QEQAKTIVPPGSKSISNRALILAALGKGTCKIKNLLHSDDTKHMLTAVQELKGASITWED 472

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLT---AAVTAAGGNATYVLDGVPR 128

+ V+ G GG+ A L+LGNAG A R LT A V ++ VL G R

Sbjct: 473 NGETVVLEHGGETLTASADP---LYLGNAGTASRFLTTLAALVNSSSKQDYVVLGTGNAR 529

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

M++RPIG LV L+ G +D P+++ GG+++L+ ++SSQY+S++LM

Sbjct: 530 MQQRPIGPLVDSLRTNGTKIDYKSEGLPLKIYTSFPFKGGRIELAAATVSSQYVSSVLM 589

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPK 246

AP A V + ++ K IS YV+MT+++ME+FG+K E S + ++I GQ Y +P

Sbjct: 590 CAPYAENPVTLALVGKPISQLYVDMTIKMMKFGIKVEVSTTEPYTYHLPKGQ-YTNPP 648

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA+TG TVTV G SLQGD +FA EVL MG KV T S
Sbjct: 649 EYIIIESDASSATYPLAFAAMTGTTVTPNIGYESLQGDARFAIEVLRPMGCKVEQTANST 708

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD-----GPTAIRDVASWRV 358
TVTGPP + LK +D M M D +T +VVA A T I +A+ RV
Sbjct: 709 TVTGPPPTGSL--RPLKHVD--MEPMTDAFLTASVVAVAHDNDTDSANVTTIEGIANQRV 764

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVTADITYDDHRMAM 408
KE R+ A+ TEL K G + +E PD I P I++YDDHR+AM
Sbjct: 765 KECNRIEAMSTELAKFGVATKELPDGIQHGINSLDLLQLPSNSTGPIGIESYDDHRVAM 824

Query: 409 AFSLAA-----CAEV-PVTIRDPGCTRKTFPDYFDVLST 441
+ SL A A++ PV I + CT KT+P ++DVL T
Sbjct: 825 SLSLLAGMVNYSKSHPAADIKPVRILERRCTGKTWPGWWDVLHT 868

>ref|XP_002836591.1| hypothetical protein [Tuber melanosporum Mel28]
emb|CAZ80782.1| unnamed protein product [Tuber melanosporum]
Length = 1554

Score = 266 bits (681), Expect = 3e-69, Method: Compositional matrix adjust.
Identities = 179/438 (40%), Positives = 250/438 (57%), Gaps = 32/438 (7%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D +ML AL LG + ++ VV G
Sbjct: 398 PGSKSISNRALVLAALGSGTCHVKNLLHSDDEHMLTALHNLGGIYQSWEEDGDVVLVVG 457

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYVLDGVPRMRERPIGDL 137
GGK +L+LGNAG A R LT+ V+ +G + + VL G RM++RPIG L
Sbjct: 458 NGGKLACGD----ELYLGNAGTAARLTSTVATLVSPSGEHSIVLTGNARMKQRPISGL 513

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G+ V+ PVRV GL GG+++L +SSQY+S++L+ AP A V
Sbjct: 514 VDALRSNGSSVEYLESQGSPLVRVPSTSGLMGGRIELEAKVSSQYVSSVLICAPYAREPV 573

Query: 198 EIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT+ +M FG+ S + + Y YK+P VE DASS
Sbjct: 574 TSLVGGKPIISQLYIDMTIAMSSFGIDVTKSTAEEYTYHIPQGSYKNPAVYVVEDASS 633

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPPREPF 315
A+Y LA AAITG TVTV G SLQGD +FA +VL MG V ++ S TV GPP
Sbjct: 634 ATYPLAIAAITGNTVTPNIGRKSLLQGDARFAVDVLRPMGCTVEQSDYSTTVRGPP---- 689

Query: 316 GRKHLKAI-DVMNKMMPDVAMTLAVVALFADG--PTAIRDVASWRVKETERMVAIRTEL 372
+ L+ + V+M M D +T +V+A A G ++I +A+ RVKE R+ A+ EL
Sbjct: 690 -KGQLRPLPHVDMPEPMTDAFLTASVLA AVAKGVERSITGIANQRVKECNRIAAMVHEL 748

Query: 373 KLGASVEE-----GPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEVPVTIR 423
K G + E G DY ++ PE + YDDHR+AM+FS ++ A PV ++
Sbjct: 749 KFGVTAGELEDGIWIQIDYNLLKTPE-----GVHCYDDHRVAMSFSVISLIAPNPVILQ 803

Query: 424 DPGCTRKTFPDYFDVLST 441
+ C KT+P ++DVLST
Sbjct: 804 ERKCVETWPGWWDVLST 821

>ref|XP_003016933.1| repressor protein [Arthroderma benhamiae CBS 112371]
gb|EFE36288.1| repressor protein [Arthroderma benhamiae CBS 112371]
Length = 1571

Score = 266 bits (680), Expect = 5e-69, Method: Compositional matrix adjust.
Identities = 181/450 (40%), Positives = 256/450 (56%), Gaps = 28/450 (6%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K + T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + + ++
Sbjct: 402 KSLQVTCTPPGSKSISNRALVLAALGSGTCRIRNLLHSDDEVMLNLEALGAATFSWEE 461

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY---VLDGVPR 128
+ VV G GKK DA +L+LGNAG A R LT T + A +L G R

Sbjct: 462 EGEVLVVNGKGGKL---DASSH-ELYLGNAGTASRFLTTVATLSNNKADVSHNILTGNAR 517

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPIGDLV LK G ++ P++V GG GG++KL+ +SSQY+S+LLM

Sbjct: 518 MKQRPIGDLVDALKANGVPIEYIEQQGSLPLKVPACGGFKGGEIKLAAKVSSQYVSSLLM 577

Query: 189 AAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPK 246
AP A V ++++ K IS Y+ MT +M+ FG+ E S + + ++I+ GQ YK+P

Sbjct: 578 CAPYAKEKVTLKLVGGKPISEAYISMTAAMMKSFGINVEKSTEEYTYHIEQGQ-YKNPP 636

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA++G T T+ G+ SLQGD +FA +VL MG V T+TS

Sbjct: 637 EYVIESDASSATYPLAIAAMSGTCTCTIPNIGSKSLQGDARFAVDVLRPMGCDVKQTDST 696

Query: 306 TVTGPPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFA----DGPTAIRDVASWRVKE 360
TVTGP LK I +V+M M D +T +V+A A T I +A+ RVKE

Sbjct: 697 TVTGPT-----DGALKPIANVDMPEMTDAFLTASVLA AVAKDKSSNTTRIYGIANQRVKE 751

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFSL--AA 414
R+ A++ EL K G + E D I +++ + + YDDHR+AM+FS+ +A

Sbjct: 752 CNRIKAMKDELAKFGVTCREHEDGIEIDGIDRMALKVPFNGVHCYDDHRVAMSFVSLASA 811

Query: 415 CAEVPVTIRDPGCTRKTTPDYFDVLSTFVK 444
+ P I + C KT+P ++D LS K

Sbjct: 812 ASSQPTLILEKECVGKTWPAWWDTLSTQTFK 841

>ref|XP_449840.1| hypothetical protein [Candida glabrata CBS 138]
emb|CAG62820.1| unnamed protein product [Candida glabrata]
Length = 1579

Score = 266 bits (680), Expect = 5e-69, Method: Compositional matrix adjust.
Identities = 191/475 (40%), Positives = 263/475 (55%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI---SGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P I + TV PGSKS+SNR L+LAAL +GT + NLL+S+D +ML A+

Sbjct: 392 DETLVYPFNNIPRDQNKTVTPPGSKSISNRALVLAALGKGTCTRIKLLHSDDTKHLMTAV 451

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT---AAVTAAG 116
+ L G ++ + + V+ G GG V E L+LGNAG A R LT A V +

Sbjct: 452 QELKGANISWEDNGETVVLEGQGGSTLVAC---ENDLYLGNAGTASRFLTSVAALVNSTS 508

Query: 117 GNATYVLVDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
+L G RM++RPIG LV L+ G +D C P++V+ GG+++L+

Sbjct: 509 QKDHVILTGARMQQRPIGPLVDSLRNNGIKIDYVKNEGCLPLKVHTDSVFKGGRIELAA 568

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
++SSQY+S++LM AP A V + ++ K ISI YVEMT+++ME+FG+K E S + + Y

Sbjct: 569 TVSSQYVSSILMCAPYAENPVTALVGGKPI SILYVEMTIKMEKFGIKVEKSTEEYTY 628

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMM 294
I Y +P +E DASSA+Y LA AA+TG TVTV G+ SLQGD +FA +VL+ M

Sbjct: 629 IIPKGHYVNPAYEVIESDASSATYPLAFAALTGTTTVTPNIGSASLQGDARFATDVLQPM 688

Query: 295 GAKVTWTETSVTVTGPPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFAD-----G 346
G VT T TS TVTGPP HLG + V+M M D +T VVA A

Sbjct: 689 GCSVTQTATSTTVTGPP-----VGHLKPLKHVDMEPMTDAFLTACVVA AVAHNDNDPTSKN 743

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----VT 396
T I +A+ RVKE R+ A+ T+L K G E PD + +N

Sbjct: 744 TTTIEGIANQRVKECNRIEAMCTQLAKFGVRTNELPDGIQVHGLHSINDLKVPSIGNEAV 803

Query: 397 AIDTYDDHRMAMAFSLAA-----CAEVPVTIRDPGCTRKTTPDYFDVLST 441
+ TYDDHR+AM+FSL A PV I + CT KT+P ++DVL T

Sbjct: 804 GVCYDDHRVAMSFSLLAGMVNSEQPNSSNPTPVRIERHCTGKTWPGWWDVLHT 858

>gb|EFY84835.1| pentafunctional AROM polypeptide [Metarhizium acridum CQMa 102]
Length = 1570

Score = 266 bits (680), Expect = 5e-69, Method: Compositional matrix adjust.

Identities = 180/441 (40%), Positives = 252/441 (57%), Gaps = 25/441 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
TV PGSKS+SNR L+LAAL G + NLL+S+D +ML A++ LG S A +
Sbjct: 406 TVTPPGSKSISNRALILAALGSGPCKIKNLLHSDDTFMLSIIQQLGGASYSWYDAGEIL 465

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG---NATYVLDGVPRMRER 132
V G G G K ++E+ L++GNAG A R LT +T N+T VL G RM+ R
Sbjct: 466 EVTGNNGKLSA--SRED--LYIGNAGTASRFLTTVLTLCSSSTQESNST-VLTGNTRMKVR 520

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+Q GA ++ P+RV+ GG GG ++L+ ++SSQY+S++LMAAP
Sbjct: 521 PIGPLVDALRQGAQIEYLEQEKSLPIRVHSTGGFQGGMIELAATVSSQYVSSILMAAPY 580

Query: 193 ALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYV 250
A V + +I K IS PY++MT+ +M FG+ S + D ++I G YK+P +
Sbjct: 581 AKTPVTLRLIGGKPISQPYIDMTISMSSFGISVTKSTTDMDTYHIPLG-AYKNPSEYVI 639

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTG 309
E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL MG V E S TVTG
Sbjct: 640 ESDASSATYPLAVAAITGTTCTIPNIGSASLQGDARFAIDVLRPMGCSVQQDEHSTTVTG 699

Query: 310 PPREPFGRKHLKAI-DVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LK + V+M M D +T +V+A A+G T I +A+ RVKE +R+ A++
Sbjct: 700 PV-----TGQLKPLPHVDMPEMTDAFLTASVLAAVANGETQITGIANQRVKECDRIAAMK 754

Query: 369 TELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFS-LAACAEVPTIR 423
+L K G + E D I+ ++ I YDDHR+AM+ S L+ A I
Sbjct: 755 EQLAKFGVTCTELDDGIQISGKSLSDIRTPNVGIHCYDDHRVAMSLSVLVVAPGSTIIT 814

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
+ C KT+P ++D L+ K
Sbjct: 815 ERECVGKTWPGWWDTLAQSFK 835

>emb|CBX30069.1| 3-phosphoshikimate 1-carboxyvinyltransferase 1 [uncultured
Desulfobacterium sp.]
Length = 444

Score = 266 bits (679), Expect = 6e-69, Method: Compositional matrix adjust.
Identities = 160/426 (37%), Positives = 238/426 (55%), Gaps = 22/426 (5%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+++PGSKS ++R+L+ +ALS+G + N L SED L ALR +G+ +E K +V
Sbjct: 37 IEVPGSKSYTHRLIASALS DGKCSLTNCLKSEDTLLTLEALRLMGVKIE--NLEKEVIV 94

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G G D ++L N+G +MR LT AA G+ Y L G RM +RPI DL+
Sbjct: 95 YGSKGLLKAYDK----PVYLANSGTSMRLLTGV--AALGDGYTLTGTERMSQRPIQDLL 148

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
GL LG + CPPV + G G + GG ++L +ISSQ+LS++L+ +P ++
Sbjct: 149 DGLNSLVGEARSVNNGCPCPVVIK-GKIKGGYIELKCNISSQFLSSVLLISPYTEKGIK 207

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I++++ +S PY++MT+ +M + GV D + F + G Q YK+ + VE D S A
Sbjct: 208 IKVVEGPVSKPYIDMTIDIMAKLGVNVSR-DGYTGFSVDGQNYKAGSFS-VEPDQSAG 265

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRK 318
YF A AAITG + V+G S QGD+K + E MG KV + + V G P
Sbjct: 266 YFWAAAATGSEIKVGITKDSRQGDCLKLTGLFEKMGCKVVFESDGIIVKGGP----- 318

Query: 319 HLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
L I+ +M+ MPD+ TLAVVA FA G T I++V + KE++R+ A+ EL+K G
Sbjct: 319 -LVGIETDMSDMPDMVPTLAVVAFAFARGTTVIKNVEHLKAKESDRLSAVINELSKTGIEA 377

Query: 379 EE-GPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFD 437
+ G D I K IDTY+DHR+AM+F++ + I D C K+FP+++D
Sbjct: 378 KSVGSDLVIKGGIPK--GARIDTYNDHRIAMSFVAVGLKTPGIIIEDKKCKVEKSFPNFW 435

Query: 438 VLSTFV 443

V + V
Sbjct: 436 VFANLV 441

>ref|YP_174720.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
dbj|BAD63759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
Length = 446

Score = 265 bits (677), Expect = 1e-68, Method: Compositional matrix adjust.
Identities = 170/444 (38%), Positives = 244/444 (54%), Gaps = 27/444 (6%)

Query: 1 MAGAEEIVLQPI-KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGA 59
+AG E + L P K I+ T+++PGSKS +NR LLLAA++ GT+ + N L S+D ++ + A
Sbjct: 15 LAGVERLRRLTPSQKRINATLEVPKSGSATNRALLAAVASGTSTLRNALKSDDTYWCIEA 74

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
L+ G+ + D V G GG F L++G+AG A R L + AA GN
Sbjct: 75 LKKTGVEIAVD--GSNVTVYGRGGVF-----HSGSLYIGSAGTAGRFLPGMLAAATGN- 125

Query: 120 TYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSIS 179
+ ++ M +RPI LV L+ LGA++ P+ ++G GL GGV +SG +S
Sbjct: 126 -WHVEASHSMNKRPIAPLVKTLQALGANIQYGSRRGHYPLSISG-EGLNGGKVNMSGQLS 183

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ++S L+AAPLA V I + D ++ YV +T+ LM FGV+ + + W +
Sbjct: 184 SQFISGCLLAAPLAKNPVSITVKDGIYQQAYVRITIDLMAAFGEVKAAPDWSLLEVN-- 241

Query: 240 QKYKSP---KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
SP + +E DAS+A YFLA AAIT G + + T + Q D+ F +L+ MG
Sbjct: 242 ---PSPYVANDIAIEADASTACYFLALAAITAGKIRIRHFSKTSQPDILFVSILKRMGC 298

Query: 297 KVTWTESTVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
+ V GP R G VNMN++ D A+TLA ++ FADGP AI V
Sbjct: 299 NFEIGPSFVEGEGPTRLRGG-----FTVNMNELSDQALTLAAISPFADGPPIAIEGVGHI 352

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAACA 416
R E +R+ AI TEL++LG VEE D + P + T ++TYDDHRMAMA +L
Sbjct: 353 RHHECDRIRAICTELSRGLIRVEERHDGLTVYPGPQ-KPTVVNTYDDHRMAMALALIGAK 411

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLS 440
+ + DPGC KT P YF +L+
Sbjct: 412 VDGIELDDPGCVAKTCPSYFSMLA 435

>ref|XP_002153704.1| pentafunctional polypeptide (AroM), putative [Penicillium marneffei
ATCC 18224]
gb|EEA18560.1| pentafunctional polypeptide (AroM), putative [Penicillium marneffei
ATCC 18224]
Length = 1573

Score = 265 bits (676), Expect = 1e-68, Method: Compositional matrix adjust.
Identities = 180/443 (40%), Positives = 247/443 (55%), Gaps = 25/443 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+++ PGSKS+SNR L+LAAL GT V NLL+S+D ML AL LG + A +
Sbjct: 399 KDLNVVCAPPGSKSISNRALVLAALGSGTVRVKNLLHSDDEVMLNALERLGAATFAWED 458

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATY-VLDGVPRM 129
+ VV G GKK +L+LGNAG A R LT+ T +G G+ Y +L G RM
Sbjct: 459 EGEVLVVGNGGKMQAS---PTELYLGNAGTASRFLTSVATLSGKGSVDYNTLTGNRM 514

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
++RPIGDLV L GA V+ P+++ GG GG++ L+ +SSQY+S+LLM
Sbjct: 515 KQRPIGDLVDALTINGAQVEYLEKAGSLPLKIAASGGFGKGRINLAAKVSSQYVSSLLMC 574

Query: 190 APLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AP A V ++++ + IS+ Y+EMT +M FG+ + S + + Y Y +P
Sbjct: 575 APYAKEPVTLLKVGGRPIISLSYIEMTTAMMRSFGIDVQKSTTEEWYHIPQGSYNPPEY 634

Query: 249 YVEGDASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKFA-EVLEMMGAKVTWTETSVTV 307
+E DASSA+Y LA AA+TG T TV G+ SLQGD +FA EVL MG KV T TS TV
Sbjct: 635 VIESDASSATYPLAIAAVTGTCTVPNIGSASLSQGDARFAVEVLPRMGCKVEQTATSTTV 694

Query: 308 TGPPREPFPGRKHLKAI-DVNMNMKMPDVAMTLAVVALFADG-----PTAIRDVASWRVKET 361
TGP L+ + +V+M M D + +V+A A G T I +A+ RVKE
Sbjct: 695 TGP-----ADGVLRLPLPNVDMPEPMTDAFLGASVLAIAAQEGGNHATRIYIGIANQVRVKEC 749

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAFS-LAACA 416
R+ A+R EL K G E PD I ++ + + YDDHR+A +FS L+ A
Sbjct: 750 NRIEAMRVELAKFGVVCREHPDGLEIDGIDRSTLRHPAGGVFCYDDHRVAFSFSILSLVA 809

Query: 417 EVPVTIIRDPGCTRKTFPDYFDVL 439
P I + C KT+P Y+D L
Sbjct: 810 PTPTLILEKECVGKWTWPTYWDAL 832

>ref|XP_001243950.1| hypothetical protein CIMG_03391 [Coccidioides immitis RS]
Length = 1543

Score = 265 bits (676), Expect = 1e-68, Method: Compositional matrix adjust.
Identities = 187/467 (40%), Positives = 260/467 (55%), Gaps = 42/467 (8%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 342 KIVLAPSIEVSPGVPKSLQVTCTPPGSKSISNRALVLAALGSGTCRIKNLLHSDDETEVML 401

Query: 58 GALRTLGLSVEA-DKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA- 115
AL LG + + ++ + VV G GG ++ + EE L+LGNAG A R LT T A
Sbjct: 402 NALERLGAATFSWEEEGEVLVHGNNGA--LKASPEE--LYLGNAGTASRFLTTVATLAN 457

Query: 116 -GGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKL 174
G ++ VL G RM++RPIG LV L+ GA V+ C P++++ GG GG++ L
Sbjct: 458 NGTVSSVTLTGNARMKQRPICALVDSL RANGAGVEYLETNGCLPLKIDASGGFAGGEISL 517

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ ISSQY+S+LLM AP A V ++++ K IS Y++MT +M FG+ + S + +
Sbjct: 518 AAKISSQYVSSLLMCAPYAKEPVTLKLVGGKPISQQYIDMTTAMMRSFGIDVKRSTTEEH 577

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKFA-EVLE 292
Y KY +P +E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL
Sbjct: 578 TYHIPQKYMNPAEYIIIESDASSATYPLAVAAITGTTCTIPNIGSKSLQGDARFAVDVLR 637

Query: 293 MMGAKVTWTETSVTVTGPPREPFPGRKHLKAI-DVNMNMKMPDVAMTLAVVALFADGP---- 347
MG +V+ +E S TVTGP LK + +V+M M D +T +V+A A G
Sbjct: 638 PMGCEVSQSEYSTTVTGP-----KDGVLKPLPNVDMPEPMTDAFLTASVLAAVATGSPNRT 692

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD-----YCIITPPEKLNVTAI 398
T I +A+ RVKE R+ A++ EL K G E D ++ PP +
Sbjct: 693 TRIFGIANQVRKECNIRAMKDELAKFGVICREHDDGLEIDGIDRSTLLQPPH-----GV 747

Query: 399 DTYDDHRMAMAFS-LAACAEVPVTIIRDPGCTRKTFPDYFDVLSTFVK 444
YDDHR+AM+FS LA A P I + C KT+P ++D L+ K
Sbjct: 748 HCYDDHRVAMSFVLAALTAPKPTLILEKECVGKTPGWWDTLAQLFK 794

>ref|XP_002847108.1| pentafunctional AROM polypeptide [Arthroderma otae CBS 113480]
gb|EEQ32026.1| pentafunctional AROM polypeptide [Arthroderma otae CBS 113480]
Length = 1571

Score = 264 bits (674), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 182/450 (40%), Positives = 256/450 (56%), Gaps = 28/450 (6%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K ++ T PGSKS+SNR L+LAAL G + NLL+S+D ML AL LG + + ++
Sbjct: 403 KPLNVCTTPPGSKSISNRALVLAALGSGVCRIRNLLHSDDETEVMLNALEALGAATFSWEE 462

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGN---ATYVLDGVPR 128
+ VV G GKG +E + E L+LGNAG A R LT T + + +L G R
Sbjct: 463 EGEVLVNGKGGK--LEASAHE--LYLGNAGTASRFLTTVATLSNEKDDVSHNILTGNAR 518

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPIGDLV LK G VD P++V GG GG ++L+ +SSQY+S+LLM
Sbjct: 519 MKQRPIGDLVDALKSNGVSVDYLEQQGSLPLKVPACGGFKGGAIELAAKVSSQYVSSLLM 578

Query: 189 AAPLALGDVEIEI-II-DKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPK 246
AP A V ++++ K IS Y+ MT +M+ FG+ E S + + ++I+ GQ YK+P
Sbjct: 579 CAPYAKEKVTLKLVGGKPISETYIAMTAAMMKSFGIDVEKSTTEEYTYHIQQGQ-YKNPP 637

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA++G T T+ G+ SLQGD +FA +VL MG V T +S
Sbjct: 638 EYIIESDASSATYPLAIAAMSGTTCIPNIGSKSLQGDARFAVDVLRPMGCDVKQTNSS 697

Query: 306 TVTGPPREPFGKRHLKAI-DVNMNKMPPDVAMTLAVVALFAD----GPTAIRDVASWRVKE 360
TVTGP LK I +V+M M D +T +V+A A+ T I +A+ RVKE
Sbjct: 698 TVTGPT-----NGALKPIANVDMPEMTDAFLTASVLAANDKSGNTTRIYGIANQVRKE 752

Query: 361 TERMVAIRTELTKLGASVEEGPDYC----IITPPEKLNVTATIDTYDDHRMAMAFSL--AA 414
R+ A++ EL K G + E D I + K+ V + YDDHR+AM+FS+ AA
Sbjct: 753 CNRIKAMKDELAKFGVTCREHDDGIEIDGIDSELKVPVNGVHCYDDHRVAMSFSVLAAA 812

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
A P I + C KT+P ++D L+ K
Sbjct: 813 AASQPTLILEKECVGKTWPAWWDALAQTFFK 842

>ref|XP_003023519.1| repressor protein [Trichophyton verrucosum HKI 0517]
gb|EFE42901.1| repressor protein [Trichophyton verrucosum HKI 0517]
Length = 1600

Score = 264 bits (674), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 180/450 (40%), Positives = 255/450 (56%), Gaps = 28/450 (6%)

Query: 13 KEISGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADK 71
K + T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++
Sbjct: 402 KSLQVCTTPPGSKSISNRALVLAALSGTCTIRNLLHSDDETEVMLNALEALGAATFSWEE 461

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY---VLDGVPR 128
+ VV G GSK DA +L+LGNAG A R LT T + A +L G R
Sbjct: 462 EGEVLVVNGKGGKL---DASSH-ELYLGNAGTASRFLTTVATLSNTKADVSHNLTGNAR 517

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPIGDLV LK G ++ P++V GG GG+++L+ +SSQY+S+LLM
Sbjct: 518 MKQRPIGDLVDALKANGVPIEYIEQQGSLPLKVPACGGFKGGEIELAAKVSSQYVSSLLM 577

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPK 246
AP A V ++++ + IS Y+ MT +M+ FG+ E S + + ++I+ GQ YK+P
Sbjct: 578 CAPYAKEKVTLKLVGGKPISETYISMTAAMMKSFGINVEKSTTEEYTYHIEQQGQ-YKNPP 636

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA++G T T+ G+ SLQGD +FA +VL MG V T+TS
Sbjct: 637 EYVIESDASSATYPLAIAAMSGTTCIPNIGSKSLQGDARFAVDVLRPMGCDVKQTDST 696

Query: 306 TVTGPPREPFGKRHLKAI-DVNMNKMPPDVAMTLAVVALFA----DGPTAIRDVASWRVKE 360
TVTGP LK I +V+M M D +T +V+A A T I +A+ RVKE
Sbjct: 697 TVTGPT-----DGALKPIANVDMPEMTDAFLTASVLAAVARDKSSNTTRIYGIANQVRKE 751

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPE----KLNVTATIDTYDDHRMAMAFSL--AA 414
R+ A++ EL K G + E D I + K+ + + YDDHR+AM+FS+ +A
Sbjct: 752 CNRIKAMKDELAKFGVTCREHEDGIEIDGIDRMALKVPINGVHCYDDHRVAMSFSVLASA 811

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ P I + C KT+P ++D LS K
Sbjct: 812 ASSQPTLILEKECVGKTWPAWWDTLSTQTFK 841

>ref|XP_001585666.1| hypothetical protein SS1G_13550 [Sclerotinia sclerotiorum 1980]
gb|EDN98691.1| hypothetical protein SS1G_13550 [Sclerotinia sclerotiorum 1980]
Length = 1576

Score = 264 bits (674), Expect = 3e-68, Method: Compositional matrix adjust.
Identities = 177/431 (41%), Positives = 247/431 (57%), Gaps = 21/431 (4%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAAKRAVVVG 80
Sbjct: 415 PGSKSISNRALVLAALGTGPCRKNLHSDDEVEFMLTSIGKLGATYAWEDAGEVLCVQG 474

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY---VLDGVPRMRERPIGDL 137
GG +L++GNAG A R LT V+ +A+ +L G RM+ RPIG L
Sbjct: 475 KGGDL----HASPTELYIGNAGTASRFLTTVSLCKPSASTKSTILTGNARMKVRPIGPL 530

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G D++ P+ V GG GG + L+ ++SSQY+S+LLM AP A V
Sbjct: 531 VDSLRLANGVDIEYLEKEHSLPLNVAASGGFTGGDINLAATVSSQYVSSLLMCAPYAKNPV 590

Query: 198 EIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT +M FG+ S + + Y YK+P+ VE DASS
Sbjct: 591 TLRLVGGKPIISQLYIDMTTAMMAAFGIHVVRSQTEETHYHIPQGVYKNPEEYVVEDASS 650

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPF 315
A+Y LA AAI+G T T+ G S+QGD +FA +VL+ MG KV T+ S TVTGP P
Sbjct: 651 ATYPLAVAAISGTTCTIPNIGCKSIQGDARFAIDVLKPMGCKVVQTDYSTTVTGP---PI 707

Query: 316 GRKHLKAI-DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASVRVKETERMVAIRTELTKL 374
G L+AI +V+M M D +T +V+ A G T IR +A+ RVKE R+ A++ EL K
Sbjct: 708 GS--LQAIEEVDMEPMTDAFLTASVLAGAVAKGTTKIRGIANQRVKECNRIKAMKDELAKF 765

Query: 375 GASVEEGPDYCI--TPPEKLNVT--IDTYDDHRMAMAFS-LAACAEVPVTIRDPGCTR 429
G + E D + P + L A I YDDHR+AM+FS L+ A PV I + C
Sbjct: 766 GVTCRELEDGIEVDGVPIKDLKHPAEGIHICYDDHRVAMSFSVLSVAASQPVLIIEERECVG 825

Query: 430 KTFPDYFDVLS 440
KT+P ++D+LS
Sbjct: 826 KTWPGWWDILS 836

>ref|XP_002478440.1| pentafunctional polypeptide (AroM), putative [Talaromyces
stipitatus ATCC 10500]
gb|EED21477.1| pentafunctional polypeptide (AroM), putative [Talaromyces
stipitatus ATCC 10500]
Length = 1577

Score = 263 bits (673), Expect = 3e-68, Method: Compositional matrix adjust.
Identities = 176/434 (40%), Positives = 246/434 (56%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + A ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTVRIKNLHSDDEVEMLNALEHLGAATFAWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATY-VLDGVPRMRERPIGDLV 138
GGK +L+LGNAG A R LT+ T +G G+ + +L G RM++RPIGDLV
Sbjct: 472 NGGKMQAS----PTELYLGNAGTASRFLTSVATLSGKGSVDNFNLTGNRMKQRPIDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA+++ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTVNGAEIEYLEKAGSLPLKIAASGGFKGGRINLAAKVSSQYVSSLLMCAPYAKEPVV 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ + IS+ Y+EMT +M FG+ + S + + Y Y +P +E DASSA
Sbjct: 588 LKLVGGRPISLSYIEMTTAMMRSFGIDVQQSTTEEWYHIPQGSYTNPAEYVIESDASSA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPF 316
+Y LA AA+TG T TV G+ SLQGD +FA +VL MG KV T TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTVPNIGSASLQGDARFAVDVLRPMGCKVEQTATSTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNMKMPDVAMTLAVVALFADGP-----TAIRDVASVRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+R E
Sbjct: 703 DGVLRPLPNVDMEPMTDAFLGASVLAAIAQGECSNHTTRIYGIANQRVKECNRIEAMRVE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E PD I ++ + + YDDHR+A +FS LA A +P I +
Sbjct: 763 LAKFGVVCREHPDGLIDGIDRSTLRHPAGGVFCYDDHRVAFSFSILALVAPMPTLILEK 822

Query: 426 GCTRKTFFDYFDVL 439
C KT+P Y+D L
Sbjct: 823 ECVGKTWPTYWDAL 836

>ref|ZP_06885153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
lentocellum DSM 5427]
gb|EFG97554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
lentocellum DSM 5427]
Length = 437

Score = 263 bits (671), Expect = 5e-68, Method: Compositional matrix adjust.
Identities = 168/427 (39%), Positives = 239/427 (55%), Gaps = 20/427 (4%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V +PGSKS++NR LL+A L++G + + L S+D + L ++ LG E D+AA V
Sbjct: 24 VSVPGSKSITNRALLIATLADGISELKGTLFSDDSRHFLQCVQELGFETEVEAACMIKV 83

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G GK P K E +++G+AG A R LTA + + G Y LD +MR+RP+ L+
Sbjct: 84 HGLKGKVP---KREAAIYVGSAGTAARFLTAFLGVSDG--VYKLDASEQMRKRPMAPLL 137

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPLALGD 196
L+ LG +VD L C P + G P K ++S +I SSQ+LSALL+A+ D
Sbjct: 138 HTLEGLGTEVDYEELEEGCFPFTRLG---KPVTKDQMSVNIKSSQFLSALLIASTCFKED 194

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
V I + + + Y++MT+++M++FG++ S + +++I GQ Y++ K +E D S+
Sbjct: 195 VTISL-EGTHGMAYIDMTIKMMKQFGLLEVRESQAH-QYFISKQTYEA-KQYQIEPDVSA 251

Query: 257 ASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
A YF AA+ G V VE SLQGD++F LE MG V T + V GP +
Sbjct: 252 ACYFYGMAALLGIEVVVENVFFDSLQGDIQFISFLEEMGCSVEETPEGICVKGPVDGKY- 310

Query: 317 RKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
K I +M+ D A+TLA +A FAD PT I+ + + +E+ R+ AI TEL K+G
Sbjct: 311 ----KGITADMHACSDQAITLAALAPFADSPTIKIGIGHIKYQESNRIKAITTELKMG I 366

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYF 436
EE D I P E ++TYDDHRMAM FSL VTI DP C RKT F YF
Sbjct: 367 RCEDEDEDGVTIYPGEP-TAARVETYDDHRMAMGFSLIGLRAEGVTISDPMCCRKTFEKFY 425

Query: 437 DVLSTFV 443
+VL V
Sbjct: 426 EVLEEVV 432

>gb|EFW96244.1| Pentafunctional arom protein [Pichia angusta DL-1]
Length = 1739

Score = 262 bits (670), Expect = 7e-68, Method: Compositional matrix adjust.
Identities = 179/459 (38%), Positives = 262/459 (57%), Gaps = 35/459 (7%)

Query: 5 EEIVLQPIKEISGTVKL--PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
+EI+++P K + V + PGSKS+SNR L++AAL +G + NLL+S+D +ML A+
Sbjct: 392 DEILVKPFKNVHQDVVVTPPGSKSISNRALVMAALGKGVCKIKNLLHSDDTAHLMTAMTA 451

Query: 63 L-GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
L +V + + V+ G GG+ D +++LG NAG A R LT+ + G N
Sbjct: 452 LKAATVSWEDKGETLVLNGNGGQLVACDE---EIYLG NAGTASRFLTSVASLVGVNGDL 507

Query: 122 ---VLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
VL G M++RPIG LV L++ G+ ++ P+++ GL GG+++L +I
Sbjct: 508 DHVVLTGKWMQKRPVIGPLVDALRENGSSIEYQNNESLPLKIRCGKGLKGRIELEATI 567

Query: 179 SSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
SSQY+S++L+ AP A V + ++ K IS Y++MT+R+M FG+ S + + Y
Sbjct: 568 SSQYVSSILICAPYADEPVTALVGGKPISQYIDMTIRMMSAFGIHVTKSTTEHTYHI 627

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFA-EVLEMMGA 296
Y +P +E DASSA+Y LA AA+ G T+ G+ SLQGD +FA EVL+ MG

Sbjct: 628 PKGSYVNPSEYVIESDASSATYPLAFAAMNGTKCTIPNIGSASLQGDSRFAVEVLKPMGC 687

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAID-VNMNKMPPDVAMTLAVVALFADGP---TAIRD 352
VT TETS TV GPP LK + V+M M D +T +VVA A+ T+I

Sbjct: 688 IVTQTETSTTVQGP-----VGQLKPLPLVDMPEPMTDAFLTASVVAIAANDQTQTTSIVG 742

Query: 353 VASWRVKETERMVAIRTELTKLGASVEE-----GPDYCIITPPEKLNVT AIDTYDDH 404
+A+ RVKE R+ A+R +L K G EE G +Y + PE+ I YDDH

Sbjct: 743 IANQRVKECNRIAMRIQLAKFGVKAELEEDGIKIYGINYKDLKTPER---PGIYPYDDH 799

Query: 405 RMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLST 441
R+AM+FSL A C + PV I++ CT KT+P ++DVL T

Sbjct: 800 RVAMSFSLLAGFCKD-PVIIQERRCTAKTWPGWWDVLHT 837

>ref|XP_001539094.1| 3-dehydroquinate synthase [Ajellomyces capsulatus NAM1]
gb|EDN09532.1| 3-dehydroquinate synthase [Ajellomyces capsulatus NAM1]
Length = 1538

Score = 261 bits (668), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 181/462 (39%), Positives = 251/462 (54%), Gaps = 31/462 (6%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML

Sbjct: 388 QIVLAPSIIEVSPGVKGLDVTCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDETVML 447

Query: 58 GALRTLGL-SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + VV G GG+ + +L++GNAG A R LT T A

Sbjct: 448 NALERLGAATFSWEDEGEVLVVGSGKGRMEASS-----ELYVGNAGTASRFLTTVATLAR 503

Query: 117 GNA--TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKL 174
++ + VL G RM++RPIGDLV L GA ++ C P+++ GG GG++ L

Sbjct: 504 KSSVDSSVLTGNARMKQRPIGDLVDALAANGASIEYLENLGLCLPLKIAASGGFAGGEINL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +SSQY+S+LLM AP A V + ++ K IS PY++MT +M FGV+ + S++ +

Sbjct: 564 AAKVSSQYVSSLLMCAPYAKTPVTLRLVGGKPI SQPYIDMTTAMMRSFGEVKKSETEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
Y Y +P VE DASSA+Y LA AAITG + TV G+ SLQGD +FA +VL

Sbjct: 624 TYHIPLGFYTNFVEYIVESDASSATYPLAAAAITGTSCTVPNIGSKSLQGDARFAVDVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGP----- 347
MG V + S VTGPP G ++NM M D +T +V+A A G

Sbjct: 684 PMGCAVDQNDFTSTRVTGPP----GGILSPLPNINMEPMTDAFLTASVLAAVARGKGSNRT 739

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDD 403
T I +A+ RVKE R+ A++ EL K G E D I ++ + + YDD

Sbjct: 740 TRIFGIANQRVKECNRIKAMKDELAKFGVVCREHDDGLEIDGIDRATLHHPSDGVVYCYDD 799

Query: 404 HRMAMAFS-LAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444

HR+AM+FS L+ A P I + C KT+P ++D LS K

Sbjct: 800 HRVAMSFVLSLVAHEPTLILEKECVGKTWPGWWDCLSQTFK 841

>ref|ZP_03754397.1| hypothetical protein ROSEINA2194_02822 [Roseburia inulinivorans DSM
16841]
gb|EEG93435.1| hypothetical protein ROSEINA2194_02822 [Roseburia inulinivorans DSM
16841]
Length = 428

Score = 261 bits (668), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 164/435 (37%), Positives = 239/435 (54%), Gaps = 21/435 (4%)

Query: 13 KEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K I V +PGSKS++NR LL+AALS+GT +D +L S+D + + +L LG V ++

Sbjct: 11 KPIDWCVTVPGSKSMTNRALLMAALSDGTVTLDGVLFSDDSRHFISLTALGFDVLVEEE 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+R V G GG P K+E ++ +G+AG A R LTA + + G +YV+ +M++R

Sbjct: 71 KRRVTVKGEGGTIP----KKEAEIDVGSAGTAARFLTAMLGMSDG--SYVIQASGQMKKR 124

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ DL V L+ GA++ PV++NG V+L S S+Q+LSA+L+ +P+
Sbjct: 125 PMKDLFVLEHTGAEIIYLEQEGFLPVKINGQRKDQKLTVRLDISRSTQFLSAMLISPM 184

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
+ I+I + Y+ +T +ME +GV+ + + + G Y K Y VE
Sbjct: 185 LPQGLHIQITSEKTDGSYIRITRNMENWGVQTQFDGK--NYEVMPGAAYH--KTTYVVE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S+A YF AAITGG VE + QGD KF +VLE +G KVT T + V GP
Sbjct: 241 PDMSAACFYFGAAAITGGKAIVENVHMDNTQGDKKFLKVLEQLGCKVTD TAKGICVEGPE 300

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
G H ID++MN D MTLA +A +AD P I + R++E++R+ AI TEL
Sbjct: 301 H---GNH--GIDIDMNDFSQTMTLAAMAPYADAPVHISHIGHIRLQESDRIHAIVTEL 355

Query: 372 TKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTR 429
+ G EE D I P P + I TY+DHRMAMAFSL + I DP C +
Sbjct: 356 RRAGIRCEEEDALTIYPGVP---HAAVIKTYEDHRMAMAFSLGLRLTDGIIIDDLCK 412

Query: 430 KTFPDYFDVLSTFVK 444
KTF +YF++ + +
Sbjct: 413 KTFENYFELFTILTQ 427

>ref|XP_003068793.1| 3-dehydroquinate synthase, putative [Coccidioides posadasii C735
delta SOWgp]
gb|EER26648.1| 3-dehydroquinate synthase, putative [Coccidioides posadasii C735
delta SOWgp]
Length = 1589

Score = 261 bits (668), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 185/467 (39%), Positives = 259/467 (55%), Gaps = 42/467 (8%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 KIVLAPSEIEVSPGVKSLQVTCTPPGSKSISNRALVLAALGSGTCRIKNLLHSDTEVML 447

Query: 58 GALRTLGLSVEA-DKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA- 115
AL LG + + ++ + VV G GG ++ + EE L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWEEEGEVLVVHNGGT--LKASPEE--LYLGNAGTASRFLTTVATLAN 503

Query: 116 -GGNATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
G ++ VL G RM++RPIG LV L+ GA V+ C P++++ GG GG++ L
Sbjct: 504 NGTVSSTVLTGNARMKQRPICALVDSL RANGAGVEYLETNGCLPLKIDASGGFAGGEISL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ ISSQY+S+LLM AP A V++++ K IS Y++MT +M FG+ + S + +
Sbjct: 564 AAKISSQYVSSLLMCAPYAKEPVTCLKLVGGKPISQQYIDMTTAMMRSFIDVVKRSTTEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
Y KY +P +E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL
Sbjct: 624 TYHIPQKYNPAEYIIIESDASSATYPLAVAAITGTTCTIPNIGSKSLQGDARFAVDVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGP---- 347
MG +V+ +E S TVT P LK + +V+M M D +T +V+A A G
Sbjct: 684 PMGCEVSQSEYSTTVTAP-----KDGVLKPLPNVDMEPMTDAFLTASVLA AVATGSPNRT 738

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD-----YCIITPPEKLNVTAI 398
T I +A+ RVKE R+ A++ EL K G E D ++ PP +
Sbjct: 739 TRIFGIANQRVKECNIRIRAMKDELAKFGVICREHDDGLEIDGIDRSTLLQPPH-----GV 793

Query: 399 DTYDDHRMAMAFS-LAACAEVPTVIRDPGCTRKTTFPDYFDVLSTFVK 444
YDDHR+AM+FS L+ A P I + C KT+P ++D L+ K
Sbjct: 794 HCYDDHRVAMSFVLSLTAPKPTLILEKECVGKTWPGWWDTLAQLFK 840

>gb|EFW20721.1| 3-dehydroquinate synthase [Coccidioides posadasii str. Silveira]
Length = 1445

Score = 261 bits (667), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 185/467 (39%), Positives = 259/467 (55%), Gaps = 42/467 (8%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 KIVLAPSIEVSPGPVKSLQVTCTPPGSKSISNRALVLAALGSGTCRIKNLLHSDDEVML 447

Query: 58 GALRTLGLSVEA-DKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA- 115
AL LG + + ++ + VV G GG ++ + EE L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWEEEGEVLVVGNGGT--LKASPEE--LYLGNAGTASRFLTATLAN 503

Query: 116 -GGNATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKL 174
G ++ VL G RM++RPIG LV L+ GA V+ C P++++ GG GG++ L
Sbjct: 504 NGTVSSTVLTGNARMKQRPICALVDSLRLANGAGVEYLETNGCLPLKIDASGGFAGGEISL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ ISSQY+S+LLM AP A V +++ K IS Y++MT +M FG+ + S + +
Sbjct: 564 AAKISSQYVSSLLMCAPYAKEPVTLLKLVGGKPISSQYIDMTTAMMRSFGIDVKRSTTEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
Y KY +P +E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL
Sbjct: 624 TYHIPQGYVNPAYEIIIESDASSATYPLAVAAITGTTCTIPNIGSKSLQGDARFAVDVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGKRHLKAI-DVNMNKMPPDVAMTLAVVALFADGP---- 347
MG +V+ +E S TVT P LK + +V+M M D +T +V+A A G
Sbjct: 684 PMGCEVSQSEYSTTVTAPK-----DGVLKPLPNVDMPEMTDAFLTASVLAAVATGSPNRT 738

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD-----YCIITPPEKLNVTAI 398
T I +A+ RVKE R+ A++ EL K G E D ++ PP +
Sbjct: 739 TRIFGIANQVRKECNIRAMKDELAKFGVICREHDDGLEIDGIDRSTLLQPPH-----GV 793

Query: 399 DTYDDHRMAMAFS-LAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
YDDHR+AM+FS L+ A P I + C KT+P ++D L+ K
Sbjct: 794 HCYDDHRVAMSFVLSLTAPKPTLILEKECVGKTWPGWWDTLAQLFK 840

>emb|CBY01360.1| similar to pentafunctional polypeptide AROM [Leptosphaeria
maculans]
Length = 1591

Score = 261 bits (667), Expect = 2e-67, Method: Compositional matrix adjust.
Identities = 178/448 (39%), Positives = 250/448 (55%), Gaps = 39/448 (8%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR+L+LAAL G + NLL+S+D ML AL + G S + K VV G
Sbjct: 416 PGSKSISNRVLVLAALGTGCRITNLLHSDDTQVMLDALAKMQGASFAWEDDGKVLVVTG 475

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
GG + +L+LGNAG A R S+TA + ++ G RM+ERPI L
Sbjct: 476 NGGNLKTSS----ELYLGNAGTAARFLTSVTALCRPVESITSTIVTGNARMKERPIAPL 531

Query: 138 VVGLKQLGADVDCFLGTDGPPVRVNGIGGLPG----GKVKLSGSISSQYLSALLMAAPLA 193
V L+ +G +++ P+R+ G G ++L+ ++SSQY+S++L++AP +
Sbjct: 532 VKSLRTMGVEIEYVEKEGGLPLRIQACSGFGSDSFTGDIELTANVSSQYVSSILLSAPYS 591

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V + ++ K+IS PY++MT+ +M FGV+ E S S Y + Y +P VE
Sbjct: 592 KKPVTLLRLVGGKVISQPYIDMTIAMMASFGVQVERSASDPNTYHIPNKPYPNPTSTYEVE 651

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPP 311
DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL MG KV ++TS TVTGPP
Sbjct: 652 DASSATYPLAIAAITGTTCTVPNIGSGSLQGDARFAIEVLRPMGCKVEQSKTSTTVTGPP 711

Query: 312 REPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFA--DG---PTAIRDVASWRVKETERMV 365
R LKA+ +++M M D +T +V+A A DG T I +A+ RVKE R+
Sbjct: 712 -----RGELKAVKEIDMEPMTDAFLTASVLAAVASSDGTSTTTIRYIGIANQVRKECNRIQ 766

Query: 366 AIRTELTKLGASVEE-----GPDYCIITPPEKLNVTAIPTYDDHRMAMAFS-LAACA 416
A+ EL K G + + G Y + TP I YDDHR+AM+F+ L+ A
Sbjct: 767 AMEDELAKFGVTCRQFDDGIEVDGKGYDLATPQ----VGIHCYDDHRVAMSFVLSLVA 821

Query: 417 EVPVTIRDPGCTRKTTPDYFDVLSTFVK 444
PV I + CT KT+P Y+D L+ K
Sbjct: 822 PAPVLILEKDKCTGKTWPGYWDSLNLQIFK 849

>ref|XP_002555600.1| KLTH0G13090p [Lachancea thermotolerans]
emb|CAR25163.1| KLTH0G13090p [Lachancea thermotolerans]
Length = 1579

Score = 261 bits (666), Expect = 2e-67, Method: Compositional matrix adjust.
Identities = 193/467 (41%), Positives = 270/467 (57%), Gaps = 38/467 (8%)

Query: 5 EEIVLQPIKEISG---TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGAL 60
+E ++ P K + T+ PGSKS+SNR L+LAAL EGT + NLL+S+D +ML A+
Sbjct: 400 DETLVYPFKTLENGQEKTIVPPGSKSISNRALILAAALGEGTCKIKNLLHSDDTKMLHAV 459

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT---AAVTAAG 116
+ L G ++ + + V+ G GG A+ L+LGNAG A R LT A V +
Sbjct: 460 QQLKGATITWEDNGETVVLKGHGGSTLQATAEP---LYLGNAGTASRFLTSAALVNSTS 516

Query: 117 GNATYVLGDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSG 176
+ VL G RM+ERPIG LV L++ G +D P+++N GG+++L+
Sbjct: 517 SQKSVLTGNARMQERPIGPLVDLSRENGISIDYLNKEKSLPLKINTDSNFKGGRIELAA 576

Query: 177 SISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHS-DSWDRF 234
++SSQY+S++LM AP A V + ++ K IS Y++MT+++ME+FG+ + S + + +
Sbjct: 577 TVSSQYVSSILMCAPYAEPTLALVGGKPIKSLYIDMTIKMMEKFGIYVKASTEENPTY 636

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
+I G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 637 HIPKGH-YVNPEYVIESDASSATYPLAAMTGTTVTVPNIGFESLQGDARFARDVLKP 695

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFA-DGP----- 347
MG VT TETS TVTGPP G K LK +D M M D +T VVA A DG
Sbjct: 696 MGCSVTQTETSTTVTGPPVG--GLKPLKHVD--MEPMTDAFLTACVVAVAHDGKEGSRN 751

Query: 348 -TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCII---TPPEKLVN-TAIDTYD 402
T I +A+ RVKE R++A+ EL K G E PD + + +KL V AI +YD
Sbjct: 752 TTTIEGIANQRVKECNRLAMVDELAKFGVEANELPDGIQVHGLSSIDKLKVPEAIHSYD 811

Query: 403 DHRMAMAFSLAA-----CAEVPVTIRDPGCTRKTTPDYFDVLST 441
DHR+AM+FSL A PV I + CT KT+P ++DVL T
Sbjct: 812 DHRVAMSFSLLAGMVGATKDALSEPVRILERSCTGKTWPGWWDVLHT 858

>ref|XP_722769.1| hypothetical protein CaO19.4704 [Candida albicans SC5314]
gb|EAL04039.1| hypothetical protein CaO19.4704 [Candida albicans SC5314]
Length = 1551

Score = 260 bits (665), Expect = 3e-67, Method: Compositional matrix adjust.
Identities = 183/443 (41%), Positives = 258/443 (58%), Gaps = 32/443 (7%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D +ML A+ +L G + + + VV G
Sbjct: 407 PGSKSISNRALILAAALNGTIVRVKNLLHSDDTKMLDAVASLKGAEISTEDNGETIVVKG 466

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT---YVLGDGVPVRMRERPIGDL 137
GG V +E L+LGNAG A R LT + G + +L G RM+ERPIG L
Sbjct: 467 NGGNL-VTSGEE---LYLGNAGTASRFLTTVASLVGKSQASDDVILTGNARMQERPIGPL 522

Query: 138 VVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L G++++ P++++ GL GG+++L+ +ISSQY+S++LM AP A V
Sbjct: 523 VDALGNSGSEIEYLNKQGSPLKISAGNGLKGRIELAAATISSQYVSSILMCAPYAKEPV 582

Query: 198 EIEIID-KLISIPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT +M+ FG++ S + + Y YK+P +E DASS
Sbjct: 583 TLALVGGKPIKSLYIDMTCAMMKSFGIEVTKSTTEFYTHIPKGYKNPSEYVIESDASS 642

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREP 315
A+Y LA AA+TG + T+ G++SLQGD KFA +VL+ MG KV T TS TVTGPP
Sbjct: 643 ATYPLAFAAMTGTSTIPNIGSSSLQGDAKFAVDVLKPMGCKVEQTTSTTVTGPP---- 698

Query: 316 GRKHLKAI-DVNMNKMMPDVAMTLAVVALFADG--PTAIRDVASWRVKETERMVAIRTELT 372
R HLK + V+M M D +T +VVA A G T+I +A+ RVKE R+ A+ TEL
Sbjct: 699 -RGHLKPLPHVDMPEPMTDAFLTASVVA AVAKGGSSTSITGIANQVRKECNRIEAMVTELA 757

Query: 373 KLGASVEEGPDYCI-----TPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVT 421
K G E PD I TP +++ + +YDDHR+ M+FSL A C E PV
Sbjct: 758 KFGVPANELPDGIEIHGIDIEDLKTP--EISKRGVSSYDDHRVGMSFSLLAGLCKE-PVL 814

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + T KT+P ++D+L + K
Sbjct: 815 ILERSTGKTWPGWWDILHSKFK 837

>ref|XP_002146148.1| 3-dehydroquinate synthase, putative [Penicillium marneffei ATCC
18224]
gb|EEA25601.1| 3-dehydroquinate synthase, putative [Penicillium marneffei ATCC
18224]
Length = 1571

Score = 260 bits (665), Expect = 3e-67, Method: Compositional matrix adjust.
Identities = 178/434 (41%), Positives = 241/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEA-DKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D ML AL LG + A + + VV G
Sbjct: 408 PGSKSISNRALVLAALGSGTVRVKNLLHSDDTFVMLNALERLGAATFAWEDEGEVLVVNG 467

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-GNATY-VLDGVPRMRERPIGDLV 138
GGK +L+LGNAG A R LT+ T +G G+ Y +L G RM++RPIGDLV
Sbjct: 468 NGGKMQAS----PTELYLGNAGTASRFLTSVATLSGKGSVDYNILTGNNRMKQRPPIGDLV 523

Query: 139 VGLKQLGADVD CFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA V+ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 524 DALTVNGAQVEYLEKAGSLPLKIAASGGFKGGRINLAAKVSSQYVSSLLMCAPYAKEPVT 583

Query: 199 IEIID-KLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS+ Y+EMT +M FG+ + S + + Y Y +P +E DASSA
Sbjct: 584 LKLVGGKPISLSYIEMTTAMMRSFGIDVQKSTTEEWYHIPQGSYTNPPEYVIESDASSA 643

Query: 258 SYFLAGAAITGGTGTVTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T TV G+ SLQGD +FA EVL MG V T TS TVTGP
Sbjct: 644 TYPLAIAAVTGTCTVTPNIGSASLQGDARFAVEVLRPMGCNVEQTATSTTVTGP-----A 698

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+R E
Sbjct: 699 DGVLRPLPNVDMPEPMTDAFLGASVLAIAAQKGNNNTTRIYGIANQVRKECNRIEAMRVE 758

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E PD I + ++ + YDDHR+A +FS L+ A I +
Sbjct: 759 LAKFGVVCREHPDGLDIDGINRSSLRHPAGGVFCYDDHRVAFSFSILSLVAPTSTLILEK 818

Query: 426 GCTRKTFPDYFDVL 439
C KT+P Y+D L
Sbjct: 819 ECVGKTWPTYWDAL 832

>ref|XP_722916.1| hypothetical protein CaO19.12175 [Candida albicans SC5314]
gb|EAL04195.1| hypothetical protein CaO19.12175 [Candida albicans SC5314]
Length = 1551

Score = 260 bits (665), Expect = 3e-67, Method: Compositional matrix adjust.
Identities = 183/443 (41%), Positives = 258/443 (58%), Gaps = 32/443 (7%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D +ML A+ +L G + + + VV G
Sbjct: 407 PGSKSISNRALILAAALGNGTVRVKNLLHSDDTKHMLDAVASLKGAESTEDNGETIVVKG 466

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT---YVLDGVPRMRERPIGDL 137
GG V +E L+LGNAG A R LT + G + +L G RM+ERPIG L
Sbjct: 467 NGGNL-VTSGEE---LYLGNAGTASRFLTTVASLVGKSQASDDVILTGNARMQERPIGPL 522

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L G++++ P++++ GL GG+++L+ +ISSQY+S++LM AP A V
Sbjct: 523 VDALGNSGSEIEYLNKQGSPLKISAGNGLKGGRIELAATISSQYVSSILMCAPYAKEPV 582

Query: 198 EIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT +M+ FG++ S + + Y YK+P +E DASS
Sbjct: 583 TLALVGGKPIISQLYIDMTCAMMKSFGIEVTKSTTEEYTYHIPKGTYNPSEYVIESDASS 642

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREP 315
A+Y LA AA+TG + T+ G++SLQGD KFA +VL+ MG KV T TS TVTGPP
Sbjct: 643 ATYPLAFAAMTGTSC TIPNIGSSSLQGDFAVDVLKPMGCKVEQTTTSTTVTGPP---- 698

Query: 316 GRKHLKAI-DVNMNMKMPDVAMTLAVVALFADG--PTAIRDVASWRVKETERMVAIRTEL 372
R HLK + V+M M D +T +VVA A G T+I +A+ RVKE R+ A+ TEL
Sbjct: 699 -RGHLKPLPHVDMPEMTDAFLTASVVA AVAKGSSSTSITGIANQRVKECNRIEAMVTELA 757

Query: 373 KLGASVEEGPDYCI-----TPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVT 421
K G E PD I TP +++ + +YDDHR+ M+FSL A C E PV
Sbjct: 758 KFGVPANELPDGIEIHGIDIEDLKT--EISKRGVSSYDDHRVGMFSLLAGLCKE-PVL 814

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + T KT+P ++D+L + K
Sbjct: 815 ILERSTTGKTPGWDILHSEFK 837

>ref|NP_010412.1| Aro1p [Saccharomyces cerevisiae S288c]
sp|P08566.1|ARO1_YEAST RecName: Full=Pentafunctional AROM polypeptide; Includes: RecName:
Full=3-dehydroquinase; Includes: RecName:
Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS; Includes:
RecName: Full=Shikimate kinase; Includes: RecName:
Full=3-dehydroquinase dehydratase;
Short=3-dehydroquinase; Includes: RecName:
Full=Shikimate dehydrogenase
emb|CAA29458.1| unnamed protein product [Saccharomyces cerevisiae]
emb|CAA88208.1| Aro1p [Saccharomyces cerevisiae]
tpg|DAA11973.1| TPA: Aro1p [Saccharomyces cerevisiae S288c]
Length = 1588

Score = 259 bits (663), Expect = 4e-67, Method: Compositional matrix adjust.
Identities = 187/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI---SGTVKLPGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQKQVVIIPGSKSISNRALLAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTS 517

Query: 117 GNATYVLGDGVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDLSLRANGTKIEYLNNEGSLPIKVYTDVSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIISKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGT--KPLKHVD--MEPMTDAFLTACVVAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTTIEGIANQRVKECNRIAMATELAKFGVKTTLPDGIQVHGLNSIKDLKVPSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAACA-----EV--PVTIRDPGCTRKTFFPDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVANPVRILRHTGKTWPGWWDVLHS 867

>gb|AAN70992.1|AF482690_1 arom polypeptide [Thanatephorus cucumeris]
Length = 1618

Score = 259 bits (663), Expect = 4e-67, Method: Compositional matrix adjust.
Identities = 192/459 (41%), Positives = 259/459 (56%), Gaps = 49/459 (10%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D M+ AL L G + + VV G
Sbjct: 422 PGSKSISNRALVLAALGNGTCRLRNLLHSDDTQVMMASALIELKGAKFAWEDGGETLVVSG 481

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGVPR 128
GG F + A +E L+LGNAG A R LT T G +++ + G R
Sbjct: 482 GGGAFITIPPAGKE--LYLGNAGTAARFLTTCVCTLVGPDSSSATASSEFPEGTYFITGNAR 539

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RP G LV L+ G+ V C P+ + G GGL GG ++L+ S+SSQY+S++L+
Sbjct: 540 MKQRPCGPLVDALRANGSKVKYIESEGCLPLHI-GAGGLKGGTIQLAASVSSQYVSSILL 598

Query: 189 AAPLALG-DVEIEIID-KLISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYIKGGQK 241
AP A DV +E++ ++IS PY++MTL +M+ FGV KAE D + I Q
Sbjct: 599 CAPYARDEDVLELVGGQVISQPYIDMTLAMKTFGVEVTRKAEDGTLDDIYDIPRAQ- 657

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTW 300
Y +P+ +E DASSA+Y LA AAITG T T+E GT+SLQGD FA VL+ MG KV
Sbjct: 658 YTNPEKYAIESDASSATYPLAVAAITGTTCTIENIGTSSSLQGDAGFAVNVLRMGCKVEQ 717

Query: 301 TETSVTVTGPPPREPFGRKHLKAID-VNMNMPDVAMTLAVVA-----LFADGP-- 347
+E TVTGP P G+ LKAI V+M M D +T VVA L +D P
Sbjct: 718 SENETTVTGP---PIGQ--LKAIGLVMETMTDAFLTAVVVAAVCGEGSAEGLESVDVPMN 772

Query: 348 -TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT-AIDTYDD 403
T I +A+ RVKE R+ A+ EL K G +E D + P E LN ++ YDD
Sbjct: 773 TTRILGIANQRVKECNRIRAMIDELAKFGVKTELDDGLEVYGPPIETLNKNVSVHCYDD 832

Query: 404 HRMAMAFSLAACAEVPVTI-RDPGCTRKTFFPDYFDVLST 441
HR+AMAFS+ A VP TI + C KT+P+++D L+
Sbjct: 833 HRVAMAFSVLATV-VPGTILEEKRCVEKTWPNWDDLTN 870

>gb|EGA63035.1| Arolp [Saccharomyces cerevisiae Fosters0]
Length = 1416

Score = 259 bits (662), Expect = 5e-67, Method: Compositional matrix adjust.
Identities = 185/475 (38%), Positives = 256/475 (53%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI----SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQKQKVIPPQSKSISNRALILAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDSLRLANGTKIEYLNNEGSLPIKVYTDVSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTALVGGKPIISKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTVPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFAD-----G 346

MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGT--KPLKHVD--MEPMTDAFLTACVVAAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCII-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +

Sbjct: 753 TTIEGIANQRVKECNRLAMATELAKFGVKTTTELPDGIQVHGLNSIKDLKVPSPDSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAAC-----AEVPVTIRDPGCTRKTFFDYFDVLST 441
+ TYDDHR+AM+FSL A PV I + CT KT+P ++DVL +

Sbjct: 813 GVCTYDDHRVAMSFSLAGMVNSQNERDEVATPVRILERHCTGKTWPGWWDVLHS 867

>gb|EGA59386.1| Aro1p [Saccharomyces cerevisiae FostersB]
Length = 1588

Score = 259 bits (662), Expect = 6e-67, Method: Compositional matrix adjust.
Identities = 185/475 (38%), Positives = 256/475 (53%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI---SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+

Sbjct: 401 DETLVYPFKDIPADQQKVVIPPGSKSISNRALILAAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + VV G GG A L+LGNAG A R SL A V +

Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+

Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDSLRLANGTKIEYLNNEGSLPIKVYTDVSFVKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +

Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIKSLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+

Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTVPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +

Sbjct: 697 MGCKITQTATSTTVSGPPVGT--KPLKHVD--MEPMTDAFLTACVVAAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCII-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +

Sbjct: 753 TTIEGIANQRVKECNRLAMATELAKFGVKTTTELPDGIQVHGLNSIKDLKVPSPDSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAAC-----AEVPVTIRDPGCTRKTFFDYFDVLST 441
+ TYDDHR+AM+FSL A PV I + CT KT+P ++DVL +

Sbjct: 813 GVCTYDDHRVAMSFSLAGMVNSQNERDEVATPVRILERHCTGKTWPGWWDVLHS 867

>gb|EDN60469.1| 3-dehydroquinate dehydratase (3-dehydroquinase) [Saccharomyces
cerevisiae YJM789]
Length = 1588

Score = 259 bits (662), Expect = 6e-67, Method: Compositional matrix adjust.
Identities = 185/475 (38%), Positives = 256/475 (53%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI---SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+

Sbjct: 401 DETLVYPFKDIPADQQKVVIPPGSKSISNRALILAAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + VV G GG A L+LGNAG A R SL A V +

Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+

Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDSLRLANGTKIEYLNNEGSLPIKVYTDVSFVKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234


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++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIISKLYVDMTIKMEKFGINVETSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGGH-YINPSEYVIESDASSATYPLAFAAMTGT'TVTPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAFLTACVVAAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTIEGIANQVRKECNRLAMATELAKFGVKTELPDGIQVHGLNSIKDLKVPSPDSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAAC-----AEVPVTIRDPGCTRKTTPDYFDVLST 441
+ TYDDHR+AM+FSL A PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVATPVRLERHCTGKTWPGWWDVLHS 867

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>gb|EAG83528.1| Arolp [Saccharomyces cerevisiae Lalvin QA23]
Length = 1588

Score = 259 bits (662), Expect = 6e-67, Method: Compositional matrix adjust.
Identities = 187/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

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Query: 5 EEIVLQPIKEI---SGTVKLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQQKVVIPPGSKSISNRALILAAALGEGQCKIKNLLHSDDTKHMILTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTX 517

Query: 117 GNATYVLVDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDSLRLANGTKIEYLNNEGSLPIKVYTDVSFVKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIISKLYVDMTIKMEKFGINVETSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGGH-YINPSEYVIESDASSATYPLAFAAMTGT'TVTPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAFLTACVVAAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTIEGIANQVRKECNRLAMATELAKFGVKTELPDGIQVHGLNSIKDLKVPSPDSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAAC-----EV--PVTIRDPGCTRKTTPDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVANPVRLERHCTGKTWPGWWDVLHS 867

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>ref|NP_594681.1| pentafunctional aromatic polypeptide Arol (predicted)
[Schizosaccharomyces pombe 972h-]
sp|Q9P7R0.1|ARO1_SCHPO RecName: Full=Pentafunctional AROM polypeptide; Includes: RecName:
Full=3-dehydroquininate synthase; Includes: RecName:
Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS; Includes:
RecName: Full=Shikimate kinase; Includes: RecName:
Full=3-dehydroquininate dehydratase;
Short=3-dehydroquinase; Includes: RecName:
Full=Shikimate dehydrogenase
emb|CAB75770.1| pentafunctional aromatic polypeptide Arol (predicted)

[Schizosaccharomyces pombe]
Length = 1573

Score = 259 bits (662), Expect = 6e-67, Method: Compositional matrix adjust.
Identities = 180/438 (41%), Positives = 249/438 (56%), Gaps = 32/438 (7%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAA+ GT + N+L+S+D +M+ AL +LG + + + VV G
Sbjct: 412 PGSKSISNRLVLAAMGNGTCRLTNMLHSDDTQFMMSALESGLAATFSWEDGGETLVVKG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYVLDGVPRMRERPIGDLV 138
GGK V KEE L+LGNAG A R LT AA+ ++ A VL G RM+ RPIG LV
Sbjct: 472 NGGKLAV--PKEE--LYLGNAGTAARFLTGTIAALVSSKDGAKVVLTGNHRMKVRPIGPLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ G +++ P+ ++ GL GG ++L+ ++SSQY+S++LM AP A V
Sbjct: 528 DALRANGCEINYLEKQGSPLDLSSKNGLGGIIELAATVSSQYVSSILMCAPYASQPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS Y++MT+ +M FGV S + + Y KY++P + +E DASSA
Sbjct: 588 LKLVGGKPISQLYIDMTIAMMASFGVNVTKSTTEENTYNIPCGKYQNPPHYEIESDASSA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AAITG TV G+ SLQGD +FA +VL MG V T TS TV GPP+
Sbjct: 648 TYPLAIAAITGKCTVPNIGSASLQGDARFACDVLPRMGCTVEQTATSTTVQGGPKGTL- 706

Query: 317 RKHLKAIDVNMNMPDVAMTLAVVALFA-----DGPTAIRDVASWRVKETERMVAIRTE 370
K L++ID M M D +T +VVA A D T I +A+ RVKE R+ A+ E
Sbjct: 707 -KPLESID--METMTDAFLTASVVAACNVSEGDVPVTRITGIANQRVKECNRIAAMVHE 763

Query: 371 LTKLGASVEE-----GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEVPVT 421
L K G E G +Y + PE+ I TYDDHR+AM+FS L+
Sbjct: 764 LAKFGVRTGELEDGIYIFGKNYKELKKPEE----GIYTYDDHRIAMSFSVLSLICPSRTL 819

Query: 422 IRDPGCTRKTFPDYFDVL 439
I D C KT+P ++DVL
Sbjct: 820 IIDKACVEKTWPYWDVL 837

>gb|AAU95677.1| arom [Sclerotinia sclerotiorum]
Length = 1590

Score = 259 bits (661), Expect = 7e-67, Method: Compositional matrix adjust.
Identities = 175/431 (40%), Positives = 245/431 (56%), Gaps = 21/431 (4%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DKAAKRAVVVG 80
PGSKS+SNR L+LAAAL G + NLL+S+DV +ML ++ LG + A + A + V G
Sbjct: 415 PGSKSISNRLVLAALGTGPCRIKNLLHSDVEFMLTSIGKLGGATYAWEDAGEVLCVQG 474

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY---VLDGVPRMRERPIGDL 137
GG +L++GNAG A R LT V+ +A+ +L G RM+ RPIG L
Sbjct: 475 KGGDL----HASPTELYIGNAGTASRFLTTVVSLCKPSASTKSTILTGNARMKVRPIGPL 530

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G D++ P+ V GG GG + L+ ++SSQY+S+LLM AP A V
Sbjct: 531 VDSL RANGVDIEYLEKEHSLPLNVAASGGFTGGDINLAATVSSQYVSSLLMCAPYAKNPV 590

Query: 198 EIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++ K IS Y++MT +M FG+ S + + Y YK+P+ VE DASS
Sbjct: 591 TLRLVGGKPISQLYIDMTTAMMAAFGIHVRSQTGEHTYHIPQGVYKNPEEYVVESDASS 650

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 315
A+Y LA AA +G T T+ G S+QGD +FA +VL+ G KV T+ S TVTGP P
Sbjct: 651 ATYPLAATAATSGTCTIPNIGCKSIQGDARFAIDVLKPTGCKVVQTDYSTTVTGP---PI 707

Query: 316 GRKHLKAI-DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G L+AI +V+M M D +T +V+ A G T IR +A+ RVKE R+ A++ EL K
Sbjct: 708 GS--LQAIEEVDMEPMTDAFLTASVLGAVAKGTTKIRGIANQRVKECNRIKAMKDELAKF 765

Query: 375 GASVEEGPDYCI--TPPEKLNVT--IDTYDDHRMAMAFS-LAACAEVPVTIRDPGCTR 429
G + E D + P + L A I YDDHR+AM+FS L+ A PV I + C

Sbjct: 766 GVTCRELEDGIEVDGVPIKDLKHPAEGIHICYDDHRVAMSFVLSVAASQPVLEERECEVG 825

Query: 430 KTFPDYFDVLS 440

KT+P ++D+LS

Sbjct: 826 KTWPGWWDILS 836

>emb|CAY78632.1| Aro1p [Saccharomyces cerevisiae EC1118]
Length = 1588

Score = 259 bits (661), Expect = 7e-67, Method: Compositional matrix adjust.
Identities = 187/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI----SGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYFPKDIPADQQKVVIPPGSKSISNRALILAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDLNRANGTKIEYLNNEGSLPIKVTYDSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNMPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGT--KPLKHVD--MEPMTDAFLTACVVAAISHDSDPNAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTTIEGIANQRVKECNRILAMATELAKFGVKTTELPDGIQVHGLNSIKDLKVPDSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAACA-----EV--PVTIRDPGCTRKTFPDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVANPVRILERHCTGKTTWPGWWDVLHS 867

>gb|EDV08178.1| 3-dehydroquinate dehydratase [Saccharomyces cerevisiae RM11-1a]
Length = 1588

Score = 259 bits (661), Expect = 8e-67, Method: Compositional matrix adjust.
Identities = 187/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI----SGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYFPKDIPADQQKVVIPPGSKSISNRALILAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQQRPIAPLVDLNRANGTKIEYLNNEGSLPIKVTYDSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPEVTLALVGGKPIKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAFLTACVVAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTIEGIANQVRKECNRLAMATELAKFGVKTTELPDGIQVHGLNSIKDLKVPSDSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAACA-----EV--PVTIRDPGCTRKTFPDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVMSFSLLAGMVNSQNERDEVANPVRILERHCTGKTWPGWWDVLHS 867

>ref|XP_002582444.1| pentafunctional AROM polypeptide [Uncinocarpus reesii 1704]
gb|EEP82352.1| pentafunctional AROM polypeptide [Uncinocarpus reesii 1704]
Length = 1580

Score = 259 bits (661), Expect = 8e-67, Method: Compositional matrix adjust.
Identities = 181/463 (39%), Positives = 254/463 (54%), Gaps = 34/463 (7%)

Query: 6 EIVLQPIKEISGTVKL-----PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S V PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 385 KIVLAPSIEVSPGVPHALEITCVPPGSKSISNRALVLAALGSGTCRIKNLLHSDDTTEVML 444

Query: 58 GALRTLGL-SVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAA 115
AL LG + ++ + VV G GG+ DA L+LGNAG A R LT T A
Sbjct: 445 SALERLGAATFSWEEEGEVLVVGKGGRLQASPD-----LYLGNAGTASRFLTTVATLA 499

Query: 116 GGNA--TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK 173
+ + +L G RM++RPIG LV L+ GA + T C P++++ GG GG +
Sbjct: 500 NKSTVDSTILTGNARMKQRPICALVDSLRTNGAGIKYMETTGCLPLKIDASGGFAGGHIS 559

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWD 232
L+ +SSQY+S+LLM AP A V +++ K IS PY++MT +M FG+ + S S +
Sbjct: 560 LAAKVSSQYVSSLLMCAPYAKEPVTLKLVGGKPISQPYIDMTTAMMRSGFIDVKKSTSEE 619

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFA-EVL 291
Y +Y +P +E DASSA+Y LA AAITG T T+ G+ SLQGD +FA +VL
Sbjct: 620 HTYHIPQGRYMNPTHEYIIESDASSATYPLAVAAITGTTCTIPNIGSKSLQGDARFAVDVL 679

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADG---- 346
MG +V + S TVTGP L A+ +V+M M D +T +V+A A
Sbjct: 680 RPMGCEVNQSSPSTTVTGP-----RNGALNALPNVDMPEPMTDAFLTASVLAAVATAGSTS 734

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----TAIDTYD 402
T I +A+ RVKE R+ A++ EL K G + E D I ++ + + YD
Sbjct: 735 TTRIFGIANQVRKECNRIKAMKDELAKEFGVTCREHEDGLEIDGIDRSALLRLPHGVYCYD 794

Query: 403 DHRMAMAFS-LAACAEPVTIRDPGCTRKTFPDYFDVLSTFVK 444
DHR+AM+FS L+ A P I + C KT+P ++D L+ K
Sbjct: 795 DHRVAMSFVSLAASHPTLILEKECVGKTWPAWWDTLAQLFK 837

>gb|EGA75607.1| Arolp [Saccharomyces cerevisiae AWRI796]
Length = 1588

Score = 259 bits (661), Expect = 8e-67, Method: Compositional matrix adjust.
Identities = 187/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI----SGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQQKVVIPPGSKSISNRALILALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIVLTGNARMQRPPIAPLVDSLRLANGTKIEYLNNEGSLPIKVYTDVSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPPVTLALVGGKPKISKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTVPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNMPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAFLTACVVAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTTIEGIANQVRVKECNRLAMATELAKFGVKTELPDGIQVHGLNSIKDLKVPDSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAACA-----EV--PVTIRDPGCTRKTFFPDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVANPVRILERHCTGKTWPGWWDVLHS 867

>gb|EEH44586.1| pentafunctional AROM polypeptide [Paracoccidioides brasiliensis
Pb18]
Length = 1538

Score = 258 bits (660), Expect = 9e-67, Method: Compositional matrix adjust.
Identities = 177/446 (39%), Positives = 247/446 (55%), Gaps = 21/446 (4%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + + ++
Sbjct: 403 KSLNVCTTPPGSKSISNRALVLAALGSGTCRIKNLLHSDDTEVMLTALERLGAATFSWES 462

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVLDGVPRMR 130
+VV G V KE L+LGNAG A R LT T A G A+ VL G RM+
Sbjct: 463 QGEVLVVNGNGGRMVASPK-----LYLGNAGTASRFLT TVATLAQKGSVASSVLTGNARMK 519

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVLKSGSISQYLSALLMAA 190
+RPIGDLV LK GAD++ P+++ GG GG+++L +SSQY+S+LLM A
Sbjct: 520 QRPIDGLVDALKANGADIEYLENPKSLPLKITASGGFAGGEMRLDAKVSSQYVSSLLMCA 579

Query: 191 PLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P A V + ++ K +S YV+MT +M FG+ + S++ + Y YK+P
Sbjct: 580 PYAKEPVTLRVLVGGKPVSQLYVDMTTAMMRSGIDVKKSETEHTYHIPRGVYKNPAEYV 639

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
VE DASSA+Y LA AA+TG + T+ G+ SLQGD +FA EVL MG V T+ S +VT
Sbjct: 640 VESDASSATYPLAIAAMTGTSTIPNIGSKSLQGDARFAIEVLRPMGCTVNQTDFTSVT 699

Query: 309 GPPREPFRKHLKAIDVNMNMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETER 363
G G K ++M M D +T +V+A A G T I +A+ RVKE R
Sbjct: 700 GTA----GGKLSLPTIDMEPMTDAFLTASVLAAVARGQGSNHTTRICGIANQVRKECNR 755

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFS-LAACAEV 418
+ A++ EL K G + E D I ++ + + YDDHR+AM+FS LA A
Sbjct: 756 IKAMKDELAKFGVTCTREHDDGLEIDGIDRSTLRHPTEGVFCYDDHRVAMSFVLAALVAPQ 815

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
P I + C KT+P +++ L+ K
Sbjct: 816 PTLILEKECEVGKTPGWWNTLAQTFK 841

>ref|XP_002561515.1| Pc16g12160 [Penicillium chrysogenum Wisconsin 54-1255]
emb|CAP93886.1| Pc16g12160 [Penicillium chrysogenum Wisconsin 54-1255]
Length = 1586

Score = 258 bits (660), Expect = 1e-66, Method: Compositional matrix adjust.
Identities = 180/445 (40%), Positives = 244/445 (54%), Gaps = 29/445 (6%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
K ++ T PGSKS+SNR L+LAAL GT V NLL+S+D ML AL LG + ++

Sbjct: 403 KSLNVTCAPPGSKSISNRALVLAALGSGTCRVKNLLHSDDETEVMLNALERLGAATFSWEE 462

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRM 129
+ VV G GKK L+LGNAG A R LT T A ++ + VL G RM

Sbjct: 463 EGEVLVVNGKGGKI----IASPTPLYLGNAGTASRFLTTVATLATPSSVDSSVLTGNRM 518

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
++RPIGDLV L GA V+ C P+++ GG GKK+ L+ +SSQY+S+LLM

Sbjct: 519 KQRPIGDLVDALTVNGAGVEYMESKGCLPLKIAASGGFAGGKINLAAKVSSQYVSSLLMC 578

Query: 190 APLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AP A V +++ K IS PY++MT +M FG+ + S + + Y Y +P

Sbjct: 579 APYAKEPVTLLKLVGGKPISQPYIDMTTAMMRSFGIDVKKSTTEHTYHIPQGHYVNPAYEY 638

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTV 307
VE DASSA+Y LA AA+TG T TV G+ SLQGD +FA +VL MG V T+TS TV

Sbjct: 639 IVESDASSATYPLAIAAVTGTCTVNPNGSKSLQGDARFAVDVLRPMGCSVVQTDSTTV 698

Query: 308 TGPPR---EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGP-----TAIRDVASWRVK 359
TGP +P DV+M M D +T +V+A A G T I +A+ RVK

Sbjct: 699 TGPTDGLVQLPL-----DVMPEMTDAFLTASVLAAVAQKGANHTTRIYGIANQRVK 751

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAA 414
E R+ A++ EL K G E D I E+ ++ + YDDHR+A +FS L+

Sbjct: 752 ECNRKAMKDELAKFGVICREHDDGLEIDGIERSSLRQPSGGVFCYDDHRVAFSFSVLSL 811

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVL 439
A I + C KT+P ++D L

Sbjct: 812 IAPQSTLILEKECVGKTWPGWWDAL 836

>gb|EEH20188.1| pentafunctional AROM polypeptide [Paracoccidioides brasiliensis
Pb03]
Length = 1603

Score = 258 bits (659), Expect = 1e-66, Method: Compositional matrix adjust.
Identities = 177/446 (39%), Positives = 247/446 (55%), Gaps = 21/446 (4%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ T PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + + ++

Sbjct: 403 KSLNVTCTPPGSKSISNRALVLAALGSGTCRIKNLLHSDDETEVMLTALERLGAATFSWES 462

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVLDGVPRMR 130
+VV G V KE L+LGNAG A R LT T A G A+ VL G RM+

Sbjct: 463 QGEVLVVNGNGGRMVASPK-----LYLGNAGTASRFLTTVATLAQKGSVASSVLTGNARMK 519

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RPIGDLV LK GAD++ P+++ GG GG+++L +SSQY+++LLM A

Sbjct: 520 QRPIDGLVDALKSNGADIEYLENPKSLPLKITASGGFAGGEMRLDAKVSSQYVTSLLMCA 579

Query: 191 PLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P A V + ++ K +S YV+MT +M FG+ + S++ + Y YK+P

Sbjct: 580 PYANEPVTLRLVGGKPVSQLYVDMTTAMMRSFGIDVKKSETEHTYHIPRGVYKNPAEYV 639

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
VE DASSA+Y LA AA+TG + TV G+ SLQGD +FA EVL MG V T+ S +VT

Sbjct: 640 VESDASSATYPLAIAAAMTGTCTVNPNGSKSLQGDARFAIEVLRPMGCTVNTDFSTSVT 699

Query: 309 GPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETER 363
G K ++M M D +T +V+A A G T I +A+ RVKE R

Sbjct: 700 GTA----GGKLSLPTIDMEPMTDAFLTASVLAAVARGQGSNHTTRICGIANQRVKECNR 755

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---TAIDTYDDHRMAMAFS-LAACAEV 418
+ A++ EL K G + E D I ++ + + YDDHR+AM+FS LA A

Sbjct: 756 IKAMKDELAKFGVTREHDDGLEIDGIDRSLRHPTTEGVFCYDDHRVAMSFVLAALVAPQ 815

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
P I + C KT+P +++ L+ K

Sbjct: 816 PTLILEKECVGKTWPGWNTLAQTFK 841

>gb|EEU09331.1| Aro1p [Saccharomyces cerevisiae JAY291]
Length = 1588

Score = 258 bits (659), Expect = 1e-66, Method: Compositional matrix adjust.
Identities = 186/475 (39%), Positives = 258/475 (54%), Gaps = 46/475 (9%)

Query: 5 EEIVLQPIKEI---SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L++AAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQQKVVIPPQSGKSLSNRALIIAALGEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACAD---PLYLGNAGTASRFLTSLAALVNSTP 517

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG 176
VL G RM++RPI LV L+ G ++ P++V GG+++L+
Sbjct: 518 SQKYIIVLTGNARMQQRPIAPLVDSLRLANGTKIEYLNNEGSLPIKVTYDSVFKGGRIELAA 577

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDR-F 234
++SSQY+S++LM AP A V + ++ K IS YV+MT+++ME+FG+ E S + +
Sbjct: 578 TVSSQYVSSILMCAPYAEPPVTLALVGGKPKISKLYVDMTIKMEKFGINVTSTTEPYTY 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFA-EVLEM 293
YI G Y +P +E DASSA+Y LA AA+TG TVTV G SLQGD +FA +VL+
Sbjct: 638 YIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTVTVPNIGFESLQGDARFARDVLKP 696

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFAD-----G 346
MG K+T T TS TV+GPP K LK +D M M D +T VVA +
Sbjct: 697 MGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAFLTACVVAISHSDSPNSAN 752

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT 396
T I +A+ RVKE R++A+ TEL K G E PD + P +
Sbjct: 753 TTTIEGIANQRVKECNRLAMATELAKFGVKTTELPDGIQVHGLNSIKDLKVPDSSSGPV 812

Query: 397 AIDTYDDHRMAMAFSLAACA-----EV--PVTIRDPGCTRKTFFDYFDVLST 441
+ TYDDHR+AM+FSL A EV PV I + CT KT+P ++DVL +
Sbjct: 813 GVCTYDDHRVAMSFSLLAGMVNSQNERDEVANPVRILRHCCTGKTWPGWWDVLHS 867

>ref|YP_003709660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Waddlia chondrophila
WSU 86-1044]
gb|ADI38654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Waddlia chondrophila
WSU 86-1044]
Length = 405

Score = 258 bits (658), Expect = 1e-66, Method: Compositional matrix adjust.
Identities = 170/421 (40%), Positives = 243/421 (57%), Gaps = 29/421 (6%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLG--LSVEADKAAKRAVVV 79
P SK+ + R L L AL++G TV+ + L ++D + AL+ LG +S++ D A +
Sbjct: 6 PPSKAHTLRLALFLGALAQGKTVLQSPILLADDQKVAIQALKQLGADISIQRDSA---TIQ 61

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G GG V+D+ LF+GN+G+ R L+A + + +DG MR+RP+ L++
Sbjct: 62 GTGGN-RVQDSGS---LFVGNSGVTCRFLSA-IAPLLCKQSVADGDLAMRKRLPTQLLI 116

Query: 140 GLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ LG D G CPP+ + GG ++G+ISSQYLSA+L+AAP A D+ +
Sbjct: 117 ALEPLGIHSDSETG--CPPLTLT-CRFTGGATSVAGNISSQYLSAILLAAPFAENDIVV 173

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
I +L S PYVE+TL +M RFG + EH S R + G++YK+ +EGD S+ASY
Sbjct: 174 SIDGELKSGPYVEITLDMRRRFGAEVEHEGSTYR--VTAGKRYKAVAPYEIEGDYSNASY 231

Query: 260 FLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGGRKH 319
FLA AAIT +T++ SLQGD K ++L+ G V+ +SVTV G P
Sbjct: 232 FLAQAAITHTRITIDRLMPNSLQGDRLKILDLKQFGCNVSRGSSSVTVEGRP----- 283

Query: 320 LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG--AS 377
L +I V M+ PD+ T+AV+A FA G T I V R KET+R+ AI +EL K+G A
Sbjct: 284 LSSICVEMSDTPDLVPTVAVIAAFAGTTKINGVGHRLRYKETDRLKAIVSELKMKGIKAF 343

Query: 378 VEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPTIRDGCTRKTFPDYFD 437
EE + P+ IDTY+DHR+AMAFS+A A + IR P C K+FPD+FD
Sbjct: 344 SEEETLWIEGGTPQ---AAEIDTYNDHRIAMAFSVAKRAIPKIVIRCPECVNKSFPDFFD 400

Query: 438 V 438
+
Sbjct: 401 L 401

>ref|YP_003878008.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Zinderia
insecticola CARI]
gb|ADM89662.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Zinderia
insecticola CARI]
Length = 435

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 156/447 (34%), Positives = 252/447 (56%), Gaps = 25/447 (5%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M I+L+ ISG + +PGSKS+SNRILL++ALS G T + NLL S+D M+ L
Sbjct: 1 MNKNKFILLKKKNNISGKINIPGSKSISNRILLISALSLGITKIKNLLISDDLIMIKCL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
+ LG+ ++ K V G KF K+ V+LF+ NAG +R LT+ ++ GN
Sbjct: 61 KKLGIKIKK--KKKIFFVYGNFIKF----LKKNVKLFVDNAGTLIRPLTSILSFMKGN-- 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
Y+L G RM +RPI DLV L +G + PP+ + S +ISS
Sbjct: 113 YILYGSKRMNKRIKDLVSSLNIGMRIKYLKNNGFPLLIKKGKIKTNIKIKS-NISS 171

Query: 181 QYLSALLMAAPL--ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
QYL+++L+++ L ++ I + ++S Y+ +T+ LM+ F V ++ + F I
Sbjct: 172 QYLTSLILSSVLINKFKEIIITNNNIVSNSYINITINLMKLFKVNVIKINN-NVFKIIT 230

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+KY SP +EGD +SASYFLA + I+ G + ++G S+QGDVKF ++LE MGAK+
Sbjct: 231 KEKYISPGIVKIEGDLTSASYFLASSVISKGPLKIKGIKNSIQGDVKFLDILEDMGAKI 290

Query: 299 TWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ + + E + K +K +++ PD+AMTL +++L+++ + +++ SW
Sbjct: 291 NYQDNEL-----EIYYNKIIKNFNIDCINFPDLAMTLMLSLYSNNISLFPKNLYSWNF 343

Query: 359 KETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAE 417
KET R+ A++ EL K+GA + + ++ PP+ + I+TY+DHR+AM FSL +
Sbjct: 344 KETNRLNAMKELNKIGAKINIINRNDILVIPKYIKSAFINTYNDHRIAMCFSLLSLNN 403

Query: 418 V-----PVTIRDGCTRKTFPDYFDVL 439
+ + I +P C KTFP+YF +
Sbjct: 404 INKLGSNILIEPNKCVFKTFPNYFKLF 430

>ref|YP_001818996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Opitutus terrae
PB90-1]
sp|B1ZMW8.1|AROAO_PITP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACB75396.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Opitutus terrae
PB90-1]
Length = 431

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 170/442 (38%), Positives = 241/442 (54%), Gaps = 37/442 (8%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V LPGSKSL+NR LLLAAL + V+ L SED M+ ALR LGL+V A++
Sbjct: 14 RPVRGEVTLPGSKSLTNRALLLAALCDHPVLTGALFSEDQLMVAALRRLGLTVFANEP 73

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
A+ V F AK V LF+G AG A R LTA + AA Y +DGV +MR+R
Sbjct: 74 ARTLAVSDQASAF---QAKAPVDLFVGLAGTAARFLTA-LCAAAPRGVYRIDGVSQMRKR 129

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ L+ LGA+V C P+ ++ GL GG V++ S SSQ LSALLM APL
Sbjct: 130 PMRGLIDALRALGA-EVRC-TEREGFFLEIHA-RGLRGGPVEIDASESSQLLSALLMVAPL 188

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-EHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A +I + + +VEMT RLM FGV+ +H+ S F +K G +Y +P +E
Sbjct: 189 ARAATQITLTSD-VRWTFVEMTFRLMAEFGRIDHAGSSTTFEMKAG-RYSAPSRYAIEP 246

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTS--LQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
DA++ASYF A + GGT+ + G LQGD F +VL + A+
Sbjct: 247 DATAASYFQALPLVVGTTALPLGRPPGDGLQGDSAFVDVLARVRARAAG----- 296

Query: 311 PREPFGKRHLKKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ ++ N +++ D +TLA + GPT I +A R +ET+R+ + E
Sbjct: 297 -----QLLEENFHEISDTFLTLAAITPLLAGPTRITGIAHTRQQETDRVAGMARE 346

Query: 371 LTKLGASVEEGPDYCIITP-PEKLNVTADITYDDHRMAMAFSLAACAEVP-----VTIR 423
L +LG V E I P P +L T I+TY DHR AM+F++ C +V ++IR
Sbjct: 347 LMQLGQRVETRGELEIHPQLRLGET-IETYGDRHFAMSFALGCRDVRGDRPWLSIR 405

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
DP C KTFP++F++L+T +
Sbjct: 406 DPACCAKTFPNFFELLATLRQK 427

>sp|P07547.3|ARO1_EMENI RecName: Full=Pentafunctional AROM polypeptide; Includes: RecName:
Full=3-dehydroquininate synthase; Short=DHQS; Includes:
RecName: Full=3-phosphoshikimate
l-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS; Includes: RecName:
Full=Shikimate kinase; Includes: RecName:
Full=3-dehydroquininate dehydratase;
Short=3-dehydroquinase; Includes: RecName:
Full=Shikimate dehydrogenase
Length = 1583

Score = 257 bits (656), Expect = 3e-66, Method: Compositional matrix adjust.
Identities = 175/439 (39%), Positives = 239/439 (54%), Gaps = 25/439 (5%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTCRIKNLLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGNA--TYVLDGVPRMRERPIGDLV 138
GG + L+LGNAG A R LT T A + + VL G RM++RPIGDLV
Sbjct: 472 KGGNLQASSSP----LYLGNAGTASRFLTTVATLANSTVDSSVLGTNNRMKQRPIDGLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA ++ T P+++ GG GG + L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGASIEYVERTGSLPLKIAASGGFAGGNINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKA-EHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ ++ K IS PY++MT +M FG+ + S + + Y +Y +P +E DASSA
Sbjct: 588 LRLVGGKPISQPYIDMTTAMMRSFGIDVQKSTTEEHTYHIPQGRYVNPAYEVIESDASSA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTS-LQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T TV G+ SLQGD +FA EVL MG V TETS TVTGP
Sbjct: 648 TYPLA-AAVTGTCTVPNIGSASLQGDARFAVEVLRPMGCTVEQTETSTTVTGP-----S 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A++ E
Sbjct: 703 DGILRPLPNVDMPEPMTDAFLGASVLAAIARGKESNHTTRIYGIANQRVKECNRIKAMKDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ N V + YDDHR+A +FS L+ P I +
Sbjct: 763 LAKFGVICREHDDGLEIDGIDRSNLRQPVGGVFCYDDHRVAFSFSVLSLVTPQPTLILEK 822

Query: 426 GCTRKTFPDYFDVLSTFVK 444
C KT+P ++D L K

Sbjct: 823 ECVGKTWPGWWDTLRQLFK 841

>ref|ZP_04452905.1| hypothetical protein GCWU000182_02215 [Abiotrophia defectiva ATCC 49176]
gb|EEP25105.1| hypothetical protein GCWU000182_02215 [Abiotrophia defectiva ATCC 49176]
Length = 437

Score = 257 bits (656), Expect = 3e-66, Method: Compositional matrix adjust.
Identities = 158/428 (36%), Positives = 241/428 (56%), Gaps = 16/428 (3%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHMLGALRTLGLSVEADKAAKRAVV 78
VK+PGSKS++NR LL+AAL+EG + + L S D M+ L +LG+ + D+ + VV
Sbjct: 21 VKVPGSKSITNRALLIAALAEGLSGALFSNDAKNMIACLSLGIKTDIDEENETIVV 80

Query: 79 VCGGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
GCGG+ PV +A V G+AG A R +TA + +GG Y LD +M++RP+ L+
Sbjct: 81 QCGGRLPVRREAGINV---GSAGTAARFITALAFSGG--VYHLDASEQMKRPMKPLL 134

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG + P ++ + GG++ L ISSQ+LSA++M L ++
Sbjct: 135 DALISLGVVISYDEKEGHFPFTLDS-REVKGGRICLDTGISSQFLSAVIMTGFLKNGLK 193

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAE--HSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
++I + S+PYV+MT+++ME FGVK + H + + +K G Y + + +E D S+
Sbjct: 194 VDIGGERESLPYVDMTVKVMGFGVKVDTVHENGLASYILKEGNGY-TAREYNIEPDVSA 252

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFG 316
A YF A A I G VE S+QGD++F ++L M AK++ + + G +
Sbjct: 253 ACYFYAMAEILGCKAQVERVHLDISIQGDIEFVKLLTKMRAKLSENSEGIVLQGA KDGNV- 311

Query: 317 RKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
+ ++ N+N D ++TLA V FA PT I VA R++E++R++AI+TEL +LG
Sbjct: 312 ----EGLEANLSNFSQSLTLAAVGAFASPTKITGVAHIRLQESDRLLAIKTELERLGI 367

Query: 377 SVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDY 435
E G I P + I+TY+DHR+AMAF+L V I++PGC+ KTF DY
Sbjct: 368 KTEIGEGETITFPMMSDSSEVEIETIEDHRVAMAFALIGLRREGVVIKNPGCSAKTFKDY 427

Query: 436 FDVLSTFV 443
F VL V
Sbjct: 428 FKVLDKIV 435

>ref|ZP_03714227.1| hypothetical protein EIKCOROL_01924 [Eikenella corrodens ATCC 23834]
gb|EEG23474.1| hypothetical protein EIKCOROL_01924 [Eikenella corrodens ATCC 23834]
Length = 311

Score = 256 bits (654), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 150/317 (47%), Positives = 195/317 (61%), Gaps = 11/317 (3%)

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK--VKLSGSISSQYLSAL 186
M ERPIGDLV L+Q+GA + PP+ + GG+ + + G++SSQ+L+AL
Sbjct: 1 MHERPIGDLVDALRQVGATIRYEGREGYPPLHIGERQA--GGQRLITVRGNVSSQFLTAL 58

Query: 187 LMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMA PL EIE+ +LIS PY+++TL+LM +FGV+ H DS F + +Y +P
Sbjct: 59 LMALPLTQGAHEIEVQGELISQPYIDITLKLMAQFGVQVAH-DSHRLFRLPETARYHAPA 117

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+VEGDAS ASYFLA + V V G G S+QGD FA LE +GA V W E +
Sbjct: 118 TLHVEGDASGASYFLAAGLLAATPVRYVYIGRHSIQGDTAFAAELEKIGAAVEWGENYIQ 177

Query: 307 VTGPPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V R P R ++ D++ N +PD AMTLAVVAL A ++R++ SWRVKET+R+ A
Sbjct: 178 VA---RRPGQR--IRPFDLDANHPIDAAMTLAVVALAAGARCSLRNIGSWRVKETDRITA 232

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACAEVPVTIRDP 425

+ EL KLGA VEE + ITPP +L A IDTYDDHRMAM FSL + VPV I DP
Sbjct: 233 MAAELRKLGARVEEEAEIHTPPRLAANARIDTYDDHRMAMCFSLVSLLGVPVYINDP 292

Query: 426 GCTRKTFPDYFDVLSTF 442
C KTFPDYF + +

Sbjct: 293 QCVNKTFPDYFRLFESM 309

>gb|AAV64002.1| AroA [Actinobacillus suis ATCC 33415]
Length = 285

Score = 256 bits (654), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 146/298 (48%), Positives = 188/298 (63%), Gaps = 15/298 (5%)

Query: 57 LGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
L AL+ LG++ + V G GG F ++ + LFLGNAG AMR LTAA+ G
Sbjct: 1 LNALKALGVNYSLEDKTVCTVEGIGGAFNWQNG---LSLFLGNAGTAMRPLTAALCLKG 57

Query: 117 G-NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS 175
A +L G PRM+ERPI LV L+Q GA V PPV + GL GGKV++
Sbjct: 58 ATEAEVILTGEPRMKERPIKHLVDALRQAGASVQYLENEGYPVAIRN-SGLKGGKVQID 116

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
GSISSQ+L+ALLMAAPLA GD+EIEII +L+S PY+++TL +M+ FGV E+ + + F
Sbjct: 117 GSISSQFLTALLMAAPLAEGDMEIEIIGELVSKPYIDITLMMKDFGVNVENQN-YQTFV 175

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+KG Q Y SP+ VEGDASSASYFLA AI G V V G G S+QGD FA VLE MG
Sbjct: 176 VKGNQSYISPEKYLVEGDASSASYFLAAGAIK-GKVKVPGIGKNSIQGDRLFANVLEAMG 234

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
AK+TW + + + LK +D++MN +PD AMT+A ALFA+G T IR++
Sbjct: 235 AKITWGDDFIQAE-----QGELKGVMDMNHIPDAAMTIATTALFAEGETVIRNI 284

>ref|ZP_05791383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Butyrivibrio
crossotus DSM 2876]
gb|EFF69404.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Butyrivibrio
crossotus DSM 2876]
Length = 431

Score = 255 bits (652), Expect = 8e-66, Method: Compositional matrix adjust.
Identities = 159/430 (36%), Positives = 236/430 (54%), Gaps = 18/430 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V +PGSKS++NR LLLA LSE +V+ +L S+D + L L++LG +E D+ K
Sbjct: 13 LKGVVTVPGSKSMTNRALLLATLSEESVLRGVLFSDSRHFLACLQSLGFLLEIDENEK 72

Query: 75 RAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G GG+ P + +V G+AG A R LTA + + G T + +M +RP+
Sbjct: 73 VVKIKGTGGRIPYKTGTIDV---GSAGTAARFLTAMLALSDGEYTMCS--EQMEKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+L L ++GA + P +V G GG+ + + S S+Q+LSA+LM P+
Sbjct: 127 AELFNVLTGEMGARFEYLKNEGHLPAKVIENGVCCK-DITMDISRSTQFLSAMLVTPVTR 185

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ I I + + Y+E+T+ ++ FG+ YI G + + Y+E D
Sbjct: 186 SGIRIRITSEKKTGAYIEITMDMLREFGINVTFDGE---YIVDGNQKAVIGDYIEPDV 242

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+A YF A AA+TGG +TV +S+QGD+KF VL MG +VT T+ +TV+
Sbjct: 243 SAACYFYAMAAVTGGKITVRNVFESSQGDMKFLNLVAEMGCEVTEKDGITVSRG--- 299

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
LK IDVNMN D A+TLA +A FADG T IR+V R +E +RM AI ELTK
Sbjct: 300 ----GLKGIDVNMNNSDQALTLAAIAPFADGDTVIRNVGHIRGQECRMAAIINELTKC 355

Query: 375 GASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDGCTRKTTFPD 434
G + D I+ + I+TYDDHR+AMAF++ + I +P C RKTf +
Sbjct: 356 GVACHISGDDIFISSGAA-HGAEIETYYDDHRVAMAFVTGTGLVTGGMIIIDNPMCCRKTfEN 414

Query: 435 YFDVLSTFVK 444
Y++VL ++
Sbjct: 415 YFEVLEKLE 424

>ref|YP_846833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophobacter
fumaroxidans MPOB]
sp|A0LLU6.1|AROASYNFM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK18398.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophobacter
fumaroxidans MPOB]
Length = 423

Score = 255 bits (652), Expect = 9e-66, Method: Compositional matrix adjust.
Identities = 167/439 (38%), Positives = 240/439 (54%), Gaps = 27/439 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++PI I + +PGSKS+++R L+LAAL++ + + N L ++D AL +G+ V+
Sbjct: 5 IEPISGIKAQLSVPGSKSITHRALMLAALADDESEIRNPLVADDTTITADALVQMGVGVQ 64

Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V+V K ++ + LGN+G + R L A AA G + DG PR
Sbjct: 65 WKPGS---VLVAPPSK---RWSQPSEPIILLGNSGTSTRLLLA--LAATGVGDFTFDGAPR 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R+RP+ LV L+ LGA DC P+RV GL GGVK + S Q+LSA+LM
Sbjct: 117 LRQRPVKPLVSALEMLGARFDCETETDGFLLPLRVIA-HGLSGGKVLVDARQSGQFLSAVLM 175

Query: 189 AAPALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAP A G+V +E ++ + S PYV MTL +M G+ D +R + Q+Y +
Sbjct: 176 AAPCAGGEVTVWELEPVASYPYVAMTLAMMGERGIDF-RKDRANRVIVPAPQRYAGGRWT 234

Query: 249 YVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VE D SSASY A AA+TGG V SLQGD +F +LE MG +VTW E V V
Sbjct: 235 -VEADCSSASYLWAAAALTGGDVLTHPLSPDSLQGDRCFLGILERMGCRTVWEEDGVRVV 293

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
L+ +D+++N+MPD+ TLA++A FA G + IR+VA RVKE++R+ A+
Sbjct: 294 S-----SGELRPVLDLNLNEMPDMPVPTLAILAAAFAGGVSRIRNVHLRVKESDRLQAVS 346

Query: 369 TELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+EL KLG E PD I T P+ ID +DDHR+AMAF++A V I
Sbjct: 347 SELGKLGVPNRELDPGLEIRGGAATSPK----VGIDPHDDHRIAMAFVAGLRVGGVEIE 402

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
D K+FP +++
Sbjct: 403 DAEVVAKSFPPTFWETFEKL 421

>ref|XP_001728822.1| hypothetical protein MGL_3989 [Malassezia globosa CBS 7966]
gb|EDP41608.1| hypothetical protein MGL_3989 [Malassezia globosa CBS 7966]
Length = 1611

Score = 255 bits (652), Expect = 9e-66, Method: Compositional matrix adjust.
Identities = 185/459 (40%), Positives = 251/459 (54%), Gaps = 50/459 (10%)

Query: 18 TVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGAL---RTLGLSVEADKAAK 74
T+ PGSKS+SNR L+LAALS GT + +LL+S+D M+ AL R + E + A
Sbjct: 431 TIHTPGSKSVSNRALVLAALSGGTCRLRHLLHSDDTQVMMQALQRAADFAWEDNGAT- 489

Query: 75 RAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG-----NATYVL 123
VV G GG+ D ++L NAG A R +TA A + L
Sbjct: 490 -LVVHGQGGRRVLASDEP---VYLQNAGTAARFVTAVACLAASSASCSGSDSSCHGVVHL 544

Query: 124 DGVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RM++RPIG LV L+ GA +D ++C P+ V G L GG+++L+ +SSQY+
Sbjct: 545 TGNARMQRPPIGLVDAALRSNGARIDYVEQSNCLPLNVTASGALQGGRIELAADVSSQYV 604

Query: 184 SALLMAAPALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242

SA+L+ AP A DVE+ ++ K+IS PY++MT+ +M+ FGV+ E + Y Y
Sbjct: 605 SAVLLCAPYAQNDELALVGGKVISQPYIDMTIAMMQSFGVRVERVA--EHVYRIPRTTY 662

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWT 301
+P VE DASSA+Y LA AAITG TVTV G SLQGD FA +VL MG +V
Sbjct: 663 VAPSTYEVECDASSATYPLAIAAITGTTVTPSLGRASLQGDAAFARKVLAPMGCQVEQN 722

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGP----- 347
+ S TVTGPP K L AID M M D +T A++ A P
Sbjct: 723 DVSTTVTGPPVGML--KALGAID--MESMTDAFITAMLFATAPCDEYASSSTSASPS 778

Query: 348 -TAIRDVASWRVKETERMVAIRTELTKLGA-SVEEGPDYCIITPP--EKLNVTAIDTYDD 403
T I +A+ RVKE +R+ A+ TEL KLG +VE + + P + L +I YDD
Sbjct: 779 STRITGIANQVRKECDRLRAVVTTELAKLGVRAVEHDDGIEVFSTPISQLPHASIYCYDD 838

Query: 404 HRMAAFSLAACAEVP---VTIRDPGCTRKTFPDYFDVL 439
HR+AMAFS+ AC VP I++ C KT+P ++DVL
Sbjct: 839 HRIAMAFSVLACV-VPGAGTEIQEKRCVEKTWPSWWDVL 876

>emb|CBK80210.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coproccoccus catus
GD/7]
Length = 434

Score = 255 bits (651), Expect = 1e-65, Method: Compositional matrix adjust.
Identities = 164/442 (37%), Positives = 232/442 (52%), Gaps = 18/442 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I P T+ PGSKS++NR L+LAAL+ G T++ L S+D + L L+ LG
Sbjct: 7 QPIFSHPHPFELTIDAPGSKSITNRALMLAALANGETLLKGALFSDSRHFLQCLKDLG 66

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D+ A V G GG+ P KE + +G+AG A R LTA + A G + LD
Sbjct: 67 FDVVVDEPAHTVRVTGLGGRIP---KETAAINVGSAGTAARFLTAMLGCAKG--VWHLD 120

Query: 125 GVPRMRERPIGLDLVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
+M++RP+ L+ L LG +DC P + G+ + + SSQ+LS
Sbjct: 121 ASEQMKKRPMALLNLTLDLGCRLDCEKEGYFPFTIYS-EGITASEATVDIGDSSQFLS 179

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAA + D I I Y+ MT +M +FGV+ SD + I G Y+S
Sbjct: 180 ALLMAAVMMDHDFAIHITGNH-GFSYIHMTTAMMRQFGEISVSDD-QTWRIPGNAAYQS 237

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
++ +E D S+A+YF A ++GG V V SLQGDV E MG T
Sbjct: 238 -QDYQIEPDVSAAYFYGMVLSGGNVLRHVHFDLSLQGDVALLRTFEKMGCSAEDTPEG 296

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ +TGP + GR H ID++M+ D A+T+A +A FAD PT IR + R++E++RM
Sbjct: 297 IRLTGPAQ---GRLH--GIDIDMSSFSQALTMAAIAPFADSPTFIRGIGHIRLQESDRM 351

Query: 365 VAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIR 423
AI L+++G +G D I P + I+TYDDHR+AMAFSL + I
Sbjct: 352 AAIVENLSRMGIHAAIQGND--IYIEPGTPHAATIEYDDHRVAMAFSLTGLRTPGIIS 409

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
+P C RKTF +YFDVL +N
Sbjct: 410 NPLCCRKTFENYFDVLDACRN 431

>ref|XP_003026716.1| hypothetical protein SCHCODRAFT_83545 [Schizophyllum commune H4-8]
gb|EF191813.1| hypothetical protein SCHCODRAFT_83545 [Schizophyllum commune H4-8]
Length = 1635

Score = 255 bits (651), Expect = 1e-65, Method: Compositional matrix adjust.
Identities = 182/457 (39%), Positives = 244/457 (53%), Gaps = 55/457 (12%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-LSVEADKAAKRA 76
++K PGSKS+SNR LLLAALS GTT + NLL+S+D M AL +G + + +
Sbjct: 446 SLKTPGSKSISNRALLAALSSGTTKLRLNLLHSDTRVMRAALGEMGGATFTWEDGGETL 505

Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN----- 118
VV G GG DA +EV +LGNAG A R LT G
Sbjct: 506 VVHGRGGS LHAPDAGKEV--YLG NAGTAARFLTTVCALVDGQWSVEIRMSCHADRPAAATE 563

Query: 119 --ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
T + G RM++RPIG LV L++ GA ++ G C P+RV GL GG +KL+
Sbjct: 564 SAKTTTTITGNKRMKQRPPIGPLVDALRENGASIEYREGEGCLPLRVGAGQGLAGGHIKLA 623

Query: 177 SISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
SISSQY+S++L+ AP A V +E++ ++IS PY++MTL +M FGV+A D +
Sbjct: 624 SISSQYVSSILLCAPYAKEPVTLELVGGQVISQPYIDMTLGMMAFGVRATRRPGTDIYD 683

Query: 236 I-----KGGQKYKSPKNAY-VEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKF 287
I GG+K Y V DASSA+Y LA AAITGG TVE GT SLQGD F
Sbjct: 684 IPRGVYRC DGGEK----STVYTVFSDASSATYPLALAAITGGKCTVEAIGTRSLQGDAGF 739

Query: 288 AE-VLEMMGAKVTWTETSVTVTGPPPEPFGRKHLKAIDVNMNKM P DVAMTLAVVALFADG 346
A VL +G +V+ TE TV +++M M D +T V+A + G
Sbjct: 740 ATGVLAGLGCEVSQTERETT VR-----ELDMETMTDAFLTATVLA AVSKG 784

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLN V-TAIDTYDD 403
T I +A+ RVKE R+ A+ EL K G E P +I P E+L + TYDD
Sbjct: 785 TTRIIGIANQRVKECNRIKAMVDELAKFGVECSELP TGLVIHGRPV EELKRGV VVHTYDD 844

Query: 404 HRMAFAFLAACAEPVPTIRDPGCTRKTFPDYFDVLS 440
HR+AMAFS+ A + + C KT+P+++D LS
Sbjct: 845 HRVAMAFSVLA AVVP GTVLEEKRCVEKTWPNWDDLS 881

>ref|XP_003192257.1| aromatic amino acid family biosynthesis-related protein
[Cryptococcus gattii WM276]
gb|ADV20470.1| Aromatic amino acid family biosynthesis-related protein, putative
[Cryptococcus gattii WM276]
Length = 1610

Score = 255 bits (651), Expect = 1e-65, Method: Compositional matrix adjust.
Identities = 179/453 (39%), Positives = 250/453 (55%), Gaps = 37/453 (8%)

Query: 18 TVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+ PGSKS+SNR L+LAAL +GT V NLL+S+D M+ AL L +V + + +
Sbjct: 415 TMAPGSKSISNRALVLAALGKGTCRVNLLHSDDTAVMMNALVELKGAVFSWEDGGDTI 474

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY----VLDGVPRMRERP 133
VV GG AK + +L+LGNAG A R LT G+A+ ++ G RM++RP
Sbjct: 475 VVEGGGGILSTPAK GK-ELYLGNAGTASRFLTTVCAMVSGSASSERSTIITGNARMKQRP 533

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV L GA V T C P+ + G GG ++L+ S+SSQY+S++L+ AP A
Sbjct: 534 IGPLVDALTANGAKVKYLESTGCLPLDIE-TDGRFGGHIQLAASVSSQYVSSILLCAPYA 592

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYIKGGQKYKSPKN 247
V +E+ ++IS PY++MT+ +ME+FG K E + D Y+ Y +P
Sbjct: 593 AEQVTLELTGGQVISQPYIDMTIAMMEQFGATVERQKDEQGNLLD-IYVIPKCTYVNP AE 651

Query: 248 AYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFA-EVLEMMGAKVTWTETSVT 306
VE DASSA+Y LA AAITG T T+ G++SLQGD +FA EVLE MG V T TS
Sbjct: 652 YSVESDASSATYPLAIAAITGTCTISNIGSSSLQGDARFAKEVLEPMGCTVEQTLTSTK 711

Query: 307 VTGPPPEPFGRKHLKAI-DVNMNKM P DVAMTLAVVALFADGP-----TAIR 351
VTGPP L+A+ +V+M M D +T +V+A A P + I
Sbjct: 712 VTGPP-----VGTLRALGNVDM EPM TDAFLTASVLA AVAVK PCLPERRVEGLPETASRIY 766

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEK--LNVTAIDTYDDHRMAM 408
+A+ RVKE R+ A+R +L K +E D II PE +I YDDHR+AM
Sbjct: 767 GIANQRVKECNRIQAMRDQLAKFSVETDEFDDGIIIFGKPEASLFRGASIH CYDDHRVAM 826

Query: 409 AFSLAACAEPVPTIRDPGCTRKTFPDYFDVLS 441
AF++ +C I + C KT+P+++D L
Sbjct: 827 AFAVLSCIIDKTIIEEKRCVEKTWPNFWDDLQN 859

>ref|XP_569127.1| aromatic amino acid family biosynthesis-related protein
[Cryptococcus neoformans var. neoformans JEC21]
ref|XP_777142.1| hypothetical protein CNBB3730 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|EAL22495.1| hypothetical protein CNBB3730 [Cryptococcus neoformans var.
neoformans B-3501A]
gb|AAW41820.1| aromatic amino acid family biosynthesis-related protein, putative
[Cryptococcus neoformans var. neoformans JEC21]
Length = 1611

Score = 255 bits (651), Expect = 1e-65, Method: Compositional matrix adjust.
Identities = 179/453 (39%), Positives = 252/453 (55%), Gaps = 37/453 (8%)

Query: 18 TVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+ PGSKS+SNR L+LAAL +GT V NLL+S+D M+ AL L +V + + +
Sbjct: 415 TMATPGSKSISNRALVLAALGKGTCTVRNLLHSDDTAVMMNALVELKGAVFSWEDGGDTI 474

Query: 78 VVCGGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY----VLDGVPRMRERP 133
VV GG AK + +L+LGNAG A R LT G+A+ V+ G RM++RP
Sbjct: 475 VVEGGGILSTPAKKG-ELYLGNAGTASRFLT TVCAMVSGSASSERSTVITGNARMKQRP 533

Query: 134 IGD LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV L GA V T C P+ ++ G GG ++L+ S+SSQY+S++L+ AP A
Sbjct: 534 IGPLVDALTANGAKVKYLESTGCLPLDID-TDGFRRGHIQLAASVSSQYVSSILLCAPYA 592

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYIKGGQKYKSPKN 247
V +E+ ++IS PY++MT+ +M++FG K E + D Y+ Y +P
Sbjct: 593 AEQVTELELTGGQVISQPYIDMTIAMMKQFGATVERQKDEQGNLLD-IYVIPKCTYVNPPE 651

Query: 248 AYVEGDASSASYFLAGAAITGGT VTVGCGTTS LQGDVKFA-EVLEMMGAKVTWTETSVT 306
VE DASSA+Y LA AAITG T T+ G++SLQGD +FA E+LE MG V T TS
Sbjct: 652 YSVESDASSATYPLAIAAITGTTCTISNIGSSSLQGDARFAKEILEPMGCIVEQTLTSTK 711

Query: 307 VTGPPPREPFGRKHLKAI-DVNMNKM PDMVAMTLAVVALFADGP-----TAIR 351
VTGPP L+A+ +V+M M D +T +V+A A P + I
Sbjct: 712 VTGPP-----VGTLRALGNVDMPEPMTDAFLTASVLA AVKPKCLPERKVEGLPETASRIY 766

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEK--LNVTAIDTYDDHRMAM 408
+A+ RVKE R+ A+R +L K G +E D II PE +I YDDHR+AM
Sbjct: 767 GIANQRVKECNRIQAMRDQLAKFGIETDEFDDGIIIFGKPEASLFRGASIH CYDDHRVAM 826

Query: 409 AFSLAACAEVPVTIRDPGCTRTFPDYFDVLST 441
AF++ +C I + C KT+P+++D L
Sbjct: 827 AFAVLSCIIDEITIEEKRCVEKTWPNFWDLLQN 859

>gb|EEH08604.1| pentafunctional AROM polypeptide [Ajellomyces capsulatus G186AR]
Length = 1595

Score = 254 bits (649), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 178/462 (38%), Positives = 251/462 (54%), Gaps = 31/462 (6%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 QIVLAPSIIEVSPGPVKGLDVTCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDTVEVML 447

Query: 58 GALRTLGL-SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + VV G GG+ + +L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWEDEGEVLVVS GKGGRMEASPS----ELYLGNAGTASRFLT TVATLAR 503

Query: 117 GNA--TVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKL 174
++ + VL G RM++RPIGDLV L GA ++ C P+++ GG GG++ L
Sbjct: 504 KSSVDSSVL TGNARMKQRP IGD LVDALAANGASIEYLENLGLPLKIASSGGFAGGEINL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +SSQY+S+LLM AP A V + ++ K IS PY++MT +M FGV+ + S++ +
Sbjct: 564 AAKVSSQYVSSLLMCAPYAKTPVTLRLVGGKPI SQPYIDMTTAMMRSFGVEVKKSETEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVGCGTTS LQGDVKFA-EVLE 292
Y Y +P VE DASSA+Y LA AAITG + TV G+ SLQGD +FA +VL
Sbjct: 624 TYHIPLGFYTNPVEYIVESDASSATYPLAAAAITGTSCTVPNIGSKSLQGDARFAVDVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGP----- 347
MG V ++ S VTGPP G +++M M D +T +V+A A G
Sbjct: 684 PMGCAVDQSDFSTRVTGPP----GGILSPLNIDMEPMTDAFLTASVLAAVARGKGSNHT 739

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDD 403
T I +A+ RVKE R+ A++ EL + G E D I ++ + + YDD
Sbjct: 740 TRIFGIANQRVKECNRIKAMKDELAEEFVVCREHDDGLEIDGIDRATLHHPSDGVVYCYDD 799

Query: 404 HRMAMAFS-LAACAEVPTTIRDPGCTRKTFPDYFDVLSTFVK 444
HR+AM+FS L+ P I + C KT+P ++D L+ K
Sbjct: 800 HRVAMSFSVLSLVTPEPTLILEKECVGKTWPGWWDLSAQTFK 841

>ref|XP_002375788.1| pentafunctional polypeptide (AroM), putative [Aspergillus flavus NRRL3357]
ref|XP_001727508.2| shikimate dehydrogenase [Aspergillus oryzae RIB40]
gb|EED54516.1| pentafunctional polypeptide (AroM), putative [Aspergillus flavus NRRL3357]
Length = 1578

Score = 253 bits (647), Expect = 3e-65, Method: Compositional matrix adjust.
Identities = 174/434 (40%), Positives = 241/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTCRVKNLLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + +L+LGNAG A R LT T A ++ + +L G RM++RPIGDLV
Sbjct: 472 KGGNLQASPS----ELYLGNAGTASRFLTTVATLANASSVDSSILTGNRMKQRPIDGLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA V+ P++V GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGASVEYVERKGSPLKVAASGGFAGGRINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P +E DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVQKSTTEEHTYHIPQGRYVNPAYEVIESDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AAITG T TV G+ SLQGD +FA EVL MG V T+TS TV GP
Sbjct: 648 TYPLAIAAITGTCTVPNIGSKSLQGDARFAVEVLGPMGCTVKQTDSTTVVGP-----S 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADG-----PTAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D +T +V+A A G T I +A+ RVKE R+ A++ E
Sbjct: 703 DGILRPLPNVMEPMTDAFLTASVLAAVARGDGASHTRIYGIANQRVKECNRIKAMKDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAFS-LAACAEVPTTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVYCYDDHRVAFSFSVLSLVAPOPTLILEK 822

Query: 426 GCTRKTFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>dbj|BAE60669.1| unnamed protein product [Aspergillus oryzae]
Length = 1595

Score = 253 bits (647), Expect = 3e-65, Method: Compositional matrix adjust.
Identities = 174/434 (40%), Positives = 241/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT V NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTCRVKNLLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + +L+LGNAG A R LT T A ++ + +L G RM++RPIGDLV
Sbjct: 472 KGGNLQASPS----ELYLGNAGTASRFLTTVATLANASSVDSSILTGNRMKQRPIDGLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA V+ P++V GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGASVEYVERKGSPLKVAASGGFAGGRINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P +E DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVQKSTTEEHTYHIPQGRYVNPAYEVIESDASSA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AAITG T TV G+ SLQGD +FA EVL MG V T+TS TV GP
Sbjct: 648 TYPLAIAAITGTTCTVPNIGSKSLQGDARFAVEVLGPMGCTVKQTDSTTVVGP-----S 702

Query: 317 RKHLKAI-DVNMNKMPPDVAMTLAVVALFADG-----PTAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D +T +V+A A G T I +A+ RVKE R+ A++ E
Sbjct: 703 DGILRPLPNVDMPEPMTDAFLTASVLAAVARGDGASHTTRIYGIANQRVKECNRIKAMKDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQFAGGVYCYDDHRVAFSFSVLSLVAPQPTLILEK 822

Query: 426 GCTRKTFFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>ref|XP_001931677.1| pentafunctional AROM polypeptide [Pyrenophora tritici-repentis
Pt-1C-BFP]
gb|EDU40782.1| pentafunctional AROM polypeptide [Pyrenophora tritici-repentis
Pt-1C-BFP]
Length = 864

Score = 253 bits (647), Expect = 3e-65, Method: Compositional matrix adjust.
Identities = 173/432 (40%), Positives = 245/432 (56%), Gaps = 39/432 (9%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
PGSKS+SNR+L+LAAL G+ + NLL+S+D ML AL + G S + K VV G
Sbjct: 417 PGSKSISNRVLVLAALGTGSCRITNLLHSDDTQVMLDALAKMQGASFAWENDGKELVVTG 476

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
GG +L+LGNAG A R S+TA + ++ G RM+ERPIG L
Sbjct: 477 NGGNLKASSN----ELYLGNAGTAARFLTSTALCQPVEDTTSTIVTGNARMKERPIGPL 532

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG----GKVKLSGSISSQYLSALLMAAPLA 193
V L+ +G ++D P+R++ GG G ++L+ ++SSQY+S++L++AP +
Sbjct: 533 VKSLRTMGVEIDYQEKEGSLPLRISACGGFGSDSFTGDIELTANVSSQYVSSILLSAPYS 592

Query: 194 LGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V + ++ KIS PY++MT+ +M FGV+ E S+S Y + Y +P VE
Sbjct: 593 KKPVTTLRLVGGKVISQPYIDMTIAMMAAFGVQVERSESDLNTYHIPNKPYPNPEYEVES 652

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPP 311
DASSA+Y LA AAITG T TV G+ SLQGD +FA EVL+ MG KV ++TS TVTGPP
Sbjct: 653 DASSATYPLAIAAITGTTCTVPNIGSGSLQGDARFAVEVLKPMGCKVEQSKTSTTVTGPP 712

Query: 312 REPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFA--DGPTA---IRDVASWRVKETERMV 365
R LKA+ +++M M D +T +V+A A +G T+ I +A+ RVKE R+
Sbjct: 713 -----RGELKAVKEIDMEPMTDAFLTASVLAAVASSNGSTSTTRIYGIANQRVKECNRIQ 767

Query: 366 AIRTELTKLGASVEE-----GPDYCIITPPEKLNVT AIDTYDDHRMAMAFS-LAACA 416
A+ EL K G + + G Y + P I YDDHR+AM+F+ LA A
Sbjct: 768 AMEDELAKFGITCRQFDDGIEVDGRGYQLDAPK-----VGIHCYDDHRVAMSFVLAALVA 822

Query: 417 EVPVTIRDPGCT 428
PV I + CT
Sbjct: 823 PEPVLILEKECT 834

>ref|XP_455965.1| hypothetical protein [Kluyveromyces lactis NRRL Y-1140]
emb|CAG98673.1| KLLA0F19712p [Kluyveromyces lactis]
Length = 1578

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 186/466 (39%), Positives = 259/466 (55%), Gaps = 35/466 (7%)

Query: 4 AEEIVLQPIKEI----SGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGA 59
++E ++ P I + + PGSKS+SNR L+LAAL +GT + NLL+S+D +ML A
Sbjct: 401 SDETLLVHPFNNIPEQGQNKVITPPGSKSISNRALILAAALGKGTCKIKNLLHSDDTKHLNA 460

Query: 60 LRTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--- 115
++ L G ++ + + VV G GG ++ L+LGNAG A R LT A
Sbjct: 461 VQQLKGATISWEDDGETVVVHGQGGSTLTAPSE---ALYLGNAGTASRFLTVAALAKKD 517

Query: 116 GGNATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLS 175
G N +L G RM+ERPIG LV L+ G +D P+++N GGK++L+
Sbjct: 518 GKNDHVILTGNARMQERPIGPLVDSLRSNGLKIDYLNRRQGSPLKINTETNFKGGKIELA 577

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
++SSQY+S++LM AP A V + +I K IS YV+MT+++M+ FG+K S +
Sbjct: 578 ATVSSQYVSSILMCAPYAEFPVTLSLIGGKPISQLYVDMTIKMMDAFGIKVTTSTTEPFT 637

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFA-EVLEM 293
Y Y +P +E DASSA+Y L+ AAITG TVTV G+ SLQGD +FA +VL
Sbjct: 638 YHIPKGNINPAEYTIESDASSATYPLSFAAITGTTVTPNIGSASLQGDARFAVDVLRP 697

Query: 294 MGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNMPDVMATLAVVALFA----DGPTA 349
MG +VT T TS TVTGPPR K LK +D M M D +T +VVA T
Sbjct: 698 MGCEVTQTATSTTVTGPPRGQL--KPLKHVD--MEPMTDAFLTASVVAICNNGTTNTTT 753

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPD-----YCIITPEKLNVTIAIDTYDD 403
I +A+ RVKE R+ A+ T+L K G E PD I+ + + I+TYDD
Sbjct: 754 IEGIANQRVKECNRIEAMVTQLAKFGVRANELPDGIQIHGVNSISELRQPSDAGIETTYDD 813

Query: 404 HRMAFSLAACA-----EVPVTIRDPGCTRKTFPDYFDVLST 441
HR+AM+FSL A E V I + CT KT+P ++DVL +
Sbjct: 814 HRVAMSFSLLAGMVNSDKKDESSVRILERQCTGKTWPGWWDVLHS 859

>ref|ZP_04624288.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia kristensenii
ATCC 33638]
gb|EEP91176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia kristensenii
ATCC 33638]
Length = 287

Score = 253 bits (646), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 147/273 (53%), Positives = 186/273 (68%), Gaps = 8/273 (2%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L PI I+GTV LPGSKS+SNR LLLAAL+EGTT ++NLL+S+D+ +ML AL+ LG
Sbjct: 3 ESLTLHPIALINGTVNLPGSKSVSNRALLLAALAEGTTQLNNLLSDDIRHMLNALQALG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V G GSK A + V+LFLGNAG AMR L AA+ GN +L
Sbjct: 63 VKFRLSADRTCEVDGLGGKLV--ADQPVELFLGNAGTAMRPLAALCL--GNNDIILT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D + PP+R+ GG GSK+ + GS+SSQ+L+
Sbjct: 118 GEPRMKERPIGHLVDALRQGAQIDYLEQENYPPRLRLR--GGFRGGKLTVDGSVSSQFLT 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D +I+I +L+S PY+++TL LM+ FGV H +++ F+IKGGQ Y S
Sbjct: 176 ALLMTAPLAEQDTDIQIGELVSKPYIDITLHLMKTFGVDVVH-ENYQVFIKGGQTYHS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCG 277
P VEGDASSASYFLA AAI GGT V G G
Sbjct: 235 PGTYLVEGDASSASYFLAAAAIKGGTVRVTGIG 267

>ref|ZP_06933986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
polysaccharea ATCC 43768]
gb|EFH23046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria
polysaccharea ATCC 43768]
Length = 272

Score = 253 bits (646), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 132/274 (48%), Positives = 176/274 (64%), Gaps = 7/274 (2%)

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
+ + G++SSQ+L+ALLMA PL EI ++ +LIS PY+++TL+LM +FGV+ ++++
Sbjct: 2 IPIKGNVSSQFLTALLMALPLTGQAFEIRMVGEISKPYIDITLKLMAQFGVQVA-NENY 60

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 291
F I Y +P++ +VEGDAS ASYFLA I + V G G S+QGDV FA L
Sbjct: 61 RVFKIPADAHYHAPEHLHVEGDASGASYFLAAGLIAATPIRVTVGIGANSIQGDVAFACEL 120

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR 351
E +GA V W E V V+ P + ++A D++ N +PD AMTLA+VAL +R
Sbjct: 121 EKIGANVVWGENFVEVSRP-----KERAVQAFDLNANHIPDAAMTLAIVALATGQTCTLR 175

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAF 410
++ SWRVKET+R+ A+ EL KLGA V E + ITPPE L A IDTYDDHRMAM F
Sbjct: 176 NIGSWRVKETDRIAAMANELRKLGAKVAEEAEAIHITPPETLTPDAVIDTYDDHRMAMCF 235

Query: 411 SLAACAEVPVTIRDPGCTRKTFFDYFDVLSTFVK 444
SL + VPV I DP CT KTFP YFDV S+ +
Sbjct: 236 SLVSLLGVPVVINDPKCTHKTFPTYFDVFSSLTE 269

>ref|YP_003769882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Amycolatopsis
mediterranei U32]
gb|ADJ49480.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Amycolatopsis
mediterranei U32]
Length = 412

Score = 252 bits (644), Expect = 7e-65, Method: Compositional matrix adjust.
Identities = 171/432 (39%), Positives = 226/432 (52%), Gaps = 37/432 (8%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V++PGSKS++ R L LAA + GTTV+ L+S+D L LG V D+ +
Sbjct: 4 VEIPGSKSVTARGFLFLAAAAGTTVLGRPLHSDDTEGFAEGLAELGYRV--DRQPGEWTI 61

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P E +F + R L A AA G T+ D +MR RP+G L
Sbjct: 62 EG----RPSGPGVAEADVFCRDGATTARFLPA--LAAAGTGTFRFDASGMRRRPLGPLT 115

Query: 139 VGLKQLGADVDCFLGTDGCPP--VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L++LG +++ P VR NGI GG++ L +SSQ+L+ALL+ PL
Sbjct: 116 DALQELGVELEFRGEPGHHPLTVRANGI---KGGELTLDAGLSSQFLTALLLVGPLTAEG 172

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-----V 250
+ I + D L+S+PYVE+TL +M RFGV GQ + P Y V
Sbjct: 173 LRITVTD-LVSVPYVEITLMMRRFGVDVRE-----GQTFVVPAPQYQACEYPV 221

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTG 310
E DAS+ASYFLA AA+TG TVT+ G G+ +LQGDVKFA+VL MGA V SVTV GP
Sbjct: 222 EPDASTASYFLAAAALTGRTVTIPGLGSEALQGDVKFADVLREMGAVDLGPDSTVAGP 281

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L+ I VNM + D TLA +A FA GP I DV + R+KE +R+ A
Sbjct: 282 -----SDGLRGITVNMRIISDTVPTLAAIAPFASGVPRIEDVYNTRIKECDRLDACEEN 335

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
L +G +VE G D+ I P T + DHR+AMAFS+ VT+ DP C +K
Sbjct: 336 LRAMGIAVETGRDWIEIQPGRPTG-TLVSCRDRHRIAMAFSITGLLVGVTLDGPDPCVKK 394

Query: 431 TFPDYFDVLSTF 442
TFP + L T
Sbjct: 395 TFPGFHQALGTL 406

>ref|XP_001268882.1| pentafunctional polypeptide (AroM), putative [Aspergillus clavatus
NRRL 1]
gb|EAW07456.1| pentafunctional polypeptide (AroM), putative [Aspergillus clavatus
NRRL 1]

Length = 1587

Score = 252 bits (643), Expect = 8e-65, Method: Compositional matrix adjust.
Identities = 172/434 (39%), Positives = 240/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL +G + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTCRIKNLLHSDDETEVMLNALERIGAATFSWEEEGEVLVVG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT-AAGGNATY-VLDGVPRMRERPIGDLV 138
GG + +L+LGNAG A R LT T A N + +L G RM++RPIGDLV
Sbjct: 472 KGGALQAHP-----ELYLGNAGTASRFLTTVATLATPSNVDFSILTGNRMKQRPIDLV 527

Query: 139 VGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA V+ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 EALIANGAQVEYMESKSLPLKIAASGGFTGGQINLAQVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVQKSTEEHTYHIPQGRYTNPAEYVVEDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T TV G+ SLQGD +FA +VL MG V T+TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTVPNIGSKSLQGDARFAVDVLRPMGCTVEQTDSTTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNKMPPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+ E
Sbjct: 703 DGVLRPLPNVDMPEPMTDAFLGASVLAAIARGESNHTTRIYGIANQRVKECNRIKAMHDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ N+ + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHEDGLEIDGIDRANLRQPAGGVFCYDDHRVAFSFSVLSLVAPKPTLILEK 822

Query: 426 GCTRKTFFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>ref|YP_001047210.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanoculleus
marisnigri JR1]
sp|A3CV28.1|AROAMETMJ RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABN57228.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanoculleus
marisnigri JR1]
Length = 422

Score = 252 bits (643), Expect = 9e-65, Method: Compositional matrix adjust.
Identities = 166/418 (39%), Positives = 228/418 (54%), Gaps = 19/418 (4%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 81
P SKS ++R L+ AL+ G T + L + D L LG+ +E V GC
Sbjct: 18 PPSKSYTHRALIAGALALGRTRIARPLRAADTELTAARGLEALGVPLE--WLPGEIAVAGC 75

Query: 82 GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGL 141
G FP A EV + GN+G +R LT+A + VL G PRM ERP+G L L
Sbjct: 76 SGTFP---AAGEVTIDCGNSGTTLRLTLTSAALLS--QHPVVLTGSPRMLERPVGPLAGAL 130

Query: 142 KQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEI 201
+ LG DV PP+R++G L GG+ + GSISSQ++S++LMAAP A DVE+ +
Sbjct: 131 RALGGDVAFTGQPGYPPIRISGR--LRGGRATIDGSISSQFVSSILMAAPYAEEDVELTL 188

Query: 202 IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL 261
S Y+++T +M RFG E +DRF ++ G+ Y+ ++ VEGD SSASY
Sbjct: 189 PATPASRSYLDVTADVMLRFGAHER-QGYDRFRVESGRAYRG-RDYRVEGDYSSASYLF 246

Query: 262 AGAAITGGTGTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
A AA+ GG V V G TS+QGD +F + LE MG V +VTV E G LK
Sbjct: 247 AVAAVCGRRVAVTGLNPTSVQGDRRFLDALEAMGCSVAAGTDAVTV-----ERTG--DLK 299

Query: 322 AIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEG 381
I+++M+ PD TLA VA A PT I A + KE++R+ L ++GA VE
Sbjct: 300 GIEIDMSSSPDTVQTAAVAATAGSPTTITGTAHLQYKESDRVGVGTADTLRRMGAGVEVT 359

Query: 382 PDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
D IT P L+ A+D +DDHR AMAF++ A + IRDP C K+FP +++ L
Sbjct: 360 EDSLTTIT-PAPLHGVAVDPHDDHRTAMAFVLGLAVGGMAIRDPECVEKSFPGFWEAL 416

>gb|EER42257.1| pentafunctional AROM polypeptide [Ajellomyces capsulatus H143]
Length = 1595

Score = 251 bits (640), Expect = 2e-64, Method: Compositional matrix adjust.
Identities = 177/462 (38%), Positives = 250/462 (54%), Gaps = 31/462 (6%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 QIVLAPSIIEVSPGVKGLDVTCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDEVTML 447

Query: 58 GALRTLGL-SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + VV G GG+ + +L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWEDEGEVLVVSGKGRMEASPS----ELYLGNAGTASRFLTTVATLAR 503

Query: 117 GNA--TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
++ + VL G RM++RPIGDLV L GA ++ C P+++ GG GG++ L
Sbjct: 504 KSSVDSSVLTGNARMKQRPIGDLVDALAANGASIEYLENLGCLPLKIAASGGFAGGEINL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +SSQY+S+LLM AP A V + ++ K IS Y++MT +M FGV+ + S++ +
Sbjct: 564 AAKVSSQYVSSLLMCAPYAKTPVTLRLMGGKPIQSQYIDMTTAMMRSFGVEVKKSETEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
Y Y +P VE DASSA+Y LA AAITG + TV G+ SLQGD +FA +VL
Sbjct: 624 TYHIPLGFYTNPEYIIVESDASSATYPLAAAAITGTSCTVPNIGSKSLQGDARFAVDVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGP----- 347
MG V ++ S VTGPP G +++M M D +T +V+A A G
Sbjct: 684 PMGCAVDQSDFSFTRVTGPP----GGILSPLPNIDMEPMTDAFLTASVLASVARGKGSNHT 739

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDD 403
T I +A+ RVKE R+ A++ EL + G E D I ++ + + YDD
Sbjct: 740 TRIFGIANQRVKECNRIKAMKDELAQFVGVCREHDDGLEIDGIDRATLHHPDGVYCYDD 799

Query: 404 HRMAMAFS-LAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
HR+AM+FS L+ P I + C KT+P ++D L+ K
Sbjct: 800 HRVAMSFVLSLVTPEPTLILEKECVGKTWPGWWSLAQTFK 841

>gb|EEQ84223.1| 3-dehydroquinate synthase [Ajellomyces dermatitidis ER-3]
Length = 1597

Score = 251 bits (640), Expect = 2e-64, Method: Compositional matrix adjust.
Identities = 181/463 (39%), Positives = 252/463 (54%), Gaps = 33/463 (7%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 QIVLAPSIIEVSPGVKPNLNVCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDEVTML 447

Query: 58 GALRTLGLSVEA-DKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + + VV G GSK +L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWENEGEVLVVNGKGGKMKASPD----ELYLGNAGTASRFLTTVATLAQ 503

Query: 117 GNA--TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
++ + VL G RM++RPIGDLV L GA V+ + P+++ GG GG++ L
Sbjct: 504 KSSVDSSVLTGNARMKQRPIGDLVDALAANGAGVEYLENSGSLPLKIAASGGFAGGEINL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +SSQY+S+LLM AP A V + ++ K IS Y++MT +M FG+ + S++ +
Sbjct: 564 AAKVSSQYVSSLLMCAPYAKKPVTLRLVGGKPISTYIDMTTMMRSFGIDVKKSETEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292

Y Y SP VE DASS++Y LA AAITG + TV G+ SLQGD +FA EVL
Sbjct: 624 TYHIPLGFYISPAEYIVESDASSSTYPLAVAAITGTSTVNPISGSKSLQGDARFAVEVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADG----- 346
MG V + S TVTGP L+ + +V+M M D +T +V+A A G
Sbjct: 684 PMGCTVDQKDFSTTVTGP-----ANGILRPLPNVDMPEMTDAFLTASVLAAVARGGGSNH 738

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYD 402
T I +A+ RVKE R+ A++ EL K G + E D I ++ + + YD
Sbjct: 739 TTRIFGIANQVRKECNRIKAMKDELAKFGVTCREHDDGLEIDGIDRSTLRHPSDGVYCYD 798

Query: 403 DHRMAMAFS-LAACAEPVPTIRDPGCTRKTTPDYFDVLSTFVK 444
DHR+AM+FS L+ A P I + C KT+P ++D L+ K
Sbjct: 799 DHRVAMSFVLSLVAPQPTLILEKECVGKTWPGWWSLAQTFK 841

>ref|XP_002626822.1| 3-dehydroquinate synthase [Ajellomyces dermatitidis SLH14081]
gb|EEQ76475.1| 3-dehydroquinate synthase [Ajellomyces dermatitidis SLH14081]
Length = 1597

Score = 251 bits (640), Expect = 2e-64, Method: Compositional matrix adjust.
Identities = 181/463 (39%), Positives = 252/463 (54%), Gaps = 33/463 (7%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
+IVL P E+S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 388 QIVLAPSIIEVSPGVKPNLNVCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDETEVML 447

Query: 58 GALRTLGLSVEA-DKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + + VV G GSK +L+LGNAG A R LT T A
Sbjct: 448 NALERLGAATFSWENEGEVLVVGKGGKMKASPD----ELYLGNAGTASRFLTTVATLAQ 503

Query: 117 GNA--TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKL 174
++ + VL G RM++RPIGDLV L GA V+ + P+++ GG GG++ L
Sbjct: 504 KSSVDSSVLTGNARMKQRPIGDLVDALAANGAGVEYLENSGSLPLKIAASGGFAGGEINL 563

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +SSQY+S+LLM AP A V + ++ K IS Y++MT +M FG+ + S++ +
Sbjct: 564 AAKVSSQYVSSLLMCAPYAKKPVTLRLVGGKPISTYIDMTTMMRSFGIDVKKSETEEH 623

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
Y Y SP VE DASS++Y LA AAITG + TV G+ SLQGD +FA EVL
Sbjct: 624 TYHIPLGFYISPAEYIVESDASSSTYPLAVAAITGTSTVNPISGSKSLQGDARFAVEVLR 683

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADG----- 346
MG V + S TVTGP L+ + +V+M M D +T +V+A A G
Sbjct: 684 PMGCTVDQKDFSTTVTGP-----ANGILRPLPNVDMPEMTDAFLTASVLAAVARGGGSNH 738

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYD 402
T I +A+ RVKE R+ A++ EL K G + E D I ++ + + YD
Sbjct: 739 TTRIFGIANQVRKECNRIKAMKDELAKFGVTCREHDDGLEIDGIDRSTLRHPSDGVYCYD 798

Query: 403 DHRMAMAFS-LAACAEPVPTIRDPGCTRKTTPDYFDVLSTFVK 444
DHR+AM+FS L+ A P I + C KT+P ++D L+ K
Sbjct: 799 DHRVAMSFVLSLVAPQPTLILEKECVGKTWPGWWSLAQTFK 841

>gb|EGC43649.1| 3-dehydroquinate synthase [Ajellomyces capsulatus H88]
Length = 1574

Score = 249 bits (635), Expect = 8e-64, Method: Compositional matrix adjust.
Identities = 176/462 (38%), Positives = 250/462 (54%), Gaps = 31/462 (6%)

Query: 6 EIVLQPIKEISG-----TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
+IVL P ++S T PGSKS+SNR L+LAAL GT + NLL+S+D ML
Sbjct: 367 QIVLAPSIKVSPPVKGLDVTCTPPGSKSISNRALVLAALGSGTCRLKNLLHSDDETEVML 426

Query: 58 GALRTLGL-SVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
AL LG + + + + VV G GG+ + +L+LGNAG A R LT T A
Sbjct: 427 NALERLGAATFSWEDEGEVLVVGKGGRMEASPS----ELYLGNAGTASRFLTTVATLAR 482

Query: 117 GNA--TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKL 174

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      ++ + VL G RM++RPIGDLV L GA ++ C P+++ GG GG++ L
Sbjct: 483 KSSVDSSVLGTGNARMKQRPIGDLVDALAANGASIEYLENLGCLPLKIAASGGFAGGEINL 542

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
      + +SSQY+S+LLM AP A V + ++ K IS Y++MT +M FGV+ + S++ +
Sbjct: 543 AAKVSSQYVSSLLMCAPYAKTPVTTLRLMGGKPISQSYIDMTTAMMRSFGEVKKSETEEH 602

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
      Y Y +P VE DASSA+Y LA AAITG + TV G+ SLQGD +FA +VL
Sbjct: 603 TYHIPLGFYTNPVEYIVESDASSATYPLAAAAITGTSTCTVFNIGSKSLQGDARFAVDVLR 662

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGP----- 347
      MG V ++ S VTGPP G +++M M D +T +V+A A G
Sbjct: 663 PMGCAVDQSDFTSTRVTGPP----GGILSPLNIDMEPMTDAFLTASVLASVARGKGSNHT 718

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDD 403
      T I +A+ RVKE R+ A++ EL + G E D I ++ + + YDD
Sbjct: 719 TRIFIGIANQRVKECNRIKAMKDELAQFGVVCREHDDGLEIDGIDRATLHHPSDGVYCYDD 778

Query: 404 HRMAMAFS-LAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
      HR+AM+FS L+ P I + C KT+P ++D L+ K
Sbjct: 779 HRVAMSFVLSLVTPEPTLILEKECVGKTWPGWWSLAQTFK 820

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>ref|YP_001122070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
      tularensis subsp. tularensis WY96-3418]
gb|ABO46949.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
      tularensis subsp. tularensis WY96-3418]
      Length = 425

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Score = 248 bits (634), Expect = 1e-63, Method: Compositional matrix adjust.
Identities = 157/440 (35%), Positives = 228/440 (51%), Gaps = 18/440 (4%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      ++ +LQ +I V L GSKS+SNR L++AA+++G T +NL NS DV + AL+ LG
Sbjct: 2 KDFILQIKSQKQVYLDGSKSISNRSLIIAAMAQQQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +E + +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSRDSKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYVY 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMHRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      + VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
      A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIYVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFPDYFDVLSTFV 443
      + KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

```

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>emb|CAD29607.2| pentafunctional arom polypeptide [includes: 3-dehydroquinat
      synthase], putative [Aspergillus fumigatus]
      Length = 1582

```

Score = 248 bits (634), Expect = 1e-63, Method: Compositional matrix adjust.

Identities = 170/434 (39%), Positives = 239/434 (55%), Gaps = 25/434 (5%)

```
Query: 22  PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
          PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTVRIKLLHSDDEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81  CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
          GG + L+LGNAG A R LT T A ++ + VL G RM++RPIGDLV
Sbjct: 472 KGGALQAHPSP---LYLGNAGTASRFLTTVATLATASSVDSSVLTGNRMQRPIGDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
          L GA ++ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGAQIEYVENKGSPLKIAASGGFTGGQINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
          ++++ K IS PY++MT +M FG+ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVKKSTEEHTYHIPQGRYINPAEYVVESDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREFPG 316
          +Y LA AA+TG T T+ G+ SLQGD +FA +VL MG V T+TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTIPNIGSKSLQGDARFAVDVLRPMGCTVEQTDSTTTVTGP----A 702

Query: 317 RKHLKAI-DVNMNKMPPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
          L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+ E
Sbjct: 703 DGVLRPLPNVMEPMTDAFLGASVLAAIARGKDSNHTTRIYGIANQRVKECNRIKAMHDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPTVIRDP 425
          L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVFCYDDHRVAFSFSVLSLIAPKPTLILEK 822

Query: 426 GCTRKTFFPDYFDVL 439
          C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836
```

>ref|XP_001879572.1| predicted protein [Laccaria bicolor S238N-H82]
gb|EDR10187.1| predicted protein [Laccaria bicolor S238N-H82]
Length = 1606

Score = 248 bits (633), Expect = 1e-63, Method: Compositional matrix adjust.
Identities = 177/435 (40%), Positives = 248/435 (57%), Gaps = 25/435 (5%)

```
Query: 22  PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKRAVVVG 80
          PGSKS+SNR L+LAAL +GT + NLL+S+D M+ AL L G S + A + VV G
Sbjct: 418 PGSKSISNRALVLAALGKGTCRLKNLLHSDDTQVMMALNELKGASFAWEDAGETLVVKG 477

Query: 81  CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT---AAGGNATY-VLDGVPRMRERPIG 135
          G V +E L+LGNAG A R LT T + NA Y V+ G RM++RPIG
Sbjct: 478 GEGSLSVPPKGKE--LYLGNAGTAARFLTTVCTLVQSSPDNAEYTVITGNARMQRPIG 535

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
          LV L+ G+ +D C P+ + GL G +++L+ S+SSQY+S++L+ AP A
Sbjct: 536 PLVTALQANGSKIDFLESEGCLPLAI-APQGLKGSQQLAASVSSQYVSSILLCAPYAE 594

Query: 196 DVEIEIID-KLISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYIKGGQKYKSPKNAY 249
          + +E+I ++IS PY++MT+ +M+ FGV K + + Y Y +P
Sbjct: 595 PITLELIGGQVISQPYIDMTVAMMKTFGVDVVRKDPVTGKFLDVYEIPKAVYTNPEYN 654

Query: 250 VEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVT 308
          +E DASSA+Y LA AA+TG + T++ G+ SLQGD KFA EVLE MG +V+ T T TV
Sbjct: 655 IESDASSATYPLAIAAVTGTSTCTIQNIGSASLQGDAKFAKEVLEKMGCVSQTATETTVQ 714

Query: 309 GPPREFPGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
          GP P G+ LKAI +V+M M D +T +A A+G T I +A+ RVKE R+ A+
Sbjct: 715 GP---PIGQ--LKAIEEVDMEVMTDAFLTATALAAVANGKTRIIGIANQRVKECNIRAM 769

Query: 368 RTELTKLGASVEEGPD--YCIITPPEKLNVT-TAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
          EL K G E D I P L ++ YDDHR+AMAFS+ + I +
Sbjct: 770 IDELAKFGVETIELDDGLEIIGKPIISDLKRGVSVHCYDDHRVAMAFSVLSTVVEGTIIEE 829

Query: 425 PGCTRKTFFPDYFDVL 439
```


C KT+P+++D L
Sbjct: 830 KRCVEKTWPNWDDL 844

>ref|XP_752744.1| pentafunctional polypeptide (AroM) [Aspergillus fumigatus Af293]
gb|EAL90706.1| pentafunctional polypeptide (AroM), putative [Aspergillus fumigatus Af293]
Length = 1605

Score = 248 bits (633), Expect = 1e-63, Method: Compositional matrix adjust.
Identities = 170/434 (39%), Positives = 239/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTVRIKNNLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + L+LGNA G A R LT T A ++ + VL G RM++RPIGDLV
Sbjct: 472 KGGALQAHPSPP---LYLGNA GTASRFLTTVATLATASSVDSSVLTGNNRMKQRPIDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA ++ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGAQIEYVENKGSPLKIAASGGFTGGQINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVKKSTTEEHTYHIPQGRYINPAEYVVESDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T T+ G+ SLQGD +FA +VL MG V T+TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTIPNIGSKSLQGDARFAVDVLRPMGCTVEQTDSTTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+ E
Sbjct: 703 DGVLRPLPNVDMPEPMTDAFLGASVLAAIARGKDSNHTTRIYGIANQRVKECNRIKAMHDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVFCYDDHRVAFSFSVLSLIAPKPTLILEK 822

Query: 426 GCTRKTFFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWDDL 836

>gb|EDP56612.1| pentafunctional polypeptide (AroM), putative [Aspergillus fumigatus All63]
Length = 1605

Score = 248 bits (633), Expect = 1e-63, Method: Compositional matrix adjust.
Identities = 170/434 (39%), Positives = 239/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTVRIKNNLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + L+LGNA G A R LT T A ++ + VL G RM++RPIGDLV
Sbjct: 472 KGGALQAHPSPP---LYLGNA GTASRFLTTVATLATASSVDSSVLTGNNRMKQRPIDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA ++ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGAQIEYVENKGSPLKIAASGGFTGGQINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVKKSTTEEHTYHIPQGRYINPAEYVVESDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T T+ G+ SLQGD +FA +VL MG V T+TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTIPNIGSKSLQGDARFAVDVLRPMGCTVEQTDSTTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+ E
Sbjct: 703 DGVLRPLPNVDMPEPMTDAFLGASVLAIAIARGKDSNHTTRIYGIANQRVKECNRIKAMHDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVFCYDDHRVAFSFSVLSLIAPKPTLILEK 822

Query: 426 GCTRKTFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>ref|XP_001264384.1| pentafunctional polypeptide (AroM), putative [Neosartorya fischeri
NRRL 181]
gb|EAW22487.1| pentafunctional polypeptide (AroM), putative [Neosartorya fischeri
NRRL 181]
Length = 1578

Score = 248 bits (633), Expect = 1e-63, Method: Compositional matrix adjust.
Identities = 170/434 (39%), Positives = 239/434 (55%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALGSGTVRIKNLLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + L+LGNAG A R LT T A ++ + VL G RM++RPIGDLV
Sbjct: 472 KGGALQAHPSP----LYLGNAGTASRFLTTVATLATASSVDSVLTGNNRMKQRPPIGDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA ++ P+++ GG GG++ L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANGAQIEYVENKGSPLKIAASGGFTGGQINLAAKVSSQYVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY++MT +M FG+ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISQPYIDMTTAMMRSFGIDVKKSTEEHTYHIPQGRYINPAEYVVESDASSA 647

Query: 258 SYFLAGAAITGGTGTVEGCGTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T T+ G+ SLQGD +FA +VL MG V T+TS TVTGP
Sbjct: 648 TYPLAIAAVTGTCTIPNIGSKSLQGDARFAVDVLRPMGCTVEQTDSTTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A+ E
Sbjct: 703 DGVLRPLPNVDMPEPMTDAFLGASVLAIAIARGKDSNHTTRIYGIANQRVKECNRIKAMHDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ A P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVFCYDDHRVAFSFSVLSLVAPKPTLILEK 822

Query: 426 GCTRKTFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>ref|YP_001538010.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora arenicola
CNS-205]
gb|ABV99019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora arenicola
CNS-205]
Length = 414

Score = 248 bits (632), Expect = 2e-63, Method: Compositional matrix adjust.
Identities = 166/427 (38%), Positives = 236/427 (55%), Gaps = 22/427 (5%)

Query: 20 KLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
++PGSKSL+NR L +AA+++G T +DN L S+D AL LG+ VE + A+R V
Sbjct: 7 RVPGSKSLTNRALAIAAMADGVTELDNPLVSDDTSAFADALVALGVPVE--RQARRWTVT 64

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G V + ++ +AG A R L V AAGG + DG ++R RP+ L+

Sbjct: 65 GSRSGPRVRSGR----VWCEDAGTAARFLPPMVAAGG--VFDFDGTDLRLARPLHPLID 118

Query: 140 GLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ LGA V+ P R+ GL GG+V L+ SSQYLS LLMA PL L +

Sbjct: 119 ALRALGATVEPSGDGGGLPFRLVS-DGLTGGEVTLASGTSSQYLSGLLMAGPL-LSNPLT 176

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
+ +L+S PYV+MT+ +M RFGV+ + DRF + G+ ++ VE DAS+ASY

Sbjct: 177 VVAPELVSRPYVDMTIAVMARFGVQVTEARP-DRFTVHPGRYTRA--RYLVEPDASTASY 233

Query: 260 FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVITVTGPPREPFGGRKH 319
LA AA+TG V+V+G G+ S QGD +F +VL +GA VT VTV GP +H

Sbjct: 234 VLAAAVTGKEVSVDGLGSASPQGD RR FVDVLSQLGATVTADRDRVTVRGP-----RH 286

Query: 320 LK-AIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
L+ +V+M + D MTLA +A AD P I V R+KE++R+ A+ L G V

Sbjct: 287 LRGGFEVDMGSISDTFMTLAAIAPLADAPIRITGVGHARLKESDRIDAMAQNLVACGVFPV 346

Query: 379 EEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDV 438
GPD+ I+P + + I DHR+AM+FS+ + + DP C KTFP + D

Sbjct: 347 RTGPDWIEISPTDP-SPAPIHCRRDHRIAMSF SVLGLRVSGLLDDPACVSKTFPGFHDE 405

Query: 439 LSTFVKV 445
L+ +

Sbjct: 406 LARLFAD 412

>ref|ZP_04989980.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida
GA99-3548]
gb|EDN37872.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida
GA99-3548]
Length = 425

Score = 247 bits (630), Expect = 3e-63, Method: Compositional matrix adjust.
Identities = 157/440 (35%), Positives = 228/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ + Q +I V L GSKS+SNR L++AA++G T +NL NS DV + AL+ LG

Sbjct: 2 KDFIPQIKSQIKQVYLDGSKSISNRSLIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + +K V+ GC G F DAK +F +G R + + A Y +

Sbjct: 62 CQLEHSRDSKTLVIQGC SGVFANLDAK----IFCNE SGTLTRFIIPML-AVQSTGKYVYV 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S

Sbjct: 117 AKQRMMDRPLADQLKPLEKGLMLANYHQRAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S

Sbjct: 176 GLLMAAPFMHRLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +

Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIKFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+

Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVT AIDTYDDHRMAMAFSLAACAEVPTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +

Sbjct: 345 AAMAEGLSKLGIYVETQDSILISPARSKFKPAEVD SHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFPDYFDVLSSTFV 443
+ KT PDYFD + T V

Sbjct: 405 NAAAVSKTCPDYFDRMRTL 424

>ref|ZP_03727185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Opitutaceae bacterium
TAV2]

gb|EEG18802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Opitutaceae bacterium TAV2]
Length = 489

Score = 246 bits (628), Expect = 5e-63, Method: Compositional matrix adjust.
Identities = 180/479 (37%), Positives = 244/479 (50%), Gaps = 47/479 (9%)

Query: 9 LQPIKE-ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++P + + G V LPGSKSL+NR LLLAAL ++ L SED M ALR LG V
Sbjct: 12 IKPFRHPVRGEVLLPGSKSLTNRALLLAALCRDPVLLTGALFSEDTRLMAEALRRLGFRV 71

Query: 68 EADKAAKRAVVVGCGGKFP-----VEDAKE--EVQLFLGNAGIAMRSLTAAVTAAG 116
EAD+AA A V G D +E V+LF+G AG A R LTA AA
Sbjct: 72 EADEAAGTARVEQENALKGNVGGGGGEARTQEVQAVELFVGLAGTAARFLTALCAAAR 131

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
G Y +DG+ +MR+RP+ L+ L+ LGAD+ C P+ ++ GL GG V +
Sbjct: 132 GG-VYRIDGIAQMRKRPMRGLIEALRTLGLADIRCTGEEGFFPIEIIHA-RGLRGGPVTIDA 189

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S SSQ LSA+LM APLA VE+ I + P+V+MT RLME FG A + DR +
Sbjct: 190 SESSQMLSAVLMVAPLADAPVEVTIAGG-VRWPFVQMTTRLMEHFGQPAVQRLADDRLRV 248

Query: 237 KGGQKY-----KSPKNAY--VEGDASSASYFLAGAAITGGTV--TVEGCGTSLQ 282
G + + +NA +E DA++ASYFLA +TGG + LQ
Sbjct: 249 VSGHPWGLQAAAAGGRRGERNAVYAIEPDATAASYFLALPLVTGGELDLPLGRGPGGGLQ 308

Query: 283 GDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHL-----KAIDVNMNMKMPD 332
GD +F VL+ +GA VT TE F + L + N N+ D
Sbjct: 309 GDTRFVSVLQVRGAVVTETEGGGGRG--LHVAFSVEKLAGGATAGGTRTGVTENFNEFSD 366

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK 392
+TLA +A DGPT I +A R +ET+R+ + EL +LG V E D I P
Sbjct: 367 TFLTAAIAPLLDGPTRISGIAHTRKQETDRVAGMARELRLRLQQVIEEEDSLEIHPRL 426

Query: 393 LNVTAIDTYDDHRMAMAFSLAACAEVP-----VTIRDPGCTRKTFPDYFDVLSTFVKN 445
L I+TY DHR AM+F + C ++ ++I+DP C KTFP +F++L + K
Sbjct: 427 LAGQEIETYGDRHFAMSFILGCHDLHGDGRPWLSIKDPACCAKTFPHFFELLESRLKK 485

>ref|YP_169611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis SCHU S4]
ref|YP_666743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis FSC198]
ref|ZP_03665258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis MA00-2987]
ref|ZP_04986227.1| hypothetical protein [Francisella tularensis subsp. tularensis FSC033]
ref|ZP_05247239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis MA00-2987]
emb|CAG45221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis SCHU S4]
emb|CAL08604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis FSC198]
gb|EDN34119.1| hypothetical protein FTBG_01342 [Francisella tularensis subsp. tularensis FSC033]
gb|EET18964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis MA00-2987]
gb|ADA78274.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. tularensis NE061598]
Length = 425

Score = 246 bits (627), Expect = 7e-63, Method: Compositional matrix adjust.
Identities = 156/440 (35%), Positives = 228/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ +LQ +I V L GSKS+SNR L++AA+++G T +NL NS DV + AL+ LG
Sbjct: 2 KDFILQIKSIKQVYLDGSKSISNRSLIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E +K V+ GC G F A +V++F +G R + + A Y +

Sbjct: 62 CQLEHSWDSKTLVIQGC SGVF----ANLDVKIFCNESGTLTRFIIPML-AVQSTGKYYVY 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTD CPPVRVNGIGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S

Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S

Sbjct: 176 GLLMAAPFMHRLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +

Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIKFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+

Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +

Sbjct: 345 AAMAEGLSKLGIYVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFPDYFDVLSTFV 443
+ KT PDYFD + V

Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|YP_002929840.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium eligens
ATCC 27750]
gb|ACR71393.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium eligens
ATCC 27750]
Length = 431

Score = 245 bits (625), Expect = 1e-62, Method: Compositional matrix adjust.
Identities = 156/429 (36%), Positives = 243/429 (56%), Gaps = 20/429 (4%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I TV++PGSKS++NR LL+AALS+G + +L S+D + L +L LG +E ++ +

Sbjct: 13 IHCTVEVPGSKSITNRALLMAALSQGECTLKGVLFSDSRHFLSLIALGYIIEVNEVER 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G P K+ + +G+AG A R LTA + + G Y ++ +M++RP+

Sbjct: 73 YVIIHGHRDIP---KKRATINVGSAAGTAARFLTAMLALSDGE--YTIEASEQMKKRPM 126

Query: 135 GDLVVLGKQLGADVDCFLGTD CP-PVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAA 190
L L+ +GA+++ FL D PV V G G P V +S S S+Q+LSAL+M +

Sbjct: 127 LPLFEALQSMGAEIE-FLEKDGHLPVNVKGAAAYGGKKPQNHVSISSISESTQFLSALMMTS 185

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P+ + + I YV +T ++ME+FG +H + + + G Y P+ Y+

Sbjct: 186 PMLEEGIHVHITSNKTEGSYVRITAKMMEQFGCVVDHKGA--EYVVPAGSGY-YPQTYI 242

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS SVTVTGP 310
E D S+A YF A AA+ GGT V+G + S+QGD+KF +VL+ MG VT + V+GP

Sbjct: 243 EPDVSAACYFYAAAALIGGTAIVKGVHSNSMQGDLKFIDVLKQMGCAVTEEREGICVSGP 302

Query: 311 PREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ +DV+MN D +MTLA +A FA T I+++ R++E++R+ A+ E

Sbjct: 303 KDGEYC-----GVDVDMNDFSQSMTLAAIAPFAKTTTVIKNIEHIRLQESDRIEAMVNE 357

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
L LG V+EG D I+P + +DTY+DHRMAM+F+L + I + C K

Sbjct: 358 LNNLGVDVKEGRDRIEISPA-NVKPGVVDTYNDHRMAMSFALIGLRVDGIIIDNYECCCK 416

Query: 431 TFPDYFDVL 439
TF +YF+VL

Sbjct: 417 TFENYFEVL 425

>ref|YP_898731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. novicida U112]

ref|ZP_03057429.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. novicida FTE]
gb|ABK89977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida U112]
gb|EDX19499.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. novicida FTE]
Length = 425

Score = 245 bits (625), Expect = 1e-62, Method: Compositional matrix adjust.
Identities = 156/440 (35%), Positives = 227/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTL 64
++ + Q +I V L GSKS+SNR L++AA++G T +NL NS DV + AL+ LG
Sbjct: 2 KDFIPQIKSQIKQQVYLDGSKSISNRSLIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSRDSKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYVY 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMHRLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNKQGDIFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ L+KLG VE D +I+P K +D++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIVVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFFPDYFDVLSTFV 443
+ KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|ZP_06048035.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae CT 5369-93]
gb|EEY52822.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Vibrio cholerae CT 5369-93]
Length = 211

Score = 245 bits (625), Expect = 1e-62, Method: Compositional matrix adjust.
Identities = 120/214 (56%), Positives = 146/214 (68%), Gaps = 8/214 (3%)

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
+ F I GQ Y SP VEGDASSASYFLA AAI GG V V G G S+QGD++FA+
Sbjct: 6 YQEFVIPAGQSYVSPGQFLVEGDASSASYFLAAAAIKGGEVKVTGIGKNSIQGDIQFADA 65

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAI 350
LE MGA++ W + V R L A+D++ N +PD AMT+A ALFA G TAI
Sbjct: 66 LEKMQAGIEWGDDYVIAR-----RGELNAVLDLDFNHIPDAAMTIATTALFAKGTTAI 117

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF 410
R+V +WRVKET+R+ A+ TEL K+GA+VEEG D+ +ITPP KL AIDTYDDHRMAM F
Sbjct: 118 RNVYNWRVKETDRLAAMATELRKVGATVEEGEDFIVITPPTKLIHAAIDTYDDHRMAMCF 177

Query: 411 SLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
SL A ++ PVTI DP CT KTFPDYFD + +
Sbjct: 178 SLVALSDTPVTINDPKCTSKTFPDYFDKFAQLSR 211

>gb|ABK26355.1| unknown [Picea sitchensis]

Length = 148

Score = 243 bits (621), Expect = 4e-62, Method: Compositional matrix adjust.
Identities = 120/146 (82%), Positives = 125/146 (85%), Gaps = 4/146 (2%)

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDV 353
MGAKVTWTE SVTVTG + K L IDVNMNMPDVAMTLAVVALFADGPTAIRDV
Sbjct: 1 MGAKVTWTENSVTVTGAQKG---KRLHGIDVNMNMPDVAMTLAVVALFADGPTAIRDV 56

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
A+WRVKETERMVAI TEL KLGA+VEEG DYCIIITPPEKL +IDTYDDHRMAMAFSLA
Sbjct: 57 ANWRVKETERMVAICTELRKLGATVEEGHDYCIITPPEKLRASIDTYDDHRMAMAFSLA 116

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVL 439
AC +VPVTI DP CTRKTFPDYFDV
Sbjct: 117 ACGDVPVTINDPSCTRKTFPDYFDVF 142

>ref|ZP_03247089.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida
FTG]
gb|EDZ90500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida
FTG]
Length = 425

Score = 243 bits (620), Expect = 4e-62, Method: Compositional matrix adjust.
Identities = 155/440 (35%), Positives = 226/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ + Q +I V L GSKS+SNR L++AA+++G T +NL NS DV + L+ LG
Sbjct: 2 KDFIPQIKSQIKQQVYLDGSKSISNRLIIAAMAQQQTGFENLPNSADVLACIAVLKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSRDSKTLVIQCGSGVFANLDAK---IFCNESGTLTRFIIPML-AVQSTGKYYVY 116

Query: 125 GVPRMRERPIGLDLVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTILA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMHRLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIKFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIYVETTQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFPDYFDVLSTFV 443
+ KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|YP_502500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanospirillum
hungatei JF-1]
sp|Q2FQ54.1|AROA_METHJ RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABD40781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanospirillum
hungatei JF-1]
Length = 430

Score = 243 bits (619), Expect = 5e-62, Method: Compositional matrix adjust.

Identities = 159/428 (37%), Positives = 234/428 (54%), Gaps = 23/428 (5%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGC 81
P SKS ++R L++AAL++G + + L+++D AL LG+ ++ + R V G
Sbjct: 18 PPSKSYTHRALIIAALADGQSEIIGQLDADDTRMTARALMQLGVRLDWSRENIR--VQGT 75

Query: 82 GG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
GG K PVE ++ + ++G +MR LT A G VL G RM+ERP+G L+
Sbjct: 76 GGHLKAPVE-----EINIQDSGTSMRLLTGVSLLADG--PVVLTGSGRMQERPLGPLID 127

Query: 140 GLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L GA + C CPPVR++G P G + + GSISSQ++S+LL+AAP A DV I
Sbjct: 128 TLNNAGAKITCLKNPGCPPVRIDGT--FPAGDMYVDGSISSQFISSLLIAAPYADNDVHI 185

Query: 200 EIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ +S+PY+ MT+ M FG V + D F I ++YK P+ +EGD SS+
Sbjct: 186 HLTGDPVSLPYIMMTIDSMRAFGAEVLVDGDDKEPVFTISSQRRYK-PQTYGIEGDFSSS 244

Query: 258 SYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
SY+ A AAI GG+ T+ G S QGD + E+L MG +T S+ ++ R+P
Sbjct: 245 SYWFALAAICGGSATISGLNPQSAQGDRLLEILVNMGCSTIEKRESIILS---RDP--D 299

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
LK I V+M PD+ T+ +VA + PT I V R+KE++R+ AI LT LG
Sbjct: 300 VLLKGIKVDMADCPDIVQTVCMVAAVSSSPTRITGVHHLRMKESDRIAAIANGLTTLGGR 359

Query: 378 VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFD 437
VE D I+ P L+ I +DHR AM+F++ C VTI D C K++P +++
Sbjct: 360 VETEEDV-IVIHAPPLHGGIIHPENDHRTAMSAFVLGCFIGDVTILDAECVTKSYPGFWE 418

Query: 438 VLSTFVKN 445
L +N
Sbjct: 419 ELRRIWQN 426

>ref|YP_001891424.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. mediasiatica FSC147]
gb|ACD30646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. mediasiatica FSC147]
Length = 425

Score = 242 bits (618), Expect = 7e-62, Method: Compositional matrix adjust.
Identities = 154/440 (35%), Positives = 226/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++ + Q +I V L GSKS+SNR L++A +++G T +NL NS DV + +L+ LG
Sbjct: 2 KDFIPQIKSQIKQVYLDGSKSISNRLIIAVMAQQQTKFENLPNSADVLACIASLKLGL 61

Query: 65 LSVEADKAAKRAVVVGC GCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSRDSKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYVYV 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIEIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMHRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIFLEVLEKIGQVNYNDG 291

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIVVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFFPDYFDVLSTFV 443
+ KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|ZP_04988536.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. novicida GA99-3549]
gb|EDN36428.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella novicida
GA99-3549]
Length = 425

Score = 242 bits (617), Expect = 1e-61, Method: Compositional matrix adjust.
Identities = 156/440 (35%), Positives = 226/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ + Q +I V L GSKS+SNR L++AA+++G T +NL NS DV + AL+ LG
Sbjct: 2 KDFIPQIKSQIKQQVYLDGSKSISNRSLIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSWDSKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYYVY 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYTMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMQRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 PSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIKFLEVLEKIGCQVNYNDG 291

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAACAEVPTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIVVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFFPDYFDVLSTFV 443
+ KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|YP_001159802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora tropica
CNB-440]
gb|ABP55424.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora tropica
CNB-440]
Length = 414

Score = 242 bits (617), Expect = 1e-61, Method: Compositional matrix adjust.
Identities = 164/421 (38%), Positives = 232/421 (55%), Gaps = 20/421 (4%)

Query: 20 KLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
++PGSKSL+NR L +AA+++G T +DN L S+ AL LG SVE + A+R V
Sbjct: 7 RVPKSGKSLTNRLAIAAMADGVTELDNPLVSDGTTAFADALVALGASVE--RHAQRWTVT 64

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G G + + ++ +AG A R L AAGG + DG ++R RP+ L+
Sbjct: 65 GSGAGTRLRSGR---VWCEDAGTAARFLPPMAAAAGG--VFDFDGTDLRLARPLHLID 118

Query: 140 GLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ LGA V+ + P R+ GL GG+V L+ SSQYLS LLMA PL L +
Sbjct: 119 ALRALGATVEPSGDGEGLPFRLVS-DGLTGGEVVLASGTSSQYLSGLLMAGPL-LSNPLT 176

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
+ +L+S PYV+MT+ +M RFG + + RF ++ G+ ++ VE DAS+ASY

Sbjct: 177 VVAPELVSRPYVDMTIAVMARFGAQVAEAIIP-GRFTVRPGRYTRT--QFLVEPDASTASY 233

Query: 260 FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKH 319
LA AA+TG V+V+G G+ SLQGD +F +VL +GAKVT VTV GP R+

Sbjct: 234 VLA-AAVVGKEVSVDGLGSASLQGDRRFVDVLSQLGAKVTADRDRVTVRGP-----RQL 287

Query: 320 LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
V+M + D MTLA +A AD P I V R+KE++R+ AI L G V

Sbjct: 288 RGGFAVDMGPISDFTFMTLAAIAPLADAPIRITGVGHARLKESDRIDAIAQNLVSCGVPVR 347

Query: 380 EGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVVPVTIRDGCTRKTFPDYFDVL 439
G D+ I+P + + I DHR+AM+FS+ + + DP C KTFP + D L

Sbjct: 348 TGADWIEISPADP-SAALIRCRRDHRIAMSFSVLGLRVPGLVLDPAACVSKTFPGFHDEL 406

Query: 440 S 440
+

Sbjct: 407 A 407

>ref|ZP_02026168.1| hypothetical protein EUBVEN_01424 [Eubacterium ventriosum ATCC 27560]
gb|EDM51516.1| hypothetical protein EUBVEN_01424 [Eubacterium ventriosum ATCC 27560]
Length = 430

Score = 241 bits (616), Expect = 1e-61, Method: Compositional matrix adjust.
Identities = 154/430 (35%), Positives = 234/430 (54%), Gaps = 23/430 (5%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V +PGSKS++NR L+LAA+S+G ++ +L S D L L +LG SV+ D+ + V+

Sbjct: 17 VSVPGSKSITNRALMLAAMSDGICTLNGVLFSSDSRAFLDCLISLGSVQIDEESANVVI 76

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G G+ P A VQ +AG A R +T + AGG+ Y L +M++RP+ +L+

Sbjct: 77 KGENGRIPNRKATINVQ----SAGTAARFMTVFLAVAGGD--YTLQSSEQMKKRPMSELL 130

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L G ++ C P ++ G+ G +K+ + SSQY SALLMA+ + +

Sbjct: 131 GSLTAKGVEIKCLEEEGHFPFEIHS-KGIKSGNIKIDTTSSQYASALLMAS--VMNGMN 187

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGDASSA 257
+E+ + Y+++T ++++F + D YI Q Y N Y VE D S+A

Sbjct: 188 VELTGSRVGDGAYIKITTNMLKQFDIDF---DREGNTYIIKKQSYIC--NVYNVEPDMSAA 242

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGR 317
YF A AAI G V+G S+QGD+KF LE +G +T + V G +

Sbjct: 243 CYFYAMAAILGVKSIVKGIHKDSMQGDIKFIYALERIGCVITDKPEGLEVDGISAVGY-- 300

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ ID++M+ D A+T+AVVA F T IR++ R +E++R+ I EL ++G

Sbjct: 301 ---EGIDIDMSDFSDQALTMVVAFAFGKTETIRNIGHIRQESDRVQVIVNELNRMGCD 357

Query: 378 ---VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVVPVTIRDGCTRKTFPD 434
VEEG +I P KL+ I+TYDDHR+AM+F++A A + I++P C RKTF +

Sbjct: 358 AKIVEEGGSTDVIITPGKLHGAEIETYDDHRVAMSAFVAGLAVDGIVIKNPMCCRKTFEN 417

Query: 435 YFDVLSTFVK 444
YFDVL T K

Sbjct: 418 YFDVLETIEK 427

>ref|ZP_04985218.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. holarctica FSC022]
gb|EDO66296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella tularensis subsp. holarctica FSC022]
Length = 425

Score = 241 bits (616), Expect = 1e-61, Method: Compositional matrix adjust.
Identities = 155/440 (35%), Positives = 226/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64

Sbjct: 2 ++ + Q +I V L GSKS+SNR L++AA+++G T +NL NS DV + AL+ LG
KDFIPQIKSQIKQQVYLDGSKSISNRSIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + K V+ GC G F DAK +F +G R + + A Y +

Sbjct: 62 CQLEHSRDLKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYVYV 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + + P+ + L GG +++ G SSQ+ S

Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQSYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S

Sbjct: 176 GLLMAAPFMHRLRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +

Sbjct: 232 TSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIFLEVLKIGCQVNYNDG 291

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+

Sbjct: 292 IEVT-----GNNQLRGIQVNMNRNFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTATIDTYDDHRMAMAFSLAACAEVPVTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +

Sbjct: 345 AAMAEGLSKLGIIYVETTQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFFPDYFDVLSTFV 443
+ KT PDYFD + V

Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|YP_001678243.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
philomiragia subsp. philomiragia ATCC 25017]
gb|ABZ87742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
philomiragia subsp. philomiragia ATCC 25017]
Length = 426

Score = 241 bits (615), Expect = 2e-61, Method: Compositional matrix adjust.
Identities = 151/431 (35%), Positives = 227/431 (52%), Gaps = 18/431 (4%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ +V L GSKS+SNR L++AA+++G T +NL NS DV +GAL+ LG ++ ++ +

Sbjct: 11 KVKHSVYLDGSKSISNRSIIAAMAQQGQTTFFENLPNSADVLACVGAALKELGCQLKHNQES 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
K V+ GC GKF +AK +F +G R + + A Y + RM +RP

Sbjct: 71 KTLVIQCGSGKFANSNAK----IFCNESGTLTRFIIPML-AIQTGQYVYAKQRMMDRP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ D ++ L++LG P+ + L GG +++ G+ SSQ+ S LLMAAP

Sbjct: 126 LADQLIPLEKLGMSALYHQKEHAMPLTIEA-KSLNGGDIEVDGAKSSQFASGLLMAAPFM 184

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+++ I PY++MT ++M FG+ + Y Y SP VE D

Sbjct: 185 TKGLQLNSITDHKQ-PYLDMTAKVMAEFGINVNIDGN---IYSANNSSYVSPDKYVVEPD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+ASYF A AAITG + V S QGD+KF EVL+ +G +V + + + V G

Sbjct: 241 VSTASYFWAFAAITGSAIKVMNVTQKSKQGDIFLEVLKKIGCQVNYFDDGIEVIGIDS- 299

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L I+VNM D MTLA +A FA+ T I ++ R +E++R+ AI LTK

Sbjct: 300 -----LSGIEVNMRNFSDTFMTLAAIACFANSDTHISGLSHTRGQESDRVDAIAEGLTK 353

Query: 374 LGASVEEGPDYCIITPPE-KLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 432
LG VE D +I+P K +D+++DHR+AM+ +L V I + G KT

Sbjct: 354 LGIYVETTQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLRYDGVVINNAGAVSKTC 413

Query: 433 PDYFDVLSTFV 443
PDYFD + + V

Sbjct: 414 PDYFDRMRLV 424

>emb|CBQ73986.1| probable ARO1-Pentafunctional AROM polypeptide [Sporisorium reilianum]
Length = 1715

Score = 241 bits (615), Expect = 2e-61, Method: Compositional matrix adjust.
Identities = 178/465 (38%), Positives = 244/465 (52%), Gaps = 47/465 (10%)

Query: 11 PIKEISGTVKL---PGSKSLSNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
PI E T K+ PGSKS+SNR L+LAAL+ T + N+L+S+D M+ L L +
Sbjct: 436 PILEQPN TAKVTLSTPGSKSISNRALVLAALAGNTCRLRNMLHSDDTQVMMAGLHDLQAA 495

Query: 67 -VEADKAAKRAVVVCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNAT 120
E + + VV G GG P + Q++L NAG A R + V+ G
Sbjct: 496 RFEFEDGGETIVVHGNGGALARPANNK---QIYLQNAGTAARFMATVVS LVHNDGNQQP 551

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGI--GGLPGGKVKLSGSIS 179
V+ G RM+ERPIG LV L+ G +D G C P+ V G G GGK++LS +IS
Sbjct: 552 VVITGNKRMKERPIGALVDALRSNGTSIDYLEGQGCPLAVKGTTHGFKGGKIQLSATIS 611

Query: 180 SQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SQY+S++L+ AP A +V +E++ ++IS Y++MT+ +M FGVK E D +
Sbjct: 612 SQYVSSILLCAPYAAEEVVLVGGQVISQLYIDMTIAMMATFGVKVERL--LDPATGRP 669

Query: 239 GQKYKSPKNAYV-----EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EV 290
Y+ PK+ YV E DASSA+Y LA AAITG TV G+ SLQGD +FA EV
Sbjct: 670 SNTYRIPKDHVSPDIYDIESDASSATYPLAIAAITGTECTVPNIGSASLQGDARFAKEV 729

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTA- 349
LE MG V T TS TV GP + L V+M M D +T +V+ A P A
Sbjct: 730 LEPMGCTV VQTATSTTVIGPKVGQLRQIGL----VDMEPMTDAFLTASVLLAVAAQPAAN 785

Query: 350 -----IRDVASWRVKETERMVAIRTELTKLGASVEEGPD----YCIITPPEKLN 394
I +A+ RVKE R+ A+ EL K G +E D + I + N
Sbjct: 786 GSTSTSRPSTRITIGIANQRVKECNIRIAMMDELAKFGVDTKEHDDGLEIFGIDYRQLRAN 845

Query: 395 VTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVL 439
V + YDDHR+AMAFS+ A + + C KT+P+++D L
Sbjct: 846 VR-VHCYDDHRVAMAFSVLASLAPGAILEEKRCVEKTWPNWDDL 889

>ref|XP_002171624.1| pentafunctional AROM polypeptide [Schizosaccharomyces japonicus yFS275]
gb|EEB05331.1| pentafunctional AROM polypeptide [Schizosaccharomyces japonicus yFS275]
Length = 1584

Score = 240 bits (613), Expect = 2e-61, Method: Compositional matrix adjust.
Identities = 175/443 (39%), Positives = 237/443 (53%), Gaps = 32/443 (7%)

Query: 22 PGSKSLSNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGC 81
PGSKS+SNR L+LAA+++GTT + N+L+S+D M+ AL LG + + + +V
Sbjct: 412 PGSKSISNRALILAAAKGTTKLTNMLHSDDTQVMMAALEELGAATFSWEDNGETLVVNG 471

Query: 82 GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT---YVLDGVPRMRERPIGDLV 138
GGKF +L+L NAG A R LT G N VL G RM+ RPIG LV
Sbjct: 472 GGKFKTPSK----ELYLSNAGTAARFLTVAALVGENEQGGEVVL TGNHRMKVRPIGPLV 527

Query: 139 VGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ G + P+++ GL GG ++L+ ++SSQY+S++LM AP A V
Sbjct: 528 DALRANGCSISYLEREGSLPLKMIPQNGLRGGVIELAATVSSQYVSSILMCAPYAQEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS YV+MT+ +M+ FGV S++ Y Y SP + +E DASSA
Sbjct: 588 LKLVGGKPIQLYVDMTIAMMKGFVNVVKSETEAYTYHIPKANYTSPGDYIESDASSA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AAITG TV G+ SLQGD +FA +VL MG V T TS TV GPP
Sbjct: 648 TYPLAFAAITGKTCTVPNIGSASLQGDARFARDVLAPMGCTVEQTPTSTTVQGPMPGQL- 706

Query: 317 RKHLKAIDVNMNMPDVAMTLAVVALFA-----DGPTAIRDVASWRVKETERMVAIRTE 370
K L+++D M M D +T +A A + T I +A+ RVKE R+ A+ E
Sbjct: 707 -KPLESVD--METMTDAFLTATALAAVACNSSGNEHITRITGIANQRVKECNRIAAMVHE 763

Query: 371 LTKLGASVEE-----GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEPVPT 421
L K G E G Y + PE+ I TYDDHR+AMAFS L P
Sbjct: 764 LAKFGVKAGELEDGIFIHGQSYKDLKTPEE----GIYTYDDHRVAMAFSILTLVTPKPTV 819

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I D C KT+P ++DVL K
Sbjct: 820 ILDKACVVKTWPYWWDLRNSFK 842

>ref|ZP_04755889.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
philomiragia subsp. philomiragia ATCC 25015]
ref|ZP_05249554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
philomiragia subsp. philomiragia ATCC 25015]
gb|EET21279.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
philomiragia subsp. philomiragia ATCC 25015]
Length = 426

Score = 240 bits (612), Expect = 3e-61, Method: Compositional matrix adjust.
Identities = 152/431 (35%), Positives = 226/431 (52%), Gaps = 18/431 (4%)

Query: 14 EISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ V L GSKS+SNR L++AA+++G T +NL NS DV +GAL+ LG ++ ++ +
Sbjct: 11 KVKHLVYLDGSKSISNRSLIIAAMAQQOTTFFENLPNSADVLACVGALKELGCQLKHNQES 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERP 133
K V+ GC GKF +AK +F +G R + + A Y + RM +RP
Sbjct: 71 KTLVIQCGSGKFANSNAK----IFCNESGTLTRFIIIPML-AIQTGQYYVYAKQRMMDRP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ D ++ L++LG P+ + L GG +++ G+ SSQ+ S LLMAAP
Sbjct: 126 LADQLIPLEKLGMSALYHQKEHAMPLTIEA-KSLNGGDIEVDGAKSSQFASGLLMAAPFM 184

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+++ I PY++MT ++M FG+ + Y Y SP VE D
Sbjct: 185 TKGLQLNSITDHQK-PYLDMTAKVMAEFGINVNIDGN--IYSVNNFSYVSPDKYVVEPD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPE 313
S+ASYF A AAITG + V S QGD+KF EVLE +G +V + + + V G
Sbjct: 241 VSTASYFWAAAITGSAIKVMNVTQKSKQGDIKFLEVLEKIGCQVNYFDDGIEVIGIDS- 299

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L I+VNM D MTLA +A FA+ T I ++ R +E++R+ AI LTK
Sbjct: 300 -----LSGIEVNMRNFSDTFMTLAAIACFANSDTHISGLSHTRGQESDRVDAIAEGLTK 353

Query: 374 LGASVEEGPDYCIITPPE-KLNVTIAIDTYDDHRMAMAFSLAACAEPVPTIRDPGCTRKTF 432
LG VE D +I+P K +D+++DHR+AM+ +L V I + G KT
Sbjct: 354 LGIYVETQDSILISPARSKFKPAEVDSHNDHRIAMSLALLGLRYDGVVINNAGAVSKTC 413

Query: 433 PDYFDVLSTFV 443
PDYFD + + V
Sbjct: 414 PDYFDRMRSVLV 424

>ref|YP_513574.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica LVS]
ref|YP_763402.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica OSU18]
ref|YP_001428336.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica FTNF002-00]
ref|ZP_02274682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica FSC200]
ref|ZP_04983564.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica 257]
ref|ZP_06557581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica URFT1]
ref|ZP_06804404.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella

tularensis subsp. holarctica URFT1]
emb|CAJ79291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica LVS]
gb|ABI82765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica OSU18]
gb|EBA52448.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica 257]
gb|ABU61380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Francisella
tularensis subsp. holarctica FTNF002-00]
Length = 425

Score = 239 bits (611), Expect = 4e-61, Method: Compositional matrix adjust.
Identities = 155/440 (35%), Positives = 225/440 (51%), Gaps = 18/440 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ + Q +I V L GSKS+SNR L++AA++G T +NL NS DV + AL+ LG
Sbjct: 2 KDFIPQIKSQIKQQVYLDGSKSISNRLIIAAMAQQGQTKFENLPNSADVLACIAALKELG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E +K V+ GC G F DAK +F +G R + + A Y +
Sbjct: 62 CQLEHSWDSKTLVIQCGSGVFANLDAK----IFCNESGTLTRFIIPML-AVQSTGKYVY 116

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RM +RP+ D + L++LG + P+ + L GG +++ G SSQ+ S
Sbjct: 117 AKQRMMDRPLADQLKPLEKLGMLANYHQKAYAMPLTIIA-KSLDGGYIEVDGEKSSQFAS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAAP + + I PY++MT ++M FGV D + Y +Y S
Sbjct: 176 GLLMAAPFMHCGRLNSITDHKQ-PYLDMTTKVMAEFGVTV---DIDENIYTANKSQYIS 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N VE D S+ASYF A AAITG T+ V S QGD+KF EVLE +G +V +
Sbjct: 232 TSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIFLEVLEKIGCQVNYNDG 291

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ VT G L+ I VNM D MTLA +A FA G T I ++ R +E++R+
Sbjct: 292 IEVT-----GNNQLRGIQVNMNRFSDTFMTLAAIACFAKGDTHISGLSHTRGQESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPE-KLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
A+ L+KLG VE D +I+P K +D+++DHR+AM+ +L V +
Sbjct: 345 AAMAEGLSKLGIYVETTDQSDILISPARSKFKPAEVDSHNDHRIAMSLALLGLKYQGVIVN 404

Query: 424 DPGCTRKTFFPDYFDVLSFV 443
+ KT PDYFD + V
Sbjct: 405 NAAAVSKTCPDYFDRMRALV 424

>ref|YP_389974.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
gb|ABB40279.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
Length = 442

Score = 238 bits (608), Expect = 1e-60, Method: Compositional matrix adjust.
Identities = 166/444 (37%), Positives = 231/444 (52%), Gaps = 35/444 (7%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
S TV P SKS+S+R+++ AAL+ GT+ + N+L S+D+ + ++T G + + A R
Sbjct: 3 SKTVTAPASKSVSHRMVIGAAALAGSTLTNLVLESDDLTRTVEIMKTCGADI-VRQGAGR 61

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
V G G P + E ++ +G R LTA V A G T+ + GVPRM ERPIG
Sbjct: 62 YSVRGVAGT-PRGGSTEPASCYVHESGTTTCRLLTAVV--ACGLGTFRIHGVPRMHERPIG 118

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+LV L+ GADV PP+ V +G L GG V + SSQYLS LL+AAP A
Sbjct: 119 ELVTALRMAGADVRYEQHEGFPLIVEALG-LSGGMVTIGLDESSQYLSGLLLAAPQARS 177

Query: 196 DVEIEIIDKLISIPYVEMTLRLME----RFGVKAHSDSWDRF-----YIKGGQKYKS 244
K++S PYV +TL+ ME RF V+ + + W + + G ++
Sbjct: 178 MTITVGGAKVSWPYVGLTLQAMEDFGLRFSVETKDEGWHKTDWRTVKDIVGRVRFVV 237

Query: 245 PKNAY-----VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
P Y VEGD SS+SYFLA A VTV G SLQGD ++L MGA V
Sbjct: 238 PPGMYRAGDYTVEGDWSSSSYFLAAGAAGQVPVTVRGLRRDSLQGDRAMLDILRRMGAGV 297

Query: 299 TWTETSVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
W +VTV+ P LK I V+M PD+ T+A VA FA G T I +V R+
Sbjct: 298 AWDGDAVTVSPAP-----LKGIADVDMGHCPDLVPTVATVAAFASGDTTISNVGHLRI 349

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFSLA 413
KE +R+ + EL + G E D ++ + N+ T TY DHRMAM+ ++
Sbjct: 350 KECDRLASPAELARAGVQCEVRDDGLVVHGAGRENIRIAPGTVFSTYADHRMAMSMMAVL 409

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFD 437
A PVT+ DP C K+FP +++
Sbjct: 410 EMAGQPVTVDDPACVGKSFPAPWE 433

>emb|CAA28836.1| arom polypeptide [Emericella nidulans]
Length = 1586

Score = 238 bits (608), Expect = 1e-60, Method: Compositional matrix adjust.
Identities = 165/435 (37%), Positives = 226/435 (51%), Gaps = 16/435 (3%)

Query: 22 PGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL+S+D ML AL LG + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALSGTCTRIKNNLHSDDETEVMLNALERLGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA--TYVLDGVPRMRERPIGDLV 138
GG + L+LGNAG A R LT T A + + VL G RM++RPIGDLV
Sbjct: 472 KGGNLQASSSP---LYLGNAGTASRFLT TVATLANSSTVDSSVL TGNNRMKQRP I GDLV 527

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L ++ G P+++ GG GG + L+ +SSQY+S+LLM AP A V
Sbjct: 528 DALTANVLPLNTSKGRASLPLKIAASGGFAGGNINLAAKVSSQYVSSLLMCAPIYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ ++ K IS PY++MT +M FG+ + S + + Y +Y +P +E DAS A
Sbjct: 588 LRLVGGKPISQPYIDMTTAMMRSFGIDVQKSTTEEHTYHIPQGRYVNPAYEVIESDASCA 647

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREPFG 316
+Y LA AA+TG T TV G+ SLQGD +FA EVL MG V TETS TVTGP
Sbjct: 648 TYPLAFAAVTGTCTVPNIGSASLQGDARFAVEVL RMPGCTVEQTETSTTVTGPSDGILR 707

Query: 317 RKHLKAIDVNMNMPDVAMTLAVVALFADG--PTAIRDVASWRVKETERMVAIRTELTKL 374
+ N +P T + + P +A+ RVKE R+ A++ EL K
Sbjct: 708 ATSKRGYGTNDRCVPRCFRTGSHRPMESQTTTPVSSGIANQRVKECNRIKAMKDELAKEF 767

Query: 375 GASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFS-LAACAEVPVTIRDPGCTR 429
G E D I ++ N V + YDDHR+A +FS L+ P I + C
Sbjct: 768 GVICREHDDGLEIDGIDRSNLRQPVGGVFCYDDHRVAFSFSVLSLVTPQPTLILEKECVG 827

Query: 430 KTFPDYFDVLSTFVK 444
KT+P ++D L K
Sbjct: 828 KTWPGWWDTLRQLFK 842

>ref|YP_002992653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
salexigens DSM 2638]
gb|ACS81114.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
salexigens DSM 2638]
Length = 444

Score = 238 bits (607), Expect = 1e-60, Method: Compositional matrix adjust.
Identities = 167/439 (38%), Positives = 230/439 (52%), Gaps = 34/439 (7%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
VK P SKSLS+R L+ ALSEG+TVV + L+S D++ + L T+G D A V
Sbjct: 9 VKAPSSKSLSHRALIAGALSEGSTVVLDPLDSNDINRTMDCLSTMGAKFNIDGTA--TTV 66

Query: 79 VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138

Sbjct: 67 G G P AKE L + ++G R +TA A G + + G PRM +RPIG L
TGMDGG-PKGGAKEPAVLEMRDSGTTTCRLITA--LAGAGKGLFRVQGTPRMHDRPIGALT 123

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ G V PPV + G G ++ +S SSQYLS LL+ APLA

Sbjct: 124 SALESQGTKVTFSKQGYPPVTLEA-SGFKGKQMDISLEESSQYLSGLLLGAPLADETTI 182

Query: 199 IEII-DKLISIPYVEMTLRLME----RFGVKAHSDSWDRFYIKGGQKY----- 242
I +I +K +S PYV +TL +ME +F V+A+ W + + +K

Sbjct: 183 INVIGEKAVSWPYVALTLNVMEDFRVKFEVQAKKDGWVKKTDWRKVEKVVPEIRFVVEP 242

Query: 243 -KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K ++ Y VEGD S+ASYFLA A+ V +EG SLQGD +LE MGAKE

Sbjct: 243 SKFDRDEYRVEGDWSNASYFLAAGAVGNPNVKIEGMNVNSLQGDRAIMYILESMGAKIES 302

Query: 301 TETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ SVTV P + L ++V+M+K PD+ T+AV A FAD PT I +VA R+KE

Sbjct: 303 DHHSVTYV-PSK-----LHGVEVDMSKCPDLVPTVAVAAAFADSPITTITNVAHLRIKE 354

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEV 418
+R+ A E+ + G E D I P +K DTYDDHR+AM ++ A A +

Sbjct: 355 CDRLEASAAEVMRAGGKAEITADSITIIPAPLKKGERIVFDTYDDHRLAMCTAIFAMAGI 414

Query: 419 PVTIRDPGCTRKTFPDYFD 437
+PGC K+FP ++D

Sbjct: 415 ESIPAEPGCVAKSFPGFWD 433

>gb|ADQ43380.1| putative EPSP synthase [Streptomyces cinnamonensis]
Length = 425

Score = 238 bits (606), Expect = 2e-60, Method: Compositional matrix adjust.
Identities = 177/427 (41%), Positives = 240/427 (56%), Gaps = 32/427 (7%)

Query: 20 KLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
++PGSKSL+NR+LLLLAA ++GT+ + L SED AL G+ V++ V

Sbjct: 14 RVPGSKSLTNRLLLLLAAADGTSTLRAPLVSEDTVAFREALGVSGIPVKSGPDDAFWQVT 73

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G G + P A+ + +AG A R L AA G+ T++ DG ++R RP L+

Sbjct: 74 GTG-RGPAGPARP---WCADAGTAARFLPP--FAATGHGTFLFDGSSQLRARPQRPLIE 126

Query: 140 GLKQLGADVDCFLGTDCPP-VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LGAD++ G P +R +GI GG++ + S+SSQYLS LLMAAPL ++

Sbjct: 127 ALRALGADLEPGPGNGLPLLIRAHGI---EGGELSVDSSLSSQYLSGLLMAAPLMRRGLQ 183

Query: 199 IEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ L+S PYV+MT+ LM RFG + E S ++ G Y + + VE DASSAS

Sbjct: 184 VRTGSSLVSRPYVDMTVALMRRFGARVEESAD-GTLSVRPG-AYDA-TDVVVEPDASSAS 240

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW--TETSVTVTGPPREPFG 316
Y A AA+TG TVTV G GT SLQGD++F EVL GA+V T T+V+ TGP R F

Sbjct: 241 YIFAAAATVTRTVTPGLGTDLSLQGLRFVEVLGQAGAEVQVGPTATTVSGTGPLRGGF- 299

Query: 317 RKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
V+M ++ D MTLA +A AD P IR VA R+KE++R+ A+ L G

Sbjct: 300 -----TVDMGEISDTFMTLAAIAPLADAPITIRGVAHARLKESDRVAAMAENLRACGI 352

Query: 377 SVEEGPDYCIITP--PEKLNVTADTYDDHRMAMAFSLAACAEVPTIR--DPGCTRKTF 432
EG D+ + P P T I + DHR+AM+FS+ A VP TI DP C KTF

Sbjct: 353 ETSEGKDWITVRPGVPRP---TRIACHRDHRIAMSFSVLGLA-VPDTISLDDPACVAKTF 408

Query: 433 PDYFDVL 439
PD+ D L

Sbjct: 409 PDFHDEL 415

>ref|ZP_04696613.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces
roseosporus NRRL 15998]
ref|ZP_04711804.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces
roseosporus NRRL 11379]

ref|ZP_06587528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces roseosporus NRRL 15998]
gb|EFE77989.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces roseosporus NRRL 15998]
Length = 426

Score = 237 bits (604), Expect = 3e-60, Method: Compositional matrix adjust.
Identities = 170/437 (38%), Positives = 232/437 (53%), Gaps = 28/437 (6%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+++PGSKS++ R L LAA ++GTT + L S+D LR LG +VE + A R V
Sbjct: 4 IEIPGSKSVTARALFLAAAADGTTTLRLPLRSDDTEGFAEGLRNLGYAVE--QEADRWRV 61

Query: 79 VGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P A E ++ + R L + AA + TY D +MR RP+ L
Sbjct: 62 QG----RPAGPAATEADVCRDGATTARFL-PTLAAAAASGTYRFDASAQMRRRPLAPLT 116

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG D+ P+ V G+ GG++ L SSQYL+ALLM PL +
Sbjct: 117 RALTALGVDLRHEGADGHPLTVRA-AGIEGGELTLDAGESSQYL TALLMLGPLTTTKGLR 175

Query: 199 IEIIDLKISIPYVEMTLRLMERFGVKAHE-----SDSWDRFYIKGGQ--KYKSPKNA 248
IE+ + L+S PYVE+TL +M FGV+ E S S +GG Y++ A
Sbjct: 176 IEVTE-LVSAPYVEITLAMMRDFGVEVEREGNTFTVPSPSSRLRSNRGGPIGGYRATTYA 234

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VE DAS+ASYF A AA+TG VTV G GT +LQGD++F +VL MGA+V+ + TV
Sbjct: 235 -VEPDASTASYFFAAAALTGREVTVPGLGTGALQGD LRFVDVLRMGAEVSVGPDATTVR 293

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L+ I VNM + D TLA +A +ADGP I DVA+ RVKE +R+ A
Sbjct: 294 STGR-----LRGITVNMNRDISDTMPTLAAIAPYADGPVIEDVANTRVKECDRLEACA 346

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
L +G +V GPD I P T I T+ DHR+ M+F++A +T DPGC
Sbjct: 347 ENLRAMGITVHTGPDRIEIHGTP-KPTGIATHGDHRIVMSFAVAGLRTPGLTYDDPGCV 405

Query: 429 RKTFFPDYFDVLSTFVKV 445
RKTFF + +V + F +
Sbjct: 406 RKTFFPRFHEVFADFADH 422

>ref|XP_759754.1| hypothetical protein UM03607.1 [Ustilago maydis 521]
gb|EAK84510.1| hypothetical protein UM03607.1 [Ustilago maydis 521]
Length = 1715

Score = 236 bits (602), Expect = 5e-60, Method: Compositional matrix adjust.
Identities = 174/454 (38%), Positives = 241/454 (53%), Gaps = 43/454 (9%)

Query: 18 TVKLPKSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLS-VEADKAAKRA 76
T+ PGSKS+SNR L+LAAL+ T + N+L+S+D M+ L L + E + +
Sbjct: 447 TLSTPGSKSISNRALVLAALATNTCLRLNMLHSDDTQVMMAGLHDLQAARFEFEDGGGETI 506

Query: 77 VVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAA---GGNATYVLDGVPRMRE 131
VV G G P D Q++L NAG A R + V+ G V+ G RM+E
Sbjct: 507 VVHGAGALARPANDK----QIYLNAGTAARFMATVVS LVHNDGNQHPVVITGNKRMKE 562

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGI--GGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L+ G +D G C P+ V G G GGK++LS +ISSQY+S++L+ A
Sbjct: 563 RPIAALVDALRSNGTSIDYLEGHGCLPLAVKGTTHGFKGGKIQLSATISSQYVSSILLCA 622

Query: 191 PLALGDVEIEIIDL-KLISIPYVEMTLRLMERFGVKAHESDSWDRFYIKGGQKYKSPKNAY 249
P A V +E++ ++IS Y++MT+ +M FG+K E D + Y+ PK Y
Sbjct: 623 PYAAEQVVLVLVGGQVISQLYIDMTIAMMATFGIKVERL--LDPTTGRPSNTYRIPKGHY 680

Query: 250 V-----EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWT 301
V E DASSA+Y LA AAITG TV G+ SLQGD +FA EVLE MG V T
Sbjct: 681 VSPDVYDIESDASSATYPLAIAAITGTCTVPNIGSASLQGDARFAKEVLEPMGCTVVQT 740

Query: 302 ETSVTVTGPPREPFGFRKHLKAID-VNMNMPDVAMTLAV-VALFADGP-----T 348
TS TV GP G+ L+ I V+M M D +T +V +A+ A P T

Sbjct: 741 ATSTTVIGP---KLGQ--LRQIGLVDMPEMTDAFLTASVLLAVAAHSPANGSTSNA RPST 795

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A---IDTYDDHR 405

I +A+ RVKE R+ A+ EL K G + +E D I + + A + YDDHR
Sbjct: 796 RITGIANQRVKECNRIRAMMDELAKFGVNTKEHDDGLEIFGIDYRQLHANVRVHCYDDHR 855

Query: 406 MAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439

+AMAFS+ A + + C KT+P+++D L
Sbjct: 856 VAMAFSVLASLAPGAILEEKRCVEKTWPNWDDL 889

>ref|ZP_01292020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
gb|EAT01567.1| 3-phosphoshikimate 1-carboxyvinyltransferase [delta proteobacterium
MLMS-1]
Length = 405

Score = 236 bits (601), Expect = 7e-60, Method: Compositional matrix adjust.
Identities = 141/351 (40%), Positives = 202/351 (57%), Gaps = 15/351 (4%)

Query: 95 QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGT 154

++FLGN G A R LT+ AA G+ +++G RM ERPIG L+ L GAD+
Sbjct: 66 EIFLGNNGTATRFLTS--VAALGHGIFLINGDERMSERPIGPLLSALAGWGADIRSLRNN 123

Query: 155 DCPFVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMT 214

CPP+ + GL GG L SSQYLS+LL+ AP ++ + +++S PYV MT
Sbjct: 124 GCPPLEIQA-AGLKGATVLPAGKSSQYLSLLLVAPYTAQPAQLRVEGEVLSKPYVRMT 182

Query: 215 LRLMERFGVKAHSDSWDRFYIKGGQYKSPKNAYVEGDASSASYFLAGAAITGGT VTVE 274

+ +M FG++ E ++ + F I G + + VEGDASSASYF A AA+TGGT VTVE
Sbjct: 183 MAVMRAFGIEVEANEQLNHFRIPQGSYQR--REYAVEGDASSASYFWAAA VTGGT VTVE 240

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVA 334

SLQGD ++LE MG +V+ +TV+ P + L+ ++V M PDV
Sbjct: 241 NVPAPSLQGD TALVDILEKMGCVRVSRGADGITVSAP-----EELRGVEVEMADCPDVV 293

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT---PPE 391

TLAVVA A G T I ++A R+KE +R+ + EL +LG EEGPDY +I
Sbjct: 294 PTLAVVAALARGRTTISNIAHLRIKECDRLAVMARELARLGV RTEEGPDYLVIEGRGRAH 353

Query: 392 KLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442

+ AI T++DHR+AM F++A + I +P C +K+FPD++ +T
Sbjct: 354 DYHGAAIATHNDHRIAMCFAVAGLVIPGIRIENPDCVKKSFPDFWQRFATL 404

>ref|NP_243579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus halodurans
C-125]
sp|Q9K9D5.1|ARO A2_BACHD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 2;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase 2; Short=EPSP synthase 2; Short=EPSPS 2
dbj|BAB06432.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus halodurans
C-125]
Length = 447

Score = 235 bits (599), Expect = 1e-59, Method: Compositional matrix adjust.
Identities = 148/431 (34%), Positives = 233/431 (54%), Gaps = 25/431 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72

+ + G++ LPGSKSL+NR L+++AL+ +++ +L S+D ++ + AL+ LG V+ +
Sbjct: 28 QRLDGSITLPGSKSLTNRALIISALANSDSMLTGMLKSDDTYWC IQALKRLG--VQINVQ 85

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132

+ + G GG++ + L++G AG R L A+ A + + ++ M +R
Sbjct: 86 GETTSIRGIGGQW-----KSSSLYIGAAGTLARFLLGAL-AISRS GNWEIEASQSMSKR 138

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192

PI LV L++LGA + P+ ++G GL GG V+LSG +SSQY+S LL+AAP
Sbjct: 139 PIEPLVGVLR ELGATIH YLRREGFYPLSIHG-NLAGGTVRLSGQMSSQYISGLLIAAPY 197

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP---KNAY 249

A V I + ++ YV +TL LM+ FG + E+ + + +P ++

Sbjct: 198 ADTPVTITVQGSIVQHAYVFLTLHLMKSFGAQVEYDQQLQTIVV-----HPTPYTCQDID 252

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E DAS+A YFLA AA+T G + + ++ Q D+ V E MG VT + + + G

Sbjct: 253 LEADASTACYFLAALTKGRIRLNNLTASTTQPDLMHMLTFEKMGTCTVTRGSSFIELEG 312

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ G ++MN+M D A+TLA +A FADGP I DV R E++R+ I

Sbjct: 313 VSQKGG-----FQISMNEMSDQALTLAAIAPFADGPITITDVEHIRYHESDRIAVICE 366

Query: 370 ELTKLGASVEEGPDYCIITP-PEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
LT+LG V+E D + P K + + TYDDHR+AM+ SL + + DPGC

Sbjct: 367 ALTRLGIQVDEFEDGLTVYPGTPKPTLHPLSTYDDHRVAMSLSLIGTKVKGLRLNDPGCV 426

Query: 429 RKTFFPDYFDVL 439
KT P YF +L

Sbjct: 427 AKTCPSYFQLL 437

>ref|YP_003895882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanoplanus
petrolearius DSM 11571]
gb|ADN37444.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanoplanus
petrolearius DSM 11571]
Length = 423

Score = 233 bits (595), Expect = 3e-59, Method: Compositional matrix adjust.
Identities = 160/436 (36%), Positives = 232/436 (53%), Gaps = 24/436 (5%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
IV+ +++ T P SKS ++R L AAL++G +++N L S D AL LG+

Sbjct: 4 IVINRHRDVLTFSAAPSKSYTHRALFCAALADGISIIENPLYSGDTEVTCRALGQLGVR 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E + A +V GCGG P +V + +G ++R L G T L G

Sbjct: 64 TE--RTADGIIVDGCGGVMP---PGGDVTIDCEGSGTSLRFLATFALLYPGRVT--LTGS 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM+ERP+G+L L+++G D+ PPV ++G L GG V + S SSQ++S++

Sbjct: 117 PRMKERPVGELTGALREIGGDIRFTERPGFPPVEISG--ELSGGSVSIDASKSSQFISSM 174

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+ AP A V+I + S Y+++T+ +ME+FG E F++ G P+

Sbjct: 175 LIPAPYAEDPVDIIPEGHVASESYLDITVDVMEKFGAAVERMPDGG-FHVP SGAYV--PR 231

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD SSASY A AAI GGTVTV S+QGD FA L MG +VT SVT

Sbjct: 232 DYRVEGDYSSASYLFAIAAICGGTVTVNNLNPDVSVQGDATFAGALASMGCRVTKDAGSVT 291

Query: 307 VT--GPPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VT GP L +D++M+ PD TLA VA+FAD PT I V+ KE++R+

Sbjct: 292 VTRKGP-----LSGVDIDMSSSPDVTQTLAAVAVFADSPTRITGVSHLIYKESDRI 342

Query: 365 VAIRTELTKLGASVEEGPDYC-IITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
AI + GA E + I+ P K++ +D DDHR AM+ ++ VTI+

Sbjct: 343 GAIGRMVEGCGAGFEYNDNEGEIVITPGKIHGFVLDPVDDHRTAMSGAVIGLGAGGVTIK 402

Query: 424 DPGCTRKTFFPDYFDVL 439
DP C K++P ++D L

Sbjct: 403 DPECVGKSYPGFWDEL 418

>gb|ADI21744.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured
actinobacterium HF0130_15N16]
Length = 647

Score = 233 bits (594), Expect = 5e-59, Method: Compositional matrix adjust.
Identities = 167/426 (39%), Positives = 238/426 (55%), Gaps = 23/426 (5%)

Query: 17 GTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS--VEADKAAK 74
G+ +PGSKS +NR+LL AAL++G + + L ++D ML A+R LG + D+

Sbjct: 15 GSANVPGSKSHTNRVLLCAALADGASRISGALFADDTEAMLEAVRALGAKTVIVEDEEIL 74

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG +F + + ++G R L + A G+ T V+DG ++R RP
Sbjct: 75 EINGVGKPPRF-----NLTVDFRSSGTTSRFLIPVI--AAGHGTAVVDGSEQLRSRPF 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G+ + L LGA + +D P+ ++ G+ GG++++SG SSQ++S LLMAAPL
Sbjct: 127 GEQLAALNALGAQISSLNDSDELPLEIHA-RGVKGGIEVSGEASSQFISGLLMAAPLFE 185

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ +++ +L+S PYV++T+ +M FGV E D D ++ Q Y +P N +E DA
Sbjct: 186 EGLTLKVPGRVLVSRPYVDLTVEVMSDFGVFVEMPD--DSTFVVRPQTY-APSNILIEPDA 242

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+ASYF A AAITGGT VEG SLQGD++F VLE +GAKV W + + V G
Sbjct: 243 SAASYFFAAAAITGGTARVEGLNAASLQGDIEFVRVLEKLGAKVVWDDAYIQVEG----- 297

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ L +++ D A TLA VA FAD I V R KET R+ A+ +ELTK
Sbjct: 298 ---RGLSGGRFDSLDFSDTAQTLASVAADFADSEIEITGVGFIRAKETNRIALVSELTKC 354

Query: 375 GASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
G V E D ITP + L A IDTY+DHRMAM+ SL + IRDP C KTFP
Sbjct: 355 GVEVSETNDGLKITPNKWLRLGAEIDTYEDHRMAMMSLIGLRVPGLEIRDPSCVEKTFP 414

Query: 434 DYFDVL 439
+++ L
Sbjct: 415 SFYESL 420

>ref|ZP_03462611.1| hypothetical protein BACPEC_01696 [Bacteroides pectinophilus ATCC 43243]
gb|EEC57188.1| hypothetical protein BACPEC_01696 [Bacteroides pectinophilus ATCC 43243]
Length = 675

Score = 233 bits (593), Expect = 5e-59, Method: Compositional matrix adjust.
Identities = 156/425 (36%), Positives = 229/425 (53%), Gaps = 16/425 (3%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
VK+PGSKS++NR L+LAA+SE + +L S+D L L LG + D+ +R V+
Sbjct: 32 VKVPGSKSITNRALMLAAMSERRCELTVGLFSDDSRFLDCLGRLGFELIIDEENERVVI 91

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G GG P A +V+ +AG A R LT + AGG+ Y ++ +M +RP+ L+
Sbjct: 92 QGTGGVIPNNTASVDVR----SAGTAARFLTVMALAGGD--YEMNSSQMAKRPMEPLL 145

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ G + + FLG + + + V + ++SSQ+ SALLMA L ++
Sbjct: 146 KILRDGGVEFE-FLGEEGHFPFIMHSHDIHLSVTVDTTVSSQFTSALLMAGTLLDAGLD 204

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I + Y++MTL ++E+FG+ DS R + G Q Y + VE D S+AS
Sbjct: 205 INVTGSRTEGSYIKMTLSMLEQFGISYTRHDSGYR--VAGHQS Y-GLGSYVVEPDISAAS 261

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRK 318
YF + A I G V VE SLQGD+K+ E L +G + ++ + V G G
Sbjct: 262 YFYMAPILGCDVRVERVHRPSLQGDMKYVETLGTLCVLEESKEGLWVKGS-----GVS 316

Query: 319 HLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
I ++MN D MT+A VA++AD PT+I +V R +E++RM AI ELT +G
Sbjct: 317 SYHGITIDMNDSDQTMMAAVAVYADTPTSIYNVGHIRYQESDRMAAIINELTGMGIKC 376

Query: 379 EEGPDY-CIITPPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFD 437
EE P Y I P K ++TY+DHR+AMA SL V I++PGC RKTF +YF+
Sbjct: 377 EEIPQYDGIRIFPGKPQFVEVETIEDHRIAMAMSLTGLGADGVVKNPGCCRKTFENYFE 436

Query: 438 VLSTF 442
VL +
Sbjct: 437 VLDSL 441

>ref|YP_002467599.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosphaerula
palustris El-9c]
sp|B8GF70.1|ARO_A_METPE RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACL17876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosphaerula
palustris El-9c]
Length = 423

Score = 230 bits (587), Expect = 3e-58, Method: Compositional matrix adjust.
Identities = 154/419 (36%), Positives = 222/419 (52%), Gaps = 18/419 (4%)

Query: 22 PGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGC 81
P SKS ++R L++AAL++G +++ L +ED + AL+ LG + R V G
Sbjct: 18 PPSKSFTHRALLIAALADGESLIRGPLIAEDTLTLVRLALQALGADITDTPEGYR--VQGT 75

Query: 82 GGFVPEVDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGL 141
G+ D E L L N+G ++R L++ A L G PRM++RPIG+L +
Sbjct: 76 DGR---PDCAEGTVLDLKNSTSLRLLSSIALLCSSTAGVTLTGSPRMQQRPIGELGDAI 132

Query: 142 KQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEI 201
+ LG V PP V G L GG+ L GS+SSQ++S+LL+AAP A+ V++++
Sbjct: 133 RTLGGSVRYLAADGYPPCVVQG--PLVGGEATLDGSVSSQFISSLLLAAPYAVRPVDLKV 190

Query: 202 IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL 261
+ +S Y+E+T +M FGV + F ++ +Y+ + VEGD SSASYF
Sbjct: 191 ARQPVRSYLEITGAVMAAFGVPVRRV--GYTHFTVQPA--RYRG--REYTVEGDYSSASYFF 247

Query: 262 AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLK 321
A AA GG VTV S+QGD F L+ MG +VT VT+ K+L
Sbjct: 248 ALAATLGGKVTVRNLNHDVSVQGDRLFVAALKAMGCRVTRTETDGVTTIE-----RTKNLH 300

Query: 322 AIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEG 381
I ++M PD TLAVVA AD PT I V + KE++R+ L LG +V+
Sbjct: 301 GISIDMTTAPDVTQTLAVVAALADSPTTITGVHGLQYKESDRVAVTAGTLRALGCTVDIS 360

Query: 382 PDYCIITPEKLNVTIAIDTYDDHRMAMAFSLAACAEPVPTIRDPGCTRKTFPDYFDVLS 440
D I P L+ ID +DDHR AMAF++ A VTI DP C K+FP +++ L+
Sbjct: 361 AD-AITIHGPLHGGVIDPHDDHRTAMAFVLGLAVGDVTIETDPACVGKSFPKFWNALA 418

>ref|YP_002548675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium vitis
S4]
gb|ACM35669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium vitis
S4]
Length = 423

Score = 229 bits (585), Expect = 5e-58, Method: Compositional matrix adjust.
Identities = 165/442 (37%), Positives = 233/442 (52%), Gaps = 45/442 (10%)

Query: 8 VLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
+L P K ++G V PGSKS++NR+LLLA L+ GT+ + L S+D YM ALR +G++V
Sbjct: 13 ILPPAKPLTGHVSPPGSKSITNRVLLLAGLANGTSRLTGALKSDDTRYMADALRAMGVTV 72

Query: 68 EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 127
E + VV G G + A EE LFLGNAG A R LTAAG A G + +DG
Sbjct: 73 E-EPDETTFFVTGTG----LWRAPEEA-LFLGNAGTATRFLTAVALANGR--FTIDGDE 124

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
MR+RPI LV L+ LG + G CPPV ++ G +V + +SSQY+SALL
Sbjct: 125 HMRKRPIQLPLVDALQSLGVAIAAPSG--CPPVAIDAKGAFTKNRVVIDAGLSSQYVSALL 182

Query: 188 MAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAH-SDSWDRFYIKGGQKYKSP 245
MAAP+A E+E+ I Y+++TL M FG + E S + R G YK+
Sbjct: 183 MAAPMAGAAFEVLAGSEIGARGYIDLTLAAMRAFGARIEQPSQTIWRVEPTG---YKA- 238

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ ++E DAS+A+Y A +TGG + + Q D K V+
Sbjct: 239 SDFHIEPDASAATYWLAAEVLTTGGKIDIGTPAGQFTQPDAAHTVISAF----- 287

Query: 306 TVTGPFPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P P A+ ++ ++M D T+AV+A F + P +A+ RVKE +R+
Sbjct: 288 -----PTMP-----AV-IDGSQMQDAIPTIAVLAAFNETPVRVFGIANLRVKECDRI 334

Query: 366 AIRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPV 420
A+ T L + G + EEG D I P T IDT+ DHR+AM+F+LA +
Sbjct: 335 ALSTGLNAIRPGLATEEGDDLIIAADPALAGQTLPAKIDTFADHRIAMSFALAGLKISGI 394

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
TI DPGC KT+P Y+D L++
Sbjct: 395 TILDPGCVAKTYPGYWDALASL 416

>gb|EFP87557.1| pentafunctional AROM polypeptide [Puccinia graminis f. sp. tritici
CRL 75-36-700-3]
Length = 1618

Score = 229 bits (585), Expect = 5e-58, Method: Compositional matrix adjust.
Identities = 172/462 (37%), Positives = 255/462 (55%), Gaps = 43/462 (9%)

Query: 12 IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEAD 70
IKE+ T++ PGSKS+SNR L+LAAL GT + NLL+S+D M+ AL + G S +
Sbjct: 384 IKEV--TLRTPGSKSISNRALILAALGHGTCRLKNLLHSDDTQVMINALEEMKGASFWE 441

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT----AAGGNATYVLDGV 126
VV G GK + V +LGNAG A R LT + ++ V+ G
Sbjct: 442 DNGATLVVSGGAGKLSSPANGKHV--YLGNAGTAARFLTTCVSLVKSQVSNQSSTVITGN 499

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM+ERPIG LV L+ G +D C P+R++ G PGG ++L+ S+SSQY+S++
Sbjct: 500 ARMQERPIGPLVDALRTNGVQIDYLRNEGCLPLRISPEDGFPGGMIELAASVSSQYVSSV 559

Query: 187 LMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-----WDRFYIKGG 239
L++AP A V + ++ +IS PY+++T+ +M FG++ E ++ + + I G
Sbjct: 560 LLSAPFAQAPVTLVLGGTVISQPYIDITISMSTFGIQVERLNNPATGLPSNTYRIPNG 619

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKV 298
YK+P +E DASSA+Y LA AA+ G ++T+E G+ SLQGD +FA +VLE MG +V
Sbjct: 620 -TYKNPPVYEIESDASSATYPLAMAALNGLSITLETIGSGSLQGDAQFAKKVLEPMGCQV 678

Query: 299 TWTETSVTVTGPFPREPFGGRKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TA 349
TE V GP L+ + +++M +M D +T VV A P T
Sbjct: 679 IQTERETKVIGPSTV----SELRQLGEIDMEEMTDAFLTACVVLGVAVQPSEKEQKMSTR 734

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKL---NVT AIDTYDD 403
I +A+ RVKE R+ A+ EL K+G +E D + TP + L + I+ YDD
Sbjct: 735 IIGIANQRVKECNRIAMVAELGKMGIHAQELEDGIEVFGTVPDALAKRGDQVRINCYDD 794

Query: 404 HRMAMAFSLAACAEVP---VTIRDPGCTRKTFPDYFDVLST 441
HR+AMAFS+ VP + + + C KT+P ++D LST
Sbjct: 795 HRIAMAFSV--LGTVPGGKGLILNEKRCVEKTWPSWWDDLST 834

>ref|YP_001823336.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces
griseus subsp. griseus NBRC 13350]
dbj|BAG18653.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces
griseus subsp. griseus NBRC 13350]
Length = 415

Score = 225 bits (574), Expect = 1e-56, Method: Compositional matrix adjust.
Identities = 166/427 (38%), Positives = 225/427 (52%), Gaps = 21/427 (4%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ +PGSKS++ R L LAA ++GTT + L S+D L+ LG +VE + A R V
Sbjct: 7 IDIPGSKSVTARALFLAAAADGTTTLRLPLRSDDTEGFAEGLKNLGYAVE--QEADRWRV 64

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P A + ++ + R L V AA + TY D +MR RP+ L
Sbjct: 65 EG----RPDGPAAPDADVCRDGATTARFLPTLV-AAAASGTYRFDASQMRRRPLAPLT 119

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG D+ P+ V G+ GG V L SSQYL+ALLM PL +
Sbjct: 120 RALTALGVDLRHGGEGHHPLTVRA-AGIEGGDVVLDALESSQYLTALLMLGPLTAKGLR 178

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
IE+ D L+S PYVE+TL +M FGV S + F + G Y++ A VE DAS+AS
Sbjct: 179 IEVTD-LVSAPYVEITLAMMRDFGVDV--SREGNTFTVPSG-GYRATAYA-VEPDASTAS 233

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRGK 318
YF A AA+TG VTV G G +LQGD++F +VL MGA+V+ + TV R
Sbjct: 234 YFFAAAALTGREVTVPLGLGIGALQGDLRFDVLRDMGAEVSVGPDATTVRSTGR----- 287

Query: 319 HLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
L+ I V M + D TLA +A ADGP I DVA+ RVKE +R+ A L +G +V
Sbjct: 288 -LRGITVTMRDISDTMPTLAAIAPHADGPFVRIEDVANTRVKECDRLEACAQNLRAMGITV 346

Query: 379 EEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDV 438
G D+ I P T I T+ DHR+ M+F++A +T DPGC RKTFP + +V
Sbjct: 347 HTGHDWIEILPGTP-KPTGIATHGDHRIVMSFAVAGLLTPGLTYDDPGCVRKTFPRFHEV 405

Query: 439 LSTFVK 445
+ F +
Sbjct: 406 FADFAAS 412

>ref|YP_002543594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium
radiobacter K84]
gb|ACM25668.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium
radiobacter K84]
Length = 418

Score = 225 bits (573), Expect = 1e-56, Method: Compositional matrix adjust.
Identities = 160/450 (35%), Positives = 240/450 (53%), Gaps = 47/450 (10%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A+ ++ P K + G PGSKS++NR LLLA L++GT+ + L S+D YM AL
Sbjct: 2 MGRAKLTIIPPKPLVGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMAEAL 61

Query: 61 RTLGSLVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R +G+++ D+ +V GK ++ A E LFLGNAG A R LTAA G
Sbjct: 62 RAMGVTTI--DEPDDTTTFTVTSK--LQPAEEP--LFLGNAGTATRFLTAAALVDGKV- 114

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
V+DG MR+RPIG LV L+ LG +D T CPPV VNG G +V++ G +SS
Sbjct: 115 -VVDGDAHMRKRPIGPLVEALRSLG--IDASTETGCPPVTVNGTGRFEASRVQIDGGLSS 171

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIK 237
QY+SALM A V++E++ + I ++ Y+++T+ M FG K E + +W R
Sbjct: 172 QYVSALLMMAASGDRPVDVELLGEHIGALGYIDLTVAAAMRAFGAKVERTSPVTW-RVEPT 230

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Y + + +E DAS+A+Y A A+TG + + Q D + E++
Sbjct: 231 G---YHA-ADFLIEPDASAATYLWAAEALTGGKIDLGTPAAEFSQPDARAYELISQF--- 283

Query: 298 VTWTETSVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWR 357
HL A+ ++ ++M D TLAV+A F + P + + R
Sbjct: 284 -----PHLPAV-IDGSMQDAIPTLAVLAAFNETPVRVFGIENLR 322

Query: 358 VKETERMVAIRTELTKL--GASVEEGPDYCIITPPE---KLNVTADITYDDHRMAMAFSL 412
VKE +R+ A+ + L+++ G EEG D + + P K+ ID++ DHR+AM+F+L
Sbjct: 323 VKECDRVRALSSGLSRIVPGLGTEEGDDLVSADPSLAGKVLPAEIDSFADHRIAMSFAL 382

Query: 413 AACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A +TI DP C KTFP Y+ VL++
Sbjct: 383 AGLKIGGITILDPDCVAKTFPAYWQVLASL 412

>ref|YP_003196997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfohalobium
retbaense DSM 5692]
gb|ACV67419.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfohalobium
retbaense DSM 5692]

Length = 444

Score = 224 bits (572), Expect = 1e-56, Method: Compositional matrix adjust.
Identities = 158/440 (35%), Positives = 225/440 (51%), Gaps = 40/440 (9%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V +P SKSLs+R L+ A L+ G + V+N+L+S+D+ L LG E + A VV
Sbjct: 6 VTVPASKSLSHRALICAGLALGVSRVENVLDSQDLDRTRACLEALGTQFEVE--ADGLVV 63

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G GG V A +V G +G R LTA AA G+ + L G RM +RPI L
Sbjct: 64 RGRGGIGQVNVQASLDV----GESGTTCRLLTA--VAAAGSGVFSLAGQGRMHQRPPIAPLA 117

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L QLG + P RV+ GL GG+ ++ SSQ+LS LL+A+PLA +
Sbjct: 118 SALHQLGCRFEWLEADGFLPCRVS--SGLKGGQTTVALDESSQFLSGLLLASPLACDPLT 176

Query: 199 IEII-DKLISIPYVEMTLRLMERFG----VKAHSDSWD-----RFYIKG 238
I I + +S PYV +TL +M FG ++ H + W RF
Sbjct: 177 IGIGGQRAVSWPYVALTLEVMRFFGQEPFILEQAHGERWHSVPFESNPSIEPSKTRFRCHP 236

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
G SP+ VEGD S+ASYF+A AI V + G S QGD ++++ GA V
Sbjct: 237 G--VYSPQRYRVEGDWSNASYFVAAGAIGPRPVRLRGLYKDSRQGDRIVIDIVKQFGAYV 294

Query: 299 TWTETSVTVTGPPEPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
W S+ V P L+ +++M PD+ T+AV+A A+GPT I+++A ++
Sbjct: 295 EWGRESLVVAPGP-----LQGQELDMGPCPDLPVTVAVMASLAEGPTVIKNIAHLQL 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITP-PEKLNVTATIDYDDHRMAMAFSLAACAE 417
KE++R+ + EL K GA V D I P P + TYDDHRMAMA SL A
Sbjct: 347 KESDRLNGVANELRKAGAETVEADTLTIIPCPLGKPLRLSTYDDHRMAMALSFLQLAG 406

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
+ + + +PGC K+FP +++
Sbjct: 407 LHLQLDNPGCAKSFPRFWE 426

>ref|ZP_06279329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACT-1]
gb|EFB81832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACT-1]
Length = 415

Score = 224 bits (570), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 164/433 (37%), Positives = 221/433 (51%), Gaps = 33/433 (7%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ +PGSKS++ R L LAA ++GTT + L S+D L+ LG +VE + A R V
Sbjct: 7 IDIPGSKSVTARALFLAAAADGTTTLRLPLRSDDTEGFAEGLKNLGYAVE--QEADRWRV 64

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P A + ++ + R L V AA + TY D +MR RP+ L
Sbjct: 65 EG---RPDGAAPDADVYCRDGATTARFLPTLV-AAAASGYRFDASVQMRRRPLAPLT 119

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG D+ P+ V G+ GG V L SSQYL+ALLM PL +
Sbjct: 120 RALTALGVDLRHGEGEGHHPLTVRA-AGIEGGDVVLDAESSQYL+ALLMLGPLTAKGLR 178

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-----VEG 252
IE+ D L+S PYVE+TL +M FGV + G + P Y VE
Sbjct: 179 IEVTD-LVSAPYVEITLAMMRDFGVVD-----TREGNTFTVPSGGYRATAYAVEP 227

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 312
DAS+ASYF A AA+TG VTV G G +LQGD++F +VL MGA+V+ + TV R
Sbjct: 228 DASTASYFFAAAALTGREVTVPGLGIGALQDLRFVDVLRDMGAEVSVGPDATTVRSTGR 287

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
L+ I V M + D TLA +A ADGP I DVA+ RVKE +R+ A L
Sbjct: 288 -----LRGITVTMRDISDTMPTLAAIAPHADGPVRIEDVANTRVKECDRLEACAQNL 340

Query: 373 KLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVPVTIRDGPCTRKTF 432
+G +V G D+ I P T I T+ DHR+ M+F++A +T DPGC RKTF
Sbjct: 341 AMGITVHTGHDWIEILPGTP-KPTGIATHGDHRIVMSFAVAGLLTPGLTYDDPGCVRKTF 399

Query: 433 PDYFDVLSTFVK 445
P + +V + F +
Sbjct: 400 PRFHEVFADFAAS 412

>ref|ZP_06270491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACTE]
gb|EFB69621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACTE]
Length = 412

Score = 224 bits (570), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 167/434 (38%), Positives = 227/434 (52%), Gaps = 41/434 (9%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ +PGSKS++ R L LAA ++GTT + L+S+D L LG V + R +
Sbjct: 4 IHIPGSKSVTARALFLAAAADGTTTLRLPLSSDDEGFAEGLTRLGHGVT--REPDRWHI 61

Query: 79 VGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P A E ++ + R L + AA TY D +MR RP+G L
Sbjct: 62 EG---RPDGPVTEAEVHCRDGAATTARFL-PTLAAAAPRGTYRFDASAQMRRLPLGLT 116

Query: 139 VGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LG D+ P+ V G+ GG++ L+ SSQYL+ALLM PL +
Sbjct: 117 EALRALGVDLRHEGAEGHHPLTVRA-SGVKGGELTLNAGESSQYLTALLMLGPLTAEGLR 175

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-----VEG 252
I + + L+S PYVE+TL +M FGV ++ G + P Y VE
Sbjct: 176 IHVTE-LVSAPYVEITLAMMRSFGVDV-----VREGNTFTVPPGGYRATTYAVEP 224

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--TGP 310
DAS+ASYF A AA+TG VTV G GT +LQGD++F +VL MGA+VT T+T TV TG
Sbjct: 225 DASTASYFFAAAALTGREVTVPLGTGALQGLRFTDVLRRMGAEVTTTDTGTTVRSTGA 284

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L + VNM + D TLA VA FA P I DVA+ RVKE +R+ A
Sbjct: 285 -----LSGLTVNMRDISDTMPTLAAAVAPFASSPVRIEDVANTRVKECDRLACARN 335

Query: 371 LTKLGASVEEGPDYCIITP--PEKLNVTDAIDTYDDHRMAMAFSLAACAEVPVTIRDGPCT 428
L +G +V GPD+ I P P +T T+ DHR+ M+F++AA VT DPGC
Sbjct: 336 LRAMGTVHTGPDWTEIHPGTTPRAEIT---TFGDHRIVMSFAVAALRVPGVTYDDPGCV 392

Query: 429 RKTFFPDYFDVLSTF 442
RKTFF++ +V + F
Sbjct: 393 RKTFFPEFHEVFARF 406

>ref|XP_001834882.2| arom polypeptide [Coprinopsis cinerea okayama7#130]
gb|EAU86952.2| arom polypeptide [Coprinopsis cinerea okayama7#130]
Length = 1677

Score = 223 bits (569), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 174/456 (38%), Positives = 249/456 (54%), Gaps = 47/456 (10%)

Query: 12 IKEISGTVKL--PGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
+K G V++ PGSKS+SNR L+LAAL++GT + NLL+S+D GA+ T
Sbjct: 416 VKGSPGEVRMSTPGSKSISNRALVLAALAKGTCRLRNLLHSDDTQ---GAVFTW----- 466

Query: 70 DKAACKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLT-----AAVTAAGGNATY 121
+ + VV G G V +E L+LGNAG A R LT A + +
Sbjct: 467 EDGGETLVVEGGEGTLTVPTPGKE--LYLGNAGTAARFLTTCALAQAPASVQPPSTNT 524

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
V+ G RM++RPIG LV L+ G + C P+ + GGK++L+ S+SSQ
Sbjct: 525 VITGNARMKQRPIGPLVDALRANGCSIGYRESEGCLPLSIPP-NSFKGGKIQLAASVSSQ 583

Query: 182 YLSALLMAAPLA--LGDVEIEIID-KLISIPYVEMTLRLMERFGVK-AEHSDS----WDR 233

Y+S++L+ AP A V +E++ ++IS PY++MT+ +M+ FGV+ +D+ D
Sbjct: 584 YVSSILLCAPYAQDANGVTLELVGGEVISQPYIDMTIAMMKTFGVEVTRRTDASGKLDDI 643

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLE 292
+ I G Y +P +E DASSA+Y LA AAITG T+E G++SLQGD KFA EVL+

Sbjct: 644 YDIPRGT-YVNPVYNIESDASSATYPLAVAAITGKTCTIENIGSSSLQGD KFAVEVLQ 702

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADG----P 347
MG +V T TV GP P G+ LKAI +V+M M D +T +V+A A+G

Sbjct: 703 KMGCEVHQTADETTVQGP---PLGQ--LKAIEEVDMEVMTDAFLTASVLA AVANGGENKA 757

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGP----DYCIITPPEKLNVT AIDTYDD 403
I +A+ RVKE R+ A+ EL K G E Y + K NV+ + YDD

Sbjct: 758 MKITGIANQRVKECNIRAMMDELAKFGVHTTEQELGLTIYAVPISQLKKNVS-VHCYDD 816

Query: 404 HRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
HR+AMAFS+ + I + C KT+P ++D L

Sbjct: 817 HRVAMAFSVLSTVVEGAIIIEKRCVEKTPGWWDLL 852

>ref|YP_001096916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C5]
sp|A4FWX2.1|AROA_METM5 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABO34701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C5]
Length = 429

Score = 223 bits (569), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 145/444 (32%), Positives = 239/444 (53%), Gaps = 25/444 (5%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDEVHYMLGALRTLGLS 66
+V++ +I G + P SKS ++R ++ A+L+ G + + N LN D A G

Sbjct: 2 LVVKKTPKIKGILSAPPSKSYTHRAVICASLANGISNLKNPLNGADCLSSAHACEMFGAE 61

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E + + VV G K P + + +GN+G +R LT +++ N VL G

Sbjct: 62 IEL--SNETWVVRGSELKTP-----DNIVDIGNSGTTLRILTGT-ISSQISNGYTVLTGD 112

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+R+RP+ L+ L QLG + CF + P+ V G + V++ G +SSQ+++

Sbjct: 113 DSIRKRPMQPLLDALNQLG--LTCFSTKNNGTAPIVVKS-GKISNNVVEIRGDVSSQFIT 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDR--FYIKGGQKY 242
+++M P + D EI + L S PY+ +T+ +++FGVK E ++ ++ + IKG QKY

Sbjct: 170 SIMMTLPFSENDSEIVLTTPLKSEPYLNITIDVLDKFGVKIEKNEEKNSGKIKGNQKY 229

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTE 302
P + +EGD SSASY +A + + ++ S QGD + E+++ MGA V E

Sbjct: 230 -LPCDYTIEGDYSSASYLVAAGVLLNSDIVIKNVFKDSKQGDREIIEIVKKMGANVEINE 288

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
V +TGP + LK I++++ +PD+ T+AV+ FADG T + + R+KE +

Sbjct: 289 DHVKITGPYK-----LKGIEIDVTDIPDLVPTIAVLGCFADGKTVVYNGEHLVRLKECD 341

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ A TEL+K+GA +EE D IIT KLN + TY DHR+ MAF++A A+

Sbjct: 342 RLAACCTELSKMGAEIEKKDGLIITGVHKLNGAKLKYHDHRLVMAFTIAGMLADGETI 401

Query: 422 IRDPGCTRKTFPDYFDVLSTFVKN 445
I + +FPD+ D + + N

Sbjct: 402 IEGEDSVKISFPDFVDNMKSIGSN 425

>ref|YP_001549512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C6]
sp|A9AAA7.1|AROA_METM6 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;

Short=EPSP synthase; Short=EPSPS
gb|ABX02280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C6]
Length = 429

Score = 223 bits (569), Expect = 4e-56, Method: Compositional matrix adjust.
Identities = 140/442 (31%), Positives = 239/442 (54%), Gaps = 21/442 (4%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+V++ +I+G + P SKS ++R ++ A+L+ G + + N LN D A G
Sbjct: 2 LVVKKTPKINGILNAPPSKSYTHRAVICASLANGSLNKNPLNGADCLSSAHACEMFGAE 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E + ++ V+ G K P + + +GN+G +R LT +++ N +L G
Sbjct: 62 IEL--SDEQWVIRGSELKTP-----DNIVDIGNSGTTLRILTG-ISSQISNGYTILTGD 112

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQLG + P+ V G + V++ G +SSQ++++L
Sbjct: 113 DSIRKRPMPQLLDALKQLGIESFSTKNNGTAPIVVK-SKISNNVVEIRGDMSSQFITSL 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR--FYIKGGQKYKS 244
+M P + D +I + L S PY+ +T+ +++++FGVK E ++ + + IKG Q+Y S
Sbjct: 172 MMTLPFSENDISKIVLTTPKSEPYLNITIDVLDKFGVKIEKNEKNKLGKIKGNQRY-S 230

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P +EGD SSASY +A + + ++ S QGD + E+++ MGA V E +
Sbjct: 231 PCEYIIIEGDYSSASYLVAAGVLLNSDIVIKNVFKNSKQGDREIIEIVKMGADVEINEDN 290

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V +TGP +LK I++++ +PD+ T+AV+ FA+G T + + R+KE +R+
Sbjct: 291 VKITGP-----YNLKGIEIDVTDIPDLVPTIAVLGCFAGKTVVYNGEHVRIKCDRL 343

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIR 423
A EL+K+GA +EE D IIT KLN + TY DHR+ MAF+++ A+ I
Sbjct: 344 AACTLELSKMGAEIEEKDGLIITGVHKLNGAKLKYHDHRLVMAFTIAGMLADGETIIE 403

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
+ +FPD+ D + + N
Sbjct: 404 GEDSVKISFPDFVDMKMSIGSN 425

>ref|ZP_04998765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. Mgl]
gb|EDX23276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. Mgl]
Length = 428

Score = 223 bits (568), Expect = 5e-56, Method: Compositional matrix adjust.
Identities = 164/433 (37%), Positives = 223/433 (51%), Gaps = 30/433 (6%)

Query: 18 TVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T ++PGSKS++NR LLLAA + G T + L S+D AL LG+ + A
Sbjct: 2 TARVPGSKSITNRALLAAAATGVTRLRAPLVSDDTLAFRTALTGLGVRIETGDAWEVT 61

Query: 78 VVGCGGKFPVEDAKEEV-----QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
G G PV +++ +AG A R L AA G +V DG ++
Sbjct: 62 GTGRG---PVAATNATDADDATDAARVWCADAGTAARFLPPF--AATGKGRFVFDGTDQL 116

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RP+ L L LGADV G P + V GL GG + L S SSQYL+ LL++
Sbjct: 117 RARPLRLPLADALTALGADVSTGPGGALP-LTVTA-DGLTGGDIPLDSSFSSQYLTGLLLS 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFG-VKAHSDSWDRFYIKGGQKYKSPKNA 248
APL + + L+S PY++MTL LM FG + EH D + G + +
Sbjct: 175 APLMSAPLTVRA-RSLVSRPYIDMTLALMRHFGALTEEHGDGAITVHPGG----YTAADL 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E DAS+ASYF A AA+TG +VTV G GT S QGD+ F EVL GA+V T ++ TVT
Sbjct: 230 TIEPDASTASYFFAAAATVGRSVTVPGGLTGSSQGD LGFVEVLRRTGAEVEITASATVT 289

Query: 309 GPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G P E + DV+M + D MTLA +A ADGP + + R+KE++R+ A+
Sbjct: 290 GRPDE----RLTGGFDVDMGNISDTFMTLAAIAPLADGPVTVTGIGHARLKESDRIGAVA 345

Query: 369 TELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
L LG EEGP+ + P P + + DHR+AMAFS+ +T+ DP
Sbjct: 346 RNLRALGIHTEGPERITVHPGVPRPAQIAC---HRDHRIAMAFSVLGLRTGGITLDDPA 402

Query: 427 CTRKTFFPDYFDVL 439
C KTFP + D L
Sbjct: 403 CVAKTFFPGFHDEL 415

>ref|ZP_07015206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfonatronospira
thiodismutans ASO3-1]
gb|EFI35356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfonatronospira
thiodismutans ASO3-1]
Length = 445

Score = 223 bits (568), Expect = 5e-56, Method: Compositional matrix adjust.
Identities = 165/443 (37%), Positives = 236/443 (53%), Gaps = 40/443 (9%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+K P SKS+S+R LL A L+ GT+V++N+L SED+ L LG D + V
Sbjct: 6 TLKAPPKSVSHRALLAAGLAGGTSVLENVLVSIEDILRTRDCLAALGAKFSGDDST--PV 63

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G GG+ + + V+L +G +G R L A V+A G ++ + G RM ERPI L
Sbjct: 64 VQGLGGRIKAP-SLDPVKLDVGESGTCRLLAAIVSA--GQGSFEISGAGRMHERPIKSL 120

Query: 138 VVGLKQLGADVDCFLGTD-CPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ G +LG D CPPVR+ GLPGG V + SSQYLS +L+A+ +A
Sbjct: 121 GQSLEGQGVRFK-YLGLDGCPPVRIES-SGLPGGVTVGLDESSQYLSGILLASTMATTS 178

Query: 197 VEIEII-DKLISIPYVEMTLRLMERFGVKA-----HSDSWD-----RFYI 236
+ I I K++S PYV +TL+ M+RFG A H+D RF +
Sbjct: 179 LVINIGGKKVSWPYVHLTLQTMQRFGNPARLQTLQEGHWRHADPDQVQVPEPKIRFVV 238

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSQGDVKFAEVLEMMGA 296
G +P VEGD S+ASY LA A+ V V G S QGD + E+LE+MGA
Sbjct: 239 HPG--VLNPVRYRVEGDYSNASYLLAAGAVGEFPVEVSGLDLESRQGDRIEILELMGA 296

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
K++ T+ V V+ P R L +D++M PD+ T+AVVA A G T I +VA
Sbjct: 297 KISETKNGVMVS-PAR-----LHGVLDLDMGTCPDLVPTVAVVASMATGTTRISNVAHL 348

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATID--TYDDHRMAMAFSLAA 414
R+KE++R+ ++ E+++ G D I P E L + + TY DHRMAM+ SL
Sbjct: 349 RIKESDRLAGVQQEVSRAAGRCGLKEDGLEIEPAELLRGSQVQFKTYGDHRMAMSLSLYE 408

Query: 415 CAEVPVTIRDPGCTRKTFPDYFD 437
A + + +P C K+FP +++
Sbjct: 409 LAGIQTALDNPACVNKSFPGFWE 431

>ref|YP_003159302.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfomicrobium
baculatum DSM 4028]
gb|ACU90886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfomicrobium
baculatum DSM 4028]
Length = 448

Score = 223 bits (568), Expect = 5e-56, Method: Compositional matrix adjust.
Identities = 165/457 (36%), Positives = 232/457 (50%), Gaps = 48/457 (10%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P+ +I+ P SKSLS+R L+ AAL+EG ++++ +L+S+D+ G LR LG +
Sbjct: 1 MKPVIDITA---PSSKSLSHRALICAALAEESLLEGVLDSQDLTRTAGCLRLGALIT 56

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V G GGG A+ V + +G +G R + VTA G Y + G R
Sbjct: 57 PQGG--KLFVRGIGGKTGAS-AEGPVMNVGESGTCRLMAGVVTAIPG--IYRIHGEGR 111

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ L L Q G V + PP+ V GL GG+V ++ SSQYLS LL+

Sbjct: 112 IHDRPVAHLTDALTQQGVRVTFEEKSGYPPM-VMSSPGLIGGEVTINLEQSSQYLSGLLL 170

Query: 189 AAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGV----KAEHSDSWD----- 232
AAPLA G I +I + + S PYV +TL M RFGV + D W

Sbjct: 171 AAPLATGTTTIRLIGRSVASWPYVALTLDTMARFGVPVILERRILDDWHSCSTHAEAAAGLP 230

Query: 233 ----RFYIKGGQKYKSPKNA---YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV 285
R + + +P A VEGD S+ASYFLA A+ V + G S QGD

Sbjct: 231 PTDIRLVV-----HPAPYRAGAMRVEGDWSNASYFLAAGAVGTAPVRISGLSRQSAQGDR 285

Query: 286 KFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD 345
E+L MGA V W + VTV L+ V+MN PD+ T+A +A FA

Sbjct: 286 FMLEILSRMGASVEWQDDVVTVF-----PSALRGTVQDMNACPDIVPTVAAMAAAFAT 337

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAD--TYDD 403
G T I A +KE +R++ TEL+K G ++E PD II L ++D TY D

Sbjct: 338 GETIISGAHLALKECDRLGPVTELSKAGVNIARPDMGIIRNGGGLLPRSVDLCTYGD 397

Query: 404 HRMAAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
HRMAM+FSL + V + +P C K+FP ++DV S

Sbjct: 398 HRMAMSFSLLELGGISVNLNPNPSCVAKSFPGFWDVWS 434

>ref|ZP_07330073.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermococcus
okinawensis IH1]
gb|EFL48897.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermococcus
okinawensis IH1]
Length = 435

Score = 223 bits (567), Expect = 6e-56, Method: Compositional matrix adjust.
Identities = 143/445 (32%), Positives = 233/445 (52%), Gaps = 21/445 (4%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I+++ EI G + P SKS ++R ++ A+LS+G + + N LNS D + R LG

Sbjct: 2 IIVKKTNEIKGNIYAPPSKSYTHRAVICASLSDGISEIKNPLNSADCLSSVHGARMLGAH 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ D K +V P E + +GN+G +R LT +++ +L G

Sbjct: 62 IDTDD--KNKWIVEGNNSP---KTPENIIDIGNSGTTLRLITG-ISSQIKKGYAILTGD 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQLG + P+ V G + V++ G +SSQ++++L

Sbjct: 116 ESIRKRPMPQLLDALKQLGIEAFSSSKMDGTAPIIVKS-GEIKNNTVRIRGDMSSQFITSL 174

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-----EHSDSWDRFYIKGGQK 241
+M P A D +I + L S PY+++TL ++ +FG+ E + F+I+G QK

Sbjct: 175 MMTLPFAKEDSKIILTTPKSAFYLDITLDVLSKFGITVKPLDNEKDKAEGFFIEGSQK 234

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
YKS N VEGD SSASY +A + +T+ S QGD + +++ MGA +

Sbjct: 235 YKSC-NYTVEGDYSSASYLIAAGVLLNSELTTNNLFKDSKQGDKEIINIVKNMGAHIKVK 293

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ V + GP +LK + V++ +PD+ T+AV+ FA+G T I + R+KE

Sbjct: 294 DDKVIINGP-----HNLKGVKVDVNIPDLVPTIAVLGCFAGGKTTIYNGEHVRLKEC 346

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPV 420
+R+ A EL+K+GA + E PD +I KL ++TY DHR+ MAF++A AE

Sbjct: 347 DRLSACAKELSKMGAKITEKPDGLVIEGVGKLKGALETYHDHRLVMAFTIAGMMAEGET 406

Query: 421 TIRDPGCTRKTFPDYFDVLSFVKV 445
IR + +FP++ DV+ + N

Sbjct: 407 IIRGEDAVKISFPNFVDVMKSIGAN 431

>ref|YP_001323039.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
vannielii SB]
sp|A6UPK5.1|AROAMETVS RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS

gb|ABR54427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
vannielii SB]
Length = 429

Score = 222 bits (565), Expect = 1e-55, Method: Compositional matrix adjust.
Identities = 138/439 (31%), Positives = 236/439 (53%), Gaps = 21/439 (4%)

Query: 7 IVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++++ E+ G + P SKS ++R ++ A+L+ G +++ N LN D A R LG
Sbjct: 2 LIVKRTSEVKGIINAPPSKSYTHRAVISASLANGLSILKNPLNGADCLSSAHACRMLG-- 59

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E ++ ++G K P + + +GN+G +R +T +++ + V+ G
Sbjct: 60 AELITNEVEKWTIIGSKLKVP-----DNIIDIGNSGTTLRITG-ISSQIPDGYAVITGD 112

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQLG + P+ V G + VK+ G +SSQ++++L
Sbjct: 113 DSIRKRPMPQLLDALKQLGIESFSTRNNGIAPPIVKA-GKITSNSVKIRGDMSSQFITSL 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAH--SDSWDRFYIKGGQKYKS 244
+M P + D EI + L S PY+ +T+ ++++FGVK E ++ + IKG Q Y+
Sbjct: 172 MMTLPFSETDSEIILTTPKSEPYLNITIDVLDKFGVKIEKIVEENKTGYKIKGKQSYR- 230

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P +EGD SSASY +A + + V+ S QGD + E+++ MGA V E +
Sbjct: 231 PCEYTIIEGDISSASYLIATGVLLNSDIEVKNVFKNKQGDREIIEIVKMGADVEINENN 290

Query: 305 VVTGTPPREPFGRKHLKAIDVMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V + GP +LK I++++ +PD+ T+AV+ FA+G T + + R+KE +R+
Sbjct: 291 VKIKGP-----YNLKGIEIDVTNIPDLVPTIAVLGCFAGKTVVYNGEHVRLKECDRL 343

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIR 423
A EL+K+GA +EE PD IIT KL + + T+DDHR+ MAF++A A+ I
Sbjct: 344 NACAVELSKMGADIEEKPDGLIITGTHKLTGSKLKTDDHRLVMAFTIAGMLADGETVIE 403

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
+ +FPD+ D + +
Sbjct: 404 GEESVKISFPDFVDKMKSI 422

>gb|EFN55352.1| hypothetical protein CHLNCDRAFT_31300 [Chlorella variabilis]
Length = 176

Score = 221 bits (564), Expect = 1e-55, Method: Compositional matrix adjust.
Identities = 123/181 (67%), Positives = 139/181 (76%), Gaps = 6/181 (3%)

Query: 266 ITGGTVTVEGCGTTSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDV 325
+TGGT+TVEGCG+ SLQGDV+FAEV+ +MGA V W S+T+TGPPR LKAID
Sbjct: 1 MTGGTITVEGCGSESLQGDVRFSAEVMGLMGATVEWQPYSITITGPPR-----GQLKAIDH 55

Query: 326 NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYC 385
N N +PD AMT AV AL ADG TAIRDV +WRVKETERM AI ELTKLGASVEEG DYC
Sbjct: 56 NCNDIPDAAMTAAVAALLADGATAIRDVYNWRVKETERMKAIVAELTKLGASVEEGHDYC 115

Query: 386 IITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
+ITPP+++ AI+TYDDHRMAMAFSL A VPVTI DPGCTRKTFF YF V T K
Sbjct: 116 VITPPKEVKPGVAIETTYDDHRMAMAFSLVAACGVPVTILDGCTRKTFFPTYFRVFETVAK 175

Query: 445 N 445
+
Sbjct: 176 H 176

>gb|ADW03091.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
flavogriseus ATCC 33331]
Length = 414

Score = 221 bits (563), Expect = 2e-55, Method: Compositional matrix adjust.
Identities = 157/433 (36%), Positives = 221/433 (51%), Gaps = 33/433 (7%)

Query: 19 VKLPGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78

Sbjct: 4 + +PGSKS++ R L LAA ++GTT + L+S+D L LG +V + R +
IDIPGSKSVTARALFLAAAADGTTTLRLPLHSDDTTEGFTGLTRLGYAVV--REPDRWHI 61

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P A + ++ + R L + AA + TY D +MR RP+ L

Sbjct: 62 EG----RPSGPAAADAHVHCRDGATTARFL-PTLAAAASGYRFDASAQMRRLPLAPLT 116

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LG D+ P+ + G+ GG + L SSQYL+ALLM PL +

Sbjct: 117 EALRTLGVDLRHDGAEGHHPLTIQA-SGVKGGGLTLDAGESSQYLTAALLMLGPLTAEGLR 175

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-----VEG 252
IE+ + L+S PYVE+TL +M FGV+ ++ G + P Y +E

Sbjct: 176 IEVTE-LVSAPYVEITLAMMRGFGVEV-----VREGNTFTVPPGGYRATTYAIEP 224

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TG VTV G GT +LQGD++F EVL M A V T S TV R

Sbjct: 225 DASTASYFFAAAALTGREVTVPGLGTGALQGLRFTFVLRMRDADVRTTSDSTTVRSDGR 284

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
L + VNM + D TLA +A +A P I DVA+ RVKE +R+ A L

Sbjct: 285 -----LAGLTVNMRLDISDTMPTLAAIAPYASSPVRIEDVANTRVKECDRLCAQNLRL 337

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTF 432
+G +V GPD+ I P T I T+ DHR+ M+F++A ++ DPGC RKTF

Sbjct: 338 SMGITVRTGPDWIEIHPGTP-RPTEIATHGDHRIVMSFAVAGLRTPGMSYDDPGCVRKTF 396

Query: 433 PDYFDVLSTFVKN 445
P + + + FV+

Sbjct: 397 PRFHEEFAAFVER 409

>sp|P39915.2|AROA2_BURPS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 463

Score = 221 bits (563), Expect = 2e-55, Method: Compositional matrix adjust.
Identities = 168/421 (39%), Positives = 220/421 (52%), Gaps = 42/421 (9%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQP + ++G ++LPG KS+SNR LLL AL+EG T V LL+S+D ML ALR LG+ +E

Sbjct: 10 LQPWRHVTGHLRLPGDKSISNRSLLLALAEVTEVTGLLDSDDARAMLNALRDLGVVIE 69

Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEV-QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R V G G + K LFLGNAG AMR L+AA+ + T L G P

Sbjct: 70 GPHQG-RCTVHGVG---LHGLKAPPGLFLGNAGTAMRPLSAALALQPFDTT--LTGDP 122

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM ERPI LV L+++GA ++ PP+ + G GS+SSQ+L+ALL

Sbjct: 123 RMSEPINRLVDALREMGAVIEYLAQEGYPPLTIRG-----GGSVSSQFLTALL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
M AP+A ++ + L+S PY+++TL +M FGV D +R + +Y SP

Sbjct: 172 MTAPMASAQIKSGL---LLSKPYIDITLNVMP-FGVPT--DHETERIFAVSAIRYPSPAV 225

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+EGDA+SASYFLA A I G V V G G S+QGD F L MGA+ + V

Sbjct: 226 LRLEGDATSASYFLAAAGIKG--VPVTGIGRHSMQGDSWFPRALRRMGARSCGSSMIVCP 283

Query: 308 TGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G R A+ + N +PD AMTLA A G R + +WRVKET+R+ A+

Sbjct: 284 RGELRA-----AVRSDSNSIPDAAMTLATXXALARGGRPRPTIFAWRVKETDRLYAM 335

Query: 368 RTELTKLGASVEEGPDY--CIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDP 425
TEL GA V G C P + D RMAM FSL A +R P

Sbjct: 336 STELGAGARVVPAGLRGC---PLGRSYYVARCRDRSRMAMCFSLPAHGG--RAVRHP 390

Query: 426 G 426
G

Sbjct: 391 G 391

>emb|CBK94981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium rectale
M104/1]
Length = 427

Score = 221 bits (563), Expect = 2e-55, Method: Compositional matrix adjust.
Identities = 147/419 (35%), Positives = 225/419 (53%), Gaps = 14/419 (3%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR LL+AAL+ G +V+ L S+D + + AL LG V D+ + + G
Sbjct: 18 VPGSKSITNRALLIAALASGRSVLKGCLFSDSRHFIDALIRLGFPVLVDEDKREITITG 77

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
GG+ P K EV++ +G+AG A R LTA + + G Y + +M++RP+ DL+V
Sbjct: 78 FGGRIP---KNEVEIDVGSAGTAARFLTALLGLSKGR--YHIVSSEQMKKRPMKDLLVS 131

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L++LGA ++ P + G V ++ SSQ+LSALL++A + + I
Sbjct: 132 LEKLGAEHYDENYHFPFTTGNTGEY-ADTV DINVDKSSQFLSALLISAIVMEKNFTIN 190

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
+ + YVEMT +M++FG+ + F I Y+S + +E D S+A YF
Sbjct: 191 VTGTH-GMAYVEMTRLMMKQFGLDVMQDKNNFSFIIPKKAAYES-LDYDIEPDVSAACYF 248

Query: 261 LAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHL 320
A + + V G SLQGDV F +VL MG ++ E V PP+ H+
Sbjct: 249 YAMSPLLHVRKSKVMGVHQNLSLQGDVAFLDVLAADMGTIS-DEADGIVCMPPK---NTHI 303

Query: 321 KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
+++ D A+TLA +A FA+ P I ++ R++E +R+ AI LT+LG VEE
Sbjct: 304 HGGSWDLSTFSDQALTLAAIAPFANFVPGIEGISHIRLQECRINAIEENLTGVRVEE 363

Query: 381 GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
+ I P E + I TYDDHR+AM+F+L V I DP C RKTf +++VL
Sbjct: 364 IENGLRIYPAECIKPKIKTYDDHRVAMSFTLPGLKAEGVEIIDPYCCRKTFENFYEV 422

>ref|YP_003134364.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Saccharomonospora
viridis DSM 43017]
gb|ACU97537.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Saccharomonospora
viridis DSM 43017]
Length = 444

Score = 221 bits (562), Expect = 2e-55, Method: Compositional matrix adjust.
Identities = 156/423 (36%), Positives = 224/423 (52%), Gaps = 23/423 (5%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKS++NR +LAALS G T+V N L+S D MLGAL LG A
Sbjct: 32 ERLDATVRVPGSKSITNRAFLAALSAGETLVRNPLDSRDARMLGALDALG-----A 84

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A AV G + P+ D EV++ LGNAG R T + AA G+ T DG P +R R
Sbjct: 85 ASHAVSDGVRVQ-PMTDGDGEVEVALGNAGTVAR-FTPPL-AALGSRTVHFDGDPAIRRR 141

Query: 133 PIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ L+ L LGAD+D G P V G GGL GG V+L S SSQ+LSALL++ P
Sbjct: 142 PVAPLLQALTDLGADIDDG-GRGTVPTVRGRGLAGGTVELDSSASSQFLSALLLSGPA 200

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V + ++ K S P++ MT+ ++ RFG E S F++ S VE
Sbjct: 201 FERGVTVRLLGKTPSEPHIAMTMDMLRRFGAAPERDGS--EFHVPPATLALS--EYTVPEP 256

Query: 253 DASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D SSA+ F+ + GG V VEG + + Q + ++ +G + +TVT
Sbjct: 257 DLSSAAPFVVAPLVAGGRVHVEGWPSSETTQPGDRLRLSLVRELGGAEVLEGDGLTVT---- 312

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
G + A ++++++ ++ LA + FADGP+ IR VA R ET+R+ A+ TEL+
Sbjct: 313 ---GTGTVAATLDLHEVGELTPVLAALLCFADGPSEIRGVAHLRGHETDRLAALATELS 369

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDGPCTRKTF 432
LG V E D I P L+ TYDDHR+ MA ++ A +T+ +P KT+
Sbjct: 370 ALGGDVTETDDGLRIH-PAPLHGGTFHTYDDHRLVMAGAVLALRVPGITVENPATVGKTY 428

Query: 433 PDY 435
P +
Sbjct: 429 PGF 431

>ref|YP_001039475.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum ATCC 27405]
ref|ZP_05430875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 2360]
ref|ZP_06247596.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum JW20]
sp|A3DK03.1|ARO_A_CLOTH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABN54282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum ATCC 27405]
gb|EEU00240.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 2360]
gb|EFB38236.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum JW20]
gb|ADU73716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 1313]
Length = 423

Score = 220 bits (561), Expect = 3e-55, Method: Compositional matrix adjust.
Identities = 153/426 (35%), Positives = 234/426 (54%), Gaps = 24/426 (5%)

Query: 16 SGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG V++PGSKS + R L A+L+EG + + + L S+D + R LG +E K +
Sbjct: 11 SGNVRIPGSKSHTIRALFFASLAEGKSEIQSPLISDDALSAVEVCRALGAKIE--KEDDK 68

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
VV G GG + E+V + +GN+G +R +TAA G+ V G ++R+RP+G
Sbjct: 69 YVVEGFGGN---PEVPEDV-INVGNSTTLR--FGIMTAALGDGCSVFTGDRQIRQRPLG 122

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
L+ + LGA+ PV V G L GG+ ++ S++SQYLS++L+ +PL
Sbjct: 123 PLLCAINNLAGAEAFSTRNNGRAPVVVKG--KLKGGRTFID-SVTSQYLSSILINSPLIPL 179

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
D E+ I+ +L +PYV+MTL +++ G+K E+ D + FYIKGGQ+Y+ P N + GD S
Sbjct: 180 DTEV-IVTRLNEVPYVDMTLWLWDKLGKIYENHD-YKTFYIKGGQRYR-PLNVTIPGDFS 236

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFP 315
SA++F AAI+G ++ T QGD +LE MGAKV SV + G E
Sbjct: 237 SATFFAVQAASIGEEFVLDNLDMTDPQGDKMVFSILEDMGAKVKVEGKSVRIKGC--ELV 294

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
GR +++MN +PD +AV FA G T + +V R+KET+R+ + +L K+G
Sbjct: 295 GR-----EIDMNAIPDALPAMAVAGCFAGGETKLLNVQPARIKETDRIHVMCEQLKKMG 348

Query: 376 ASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDGPCTRKTFPD 434
A + E D +I +L ++ Y DHR+ M+ ++A AE I TFPD
Sbjct: 349 ADITELEDGLVIR-ESRLKGCKLEGYGDHRVMSLAIAGLNAEGETVIDTAEAVNVTFPD 407

Query: 435 YFDVLS 440
+ + LS
Sbjct: 408 FVNFLS 413

>ref|YP_003128029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
fervens AG86]
gb|ACV24529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
fervens AG86]
Length = 427

Score = 220 bits (560), Expect = 4e-55, Method: Compositional matrix adjust.

Identities = 145/440 (32%), Positives = 235/440 (53%), Gaps = 19/440 (4%)

```
Query: 7   IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++++   + GTVK P SKS ++R ++ A L+EG +V+ N L   D   +   R LG
Sbjct: 2   LIVKKTDRLEGTVKAPPSKSYTHRAVIGAFLAEGESVIKNPLWGADCLSSVHGCRMLGAD 61

Query: 67  VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E DK   + +V G   K P   +   + +GN+G +R LT+ + +   +L G
Sbjct: 62  IELDKDKDKWIVKGGELKTP-----DNVIDIGNSGTTLRLITS-IASQIPKGYAILTGD 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R RP+ L+ LKQL +   P+ V   G + G KV++ G ISSQ++++L
Sbjct: 115 DSIRRRPMQPLLDALKQLNIEAFSSKMDGTAPIIVKS-GEINGNKVEIRGDISSQFITSL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M P   D EI +   L S PY+++TL ++ +FG+K + ++   F + G QKYK+
Sbjct: 174 MMLLPFNKEDTEIILTPLKSKPYIDVTLTDLKSKFGIKIDETEGK--FLVYGNQKYKAI- 230

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD SSASY +A   +   +T+E   S QGD   +++ MGA +   + V
Sbjct: 231 DYIVEGDYSSASYLIAAGVLINSNITIENTLFADSKQGDRAIIDIVKEMGADIKVKKDKVI 290

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V G   +L IDV++ +PD+ T+AV+ FA+G T I +   R+KE +R+ A
Sbjct: 291 VEG-----EYNLNGIDVDVKDIPDLVPTIAVLGCFAGKTEIYNGEHVRLKECDRLRA 343

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
EL K+GA +EE PD II +KL   ++TY+DHR+ MAF++A AE   I
Sbjct: 344 CAVELKKMGADIEEKPDGLIIRGVKKLRGAKLNTYNDHRLVMAFTVAGLKAEGETIIEGE 403

Query: 426 GCTRKTFFPDYFDVLSTFVKN 445
+ +FP++ +V+ +   N
Sbjct: 404 EAVKISFPNFVEVMRSIGAN 423
```

>pir||F64362 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) -
Methanococcus jannaschii
Length = 436

Score = 220 bits (560), Expect = 4e-55, Method: Compositional matrix adjust.
Identities = 145/440 (32%), Positives = 233/440 (52%), Gaps = 19/440 (4%)

```
Query: 7   IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++++   + G VK P SKS ++R ++ A+L++G + + N L   D   +   R LG +
Sbjct: 11  LIVKKTDRLEGIVKAPPSKSYTHRAVIGASLADGVSRINPLWGADCLSSVHGCRMLGAN 70

Query: 67  VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E DK   +V G   K P   +   + +GN+G +R LT+ + +   +L G
Sbjct: 71  IELDKKEDEWIVKGGELKTP-----DNIIDIGNSGTTLRLITS-IASQIPKGYAILTGD 123

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQL +   P+ V   G + G VK+ G ISSQ++++L
Sbjct: 124 DSIRKRFMQPLLDALKQLNIEAFSSKLDGTAPIIVKS-GKIYGNVVKIRGDISSQFITSL 182

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M P   D EI +   L S PY+++TL ++ +FG+K + +D+   F + G QKYK P
Sbjct: 183 MMLLPFNKEDTEIILTSPLKSKPYIDITLDILNKFGIKIDKTDNG--FLVYGNQKYK-PI 239

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD SSASY +A   +   +T+E   S QGD   +++ MGA +   + V
Sbjct: 240 DYIVEGDYSSASYLIAAGVLINSNITIENTLFANSKQGDKAIINIVKEMGADIKVKKDKVI 299

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G   LK IDV++ +PD+ T+AV+ FA+G T I +   R+KE +R+ A
Sbjct: 300 IEG-----EYSLKGIDVDVKDIPDLVPTIAVLGCFAGKTEIYNGEHVRLKECDRLRA 352

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
EL K+GA +EE PD II +KL   ++TY DHR+ MAF++A AE   I
Sbjct: 353 CAVELKKMGADIEEKPDGLIIRGVKKLKGAKLNTYHDHRLVMAFTIAGLKAEGETIIEGE 412

Query: 426 GCTRKTFFPDYFDVLSTFVKN 445
```

+ +FP++ DV+ + N
Sbjct: 413 EAVKISFPNFVDVMKSLGAN 432

>ref|YP_002951911.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
magneticus RS-1]
dbj|BAH74025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
magneticus RS-1]
Length = 445

Score = 220 bits (560), Expect = 4e-55, Method: Compositional matrix adjust.
Identities = 160/447 (35%), Positives = 240/447 (53%), Gaps = 46/447 (10%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ P SKS+S+R ++ A+L+ GT+ + LL+S+D+ + +G ++ ++ VV
Sbjct: 4 ITAPPSKSVSHRAVIAASLAAGTSRLTGLLDSQDISRTRDCMIAMGAAMHP-QSDGSVVV 62

Query: 79 VCGGKFPV--EDAKEE-VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
G G+ P+ ED +E V L +G +G R L A AA G +++ G RM +RPIG
Sbjct: 63 SGTAGR-PLGGDEEEHSVALDVGESGTTCTLLVA--VAAAGRGHFLVRGHRMHDRIPIG 119

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+LV L LG + + CPP+ V GL GG +S SSQYLS LL+AAP+A G
Sbjct: 120 ELVNALLPLGPCELYLEKSGCPPLAVV-TQGLAGGTTISLEDSSQYLSGLLLAAPMAAG 178

Query: 196 DVEIEII-DKLISIPYVEMTLRLMERFGV----KAEHSDSW-----DRFY 235
+ IEI K +S PYV +TL + FGV + D+W RF
Sbjct: 179 PLTIEITGKKTVSWPYVAITLSALADFGVPFTVQTRQGDWVEADWRAITDVVPGQIRFA 238

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLMMG 295
++ +Y+ P+ VE D SSASYFLA A+ VTV G SLQGD ++L MG
Sbjct: 239 MQPA-RYR-PREYAVEADWSSASYFLAAGAVGPAPVTVAGLRQDSLQGDRAIRDILARMG 296

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
A++ T +TV P E G+ +++M + PD+ T+A A FA G T I++VA
Sbjct: 297 ARIEETAEGLTVF--PSELHGQ-----ELDMGRCPDLVPTVAAAACFASGETI IKNVAH 348

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPP----EKLNVTAIDTYDDHRMAMAF 410
R+KE++R+ A+ T+ GA V PD I P +++ +A +DDHR+AM+
Sbjct: 349 LRLKESDRIEAVAENCTQAGAVVTTLPDGLRIKPKALRTDQRVEFSA---FDDHRLAMSA 405

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDYFD 437
++ A + V I +PGC K+FP ++D
Sbjct: 406 AIFELAGIDVVIDNPGCVAKSFPTFWD 432

>ref|NP_247478.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
jannaschii DSM 2661]
sp|Q57925.2|ARO_A_METJA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAB98493.1| 3-phosphoshikimate-1-carboxyvinyltransferase (aroA)
[Methanocaldococcus jannaschii DSM 2661]
Length = 429

Score = 220 bits (560), Expect = 4e-55, Method: Compositional matrix adjust.
Identities = 145/440 (32%), Positives = 233/440 (52%), Gaps = 19/440 (4%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
++++ + G VK P SKS ++R ++ A+L++G + + N L D + R LG +
Sbjct: 4 LIVKKTDRLEGIVKAPPSKSYTHRAVIGASLADGVSRIINPLWGADCLSSVHGCRMLGAN 63

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E DK +V G K P + + +GN+G +R LT+ + + +L G
Sbjct: 64 IELDKKEDWIVKGGELKTP-----DNIIDIGNSGTTLRILTS-IASQIPKGYAILTGD 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQL + P+ V G + G VK+ G ISSQ++++L
Sbjct: 117 DSIRKRPMPQLLDALKQLNIEAFSSKLDGTAPIIVKS-GKIYGNVVKIRGDISSQFITSL 175

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M P D EI + L S PY+++TL ++ +FG+K + +D+ F + G QKYK P
Sbjct: 176 MMLLPFNKEDTEIILTSPLKSKPYIDITLIDLNKFGIKIDKTDNG--FLVYGNQKYK-PI 232

Query: 247 NAYVEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVT 306
+ VEGD SSASY +A + +T+E S QGD +++ MGA + + V
Sbjct: 233 DYIVEGDYSSASYLIAAGVLINSNITIENTLFANSKQGDKAIINIVKEMGADIKVKKDKVI 292

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G LK IDV++ +PD+ T+AV+ FA+G T I + R+KE +R+ A
Sbjct: 293 IEG-----EYSLKGIDVDVKDIPDLVPTIAVLGCFAGKTEIYNGEHVRLKECDRLRA 345

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
EL K+GA +EE PD II +KL ++TY DHR+ MAF++A AE I
Sbjct: 346 CAVELKKMGADIEEKPDGLIIRGVKKLKGAKLNTYHDHRLVMAFTIAGLKAEGETIIEGE 405

Query: 426 GCTRKTFFPDYFDVLSTFVKN 445
+ +FP++ DV+ + N
Sbjct: 406 EAVKISFPNFDVDMKSLGAN 425

>ref|YP_001329672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C7]
sp|A6VGE5.1|AROA_METM7 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABR65521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis C7]
Length = 429

Score = 219 bits (559), Expect = 5e-55, Method: Compositional matrix adjust.
Identities = 143/444 (32%), Positives = 240/444 (54%), Gaps = 25/444 (5%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLS 66
+V++ +I G + P SKS ++R ++ A+L+ G + + N LN D A G
Sbjct: 2 LVVKKTPKIKGILSAPPSKSYTHRAVICASLANGVSNLKNPLNGADCLSSAHACEMFG-- 59

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E D ++ VV G K P + + +GN+G +R LT +++ + VL G
Sbjct: 60 AEIDLNDKWWVRGSEFKTP-----DNIVDIGNSGTTLRILTG-ISSQISDGYTVLTGD 112

Query: 127 PRMRERPIGDLVVLGLQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+R+RP+ L+ LKQLG ++CF + P+ V G + V++ G +SSQ+++
Sbjct: 113 DSIRKRPMQPLLDALKQLG--LNCFTKNNGTAPIVVK-SKISNNVVEIRGDMSSQFIT 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR--FYIKGGQKY 242
+L+M P + D EI + + S PY+ +T+ ++++FGVK + + ++ + IKG QKY
Sbjct: 170 SLMMTLPFSENDSEIILTTPIKSEPYLNITIDVLDKFGVKIDKIEEKNKVGYKIKGNQKY 229

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTE 302
P + +EGD SSASY +A + + ++ S QGD + E+++ MGA V E
Sbjct: 230 -LPCDYTIEGDYSSASYLVAAGVLLNSDIVIKNVFKDSKQGDREIIEIVKKMGANVEINE 288

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+V + GP + LK I++++ +PD+ T+AV+ FA+G T + + R+KE +
Sbjct: 289 DNVQIMGPYK-----LKGIEIDVTDIPDLVPTIAVLGCFAGKTVVYNGEHVRLKECD 341

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ A TEL+K+GA +EE D IIT KLN + TY DHR+ MAF++A A+
Sbjct: 342 RLAACTELKSKMGAIEEKKDGLIITGVHKLNGAKLKYHDHRLVMAFTIAGMMADGETV 401

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVKN 445
I + +FPD+ D + + N
Sbjct: 402 IEGEDSVKISFPDFVDKMKSIGSN 425

>emb|CBL11268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseburia
intestinalis XB6B4]
Length = 442

Score = 219 bits (559), Expect = 5e-55, Method: Compositional matrix adjust.
Identities = 152/450 (33%), Positives = 239/450 (53%), Gaps = 44/450 (9%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV +PGSKS++NR LL+AALS+G ++ +L S+D + L +L +LG V+ +++
Sbjct: 12 RPDVDTVDVPGSKSMTNRALLMAALSDGEVKLEGVLFSDDSRHFSLVSLGFMVDINES 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+GCGG P K++ + +G+AG A R LTA + + G Y ++ +M++R
Sbjct: 72 EKAVTVLGCGGNIP----KKQAVINVGSAGTAARFLTAMLGFSDGE--YTIEASEQMKKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-----KVKLSGSISSQ 181
P+ +L L +GA++ PV++ G G ++ L S S+Q
Sbjct: 126 PMQELFSLTLGVGANITYLETEGHLPVKICGRRNPKAGADQSKADGNPLQLSLDISKSTQ 185

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LSALL+ +P+ ++I I + Y+ +T +++ GV+ ++ GG+
Sbjct: 186 FLSALLLISPMIPQGLDIHITSEKTDGSIYIRITRMLADAGVEVKY-----GKKN 235

Query: 242 YK-SPKNAY-----VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
Y+ PK Y +E D S+A YF A AAITGG V+ + QGD+KF +VL M
Sbjct: 236 YRIDPKAVYQKKHYQIEPDVSAACYFYAAAAITGGRTLKVHVHKDNSQGDMMKFLDLVAQM 295

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVA 354
G VT + VTGP + LK I+++MN D A+TLA +A F I +
Sbjct: 296 GCTVTEKADGIEVTGPAEDT-----LKGIEIDMNFSDQALTLAAMAPFCKSDVHITHIG 350

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSL 412
R +E +R+ A+ ELTK G + E PD I P P + + TY+DHR+AM+F+L
Sbjct: 351 HIRGQECDRLHAMSEELTKRGITCTEPEDAITIKPGIP---SAGIVSTYEDHRVAMSFAL 407

Query: 413 AACAEVPTVIRDPGCTRKTFPDYFDVLSTF 442
+ I +P C RKTF +YFD+L
Sbjct: 408 LGLKVDGIVIDNPSCCRKTFENYFDLLDQL 437

>ref|ZP_03524264.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli GR56]
Length = 420

Score = 219 bits (558), Expect = 6e-55, Method: Compositional matrix adjust.
Identities = 161/448 (35%), Positives = 237/448 (52%), Gaps = 49/448 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ ++ P +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIPPAGPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMADALRAM 64

Query: 64 GLSV-EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+++ E D+ VV G G P + LFLGNAG A R LTAA AA + T +
Sbjct: 65 GVAIDEPDETT--FVVTGSGRLLP-----PKAPLFLGNAGTATRFLTAA--AALVDGTVI 115

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+DG MR+RPIG LV ++ LG DV G CPPV V G G ++ + G +SSQY
Sbjct: 116 VDGDEHMRKRPIGPLVEAMRTLIGIDVSAETG--CPPVTVRGTRFEADRILIDGGLSSQY 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGG 239
+SALLM A V+IE++ + I ++ Y+++T M+ FG K E + +W R G
Sbjct: 174 VSALLMMAAGGDRPVDIELVGEDIGALGYIDLTTAAMKAFGAKVEKTSPTW-RVEPTG- 231

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y++ + +E DAS+A+Y A ++ G + + Q D K E++
Sbjct: 232 --YRA-ADFVIEPDASAATYLWAAEVLSDGKIDLGVNDRAFTQPDAKAYEIIAKF----- 283

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
HL A +++ ++M D T+AV+A F + P +A+ RVK
Sbjct: 284 -----PHLPA-EIDGSQMQDAVPTIAVLAAFNETPVRFVGIANLRVK 324

Query: 360 ETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAA 414
E +R+ A+ T L + G +VEEG D + + P T AIDT+ DHR+AM+F+LA
Sbjct: 325 ECDRIRALSTGLNNIRQGLAVEEGDDLIVHSDPALAGQTLPAIDTFADHRIAMSFALAG 384

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+TI DP C KTFP Y+ L+
Sbjct: 385 LKIDGITILDPDCVGKTFPAYWRTLAL 412

>ref|ZP_04743620.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseburia
intestinalis L1-82]
gb|EEV01203.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseburia
intestinalis L1-82]
Length = 442

Score = 219 bits (558), Expect = 7e-55, Method: Compositional matrix adjust.
Identities = 152/450 (33%), Positives = 238/450 (52%), Gaps = 44/450 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV +PGSKS++NR LL+AALS+G ++ +L S+D + L +L +LG V+ +++
Sbjct: 12 RPVDWTVDPVPGSKSMTNRALLMAALSDGEVKLEGVLFSDSRHFLESLVSLGFMVDINES 71

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+GCGG P K++ + +G AG A R LTA + + G Y ++ +M++R
Sbjct: 72 EKA VTVLGGGNIP---KKQAVINVGAGTAARFLTAMLGFSDE--YTIEASEQMKKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-----KVKLSGSISSQ 181
P+ +L L ++GA + PV++ G G ++ L S S+Q
Sbjct: 126 PMQELFSLLRVGA KITYLETEGHLPVKICGRNPKAGADQSKADGTPLQLSLDISKSTQ 185

Query: 182 YLSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LSALL+ +P+ ++I I + Y+ +T +++ GV+ ++ GG+
Sbjct: 186 FLSALLLISPMIPQGLDIHITSEKTDGSIYIRITRKLADAGVEVKY-----GGKN 235

Query: 242 YK-SPKNAY-----VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
Y+ PK Y +E D S+A YF A AAITGG V+ + QGD+KF +VL M
Sbjct: 236 YRIDPKAVYQKKHYQIEPDVSAACYFYAAAAITGGRALVKHVHKDNSQGMKFLDVLQAQ 295

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
G VT + VTGP + LK I+++MN D A+TLA +A F I +
Sbjct: 296 GCTVTEKADGIEVTGPAEDT-----LKGIEIDMNDFSQALTLAAMAPFCKSDVHITHIG 350

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDYDDHRMAMAFSL 412
R +E +R+ A+ ELTK G + E PD I P P + + TY+DHR+AM+F+L
Sbjct: 351 HIRGQECDRLHAMSEELTKRGITCTEPPDAITIKPGIP---SAGIVSTYEDHRVAMS FAL 407

Query: 413 AACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ I +P C RKTF +YFD+L
Sbjct: 408 LGLKVDGIVIDNPSCCRKTFENYFDLLDQL 437

>ref|ZP_04588138.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. oryzae str. 1_6]
Length = 418

Score = 219 bits (557), Expect = 8e-55, Method: Compositional matrix adjust.
Identities = 153/438 (34%), Positives = 235/438 (53%), Gaps = 47/438 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAQGSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ VV G + +A ++ LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DESTFVVTSNGHW---NAPQQA-LFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G DV G CPPV ++G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDLQRMGVDSAPS--CPPVAISGKGLAAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDLKISIP-YVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G +E+ + I YV++TL M+ FG V+A +W K + +
Sbjct: 184 GKGAIEVALTGSEIGARGYVDLTLAAMQAFAEVAIGDSAW-----KVSATGYCATDFH 238

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309

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      +E DAS+A+Y  A  A+T G++ +          Q D  ++++++
Sbjct: 239 IEPDASAATYLAQAALQGSIDLGVASDAFTQPDALASQIIDLF----- 283

Query: 310 PPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
      ++ A+ ++ ++M D  TLAV+A F  P      +A+ RVKE +R+ A+
Sbjct: 284 -----PNMFAV-IDGSQMQDAIPTLAVLAFAFNRPVRFVGIANLRVKECDRISALSQ 334

Query: 370 ELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIRD 424
      L  +  G +VEEG D  +  P      T  IDT+ DHR+AM F+LA      + I+D
Sbjct: 335 GLCAIAPGLAVEEGDDLNVNANPALAGTTVDALIDTHADHRIAMCFALAGLKIKGIHQD 394

Query: 425 PGCTRKTFFPDYFDVLSTF 442
      P C  KT+P Y+D L++
Sbjct: 395 PDCVGKTYPGYWDALASL 412

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>ref|YP_766557.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium leguminosarum bv. viciae 3841]
emb|CAK06442.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium leguminosarum bv. viciae 3841]
Length = 420

Score = 218 bits (556), Expect = 1e-54, Method: Compositional matrix adjust.
Identities = 162/448 (36%), Positives = 241/448 (53%), Gaps = 49/448 (10%)

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Query: 4  AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
      A+ ++ P K +SG  PGSKS++NR LLLA L++GT+ +  L S+D YM ALR +
Sbjct: 5  AKLTIIPPGKPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMAEALRAM 64

Query: 64 GLSV-EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
      G+++ E D  +  VV G G  P      +  LFLGNAG A R LTAA  AA  + T +
Sbjct: 65 GVAIDEPDDTS--FVVTGSGRLLP-----PKAPLFLGNAGTATRFLTAA--AALVDGTVI 115

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQY 182
      +DG  MR+RPIG LV  ++ LG DV  G  CPPV V G G  +++ G +SSQY
Sbjct: 116 VDGDEHMRKRPIGPLVEAMRTLIGIDVTAKTG--CPPVTVKGTGRFQADRIRIDGGLSSQY 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGG 239
      +SALLM A      V+IE++ + I ++ Y+++T  M+ FG K E  +  +W R  G
Sbjct: 174 VSALLMMAAGGDRPVDIELVGEDIGALGYIDLTTAAMKAFGAKVEKTSPTW-RVEPTG- 231

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
      Y++  +  VE DAS+A+Y  A  +TGG + +          Q D  +  +++
Sbjct: 232 --YRA-ADFIVEPDASAATYLAQAEVLTGGAILDGVPAFAFSQPDARAYDMIA----- 281

Query: 300 WTETSVTVTGPPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
      R P      HL A +++ ++M D  TLAV+A F  + P      +A+ RVK
Sbjct: 282 -----RFP-----HLPA-EIDGSQMQDAVPTLAVLAFAFNETPVRFVGIANLRVK 324

Query: 360 ETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAA 414
      E +R+ A+ T L ++  G + EEG D  + + P  +      ID++ DHR+AM+F+LA
Sbjct: 325 ECDRIRALSTGLNRIVSGLAREEGDDLIVQSDPALVGRHLP AEIDSFADHRIAMSFALAG 384

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
      +TI DP C  KTFP Y+  L+
Sbjct: 385 LKIDGITILDPDCVGKTFPAYWRTLAAL 412

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>ref|YP_002436161.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio vulgaris str. 'Miyazaki F']
gb|ACL08693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio vulgaris str. 'Miyazaki F']
Length = 450

Score = 218 bits (556), Expect = 1e-54, Method: Compositional matrix adjust.
Identities = 163/451 (36%), Positives = 224/451 (49%), Gaps = 47/451 (10%)

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Query: 18  TVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
      TV  P SKS+S+R+L+ AAL+ G +VV+++L S D+      LR G +E  +  R
Sbjct: 9  TVAAPPSKSVSHRMLIGAALAAGDSVVEHVLESRDIERADILRAAGARIE-RQGDGRFA 67

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Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G G P V + +G R LTA + A G + + G PRM ERPIG+L
Sbjct: 68 VSGVAGT-PAGGFDAPVSCDVHESGTTTCRLLTAVLAA--GKGQFRIHGAPRMHERPIGEL 124

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ G V CPP+ ++ G+ GG + SSQYLS LL+AAPL G +
Sbjct: 125 VDVLRGRGVVRVTYEGREGCPPLIDS-DGMSGGSTAIGLGESSQYLSGLLLAAPLTSG-L 182

Query: 198 EIEII-DKLISIPYVEMTLRLMERFGVKA-----HSDSWD-----RFY 235
IE+ DK++S PYV +TL+ +E FG+ +D W RF
Sbjct: 183 TIEVSGDKVSWPYVALTLQALEDFGIGFRVETRETTPRGKWQADDWRMLREVRPGLVRV 242

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+ G Y++ N VEGD S+ASYFLA A+ V V G SLQGD ++L MG
Sbjct: 243 VSPGV-YRA-GNYRVEGDWSNASYFLAAGAVGPRPVRVAGLRVDSLQGDRAMLDILGRMG 300

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
A+ + V V L ++V+M PD+ T+A A FA G T IR+VA
Sbjct: 301 ARFERADNGVVVA-----PSSLTGVEVDMGHCPDLVPTVAATAAFAQGVTTIRNV 352

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTIDTYDDHRM 406
R+KE +R+ A EL K G VEE D I+ P V +Y DHRM
Sbjct: 353 LRIKCDRLSAPAAELRKAGVRVEELDDGLIVHGSRLRSGGPAPVIDEKVMPFLSYGDHRM 412

Query: 407 AMAFSLAACAEVPVTIRDPGCTRKTFFDYFD 437
AM+ +L A V V + DP C K+FP +++
Sbjct: 413 AMSLALLGFAGVHVLDLDPACVAKSFPHFWN 443

>gb|EFU19683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta
thermophila DSM 6578]
Length = 422

Score = 218 bits (555), Expect = 1e-54, Method: Compositional matrix adjust.
Identities = 163/439 (37%), Positives = 245/439 (55%), Gaps = 29/439 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+ +QP + +SG + +P SKS + R LL+AA + GT+ + + L S D + A+ LG
Sbjct: 2 EVSVQPGR-LSGSHIPVPPSKSHTIRALLVAAAAGGTSRIRSPLFSRDTRACMRAVSLGA 60

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTA--AGGNATYVL 123
V + A +V G GG+F V + +V+ N+G + L A+ A GG A +
Sbjct: 61 VVREEGA--DLLVEGTGGRFVSVPEDVIDVE----NSGTTL-YLAGAMAALIEGGRAVFTG 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
D ++R R G L+ L LGA + G C P+ + G L GG ++ +SQYL
Sbjct: 114 DA--QLRRRTAGPLLASLHDLGARAESTRNGCAPLVIGG--PLRGGSTSIA-CPTSQYL 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL+A PL GD +E+++ L PY++MTL ++ GV E + +DRF I GGQ Y+
Sbjct: 169 SALLLACPLGKGDLSLEVVE-LNEHPYIDMTLWWLKAQGVALER-EGYDRFRIPGGQCYR 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA--KVTWT 301
+ + + GD SSA++FL AA+TG T+T+ QGD + ++LE MG +V+
Sbjct: 227 A-FDLTIPGDYSSATFFLCAAAVTGSTLTLTNLYPDDPQGDREVLDILERMGCTVEVSPE 285

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
VT+TG P L A V+M ++PD LAV A +A+G T + + A R+KET
Sbjct: 286 RREVTITGGP-----LSATKVDMTRIPDALPALAVTACYAEGTTRLYNAAHTRLKET 337

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIDTYDDHRMAMAFSLAA-CAEVPV 420
+R+ + EL++LGA VEE PD +I P L + ++DDHR+AMA ++ A A PV
Sbjct: 338 DRIAVMAQELSRILGARVEELPDGLLIHGCPPLTGGIVSSHDDHRVAMALAVGALAARAPV 397

Query: 421 TIRDPGCTRKTFFDYFDVL 439
TI T TFP++F +L
Sbjct: 398 TIEGAEATEVTFPEFFSL 416

>emb|CBL08458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseburia
intestinalis M50/1]

Length = 442

Score = 218 bits (554), Expect = 2e-54, Method: Compositional matrix adjust.
Identities = 148/441 (33%), Positives = 236/441 (53%), Gaps = 26/441 (5%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV +PGSKS++NR LL+AALS+G ++ +L S+D + L +L +LG V+ +++
Sbjct: 12 RPVDWTVVDVPGSKSMTNRALLMAALSDGEVKLEGVLFSDDSRHFLESLSLGLFMVDINES 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+GCGG P K++ + +G+AG A R LTA + + G Y ++ +M++R
Sbjct: 72 EKAFTVLGCGGNIP----KKQAVINVGSAGTAARFLTAMLGFSDGE--YTIEASEQMKKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-----KVKLSGSISSQ 181
P+ +L L +GA++ PV++ G G ++ L S S+Q
Sbjct: 126 PMQELFSLTLTGVGANITYLETEGHLTPVKICGRRNPKAGADQSKADGNPLQLPLDISKSTQ 185

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LSALL+ +P+ ++I I + Y+ +T +++ GV+ ++ + I
Sbjct: 186 FLSALLLISPMIPQGLDIHITSEKTDGSIYIRITRKMLADAGVEVKYDYGK--NYRIDPNAV 243

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y+ K+ +E D S+A YF A AAITGG V+ + QGD+KF +VL MG VT
Sbjct: 244 YQK-KHYQIEPDVSAACYFYAAAAITGGRALVKHVHKDNSQGDGMKFLDLVLRMGCTVTEK 302

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ VTGP + LK I+++MN D A+TLA +A F + I + R +E
Sbjct: 303 ADGIEVTGPAEDT-----LKGIEIDMNDFSDQALTLAAIAPFCNSDVHITHIGHIRGQEC 357

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ ELTK G + E PD I P + TY+DHR+AM+F+L +
Sbjct: 358 DRLHAMSEELTKRGITCTEEDAITIKPGTFFP-GIVSTYEDHRVAMSFALLGLKVDGIV 416

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I +P C RKTF +YFD+L
Sbjct: 417 IDNPSCCRKTFENYFDLLDQL 437

>emb|CBK90704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium rectale
DSM 17629]
Length = 427

Score = 218 bits (554), Expect = 2e-54, Method: Compositional matrix adjust.
Identities = 146/423 (34%), Positives = 224/423 (52%), Gaps = 14/423 (3%)

Query: 21 LPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR LL+AAL+ G +V+ L S+D + + AL LG V D+ + + G
Sbjct: 18 VPGSKSITNRALLIAALASGRSVLKGCLFSDDSRHFIDALIRLGFVPLVDEDKREITITG 77

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
GG+ P K E ++ +G+AG A R LTA + + G Y + +M++RP+ DL+V
Sbjct: 78 FGGRIP---KNEAEIDVGSAGTAARFLTALLGLSKGR--YHIVSSEQMKKRPMKDLLVS 131

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L++LGA ++ P + G V ++ SSQ+LSALL++A + + I
Sbjct: 132 LEKLGAIHEYDENEYHFFFTIGNTGEY-ADTVDINVDKSSQFLSALLISAIVMEKNFTIN 190

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
+ + YVEMT +M++FG+ + F I Y+S + +E D S+A YF
Sbjct: 191 VTGTH-GMAYVEMTRLMMKQFGLDVMQDKKNSFIIPKKAAYES-LDYDIEPDVSAACYF 248

Query: 261 LAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHL 320
A + + V G SLQGDV F +VL MG ++ E V PP+ H+
Sbjct: 249 YAMSPLLHVKSKVMGVHQNLSLQGDVAFDLVLVDMGCTIS-DEADGIVCMPPK---NAHI 303

Query: 321 KAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
+++ D A+TLA +A FA+ P I ++ R++E +R+ AI L +LG VEE
Sbjct: 304 HGGSWDLSTFSDQALTLAAIAPFANAPVGIEGISHIRLQECDRKAEENLAEELGVRVEE 363

Query: 381 GPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ I P E + I TYDDHR+AM+F+L V I DP C RKTF ++++VL

Sbjct: 364 IENGLRIYPAECIKPCKIKTYDDHRVAMSFTLPGLKAEGVEIIDPYCCRKTFFENFYEVLE 423

Query: 441 TFV 443

V

Sbjct: 424 ESV 426

>ref|YP_001324353.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
aeolicus Nankai-3]
sp|A6UTB9.1|AROA_META3 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABR55741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
aeolicus Nankai-3]
Length = 433

Score = 217 bits (553), Expect = 3e-54, Method: Compositional matrix adjust.
Identities = 143/443 (32%), Positives = 235/443 (53%), Gaps = 19/443 (4%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I+++ ++I GT+ P SKS ++R ++ A+L++GT+ + + LNS D + LG
Sbjct: 2 IIIIEKTEQIKGTINAPPSKSYTHRAVICASLADGTSEIISPLNSADCLSSVHGAMMLGAE 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++A K VV G + V + GN+G +R LT + + +L G
Sbjct: 62 IDATDKNKWVVV---GNNNSPKTPNNVVDI--GNSGTTLRILTG-IASQIPEGYAILTGD 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ L+ L QLQ P+ V G + VK+ G +SSQ++++L
Sbjct: 116 SSIITRPMQPLLDALNQLGIRAFSSKTDGTAPIIEVH-GEIKNNVVKIRGDMSSQFITSL 174

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGGQKYK 243
+M P + D IE+ L S PY+++T+ ++++FGVK E + + +F IKG QKYK
Sbjct: 175 MMTMPFSKMDSTIELTTPKLSAPYLDITIDVLDKFGVKIEKVKNKNLTKFKIIKGNQKYK 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + VEGD SSASYF+A + +T+ S QGD + +++ MGA + E
Sbjct: 235 -PYSYTVVEGDSSASYFIAAGVLMNSDITINNIFKNSKQGDREIVNIVKKMGAPIIEED 293

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + GP + LK ID+++ PD+ T+A++ FA+G T I + R+KE +R
Sbjct: 294 KIIIKGPYK-----LKGIDIDVKDTPDLVPTIAILGCFAGETTTIYNGEHVRLKECDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVTI 422
++A ELTK+GA + E PD II KLN ++TY DHR+ MAF++A AE I
Sbjct: 347 LMACAKELTKMGAKITEKPDGLIIEGVGKLNGAEMETYHDHRLVMAFTVAGMMAEGKTII 406

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
+ + +FP+ + + + N
Sbjct: 407 KGEDAVKISFPNFVEAIKSIGAN 429

>ref|YP_468422.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli CFN 42]
sp|Q2KBU1.1|AROA_RHIEC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABC89695.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli CFN 42]
Length = 420

Score = 217 bits (553), Expect = 3e-54, Method: Compositional matrix adjust.
Identities = 159/447 (35%), Positives = 237/447 (53%), Gaps = 47/447 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 63
A+ ++ P K +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIPP GKPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMADALRAM 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++++ + VV G G P + LFLGNAG A R LTAA AA + T ++

Sbjct: 65 GVAID-EPDDTTFFVVTGSGRLTP-----PKAPLFLGNAGTATRFLTA--AALVDGTVIV 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV +++LG DV G CPPV V G G ++ + G +SSQY+

Sbjct: 117 DGDEHMRKRPIGPLVEAMRKLIDVSAETG--CPPVTVRGTRFEADRILIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A V+IE++ + I ++ Y+++T M+ FG K E + +W R G

Sbjct: 175 SALLMAAGGDRPVVDIELVGEDIGALGYIDLTTAAMKAFGAKVEKTSPTVW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y++ + +E DAS+A+Y A ++ G + + Q D K E +

Sbjct: 232 -YRA-ADFVIEPDASAATYLAEEVLSDGRIDLGVPNDAFTQPDAKAYETIAKF----- 283

Query: 301 TETSVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
HL A +++ ++M D T+AV+A F + P +A+ RVKE

Sbjct: 284 -----PHLPA-EIDGSQMQUAVPTIAVLAAFNETPVRFVGIANLVRKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAAC 415
+R+ A+ + L + G +VEEG D + + P T IDT+ DHR+AM+F+LA

Sbjct: 326 CDRIRALSSGLNNIREGLAVEEGDDLIVHSDPALAGQTLPAEIDTFADHRIAMSFALAGL 385

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+TI DP C KTFP Y+ L+T

Sbjct: 386 KIGGITILDPDCVGKTFPAYWRTLATL 412

>ref|YP_004058389.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanithermus profundus DSM 14977]
gb|ADR37216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanithermus profundus DSM 14977]
Length = 447

Score = 217 bits (552), Expect = 3e-54, Method: Compositional matrix adjust.
Identities = 169/440 (38%), Positives = 239/440 (54%), Gaps = 18/440 (4%)

Query: 1 MAGAEEIVLQPIK-EISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGA 59
+AG + L P + + +PGSKS++NR ++LA L+EG + + +L S+D + L A

Sbjct: 15 LAGVAAVRLAPPGPVRAELAVPGSKSVTNRAIVLAGLAEGASELAGILKSDDAWWALEA 74

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
LRTLGL VE + A + G GG++P +A ++++G AG R AA

Sbjct: 75 LRTLGLEVEV--MGETARIAGGGGRWPAGEA---EVYIGAAGTLGR-FLPPALAAAPAG 127

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+ + RM +RPI LV L+ LG VD P+ V+G GL GG+V + G +S

Sbjct: 128 RFRVRASRRMSQRPIAPLVDALRALGGRVDYAGEEGRFPLVHG-AGLAGGEVTIPGHVS 186

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+ S +L+AAP A G V + + ++ YV +TL +M FG +AE +K G

Sbjct: 187 SQFTSGVLLAAPYARGPVTVRVAGGMVQPAYVRITLAMMRAFGAAEEDAELSEISVKPG 246

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+Y+ + +E DASSA+YF A AA +GG VTV G+ +LQ D+ F VLE MGA+V

Sbjct: 247 -RYRG-QRLELEADASSAAYFFALAAASGGEVTVTNIGSATLQPDGLGFVHVLERMGARVE 304

Query: 300 WTETSVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
T TV GP K V++ M D TLA +A AD P I +VA R

Sbjct: 305 LTPRRTTVRGP-----EKLGGFTVSLKAMSDQPTTLAALAALADAPVTITEVAHVRHH 358

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDAIDTYDDHRMAMAFSLAACAEVP 419
E++R+ A+ EL KLG EE PD + P + +D +DDHR+AMA SL A A

Sbjct: 359 ESDRIAAMAAELAKLGLRAEERPDGLTVW-PGRPRPARLDPHDDHRIAMALSLALAAPG 417

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
+ I +PG T KTFP Y+D L

Sbjct: 418 LEIANPGTTSKTFPRYWDYL 437

>ref|YP_002937856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium rectale ATCC 33656]

gb|ACR75722.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium rectale
ATCC 33656]
Length = 427

Score = 217 bits (552), Expect = 3e-54, Method: Compositional matrix adjust.
Identities = 145/419 (34%), Positives = 222/419 (52%), Gaps = 14/419 (3%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR LL+AAL+ G +V+ L S+D + + AL LG V D+ + + G
Sbjct: 18 VPGSKSITNRALLIAALASGRSVLKGCFLSDDSRHFIDALIRLGFPVLVDEDKREITITG 77

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
GG+ P K E ++ +G+AG A R LTA + + G Y + +M++RP+ DL+V
Sbjct: 78 FGGRIP---KNEAEIDVGSAGTAARFLTAFLGLSKGR--YHIVSSEQMKKRPMKDLLVS 131

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L++LGA ++ P + G V ++ SSQ+LSALL++A + + I
Sbjct: 132 LEKLGAHIEYDENYHFPFTTIGNTGEY-ADTV DINVKSSQFLSALLISAIVMEKNFTIN 190

Query: 201 IIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
+ + YVEMT +M++FG+ + F I Y+S + +E D S+A YF
Sbjct: 191 VTGTH-GMAVYVEMTRLMMKQFGLDVMQDKNNFSIIPKKAAYES-LDYDIEPDVSAACYF 248

Query: 261 LAGAAITGGTIVTEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHL 320
A + + V G SLQGDV F +VL MG ++ E V PP+ H+
Sbjct: 249 YAMSPLLHVSKVMGVHQNLSLQGDVAFDLVLAADMGTIS-DEADGIVCMPPK----NAHI 303

Query: 321 KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
+++ D A+TLA +A FA P I ++ R++E +R+ AI L +LG VEE
Sbjct: 304 HGGSWDLSTFSQALTLAAIAPFAKEPVGIEGISHIRLQECDRINAIEENLAELGVRVEE 363

Query: 381 GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVL 439
+ I P E + I TYDDHR+AM+F+L V I DP C RKTf ++++VL
Sbjct: 364 TENGLRIYPAECIKPKIKTYDDHRVAMSFTLPGLKAEGVEIIDPYCCRKTFFENFYEV 422

>ref|XP_001210667.1| hypothetical protein ATEG_00581 [Aspergillus terreus NIH2624]
gb|EAU39227.1| hypothetical protein ATEG_00581 [Aspergillus terreus NIH2624]
Length = 1581

Score = 217 bits (552), Expect = 4e-54, Method: Compositional matrix adjust.
Identities = 170/434 (39%), Positives = 238/434 (54%), Gaps = 25/434 (5%)

Query: 22 PGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVG 80
PGSKS+SNR L+LAAL GT + NLL S+D M+ AL +G + ++ + VV G
Sbjct: 412 PGSKSISNRALVLAALSGTCRIKNLLYSDDTEVMMNALERIGAATFSWEEEGEVLVVNG 471

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT--YVLDGVPRMRERPIGDLV 138
GG L+LGNAG A R LT VT A + VL G RM++RPIGDLV
Sbjct: 472 KGGDIKAS---PTPLYLGNAGTASRFLTTVVTLATASTVDHVSVLTGNNRMKQRPIDLV 527

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L GA V+ P+++ GG GG++ L+ +SSQ++S+LLM AP A V
Sbjct: 528 DALTANGASVEYLEKKGSLPLKIGAGGGFAGGRINLAAKVSSQFVSSLLMCAPYAKEPVT 587

Query: 199 IEIID-KLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
++++ K IS PY+EMT +M FG++ + S + + Y +Y +P VE DASSA
Sbjct: 588 LKLVGGKPISEPYIEMTTAMMRSFGIEVQKSTEEFTYHIPQGRYVNPAYEVVESDASSA 647

Query: 258 SYFLAGAAITGGTIVTEGCGTTSLQGDVKAFA-EVLEMMGAKVTWTETSVTVTGPPPREPFG 316
+Y LA AA++G T T+ G+ SLQGD +FA +VL MG VT TETS TVTGP
Sbjct: 648 TYPLAIAAVSGTCTIPNIGSKSLQGDARFAVDVLRPMGCTVTQTETSTTVTGP-----A 702

Query: 317 RKHLKAI-DVNMNKMMPDVAMTLAVVALFADGP-----TAIRDVASWRVKETERMVAIRTE 370
L+ + +V+M M D + +V+A A G T I +A+ RVKE R+ A++ E
Sbjct: 703 DGILRPLPNVDMPEPMTDAFLGASVLAAIARGECSNHTTRIYGIANQRVKECNRIKAMKDE 762

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS-LAACAEVPVTIRDP 425
L K G E D I ++ + + YDDHR+A +FS L+ P I +
Sbjct: 763 LAKFGVVCREHDDGLEIDGIDRSTLRQPAGGVFCYDDHRVAFSFSVLSLVTPQPTLILEK 822

Query: 426 GCTRKTFFPDYFDVL 439
C KT+P ++D L
Sbjct: 823 ECVGKTWPGWWDTL 836

>ref|YP_003549473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coralimargarita
akajimensis DSM 45221]
gb|ADE55303.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coralimargarita
akajimensis DSM 45221]
Length = 453

Score = 216 bits (551), Expect = 4e-54, Method: Compositional matrix adjust.
Identities = 166/447 (37%), Positives = 229/447 (51%), Gaps = 33/447 (7%)

Query: 14 EISGTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ TV+LPGSKS++NR L+LAAL+EGTT ++ L S D ML AL+TLG + D+A+
Sbjct: 13 QLDSTVQLPGSKSITNRALILAALAEGTTRLEGALFSRDTRIMLSALKTLGFDCQVDEAS 72

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ + G GK P A +V GNAG A R LTA + G +Y LDG P MRERP
Sbjct: 73 RSITLAGGAGKIPATQASIDV---GNAGTAARFLTAFLALQPG-GSYQLDGDPMRERP 127

Query: 134 IGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ L+ L+ LGA F G P ++ G GG+ + S SSQ LSALL+AA
Sbjct: 128 MQGLIQALEDLGAEEFEFHGEAGFFPFTLHS-KGYRGGEATVDASASSQILSALLLAA-- 184

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP-KNAY-V 250
G + + + YV +TL++ E FG +D Y GQ Y++P K Y +
Sbjct: 185 PAGQQGVRLHCPVRPAYVAITLKMREAFGAPEVQADPTG-CYALDGLYQAPTCKGIYTI 243

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
E D S+ASYFLA I GG +T+ G LQGD FA+VL G +V +
Sbjct: 244 EPDISAASYFLALTLIHGGKLTLSKLGPDPLQGDALFADVLAAHGLRVDADTQQWIASNS 303

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R H +++ N D +T A+A G I + R +ET+R+ + E
Sbjct: 304 TPNAIERGHR---EIDFNTFSDTFLTYAAIAPLLGGSVRITGIGHTRHGETDRIAGMANE 360

Query: 371 LTKLGASVEEGPDYCII-TPPEKLNVT-----IDTYDDHRMAMAFSLAAC--- 415
L+KLG V+E D I P +L A I+TYDDHR AM+F++
Sbjct: 361 LSKLGQLVKEEEDALTIGQKPNELRSRALHARNHQDLLEIETYDDHRFAMSFALLGSYDL 420

Query: 416 ---AEVPVTIRDPGCTRKTFFPDYFDVL 439
E + I+DP C KTFP +F+VL
Sbjct: 421 LGDGEPWLAIKDPSCCGKTFPQFFEV 447

>ref|ZP_06369933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
FW1012B]
gb|EFC19952.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
FW1012B]
Length = 440

Score = 216 bits (551), Expect = 5e-54, Method: Compositional matrix adjust.
Identities = 159/445 (35%), Positives = 235/445 (52%), Gaps = 40/445 (8%)

Query: 18 TVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV P SKS+S+R ++ A+L+ GT+ + +L+S+D+ L +G + ++ +
Sbjct: 3 TVTAPPSKSVSHRAVIAASLAAGTSRLTGVLDSQDLTRTRECLAAMGAAFHP-QSDGSVI 61

Query: 78 VVGCGGKFPVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 135
V G G+ DA+ E + L +G +G R LTA AA G + + G RM +RPIG
Sbjct: 62 VSGTAGRPQGGDAETEDPIVLVVGESGTTTCRLTA--VAAAGRGVFEIRGHGRMHDRPIG 119

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+L+ L LG + ++CPPV + G GL GG +S SSQ+LS LL+AAP+A
Sbjct: 120 ELIRALMPLGLLEALYLKSNCPVVLVG-KGLRGGTSISLEDSSQFLSGLLLAAPMATA 178

Query: 196 DVEIEII-DKLISIPYVEMTLRLMERFGV----KAEHSDSWD-----RFY 235
+ IEI K +S PYV +TL + FGV + D+W RF
Sbjct: 179 PLTIEISGQKTVSWPYVAITLSTLSDFGVFPVETLSGDAWTATDWKKLTDVTPGKVRFA 238

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
++ P++ VEGD SSASYFLA AI VTV G SLQGD ++L MG
Sbjct: 239 MRPAGYV--PRDYAVEGDWSSASYFLAAGAIGQAPVTVTGLRADSLQGDRAMLDILIRM 296

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
A++ T +TV P E G+ D++M + PD+ T+AV A FA G T IR+VA
Sbjct: 297 ARIEMTSQGITVF--PSELVGQ-----DLDMGRCPDLVPTVAVAAACFAAGETVIRNVAH 348

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITP---PEKLNVT AIDTYDDHRMAMAFSL 412
R+KE++R+ ++ + GA V PD I P P V A + DHR+AM+ +L
Sbjct: 349 LRLKESDRIESVAENCIQAGAVVTVLPDGMRIKPRPLRGERV-AFSAFCDHRLAMSAAAL 407

Query: 413 AACAEVPVTIRDPGCTRKTFPDYFD 437
A + V + +P C K+FP+++
Sbjct: 408 FELAGIEVALDEPACVAKSFPEFWE 432

>ref|YP_001299190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides vulgatus
ATCC 8482]
gb|ABR39568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides vulgatus
ATCC 8482]
Length = 409

Score = 216 bits (550), Expect = 6e-54, Method: Compositional matrix adjust.
Identities = 145/433 (33%), Positives = 229/433 (52%), Gaps = 51/433 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ AL T ++NL + +D M+ AL
Sbjct: 11 QIHTTIQLPSSKSLSNRALIINALGNRTFQLENLSDCDDTQVMIHALN----- 58

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
D K + + AG AMR LTA ++ G T ++ G RM++RP
Sbjct: 59 -----DGKNTIDIMA--AGTAMRFLTAYLSVTPG--TRIITGTQRMQQR 99

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA+++ + PP+R+ G L + L G++SSQY+SALLM AP+
Sbjct: 100 IQVLVNALRELGAIEFYIINDGYPLRITG-HKLQKDTISLPGNVSSQYISALLMIAPIL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-DRFYIK-GGQKYKSPKNAYVE 251
+ + + ++IS PY+ +TL+LM FG +A+ W + + +K Q Y+S YVE
Sbjct: 159 SNGLTLTLTGEIISRPIINLTQLMNDFGARAK---WLNEYQLKVEPQPYQSIP-FYVE 213

Query: 252 GDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+ASY+ AA++ + + G TS QGD K AE+ +++G + + +VT+
Sbjct: 214 SDWSAASYWYQIAALSNAEIIPLGLFETSYQGDSKVAEIFQLLGIESIYGKNTVTLKK- 272

Query: 311 PREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
K + +D + PD+A T V + P + S ++KET+RM A+ E
Sbjct: 273 -----TDKITERLDYDFINQPDLAQTFVVTCLMNIPFRFSGLSLQSLKIKETDRMAALIQE 327

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVP-VTIRDPG 426
+ KLG + E D + E+ +T AIDTY+DHRMAMAF+ AC +P + I +P
Sbjct: 328 MGKLGYLHETDDRILSWEGERCCEMTADVAIDTYEDHRMAMAF-PACVVMPEIRINNPQ 386

Query: 427 CTRKTFPDYFDVL 439
K++P Y++ L
Sbjct: 387 VVSKSYPPYWEDL 399

>ref|ZP_05976382.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanobrevibacter
smithii DSM 2374]
gb|EFC92603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanobrevibacter
smithii DSM 2374]
Length = 438

Score = 216 bits (549), Expect = 6e-54, Method: Compositional matrix adjust.
Identities = 153/446 (34%), Positives = 237/446 (53%), Gaps = 35/446 (7%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ I ISG VK P SKS S+R ++LA+L++GT+ + ++L S+DV + A R LG ++

Sbjct: 5 VKTISNISGEVKAPPSKSYSHRAVILASLADGTSKIHDMLFSQDVLSSINACRALGANIT 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V+G GK EV + LGN+G +R +T+ + A + +L G

Sbjct: 65 --KKDDYLEVIGTNGKLH--NSSEVPIDLGNSGTTLRMLTSIASLA--DNEVILTGDSS 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
++ RP+ L L LG G P+ + G GG+ + G++SSQ++S++L+

Sbjct: 118 LQTRPMEILTESLASLGVCAASINGNGKAPILIKP--GYAGGETNILGNVSSQFISSILI 175

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAE-----HSDS-----WDRF 234
+APL+ V++ ++ + S PYV MT +M +FGVK E H D D F

Sbjct: 176 SAPLSENGVDLFLVLPFKSRPYVNMTCDIMAKFGVKIENEFFVRHEDCDRESKNCRIDEF 235

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
I Q+YKS + VEGD SSASY LA AI GG + S QGD +L+ M

Sbjct: 236 KILK-QEYKSC-DYVVEGDYSSASYLLAAVAIYGGNAKILNLFKDSKQGDKLILNLIKMM 293

Query: 295 GAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
GAK+ + V ++ +LK IDV+++ PD+ +T+A++A ADG T I V

Sbjct: 294 GAKIEIFDDYVKISS-----EGNLKGIDVLSNAPDLLITVAILAALADGTTNIAGVK 346

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
RVKET+R+ +EL KLG ++E D I + V +D++ DHR+AMAFSL

Sbjct: 347 HARVKETDRIATTCSELKKGCKLKEFEDGMSIEGGIRSGV--VDSHKDHLAMAFSLVG 404

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ I++ +FP++ + +S

Sbjct: 405 LKH-DIEIKNGEVFVDSFPNFIEAMS 429

>ref|YP_003873613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta
thermophila DSM 6192]
gb|ADN01340.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta
thermophila DSM 6192]
Length = 422

Score = 216 bits (549), Expect = 7e-54, Method: Compositional matrix adjust.
Identities = 161/439 (36%), Positives = 245/439 (55%), Gaps = 29/439 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+ +QP + +SG + +P SKS + R LL+AA + GT+ + + L S D + A+ LG

Sbjct: 2 EVSVQPGR-LSGHIPVPPSKSHTIRALLVAAAAGGTSRIRSPFLFSRDTRACMRAVSLGA 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTA--AGGNATYVL 123
V + A +V G GG+F V + +V+ N+G + L A+ A GG A +

Sbjct: 61 VVREEGA--DLLVEGTGGRFSVPEDVIDVE---NSGTTL-YLAGAMAALIEGGRVFTG 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
D ++R R G L+ L+ LGA + G C P+ + G L GG ++ +SQYL

Sbjct: 114 DA--QLRRRTAGPLLASLQDLGARAESTRGNGCAPLVIGGP--LRGGSTSLA-CPTSQYL 168

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL+A PL G+ +E+++ L PY++MTL ++ GV E + +DRF I GGQ Y+

Sbjct: 169 SALLLACPLGKGESLVEVVE-LNEHPYIDMTLWVWKAQGVALER-EGYDRFRIPGGQSYR 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWT-- 301
+ + + GD SSA++FL AA+TG T+T+ QGD + E+LE MG +V +

Sbjct: 227 A-FDLTIPGDYSSATFFLCAAATGSLTLTLNLYPDDPQGDREVLEILERMGCERVEVSPE 285

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E +V +TG L A +V+M ++PD LAV A +A+G T + + A R+KET

Sbjct: 286 ERAVRITG-----GSLSTATEVDMTRIPDALPALAVTACYAEGTTRLNAAHTRLKET 337

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPV 420
+R+ + EL++LGA VEE PD +I P L ++DDHR+AMA ++ A A PV

Sbjct: 338 DRIAVMAQELSRILGARVEELPDGLLIHGCPCLTGGIASSHDDHRVAMALAVGALAARAPV 397

Query: 421 TIRDPGCTRKTFPDYFDVL 439
TI TFP++F +L

Sbjct: 398 TIEGAEEAEVTFPEFFSL 416

>ref|YP_001977138.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium etli CIAT 652]
sp|B3PRH7.1|AROA_RHIE6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ACE89960.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium etli CIAT 652]
Length = 420

Score = 216 bits (549), Expect = 8e-54, Method: Compositional matrix adjust.
Identities = 158/447 (35%), Positives = 235/447 (52%), Gaps = 47/447 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ ++ P + +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIPGRPLSGRAMPPGSKSITNRALLLAGLAKGTSRMTGALKSDDTRYMADALRAM 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++++ + VV G G P + LFLGNAG A R LTAA AA + T V+
Sbjct: 65 GVAID-EPDDTTFVVTGSGRLMP-----PKAPLFLGNAGTATRFLTAA--AALVDGTVVV 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV ++ LG DV G CPPV V G G ++ + G +SSQY+
Sbjct: 117 DGDEHMRKRPIGPLVEAMRTLIGIDVSADTG--CPPVTVRGTRFEADRILIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A V+IE++ + I ++ Y+++T M+ FG + E + +W R G
Sbjct: 175 SALLMMAAGDRPVDIELVGEDIGALGYIDLTTAAMKAFGARVEKTSPTVW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y++ + +E DAS+A+Y A ++ G + + Q D K E +
Sbjct: 232 -YRA-ADFVIEPDASAATYLWAAEVLSDGQIDLGVNDFTQPDAKAYETIAKF----- 283

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
HL A +++ ++M D T+AV+A F + P +A+ RVKE
Sbjct: 284 -----PHLPA-EIDGSQMQDAVPTIAVLAAFNETPVRFVGIANLRVKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPEKLNVT---AIDTYDDHRMAMAFSLAAC 415
+R+ A+ T L + G +VEEG D + + P T IDT+ DHR+AM+F+LA
Sbjct: 326 CDRIRALSTGLNNIREGLAVEEGDDLIVHSDPALAGQTLPAEIDTFADHRIAMSFAAGL 385

Query: 416 AEVPTVIRDPGCTRKTFPDYFDVLSTF 442
+TI DP C KTFP Y+ L+
Sbjct: 386 KIDGITILDPDCVGKTFPAYWRTLAL 412

>ref|NP_353664.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium tumefaciens str. C58]
gb|AAK86449.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium tumefaciens str. C58]
Length = 425

Score = 216 bits (549), Expect = 8e-54, Method: Compositional matrix adjust.
Identities = 160/448 (35%), Positives = 234/448 (52%), Gaps = 50/448 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + P +SG V+ PGSKS++NR LLLA L++G + + L S+D YM ALR +G
Sbjct: 3 ELTITPPGHPLSGKVEPPGSKSITNRALLLAGLAKGKSHLSGALKSDDTLYMAEALREMG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V + A VV G G + E LFLGNAG A R LTAA G ++D
Sbjct: 63 VKV-TEPDATTFVVEGTGVL-----QQPEKPLFLGNAGTATRFLTAAGALVDG--AVIID 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIG-GLPGGKVKLSGSISSQYL 183
G MR+RPI LV L+ LG + D G CPPV V G G G P G V + ++SSQY+
Sbjct: 115 GDEHMRKRPIPLVQALRALGVEADAPTG--CPPVTVRGKMGFPKGSVTIDANLSSQYV 172

Query: 184 SALLMAAPLALGDVEIEII---DKLISIPYVEMTLRLMERFGVKAH-SDSWDRFYIKGG 239
SALLMAA A GD ++II +++ + Y+++T ME FG K E S++ R + G
Sbjct: 173 SALLMAA--ACGDKPVDIILKGEEIGAKGYIDLTTSAMEAFGAKVERVSNAIWRVHPTG- 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + ++E DAS+A+Y +TGG + + Q D K EV+
Sbjct: 230 ---YTATDFHIEPDASAATYLGWGAELLTGGAIDIGTPADKFTQPDAKAYEVMAQF----- 281

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
HL A +++ ++M D T+AV+A F + P +A+ RVK
Sbjct: 282 -----PHLPA-EIDGSQMQDAIPTIAVIAAFNETPVRVFGIANLRVK 322

Query: 360 ETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAA 414
E +R+ A+ L ++ G + EEG D + P T +IDT+ DHR+AM+F+LAA
Sbjct: 323 ECDRIRAVSLGLNEIREGLAHEEGDDLIVHADPSLAGQTVDSIDTFADHRIAMSFALAA 382

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ I++P C KT+P Y+ L++
Sbjct: 383 LKIGGIAIQNPACVAKTYPGYWKALASL 410

>ref|YP_003459196.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
sp. FS406-22]
gb|ADC70460.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
sp. FS406-22]
Length = 427

Score = 215 bits (548), Expect = 9e-54, Method: Compositional matrix adjust.
Identities = 145/440 (32%), Positives = 230/440 (52%), Gaps = 19/440 (4%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLS 66
++++ + G VK P SKS ++R ++ A+L+EG + + N L D + + LG
Sbjct: 2 LIVKKTDRLEGIVKAPPSKSYTHRAVIGASLAEGISRIINPLWGADCLSSVHGCKMLGAD 61

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ DK VV G K P + + +GN+G +R LT+ + + +L G
Sbjct: 62 ITLDKEKDEWVVKGGELKTP-----DNIIDIGNSGTTLRLITS-IASQIPKGYAILTGD 114

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L+ LKQL + P+ V G + G VK+ G ISSQ++++L
Sbjct: 115 ESIRKRPMPQLLDALKQLNIEAFSSKLDGTAPIIVKS-GKIDGNVVKIRGDISSQFITSL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M P D EI + L S PY+++TL ++ FG+K + +D+ F + G QKYK P
Sbjct: 174 MMLLPFNKEDTEIILTSPLKSKPYIDITLDILNNGFIKIDKTDNG--FLVYGNQKYK-PI 230

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD SSASY +A + +T+E S QGD +++ MGA V + V
Sbjct: 231 DYIVEGDYSSASYLIAAGVLINSNITIENTLFANSKQGDKAIINIVKEMGADVKKVKKDRVI 290

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G L+ IDV++ +PD+ T+AV+ FA+G T I + R+KE +R+ A
Sbjct: 291 IEG-----EYSLEGIDVDVKDIPDLVPTIAVLGCFAGKTEIYNGEHVRLKECDRLRA 343

Query: 367 IRTLTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
EL K+GA +EE PD II +KL ++TY DHR+ MAF++A AE I
Sbjct: 344 CAVELKKMGADIEEKPDGLIIRGVKKLKGAKLNTYHDHRLVMAFTIAGLKAEGETIIEGE 403

Query: 426 GCTRKTFPDYFDVLSTFVK 445
+ +FP++ DV+ + N
Sbjct: 404 EAVKISFPNFVDMKSLGAN 423

>ref|YP_002974419.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium
leguminosarum bv. trifolii WSM1325]
gb|ACS54880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium
leguminosarum bv. trifolii WSM1325]
Length = 420

Score = 215 bits (548), Expect = 1e-53, Method: Compositional matrix adjust.
Identities = 155/447 (34%), Positives = 237/447 (53%), Gaps = 47/447 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 63
A+ ++ P + +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +

Sbjct: 5 AKLTIIPGRPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMAEALRAM 64

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++++ + VV G G P + LFLGNAG A R LTAA AA + T ++

Sbjct: 65 GVTID-EPDDTTFVVVTGSGRLLP-----PKAPLFLGNAGTATRFLTA--AALVDGTVIV 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV ++ LG DV G CPPV V G G +++++ G +SSQY+

Sbjct: 117 DGDEHMRKRPIGPLVEAMRTLIGIDVSAETG--CPPVTVKGTGRFQADRIRIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A ++IE++ + I ++ Y+++T M+ FG K E + +W R G

Sbjct: 175 SALLMMAAGDRPIDIELVGEDIGALGYIDLTTAAMKAFGAKVEKTSPTVW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y + + VE DAS+A+Y A +TGG + + Q D + +++

Sbjct: 232 -YHA-ADFIVEPDASAATYLWAAEVLTTGAIDLGVPSDAFSQPDARAYDMIKAF----- 283

Query: 301 TETSVTVTGPPREPFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
HL + +++ ++M D TLAV+A F + P +A+ RVKE

Sbjct: 284 -----PHLPS-EIDGSQMQUAVPTLAVLAFAFNETPVRFVGIANLRVKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPPEKLV--TAIDTYDDHRMAMAFSLAAC 415
+R+ A+ T L ++ G + EEG D + + P + ID++ DHR+AM+F+LA

Sbjct: 326 CDRIQALSTGLNRIVSGLAREEGDDLIVQSDPALVGQHLPAEIDSFADHRIAMSFALAGL 385

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
+TI DP C KTFP Y+ L+

Sbjct: 386 KIDGITILDPCVGKTFPAYWRTLAL 412

>ref|ZP_06419979.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella buccae
D17]
gb|EFC75627.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella buccae
D17]
Length = 415

Score = 215 bits (547), Expect = 1e-53, Method: Compositional matrix adjust.
Identities = 145/438 (33%), Positives = 233/438 (53%), Gaps = 52/438 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I T+ LP SKS+SNR+L++ AL+ G T+ DNL + +D ++ AL + ++

Sbjct: 9 ERIQATINLPASKSISNRVLMIHALAGGDTLNDLSDCDDTEVIIRALAAMPYEID---- 64

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLVDGVPRMRER 132
+ AG AMR +TA ++ G ++L G RM+ R

Sbjct: 65 -----IKAAGTAMRFMTAYLSVTEGK--HLLTGTDRMKRR 97

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ LGAD+ T PP+ +NG L GG++++ G+ISSQY+SALLM P

Sbjct: 98 PIAPLVNALRYLGADIRYAGETGFPPLIING-KTLEGGRLVPGNISSQYISALLMIGPA 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+ ++ ++IS PY+++TL M+ FG +AE +D D ++ Q YKS +E

Sbjct: 157 LKEGLELHLMGEIISRPYIDLTLWTMQEFGAEAEWTDI-DIITVR-PQVYKS-HPYLIEN 213

Query: 253 DASSASYF---LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----T 303
D S++SY+ LA +G ++ ++G S QGD + ++G K T+ T

Sbjct: 214 DWSASSYWEMLALQGASGSSIKLKGLTDGSKQGDVVKYLFSLLGVKTTTFDNKEEQPT 273

Query: 304 SVTVTGPPREPFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+VT+T R L +D + PD+A T V D P +AS ++KET+R

Sbjct: 274 TVTLTR-----HRCLLRLDYDFTGSPDLAQTFVVTCALLDIPFTFTGLASLKIKETDR 327

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADTYDDHRMAMAFSLAACAEVPVT 421
+ A++ E+ KLG +++ + + E+ ++ IDTY+DHRMA+AF+ AAC +

Sbjct: 328 IEALKAEEMKKGYLKIDENNTLRWEGERCPSLQPIDTYEDHRMALAFAPAAACRFPGLR 387

Query: 422 IRDPGCTRKTFFPDYFDVL 439
I +PG K++P Y+D L

Sbjct: 388 INNPVGVSYSYPHYWDDL 405

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>ref|YP_003963006.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein
[Ketogulonigenium vulgare Y25]
gb|ADO41706.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein
[Ketogulonigenium vulgare Y25]
Length = 425

Score = 215 bits (547), Expect = 1e-53, Method: Compositional matrix adjust.
Identities = 158/445 (35%), Positives = 233/445 (52%), Gaps = 48/445 (10%)

Query: 8 VLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+ P ++G + LPGSKS++NR LL+AALS G + + L S+D +M ALR +G+ V
Sbjct: 11 IAPPAGPLTGQIALPGSKSITNRALLVAALSRGVSHLTGALASDDTRHMANALRAMGVVDV 70

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
A+ + V GK V DA LFLGNAG AMR LTAA G T VL+G
Sbjct: 71 VAEGT---TLTVTSTGKLLVPDAP----LFLGNAGTAMRFLTAACAFVDG--TVVLNGDE 121

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK----VKLSGSISSQYL 183
M++RPI LV L+ +G D+ G CPPV ++G P G V++ GS+SSQY+
Sbjct: 122 HMQKRPIAPLVNLDALRAMGVVDISAPTG--CPPVTIHGGVTPPAGGGAALVEIDGSLSSQYV 179

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SALLMAAP+A V + + D L S YV++TL M FG AE +D + ++ Y
Sbjct: 180 SALLMAAPIAPVPRVRVTGDALGSRGYVDITLATMRAFG--AEVADEGNLTWLIAPTGY 237

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
++ A +E DAS+A+Y A +T G + + Q D + +++
Sbjct: 238 RATDYA-IEPDASAATYIWAAEMLTHGKIDIGIAADAMNQPDARAFDMIKF----- 288

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
P P +++++ +M D TLAV+A+F G +A+ RVKET+
Sbjct: 289 -----PHFP-----LEIDGAQMQDAIPTLAVMAMFNGGTVRFTGLANLRVKETD 332

Query: 363 RMVAIRTELTKL--GASVEEGPDYCIITPPEKLVN---TAIDTYDDHRMAMAFSLAACAE 417
R+ A+ E+ ++ G +VEEG D + P + I TY DHR+AM+F+LA
Sbjct: 333 RVRALSNEINRILPGLAVEEGDDLIVYGDPTLIGQELPAEIFTYADHRIAMSFALAGLKL 392

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
+ I DP C KT+P Y+ +++
Sbjct: 393 RGIRILDPACVNKTYPAYWRDMASL 417

>ref|ZP_03806228.1| hypothetical protein PROPEN_04630 [Proteus penneri ATCC 35198]
gb|EEG83859.1| hypothetical protein PROPEN_04630 [Proteus penneri ATCC 35198]
Length = 241

Score = 214 bits (546), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 121/242 (50%), Positives = 164/242 (67%), Gaps = 8/242 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E + LQPI I GT+ LPGSKS+SNR LLLAAL++G T + NLL+S+D+ +ML AL+TLG
Sbjct: 2 ESLTLQPIAHIEGTINLPGSKSVSNRALLAALAKGNTRLTNLLSDDIRHMLNALKTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + G GG+F + ++LFLGNAG AMR L AA++ G+ +L
Sbjct: 62 VQYQLSNNTVCDIEGLGGEF---NTHSPLELFLGNAGTAMRPLAAALSL--GSHDIILT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G PRM+ERPIG LV L+Q GA +D TD PP+R+ GG GG V++ GS+SSQ+L+
Sbjct: 117 GEPRMKERPIGHLVDALRQGGASIDYLEQTDYPPIRLR--GGFKGGNVEVDGSVSSQFLT 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLM APLA D I I +L+S PY+++TL L+ FG K E+ D + RF IKGQ+Y+S
Sbjct: 175 ALLMTAPLAEQDTTITIKGELVSKPYIDITLALINTFGGKIENQD-YQRFVIKGGQQYQS 233

Query: 245 PK 246
P+
Sbjct: 234 PE 235
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>ref|ZP_07003703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
gb|EFI00907.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]
Length = 418

Score = 214 bits (545), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 153/438 (34%), Positives = 229/438 (52%), Gaps = 47/438 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+T G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALTNFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G +V G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEVVSAPSG--CPPVAIKGKGLEAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVENTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G VE+ + I YV++TL M+ FG V+A +W Y++ + +
Sbjct: 184 GKGPVEVALTGSEIGARGYVDLTAAAMQAFGAEVQAIGETAWK---VSATGYRA-TDFH 238

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E DAS+A+Y A A+T G + + Q D ++++
Sbjct: 239 IEPDASATYLAQAALTEGDI DLGVASDAFTQPDALASQIIASF----- 283

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
++ A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+
Sbjct: 284 -----PNMFAV-IDGSQMQDAIPTLAVLAFAFNRPVRFVGIANLRVKECDRISALSN 334

Query: 370 ELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTVIRD 424
L + G +VEEG D + P T IDT+ DHR+AM F+LA + I D
Sbjct: 335 GLCAIAPLAVEEGDILLVHANPALAGTTVDALIDTHSDHRIAMCFALAGLKIAGRILD 394

Query: 425 PGCTRKTFPDYFDVLSTF 442
P C KT+P Y+D L++
Sbjct: 395 PDCVGKTYPGYWDALASL 412

>ref|YP_002280056.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium leguminosarum bv. trifolii WSM2304]
sp|B5ZS37.1|AROARHILW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI53830.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium leguminosarum bv. trifolii WSM2304]
Length = 420

Score = 214 bits (545), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 158/447 (35%), Positives = 237/447 (53%), Gaps = 47/447 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ ++ P K +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIPPGKPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMADALRAM 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+S++ + VV G G P + LFLGNAG A R LTAA AA + T V+
Sbjct: 65 GVSID-EPDDTTFFVVTGSGRLQP-----PKAPLFLGNAGTATRFLTA--AALVDGTVVV 116

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV ++ LG DV G CPPV V G G ++++ G +SSQY+
Sbjct: 117 DGDEHMRKRPIGPLVEAMRTLIDVTAETG--CPPVTVKGTGRFQADRIRIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVENTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A +IE++ + I ++ Y+++T M+ FG K E + +W R G
Sbjct: 175 SALLMMAAGDRPFDIELVGEDIGALGYIDLTTAAMKAFGAKVEKTSPTVW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y++ + VE DAS+A+Y A +TGG + + Q D + +++
Sbjct: 232 -YRA-ADFIVEPDASAATYLWAAEVLTTGGAILDGVPSDAFSQPDARAYDMIARF----- 283

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
P+ P +++ ++M D TLAV+A F + P +A+ RVKE
Sbjct: 284 -----PQLP-----AEIDGSQMQDAVPTLAVLAAFNETPVRVFGIANLRVKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPPE---KLNVTAITDYDDHRMAMAFSLAAC 415
+R+ A+ + L ++ G + EEG D + + P K ID++ DHR+AM+F+LA
Sbjct: 326 CDRIRALSSGLNRIRPGLAREEGDDLIVKSDPALVGKRLPAEIDSFADHRIAMSFALAGL 385

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+TI DP C KTFP Y+ L+
Sbjct: 386 KIDGITILDPDCVGKTFPAYWRTLAAL 412

>ref|ZP_03395431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tomato T1]
ref|ZP_07231501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tomato Max13]
ref|ZP_07251895.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tomato K40]
ref|ZP_07256911.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tomato NCPPB 1108]
gb|EEB61670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tomato T1]
Length = 418

Score = 214 bits (545), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 153/436 (35%), Positives = 228/436 (52%), Gaps = 43/436 (9%)

Query: 13 KEISGTVKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ GN +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGN--FVVDGDEYMRKR 125

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G ++ G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEISAPSG--CPPVAIKGKGLQAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVENTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +E+ + I YV++TL M+ FG AE D + Y + + ++E
Sbjct: 184 GKGPLEVALTGSEIGARGYVDLTLAAMQAFG--AEVQAIGDAAWKVSATGYHA-TDFHIE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
DAS+A+Y A A+T G + + Q D +++++ P
Sbjct: 241 PDASAATYLWAAQALTEGNIDLGVASDAFTQPDALASQIIDSF-----P 284

Query: 312 REPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
P A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+ L
Sbjct: 285 NMP-----AV-IDGSQMQDAIPTLAVLAAFNRQPVRVFGIANLRVKECDRISALCNGL 336

Query: 372 TKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ G +VEEG D + P T IDT+ DHR+AM F+LA + I+DP
Sbjct: 337 CAIAPGLAVEEGDDLIVHANPALAGTTVNALIDTHSDHRIAMCFALAGLKIKIGIHIQDPD 396

Query: 427 CTRKTFPDYFDVLSTF 442
C KT+P Y+D L++
Sbjct: 397 CVAKTYPGYWDALASL 412

>ref|ZP_07881352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella buccae
ATCC 33574]
gb|EFU32000.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella buccae
ATCC 33574]
Length = 415

Score = 214 bits (545), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 145/438 (33%), Positives = 232/438 (52%), Gaps = 52/438 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKA 72
+ I T+ LP SKS+SNR+L++ AL+ G T+ DNL + +D ++ AL + ++
Sbjct: 9 ERIQATINLPASKSISNRVLMIHLAGGDTLPDNLSDCDDTEVIIRALAAMPYEID---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ AG AMR +TA ++ G ++L G RM+ R
Sbjct: 65 -----IKAAGTAMRFMTAYLSVTEGK--HLLTGTD RMKRR 97

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L LGAD+ T PP+ +NG L GG++++ G+ISSQY+SALLM P
Sbjct: 98 PIAPLVNALHYLGADIRYAGETGFPPLIING-KTLEGGRLVPGNISSQYISALLMIGPA 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+ ++ ++IS PY+++TL M+ FG +AE +D D ++ Q YKS +E
Sbjct: 157 LKEGLELHLMGEIISRPIYIDLTLWTMQEFGAEAEWTDMDIITVR-PQVYKS-HPYLIEN 213

Query: 253 DASSASYF---LAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----T 303
D S++SY+ LA +G ++ ++G S QGD + ++G K T+ T
Sbjct: 214 DWSASSYWEMLALQGASGSSIKLKGLTDGSKQGDVVKYLFSLLGKTTTFDNKEEGQPT 273

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+VT+T R L +D + PD+A T V D P +AS ++KET+R
Sbjct: 274 TVTLTR-----HRCLLPRLDYDFTGSPDLAQTFVVTCALLDIPFTFTGLASLKIKETDR 327

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEPVPT 421
+ A++ E+ KLG +++ + + E+ ++ IDTY+DHRMA+AF+ AAC +
Sbjct: 328 IEALKAEEMKKGYLKIDENNNTLRWEGERCPSLQPIDTYEDHRMALAFAPAACRFPGLR 387

Query: 422 IRDPGCTRKTFPDYFDVL 439
I +PG K++P Y+D L
Sbjct: 388 INNPGVVSKSYPHYWDDL 405

>ref|ZP_05255540.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
4_3_47FAA]
gb|EET15932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
4_3_47FAA]
Length = 409

Score = 214 bits (545), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 144/433 (33%), Positives = 228/433 (52%), Gaps = 51/433 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ AL ++NL + +D M+ AL
Sbjct: 11 QIHTTIQLPSSKISNRALIINALGNRIFQLENLSDCDDTQVMIHALN----- 58

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
D K + + AG AMR LTA ++ G T ++ G RM++RP
Sbjct: 59 -----DGKNTIDIMA--AGTAMRFLTAYLSVTPG--TRIITGTQRMQQR 99

Query: 134 IGD LVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA+++ + PP+R+ G L + L G++SSQY+SALLM AP+
Sbjct: 100 IQVLVNALRELGAIEIYIINDGYPLRITG-HKLQKDTISLPGNVSSQYISALLMIAPIL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-DRFYIK-GGQKYKSPKNAYVE 251
+ + + ++IS PY+ +TL+LM FG +A+ W + + +K Q Y+S YVE
Sbjct: 159 SNGLTLTLTGEIISRPIYNLTQLMNDFGARAK----WLNEYQLKVEPQPYQSIP-FYVE 213

Query: 252 GDASSASYFLAGAAITG-GTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+ASY+ AA++ + + G TS QGD K AE+ +++G + + +VT+
Sbjct: 214 SDWSAASYWYQIAALSNAEIIPLGLFETSQGD SKVAEIFQLLGIESIYGNKTVTLKK- 272

Query: 311 PREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
K + +D + PD+A T V + P + S ++KET+RM A+ E
Sbjct: 273 -----TDKITERLDYDFINQPDLAQTFVVT CALMNIPFRFSGLSLQSLKIKETDRMAALIQE 327

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEPV-VTIRDPG 426
+ KLG + E D + E+ +T AIDTY+DHRMAMAF+ AC +P + I +P

Sbjct: 328 MGKLGYLHETDDRILSWEGERCMTADVAIDTYEDHRMAMAFAPACVVMPEIRINNPQ 386

Query: 427 CTRKTFPDYFDVL 439

K++P Y++ L

Sbjct: 387 VVSKSYPPYWEDL 399

>ref|XP_002943890.1| PREDICTED: hypothetical protein LOC100495501 [Xenopus (Silurana)
tropicalis]
Length = 654

Score = 214 bits (544), Expect = 2e-53, Method: Compositional matrix adjust.
Identities = 116/249 (46%), Positives = 160/249 (64%), Gaps = 17/249 (6%)

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260

++ +LIS PY+ +TL L+ RFG++ H D W RF I G +Y+SP + +VE DASSASYF

Sbjct: 175 LVGELISKPYIHITLALLARFGIQUIAH-DGWRFTIPAGSRYQSPGSIHVEADASSASYF 233

Query: 261 LAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315

+A A+T + + ++G G S+QGD+ F E MGA +T + +

Sbjct: 234 IALGALTASSEGGQKGIKIQVGLNSIQGDIHFVEAARAMGAHITGGPNWLHIE-----R 287

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375

G L+AID++ N +PD AMTLA +AL+A+G T +R++ASWRVKET+R+ A+ EL KLG

Sbjct: 288 GIWPLQAIDLDCNHIPDAAMTLAAMALYANGTTRLRNIAASWRVKETDRIAAMAAELRKLK 347

Query: 376 ASVEEGPDYCIITP---PEKLNVTIAIDTYDDHRMAMAFSLAAC--AEVPVTIRDPGCTRK 430

A+VEE D +TP P+ +I TYDDHR+AM F+LAA A +PV I DP C K

Sbjct: 348 ATVEESADAIAVTPPAAPQDWQAASIHTYDDHRIAMCFALAAFNPARLPVRIEDPQCVAK 407

Query: 431 TFPDYFDVL 439

TFPDYF+ L

Sbjct: 408 TFPDYFETL 416

>ref|ZP_06741032.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
vulgatus PC510]
ref|ZP_07998036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_1_40A]
gb|EFG19153.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
vulgatus PC510]
gb|EFV65992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_1_40A]
Length = 408

Score = 214 bits (544), Expect = 3e-53, Method: Compositional matrix adjust.
Identities = 144/433 (33%), Positives = 228/433 (52%), Gaps = 51/433 (11%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAA 73

+I T++LP SKS+SNR L++ AL ++NL + +D M+ AL

Sbjct: 10 QIHITTIQLPSSKISNRALIINALGNRIFQLENLSDCDDTQVMIHALN----- 57

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

D K + + AG AMR LTA ++ G T ++ G RM++RP

Sbjct: 58 -----DGKNTIDIMA--AGTAMRFLTAYLSVTPG--TRIITGTQRMQQR 98

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193

I LV L++LGA+++ + PP+R+ G L + L G++SSQY+SALLM AP+

Sbjct: 99 IQVLVNALRELGAIEFYIINDGYPLRITG-HKLQKDTISLPGNVSSQYISALLMIAPIL 157

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-DRFYIK-GGQKYKSPKNAYVE 251

+ + + ++IS PY+ +TL+LM FG +A+ W + + +K Q Y+S YVE

Sbjct: 158 SNGLTTLTLTGEIISRPYINLTQLMNDFGARAK---WLNEYQLKVEPQPYSIP-FYVE 212

Query: 252 GDASSASYFLAGAAITG-GTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310

D S+ASY+ AA++ + + G TS QGD K AE+ +++G + + +VT+

Sbjct: 213 SDWSAASYWYQIAALSNAEIIILPGLFETSYQGDSKVAEIFQLLGIESIYGNKTVTLKK- 271

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370

K + +D + PD+A T V + P + S ++KET+RM A+ E

Sbjct: 272 -----TDKITERLDYDFINQPDLAQTFVVTCLMNIPIFRFSGLSLQSLKIKETDRMAALIQE 326

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVP-VTIRDPG 426
+ KLG + E D + E+ +T AIDTY+DHRMAMAF+ AC +P + I +P
Sbjct: 327 MGKLGYLHETDDRILSWEGERCMTADVAIDTYEDHRMAMAFA-PACVVMPEIRINNPQ 385

Query: 427 CTRKTFFPDYFDVL 439
K++P Y++ L
Sbjct: 386 VVSKSPYPYWDL 398

>ref|ZP_06835492.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
hansenii ATCC 23769]
gb|EFG83353.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
hansenii ATCC 23769]
Length = 427

Score = 214 bits (544), Expect = 3e-53, Method: Compositional matrix adjust.
Identities = 156/440 (35%), Positives = 223/440 (50%), Gaps = 46/440 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E + P+K G V LPSKSKS++NR+LLLA L+ GT+ + L S+D YM AL+ +G+
Sbjct: 18 EPITAPLK---GRVVLPKSKSVTNRVLLLAGLARGTSQLTGALKSDDTLYMAQALQQMGI 74

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
SVE A + VV G A LFLGNAG A+R LTAA G T V+ G
Sbjct: 75 SVEQPDAT--SFVVRSDGTLHAPQAP----LFLGNAGTAVRFLTAASALVRG--TVVVGG 126

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
M RPI LV L+ LG D G CPPV ++G G L GG+V++ S+SSQY+SA
Sbjct: 127 DANMARRPIAPLVLTALRALGIDASAPSG--CPPVTIHGTGLLSGGEVEIDASLSSQYVSA 184

Query: 186 LLMAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLM A + V I + I Y+ +T+ M FG D GG +
Sbjct: 185 LLMMAACSRTPVRISLSGPHIGAHGYIGLTIAAMRAFGASVTSGDDASWTVPAGG---YT 241

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ +E DAS+A+Y A A++GG + + Q D V++
Sbjct: 242 ATDLRIEPPDASAATYLAQALSGGEIDIGFPIGDFTPQPDAAAWHVIQSF----- 291

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
H+ A+ ++ ++M D TLAV+A+F + P + + RVKE +R
Sbjct: 292 -----PHMPAV-IDGSQMQDAIPTLAVMAMFNETPVRVFGIENLRVKECDRT 337

Query: 365 VAIRTELTKLGASV--EEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVP 419
A+ T++ ++ + E G D + P+ N I+TYDDHR+AM+F+LAA
Sbjct: 338 HALATQMRINPAYAREAGDDLVLVPHDPANTAKDVRIETYDDHRIAMSFALAALKIPG 397

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
++I +PGC KTFP Y+D L
Sbjct: 398 LSILNPGCVGKTFPAYWDTL 417

>ref|ZP_03607002.1| hypothetical protein METSMIALI_00098 [Methanobrevibacter smithii
DSM 2375]
gb|EEE41217.1| hypothetical protein METSMIALI_00098 [Methanobrevibacter smithii
DSM 2375]
Length = 438

Score = 214 bits (544), Expect = 3e-53, Method: Compositional matrix adjust.
Identities = 152/446 (34%), Positives = 236/446 (52%), Gaps = 35/446 (7%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ I I G VK P SKS S+R ++LA+L++GT+ + ++L S+DV + A R LG ++
Sbjct: 5 VKNISNIGGEVKAPPSKSYSHRAVILASLADGTSKIHDMLFSQDVLSSINACRALGANIT 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V+G GK EV + LGN+G +R +T+ + A + +L G
Sbjct: 65 --KKDDYLEVIGTNGKLH--NSSEVPIDLGNSGTTLRMLTSIASLA--DNEVILTGDSS 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
++ RP+ L L LG G P+ + G GG+ + G++SSQ++S++L+

Sbjct: 118 LQTRPMEILTESLASLGVCAASINGNGKAPILIKP--GYVGGETNILGNVSSQFISSILI 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-----HSDS-----WDRF 234
+APL+ V++ ++ + S PYV MT +M FGVE E H D D F

Sbjct: 176 SAPLSENGVDLFLVLPFKSRPYVNMTCDIMANFGVKIENEFFVRHEDCDRESKNCRIDEF 235

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
I Q+YKS + VEGD SSASY LA AI GG + S QGD ++L+ M

Sbjct: 236 KIPK-QEYKSC-DYVVEGDYSSASYLLAAVAIYGGNAKILNLFKNSKQGDKLILDILKKM 293

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
GAK+ + V ++ +LK IDV+++ PD+ +T+A++A ADG T I V

Sbjct: 294 GAKIEIFDDYVEISS-----EGNLKIDVDLSNAPDLLITVAILAALADGTTNITGVK 346

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA 414
RVKET+R+ +EL KLG ++E D I + V +D++ DHR+AMAFSL

Sbjct: 347 HARVKETDRIATTCSELKKGCKLKEFEDGMSIEGGIRSGV--VDSHKDHRMAMAFSLVG 404

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ I++ +FP++ + +S

Sbjct: 405 LKH-DIEIKNGEVFDVSFPNFIEAMS 429

>ref|YP_004277887.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium sp.
H13-3]
gb|ADY63567.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium sp.
H13-3]
Length = 425

Score = 213 bits (542), Expect = 5e-53, Method: Compositional matrix adjust.
Identities = 160/448 (35%), Positives = 235/448 (52%), Gaps = 50/448 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEVDHYMLGALRTL 64
E + P +SG V+ PGSKS++NR LLLA L++G + + L S+D YM ALR +G

Sbjct: 3 ELTITPPGHPLSGKVEPPGSKSITNRALLLAGLAKGSRLTGALKSDDTLYMAEALRAMG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V + A VV G G + E LFLGNAG A R LTAA AA + ++D

Sbjct: 63 VKV-TEPDATTFVVDGTGVL-----QQPEKPLFLGNAGTATRFLTA--AALVDGAVIID 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG-GLPGGKVKLSGSISSQYL 183
G MR+RPI LV L+ LG + D G CPPV V G G G P G V + ++SSQY+

Sbjct: 115 GDEHMRKRPIMLVEALRALGVEADAPTG--CPPVTVRGKMGFPKGSVTIDANLSSQYV 172

Query: 184 SALLMAAPLALGDVEIEII---DKLISIPYVEMTLRLMERFGVKAHE-SDSWDRFYIKGG 239
SALLMAA A GD ++II +++ + Y+++T ME FG K E S++ R + G

Sbjct: 173 SALLMAA--ACGDKPVDIILKGEEIGAKGYIDLTTSAMEAFGAKVERVSNAIWRVHPTG- 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + ++E DAS+A+Y +T G + + Q D K EV+

Sbjct: 230 ---YTATDFHIEPDASAATYLGAEELLTAGAIDIGTPADKFTQPDAKAYEVMAQF----- 281

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
HL A +++ ++M D T+AV+A F + P +A+ RVK

Sbjct: 282 -----PHLPA-EIDGSQMQDAIPTIAVLAAFNETPVRFVGIANLRVK 322

Query: 360 ETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAA 414
E +R+ A+ L ++ G + EEG D + P T +IDT+ DHR+AM+F+LAA

Sbjct: 323 ECDRIRAVSLGLNEIRNGLAHEEGDDLIVHADPALAGQTVSDASIDTFADHRIAMSFALAA 382

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ I++P C KT+P Y+ L++

Sbjct: 383 LKIGGIAIQNPACVGKTYPGYWKALASL 410

>ref|YP_233984.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. syringae B728a]
sp|Q4ZY26.1|AROAPSEU2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ35946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae

pv. syringae B728a]
Length = 418

Score = 213 bits (542), Expect = 5e-53, Method: Compositional matrix adjust.
Identities = 151/436 (34%), Positives = 226/436 (51%), Gaps = 43/436 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G +V G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEVSAPSG--CPPVAIKGKGGLGAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G VE+ + I Y+++TL M FG AE D + Y++ + ++E
Sbjct: 184 GKGPVEVALTGSEIGARGYLDLTLAAMRAFG--AEVQAIGDAAWKVSATGYRA-TDFHIE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
DAS+A+Y A A+T G + + Q D ++++
Sbjct: 241 PDASAATYLAQAALTEGAIDLGVASNAFTQPDALASQIIASF----- 283

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
++ A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+ L
Sbjct: 284 -----PNMPAV-IDGSQMQDAIPTLAVLAAFNRQPVRFVGIANLRVKECDRISALSNGL 336

Query: 372 TKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ G +VEEG D + P T IDT+ DHR+AM F+LA + I DP
Sbjct: 337 CAIAPGLAVEEGDDLIVTANPTLAGTTVDALIDTHSDHRIAMCFALAGLKIAGIRILDPD 396

Query: 427 CTRKTFPDYFDVLSTF 442
C KT+P Y+D L++
Sbjct: 397 CVAKTYPGYWDALASL 412

>ref|ZP_07263162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. syringae 642]
Length = 418

Score = 213 bits (541), Expect = 6e-53, Method: Compositional matrix adjust.
Identities = 151/436 (34%), Positives = 227/436 (52%), Gaps = 43/436 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G +V G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEVSAPSG--CPPVAIKGKGGLGAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +E+ + I Y+++TL M+ FG AE D + Y++ + ++E
Sbjct: 184 GKGPLEVALTGSEIGARGYLDLTLAAMQAAG--AEVQAIGDAAWKVSATGYRA-TDFHIE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
DAS+A+Y A A+T GT+ + Q D ++++ ++ + + G
Sbjct: 241 PDASAATYLAQAALTKGTIDLGVASDAFTQPDALASQII-----ASFDPMPAVIDG-- 292

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
++M D TLAV+A F P +A+ RVKE +R+ A+ L
Sbjct: 293 -----SQMQDAIPTLAVLAAFNRQPVRFVGIANLRVKECDRISALSHGL 336

Query: 372 TKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPG 426

+ G +VEEG D + P T IDT+ DHR+AM F+LA + I DP
Sbjct: 337 CAIAPGLAVEEGDDLIVKANPALAGTTVDALIDTHSDHRIAMCFALAGLKIAGIRILDPD 396
Query: 427 CTRKTFPDYFDVLSTF 442
C KT+P Y+D L++
Sbjct: 397 CVGKTYPGYWDALASL 412

>ref|YP_001272846.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanobrevibacter smithii ATCC 35061]
sp|A5UJV0.1|AROAMETS3 RecName: Full=Probable 3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ86478.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) [Methanobrevibacter smithii ATCC 35061]
Length = 438

Score = 213 bits (541), Expect = 7e-53, Method: Compositional matrix adjust.
Identities = 151/446 (33%), Positives = 235/446 (52%), Gaps = 35/446 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ I I G VK P SKS S+R ++LA+L++GT+ + ++L S+DV + R LG ++
Sbjct: 5 VKTISNIGGEVKAPPSKSYSHRAVILASLADGTSKIHDMLFSQDVLSSINVCRALGANIT 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
K V+G GK EV + LGN+G +R +T+ + A + +L G
Sbjct: 65 --KKDDYLEVIGTNGKLH--NSSEVPIDLGNSGTTLRMLTSIASLA--DNEVILTGDSS 117

Query: 129 MRERPIGDLVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
++ RP+ L L LG G P+ + G GG+ + G++SSQ++S++L+
Sbjct: 118 LQTRPMEILTESLASLGVCAASINGNGKAPILIKP--GYVGGETNILGNVSSQFISSILI 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-----HSDS-----WDRF 234
+APL+ V++ ++ + S PYV MT +M +FGVK E H D D F
Sbjct: 176 SAPLSENGVDLFLVLPFKSRPYVNMTCDIMAKFGVKIENEFFVRHDDCDRESKNCRIDEF 235

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
I Q+YKS + VEGD SSASY LA AI GG + S QGD +L+ M
Sbjct: 236 KI-SKQYKSC-DYVVEGDYSSASYLLAAVAIYGGNAKILNLFKDSKQGDKLILNILKMK 293

Query: 295 GAKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVA 354
GAK+ + V ++ +LK IDV+++ PD+ +T+A++A ADG T I V
Sbjct: 294 GAKIEIFDDYVEISS-----EGNLKGIDVDSLNSAPDLLITVAILAALADGTTNITGVK 346

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
RVKET+R+ +EL KLG ++E D I + V +D++ DHR+AMAFSL
Sbjct: 347 HARVKETDRIATTCSELKKLGCKLKEFEDGMSIEGGIRSGV--VDSHKDHRLAMAFSLVG 404

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ I++ +FP++ + +S
Sbjct: 405 LKH-DIEIKNGEVFVDSFPNFIEAMS 429

>ref|NP_790877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000]
sp|Q888I3.1|AROAPSESM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAO54572.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000]
Length = 418

Score = 213 bits (541), Expect = 7e-53, Method: Compositional matrix adjust.
Identities = 152/436 (34%), Positives = 228/436 (52%), Gaps = 43/436 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132

VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125
Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G ++ G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEISAPSG--CPPVAIKGKGLQAGRIEIDGNLSSQYVSALLMAGAC 183
Query: 193 ALGDVEIEIIDKLISIP-YVENTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +E+ + I YV++TL M+ FG AE D + Y + + ++E
Sbjct: 184 GKGSLEVALTGSEIGARGYVDLTLAAMQAFG--AEVQAIGDAAWKVSATGYHA-TDFHIE 240
Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
DAS+A+Y A A+T G + + Q D +++++ P
Sbjct: 241 PDASAATYLWAAQALTEGNIDLGVASDAFTQPDALASQIIDSF-----P 284
Query: 312 REPFGRLKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
P A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+ L
Sbjct: 285 NMP-----AV-IDGSQMADAIPTLAVLAAFNRQPVRFVGIANLRVKECDRISALCDGL 336
Query: 372 TKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ G +VEEG D + P T IDT+ DHR+AM F+LA + I+DP
Sbjct: 337 CAIAPGLAVEEGDDLIVHANPALAGTIVNALIDTHSDHRIAMCFALAGLKIKGIHIQDPD 396
Query: 427 CTRKTFPDYFDVLSTF 442
C KT+P Y+D L++
Sbjct: 397 CVAKTYPGYWDALASL 412

>ref|ZP_07034385.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oris C735]
gb|EF149077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oris C735]
Length = 412

Score = 212 bits (540), Expect = 8e-53, Method: Compositional matrix adjust.
Identities = 146/437 (33%), Positives = 228/437 (52%), Gaps = 46/437 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I TVKLP SKS+SNR L++ AL+ V DNL + +D ++ AL+T+ +++
Sbjct: 9 QHIDTTVKLPASKSISNRALIIQALAGDNVVPDNLSDCDDTEVIIIEALKTMPETID---- 64
Query: 73 AKRAVVVGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +G AMR +TA ++ + G +VL G RM++R
Sbjct: 65 -----IKASGTAMRFMTAYLSVSEGE--HVLGTGDRMKQR 97
Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ LGAD+ PP+R+ G L GG +++SGSISSQ++SALL+ P+
Sbjct: 98 PIAVLVDALRYLGADIAEYEGEAGFPPLRIKG--RRLEGGYLEISGSISSQFISALLLIGPM 156
Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+++ D +IS PY+++TL +M FG E +D I K + + Y+E
Sbjct: 157 LEKGLELKMTDTIISRPIYDLTLCMMRDFGAAVEWTDV---DTISVAPKPYTSRRYYIES 213
Query: 253 DASSASYFLAGAAITG---GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S+ SY+ A++ TV +EG S QGD + ++G K ++ T+ V
Sbjct: 214 DWSAGSYWYEIMALSDDSEATVRLEGLMDGSRQGDVVKYIFSLLGVKTSFETTAPCV-- 271
Query: 310 PPREFPGRKH---LKAIIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P R+H L ++ + PD+A TL V D + +A+ R+KET+R+ A
Sbjct: 272 -PNTVTLRHRKCLLPRLLEYDFTGSPDLAQTLVCCALMDIKFHFGLATLRIKETDRIEA 330
Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
++TEL KLG + D + E+ T AIDTY+DHRMA+AF+ A + I +
Sbjct: 331 LKTELRLKGYVLHNVGDNELFWDGERCEPTGEAIDTYEDHRMALAFAPVALKCPGLQINN 390
Query: 425 PGCTRKTFPDYFDVLST 441
P K++PDY+ L T
Sbjct: 391 PEVVSKSYPDYWKDLQT 407

>ref|YP_003247910.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
vulcanius M7]
gb|ACX73428.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus

vulcanus M7]
Length = 426

Score = 212 bits (539), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 140/436 (32%), Positives = 231/436 (52%), Gaps = 19/436 (4%)

Query: 8 VLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ + G+VK P SKS ++R ++ A+L++G + + N L D + + LG +
Sbjct: 1 MINKTSRLEGSVKAPPSKSYTHRAVIGASLADGVSRINPLWGADCLSSVYGCKMLGAEI 60

Query: 68 EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E K +V GGK D + +GN+G +R LT+ + + VL G
Sbjct: 61 ELKKEEDEWIV--KGGKLKTPDN---VIDIGNSGTTLRILTS-IASQIPRGYAVLTGDD 113

Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+R+RP+ L+ LKQL + P+ V G + G KVK+ G ISSQ++++L+
Sbjct: 114 SIRKRPMQPLLDALKQLNINAFSSKLDGTAPIIVKS-GKIEGNKVKIRGDISSQFITSML 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
M P D EI + L S PY+++T+ ++ FG+K + +++ F + G Q+YK+ +
Sbjct: 173 MFLPFNKEDTEIILTSPLKSKPYIDITIDILSTFGIKIKETENG--FLVYGNQYKAI-D 229

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VEGD SSASY +A + +T+E S QGD +++ MGA V + V +
Sbjct: 230 YIVEGDYSSASYLIAAGVLINSNITIEINLFANSKQGDKAIINIVKEMGADVKKDKVII 289

Query: 308 TGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G +L+ IDV++ +PD+ T+AV+ FA+G T I + R+KE +R+ A
Sbjct: 290 EG-----EYNLEGIDVDVRDIPDLVPTIAVLGCFAGKTEIYNGEHVRLECDRLNAC 342

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
TEL K+GA ++E PD II +KL ++TY DHR+ MAF++A AE I
Sbjct: 343 ATELKKMGADIKPKDGLIIRGVKKLRGAKLNTYHDHRLVMAFTVAGLKAEGKTIIEGED 402

Query: 427 CTRKTFPDYFDVLSTF 442
+ +FP++ +V+ +
Sbjct: 403 AVKISFPNFVNMKSL 418

>ref|YP_273200.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. phaseolicola 1448A]
ref|ZP_06459190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. aesculi str. NCPPB3681]
ref|ZP_06479014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. aesculi str. 2250]
sp|Q48N21.1|ARO_A_PSE14 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ35419.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. phaseolicola 1448A]
Length = 418

Score = 212 bits (539), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 152/438 (34%), Positives = 228/438 (52%), Gaps = 47/438 (10%)

Query: 13 KEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G +V G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEVSAPSG--CPPVAIKGGGLEAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G VE+ + I YV++TL M+ FG V+A +W Y++ + +
Sbjct: 184 GKGPVEVALTGSEIGARGYVDLTLAAMQAFGAEVQAIGETAWK----VSATGYRA-TDFH 238

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E DAS+A+Y A A+T G + + Q D ++++
Sbjct: 239 IEPDASAATYLWAAQALTEGDIDLGVSADFTQPDALASQIIASF----- 283

Query: 310 PPREFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
++ A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+
Sbjct: 284 -----PNMPAV-IDGSQMQDAIPTLAVLAFAFNRPVRFVGIANLRVKECDRISALSH 334

Query: 370 ELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRD 424
L + G +VEEG D + P T IDT+ DHR+AM F+LA + I D
Sbjct: 335 GLCAIAPGLAVEEGDDLLVHANPALAGTTVDALIDTHSDHRIAMCFALAGLKIAGIRILD 394

Query: 425 PGCTRKTFPDYFDVLSTF 442
P C KT+P Y+D L++
Sbjct: 395 PDCVGKTYPGYWDALASL 412

>ref|ZP_03301793.1| hypothetical protein BACDOR_03185 [Bacteroides dorei DSM 17855]
ref|ZP_04539309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
9_1_42FAA]
ref|ZP_04554742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D4]
ref|ZP_06090380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_1_33FAA]
gb|EEB24351.1| hypothetical protein BACDOR_03185 [Bacteroides dorei DSM 17855]
gb|EEO47526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides dorei
5_1_36/D4]
gb|EEO62975.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
9_1_42FAA]
gb|EEZ19592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_1_33FAA]
Length = 409

Score = 212 bits (539), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 145/433 (33%), Positives = 227/433 (52%), Gaps = 51/433 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ AL T ++NL + +D M+ AL
Sbjct: 11 QIYTTIQLPSSKSISNRALIINALGNRTFQLENLSDCDDTQVMIHALN----- 58

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
D K + + AG AMR LTA ++ G T ++ G RM++RP
Sbjct: 59 -----DGKNTIDIM--AAGTAMRFLTAYLSVTPG--TRIITGTQRMQQR 99

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA+++ + PP+R+ G L + L G+ISSQY+SALLM AP+
Sbjct: 100 IQVLVNALRELGAIEIYIINDGYPLRITG-HKLQKDTISLPGNISSQYISALLMIAPIL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-DRFYIK-GGQKYKSPKNAYVE 251
+ + + ++IS PY+ +TL+LM FG KA+ W + + +K Q Y+S YVE
Sbjct: 159 SNGLALTLTGEIISRPIINLTQLMNDFGAKAK---WLNEYQLKVEPQPYQSIP-FYVE 213

Query: 252 GDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D S+ASY+ AA++ + + G TS QGD K AE+ +++G + + VT+
Sbjct: 214 SDWSAASYWYQIAALSNAEIIPLGLFETSYQGDSKVAEIFQLLGIESIYGNKMVTLKK- 272

Query: 311 PREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
K + +D + PD+A T V + P + S ++KET+R+ A+ E
Sbjct: 273 -----TDKIAERLDYDFINQPDLAQTFVVTCLMNIPFRFSGLSLQSLKIKETDRITALIKE 327

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVP-VTIRDPG 426
+ KLG + E D + E+ +T AIDTY+DHRMAMAF+ C +P + I +P
Sbjct: 328 MGKLGYLHEIDRILSWEGERCMENTADAAIDTYEDHRMAMAF-PVCVVMPEIRINNPQ 386

Query: 427 CTRKTFPDYFDVL 439
K++P Y++ L
Sbjct: 387 VVSKSYPPYWEDL 399

>gb|EFW82034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. glycinea str. B076]
gb|EFW86346.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae

pv. glycinea str. race 4]
Length = 418

Score = 211 bits (538), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 152/438 (34%), Positives = 228/438 (52%), Gaps = 47/438 (10%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+
Sbjct: 14 RPLVGRVSPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R
Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+++G +V G CPPV + G GGL G++++ G++SSQY+SALLMA
Sbjct: 126 PIGPLVDALQRMGEVSAPSG--CPPVAIKGKGGLGAGRIEIDGNLSSQYVSALLMAGAC 183

Query: 193 ALGDVEIEIIDKLISIP-YVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G VE+ + I YV++TL M+ FG V+A +W Y++ + +
Sbjct: 184 GKGPVEVALTGSEIGARGYVDLTLAAMQAFGAEVQAIGETAWK---VSATGYRA-TDFH 238

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E DAS+A+Y A A+T G + + Q D +++++
Sbjct: 239 IEPDASAATYLAQAALTEGDIDLGVASDAFTQPDALASQIIASF----- 283

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
++ A+ ++ ++M D TLAV+A F P +A+ RVKE +R+ A+
Sbjct: 284 -----PNMPAV-IDGSQMQDAIPTLAVLAFAFNRPVRFVGIANLRVKECDRISALSH 334

Query: 370 ELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRD 424
L + G +VEEG D + P T IDT+ DHR+AM F+LA + I D
Sbjct: 335 GLCAIAPGLAVEEGDDLLVHANPALAGTTVDALIDTHSDHRIAMCFALAGLKIAGIRILD 394

Query: 425 PGCTRKTFPDYFDVLSTF 442
P C KT+P Y+D L++
Sbjct: 395 PDCVGKTYPGYWDALASL 412

>ref|ZP_06254597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oris
F0302]
gb|EFB33067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oris
F0302]
Length = 412

Score = 211 bits (538), Expect = 1e-52, Method: Compositional matrix adjust.
Identities = 146/437 (33%), Positives = 227/437 (51%), Gaps = 46/437 (10%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I TVKLP SKS+SNR L++ AL+ V DNL + +D ++ AL+T+ +++
Sbjct: 9 QHIDTTVKLPASKSISNRALIIQALAGDNVVPDNLSDCDDTEVIIIEALKTMPETID---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +G AMR +TA ++ + G +VL G RM++R
Sbjct: 65 -----IKASGTAMRFMTAYLSVSEGE--HVLGTGDRMKQR 97

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ LGAD+ PP+R+ G L GG +++SGSISSQ++SALL+ P+
Sbjct: 98 PIAVLVDALRYLGADIAYEAGEAGFPPLRIKG-RRLEGGYLEISGSISSQFISALLLIGPM 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+++ D +IS PY+++TL +M FG E +D I K + + Y+E
Sbjct: 157 LEKGELEKMTDTIISRPYIDLTLCMMDRFGAAVEWTDV---DTISVAPKPYTSRRYYIES 213

Query: 253 DASSASYFLAGAAITG---GTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S+ SY+ A++ TV +EG S QGD + ++G K ++ T V
Sbjct: 214 DWSAGSYWYEIMALSDSEATVRLEGLMDGSRQGDVVKYIFSLLGVKTSFETTDPCV-- 271

Query: 310 PPREFPGRKH---LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P R+H L ++ + PD+A TL V D + +A+ R+KET+R+ A
Sbjct: 272 -PNTVTLLRRHKCLLPRLLEYDFTGSPDLAQTLVVCCALMDIKFHFGLATLRIKETDRIEA 330

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPTIRD 424
++TEL KLG + D + E+ T AIDTY+DHRMA+AF+ A + I +
Sbjct: 331 LKTELRLKGYVLHNVGDSELFWDGERCEPTGEAIDTYEDHRMALAFAPVALKCPGLQISN 390

Query: 425 PGCTRKTFPDYFDVLST 441
P K++PDY+ L T
Sbjct: 391 PEVVSKSYPDYWKDLQT 407

>ref|YP_447541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosphaera
stadtmanae DSM 3091]
sp|Q2NH05.1|AROAMETST RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABC56898.1| AroA [Methanosphaera stadtmanae DSM 3091]
Length = 426

Score = 210 bits (535), Expect = 3e-52, Method: Compositional matrix adjust.
Identities = 145/443 (32%), Positives = 239/443 (53%), Gaps = 29/443 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ ++ I +ISG +K P SKS S+R + AAL+EG +++ + L S D L A LG
Sbjct: 2 DLQVEKINKISGVKAPASKSYSHRAFIAAALAEGQSILRDPLYADTIATLEACEQLGA 61

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY-VLD 124
+ + + +V G G + +V+ N+G ++R L++ V A A Y +
Sbjct: 62 LFQ--RYPDKCIVQGTAGYIRTPENIIDVK---NSGTSVRILSS-VAAIAPRANYTIFT 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R+RP+ DL+ L+ LG + PP+ V G G GG+ + G +SSQ++S
Sbjct: 115 GDESRLKRPMQDLIDALENLGVQISSQSNGTPPIIVKG--GFEGGQTDIKGDVSSQFIS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS----WDRFYIKGGQ 240
+++MAAP + V + + +S PYV MTL ++ +FG+ E+ + + +YI+ Q
Sbjct: 173 SIIMAAPYSKKPVTLNVKGTTFVSKPYVNMVTLVSKFGIDFEYDTTNIPEYSSYYIE-PQ 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLGQGDVKFAEVLEMMGAKVTW 300
KY++ + +EGD SSASY LA AA+ +TV+ S+QGD ++++ MGA+VT
Sbjct: 232 KYEA-TDYTIEGDYSSASYILAAAAMLPSNLTVNLYKDSMQGDKIIDIKKMGAEVTV 290

Query: 301 TETSVTVTGPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ + + E G +LKA D+N+ PD+ T++++ A+G + I V R KE
Sbjct: 291 DDDQIHI-----ESDG--NLKAFDINLEDAPDLLPTISILMAQAEGVSKITGVEHARFKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEV 418
T+R+ EL +G VEE D II K N T +D++ DHRM MAF +
Sbjct: 344 TDRVHNCAVELENVGDVEELQDGLII----KGNPTGGYVDSHMDHRMVMAFYVLGLKIG 399

Query: 419 PVTIRDPGCTRKTFPDYFDVLST 441
+ I+D C +FP++ +V+ T
Sbjct: 400 NIIKIDASCYDISFPNFLEVMHT 422

>ref|ZP_07329272.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetivibrio
cellulolyticus CD2]
gb|EFL59436.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetivibrio
cellulolyticus CD2]
Length = 422

Score = 210 bits (534), Expect = 4e-52, Method: Compositional matrix adjust.
Identities = 149/428 (34%), Positives = 227/428 (53%), Gaps = 24/428 (5%)

Query: 14 EISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++G VK+PGSKS + R L +A+L+ G + V N L S D + + LG + DK
Sbjct: 9 KVNGRVKIPGSKSHTIRALFMASLAGGESQVYNPLISSDALSAVEVCKALGAQI--DKLD 66

Query: 74 KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ + G G G P A + +GN+G +R AA G V G ++R RP
Sbjct: 67 NKYTIKGFNGS-PCTPAD---VINVGNSGTTLR--LGVYLAALGEGYTVFTGDYQVRRRP 120

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G L+ + LG + D PV V G L GGK +L S++SQ+LS++L+++PL
Sbjct: 121 LGPLIKAINNLGGEAFATRNNDMAPVVVRG--KLKGKTELD-SVTSQFLSSILISSPLV 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E+ I +L IPYV++T M++ G+K E+++ + FYI G QKY+ P N + GD
Sbjct: 178 DKDTEVNIT-RLNEIPYVDITTWMMDKLGIKENNE-YKSFYIPGNQKYQ-PFNV TIPGD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTTTETS SVTVTGPPRE 313
SSA++F AAI+G +E T QGD + +LE MGAKVT S+ + G
Sbjct: 235 FSSATFFAVLAAISGEEFVLENLDITDPQGDKEVFSILED MGAKVTRGRDSIIK G---- 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L +D++MN +PD +AV FA G T + +V R+KET+R+ + +L K
Sbjct: 291 ----DTLTGMDIDMNAIPDALPAMAVAGCFKGETRLLNVPQARLKETDRIHVMCEQLGK 346

Query: 374 LGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPG-CTRKTF 432
+GA++EE D II KL ++ DDHR+ M+ ++A TI D TF
Sbjct: 347 MGANIEELEDGLIIR-ESKLGKQVNGCDDHRIVMSLAIAGLNSEGETIIDS AEAINVTF 405

Query: 433 PDYFDVLS 440
P++ +S
Sbjct: 406 PEFVSNVS 413

>ref|YP_003708293.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus voltae
A3]
gb|ADI37320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus voltae
A3]
Length = 456

Score = 209 bits (533), Expect = 5e-52, Method: Compositional matrix adjust.
Identities = 142/462 (30%), Positives = 237/462 (51%), Gaps = 40/462 (8%)

Query: 7 IVLQPIKEISGTVKLP GSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+++ P K+I+GTV P SKS ++R ++ A L+ GT+ + L S+D L A++ LG +
Sbjct: 2 LLVNPTKKINGTVYAPPSKSYTHRAVICAGLANGTSKIIQPLKSQDCISSLNAMKALGST 61

Query: 67 VEADKAAKRAV-----VVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
++ K+ + + G V + + +GN+G +R LT+ V+ N+
Sbjct: 62 IDIKKSNDELENEVWTISSDGNLKV P---KNVIDIGNSGTTLRLITSLVVSQIPHNSIA 117

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+L+G +R+RP+G L+ L QL +V L D V + G VK++G +SSQ
Sbjct: 118 ILNGDESIRKRPMPGLIEALSQNLIEV---LSNDNKAPLVVKKSSKIDGNIVKITGDMSSQ 174

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR----- 233
++S+L+M P D +I I L S PY+ +T+ L+++FGV + + +
Sbjct: 175 FISLMLLPNTQDSKILIEGDLKSEPYLNITIDLLDKFVSIKKDEINNINNINKKNK 234

Query: 234 -----FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
+ IK Q YK+ + VEGD SSASY +A + +T++ S QGD +
Sbjct: 235 TNKKENAYLIKANTYKAT-DYIVEGDYSSASYLIALGVLLDSITIKNLFKDSKQGDKE 293

Query: 287 FAEVLEMMGAKVTTTETS SVTVTGPPREPFFGRKHLKAIDVNMNMPDVAMTLAVVALFADG 346
+++ MGA + + V + + LK ID+++ PD+ TLAV+ FA+G
Sbjct: 294 IINIVKRMGADLEIRDDEVIKN-----SKFKLKGIDIDVKNTPDVPTLAVLGCF AEG 347

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVT AIDTY 401
T I + R+KE +R++A EL K+GA +EE PD II E L ++TY
Sbjct: 348 TTTIYNGEHVRIKECDRLMACTKELKKMGAKIEEKPGLIIQGLDIDNGETLKGAELETY 407

Query: 402 DDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
DHR+ MAF++A A+ I+ +FP++ DV+ +
Sbjct: 408 HDHRLIMAFMAGMLAKGQTKIKGEEAVSISFPNFVDVIKSI 449

>ref|ZP_03206915.1| hypothetical protein BACPLE_00528 [Bacteroides plebeius DSM 17135]
gb|EDY97018.1| hypothetical protein BACPLE_00528 [Bacteroides plebeius DSM 17135]
Length = 410

Score = 209 bits (533), Expect = 5e-52, Method: Compositional matrix adjust.
Identities = 147/443 (33%), Positives = 218/443 (49%), Gaps = 52/443 (11%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I + P +I ++LP SKS+ NR L++ AL+ T +NL + +D M+ AL + +
Sbjct: 4 IEITPPADIQTCIQLPSSKSIICNRALIINALAASTCRPENLSDCDDTRVMIEALTHMPET 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ + AG AMR LTA ++ G T++L G
Sbjct: 64 ID-----IMAAGTAMRFLTAYLSVTPG--THILTGT 92

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RMR+RPI LV L LGA ++ PP+++ G L G + L G++SSQY+SAL
Sbjct: 93 ERMQRPIKILVDALTSLGAQIEYTENEGYPLKITG-KALEGHSCLPGNVSSQYISAL 151

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM P+ + +E+ ++IS PY+ +TL++M+ FG KAE + D Y P
Sbjct: 152 LMIGPMLAHGLNLEGEIISRPIYNLTLMKDFGAKAEWTS--DHTLQVAPHPYH-PI 208

Query: 247 NAYVEGDASSASYFLAGAAITG--GTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
YVE D S+ASY+ A++ VT+ G S QGD K AE+ E +G S
Sbjct: 209 PYYVESDWSAASYWYEIVALSKEAVVTLPLGLFAQSPQGDQAKVAELFEQLGVCTQREGNS 268

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
VT+ H ++ N PD+A T V P + S ++KET+RM
Sbjct: 269 VTLKK-----THPHTDRMEYNFVNQPDLAQTFVVTGAMLGIPFRFSGLSLQSLKIKETDRM 322

Query: 365 VAIRTELTKLGASVEEGPDYCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
A+ E+ KLG +EE + TP E AIDTY+DHRMAMAF+ AA
Sbjct: 323 AALIAEMRKLGVLEESEGSVLSWTGTRCTPDES---PAIDTYEDHRMAMAFAPAALCNS 379

Query: 419 PVTIRDPGCTRKTFPDYFDVLST 441
+ IR+P K++P +++ L T
Sbjct: 380 TLRIRNPHVVSYSYPRFWDLLT 402

>ref|YP_001239786.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium sp.
BTai1]
gb|ABQ35880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium sp.
BTai1]
Length = 418

Score = 209 bits (532), Expect = 6e-52, Method: Compositional matrix adjust.
Identities = 159/441 (36%), Positives = 231/441 (52%), Gaps = 43/441 (9%)

Query: 8 VIQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ P + G V PGSKS++NR LLLAAL+ GT+ + L S D M ALR +G+ V
Sbjct: 8 IIPPAHPLVGRVTPPGSKSITNRALLAALARGTSRLTGALKSRDRTLMAAALRQMGVVV 67

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D+ + VV G+ ++ + L LGNAG AMR LTAA AA + T +LDG
Sbjct: 68 --DEPDTSFVVTSPGRL----SRPDQPLMLGNAGTAMRFLTAA--AALCDGTVILDGDD 119

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
MR+RPIG L+ ++ LG + T CPPV V G G G+V++ G++SSQY+SALL
Sbjct: 120 AMRKRPIGPLLAMQSLG--IAAVAPTGCPPVTQGRGHFGSGRVEIDGALSSQYVSALL 177

Query: 188 MAAPLAGDVEIEIIDK-LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
MAA G +E+ + K L + YV++T+ M FG K E DR + +
Sbjct: 178 MAAADGQGQIEVVLGKDLARGYVDLTVAAMTAFGAKVELV---DRTTWRVAPTGYTAT 234

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VE DAS+++Y A A+T G + + Q D K A+++ M
Sbjct: 235 DFVVEPDASATYLAWEALQGRIDLGVPIEAFTQPDAKAQLIRMF----- 282

Query: 307 VTGPPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
HL + ++ ++M D TLAV+A F P +A+ RVKE +R+ A
Sbjct: 283 -----PHLPTV-IDGSQMQDAVPTLAVLAFAFNATPVRFTGIANLRVKECDRIRA 330

Query: 367 IRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPVT 421

+ TEL+++ G E+G D + P T I+TY+DHR+AM+F+LAA +
Sbjct: 331 LATELSRIRPGLGREDGDDLIVAADPGLAGQTLPARIETYEDHRIAMSFALAAALRIGGIV 390

Query: 422 IRDPGCTRKTFFPDYFDVLSTF 442
I DP C KT+P Y+D L

Sbjct: 391 ILDPACVGTKTYPGYWDALRAL 411

>ref|NP_988325.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcus
maripaludis S2]
sp|Q6LXY8.1|AROA_METMP RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAF30761.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Methanococcus
maripaludis S2]
Length = 429

Score = 209 bits (532), Expect = 6e-52, Method: Compositional matrix adjust.
Identities = 141/444 (31%), Positives = 234/444 (52%), Gaps = 25/444 (5%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+V++ I G + P SKS ++R ++ A+L+ G + + N LN D A G
Sbjct: 2 LVVKKTPYIKGILSAPPSKSYTHRAVICASLANGLSNLKNPLNGADCLSSAHACEMFG-- 59

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E ++ +V+G K P + + +GN+G +R LT +++ N VL G
Sbjct: 60 AEIGLGNEKWIWMGSELKTP-----DNIVDIGNSGTTLRILTGT-ISSQISNGYTVLTGD 112

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+R+RP+ L+ LKQLG + CF + P+ V G + V++ G +SSQ+++
Sbjct: 113 DSIRKRPMQPLLDALKQLG--LICFSTKNNGTAPIVVKSGKISSNVVEIRGDMSSQFIT 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDR--FYIKGGQKY 242
+L+M P + D EI + L S PY+ +T+ ++++FGVK + ++ + IKG Q Y
Sbjct: 170 SLMMTLPFSEDDSEIILTTPLKSEPYLNITIDVLDKFGVKIGKIEKNKSGYKIKGNQTY 229

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTE 302
K P + +EGD SSASY +A + + ++ S QGD + E+++ MGA V +
Sbjct: 230 K-PCDYTIEGDYSSASYLVAAGVLLNSDIVIKNVFKDSKQGDREIIEIVKKMGADVEIND 288

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+V +TGP L I++++ +PD+ T+AV+ FA G T + + R+KE +
Sbjct: 289 DNVKITGP-----YELNGIEIDVTDIPDLVPTIAVLGCFAGKTKVVYNGEHVRLKECD 341

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ A EL+K+GA +EE D IIT KLN + TY DHR+ MAF++A A+
Sbjct: 342 RLAACTAELSKMGARIEKKDGLIITGVHKLNGAKLKYHDHRLVMAFTIAGMLADGETI 401

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVKN 445
I + +FPD+ D + + N
Sbjct: 402 IEGEDSVKISFPDFVDKMKSIGSN 425

>ref|YP_003424319.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA
[Methanobrevibacter ruminantium M1]
gb|ADC47427.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA
[Methanobrevibacter ruminantium M1]
Length = 455

Score = 209 bits (532), Expect = 7e-52, Method: Compositional matrix adjust.
Identities = 154/456 (33%), Positives = 244/456 (53%), Gaps = 38/456 (8%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +I+GTVK P SKS S+R ++LA+LSEG + + ++L SEDV + A LG ++
Sbjct: 5 IKNFSKINGTVKAPSSKSYSHRAVILASLSEKSKLFDVLYSEDVLSTIRACEALGARID 64

Query: 69 ADK-----AAKRAVVVGCGGKFP-VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG 117
K V G GKK V D + L N+G +R +T+ AA
Sbjct: 65 KKKEIILKGDKSQTVDYLEVYGTGGKLHNVSDDPSSDMIDLANS GTTLRIMTSV--AALS 122

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+ + G ++ RP+G L+ L+ LG ++ + P+++ G GG+ + GS
Sbjct: 123 DNEVIFTGDDSLKTRPMGALIDALETGLVKIESLNENNKAPLKI--YPGYEGGQTDILGS 180

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV-----K 224
ISSQ++S++L++APL+ VE+E+ + +S PYV+MT+ ++E+FG+ K
Sbjct: 181 ISSQFISSILISAPLSENGVELEVYPFVSKPYVDMTISILEKFGISVEEEYQFHETCK 240

Query: 225 AEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
EH+D +I QKY + + VEGD SSASY LA AI GG + V+ S QGD
Sbjct: 241 KEHTDCLGVKFIVKPKQYIAS-DYIVEGDFSSASYLLAATAIAGGYIRVQNLFADSKQGD 299

Query: 285 VKFAEVLMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA 344
++LE MGA VT + V++ +LK IDVN++ PD+ +T+AV+ A
Sbjct: 300 KLILDILEEMGANVTVFDDYVSLRSDG-----NLKGIDVNLNAPDLLLTVAVLGALA 352

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDH 404
+G T I V R+KET+R+ EL KLG +EE D I ++ ++++ DH
Sbjct: 353 EGKTTISGVKHGRLKETDRIDTTCRELEKLGCKLEEFEDGMTIY-GNTISDGIVESHGDH 411

Query: 405 RMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
R+AMAFSL V + + C +FP++ + ++
Sbjct: 412 RLAMAFSLIGLKH-DVEVENGECEFDVSFPNFIEMA 446

>ref|YP_003850067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermobacter
marburgensis str. Marburg]
gb|ADL58754.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermobacter
marburgensis str. Marburg]
Length = 421

Score = 208 bits (530), Expect = 1e-51, Method: Compositional matrix adjust.
Identities = 152/422 (36%), Positives = 232/422 (54%), Gaps = 26/422 (6%)

Query: 14 EISGTVKLPKSGKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+SGTVK P SKS ++R +++AAL++G + + + L +ED + A R G+ +E ++
Sbjct: 10 ELSGTVKAPPSKSYTHRAVIVAALADGISEIRDPLVAEDTLSSVEACRAFGVDIEGNE-- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ V G GG+ D ++LGN+G +R +T+ V N T VL G +R RP
Sbjct: 68 -KWSVTGSGGELETDPDD---VVYLGNSGTTLRIMTS-VAGLAENYT-VLTGDESLRTRP 120

Query: 134 IGDVVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+ LK LG + PPV + G G GG+ + GS+SSQ++S++L+AAPL+
Sbjct: 121 MQPLLDALKPLGVEAVSSRMNGLPPVIK--GFRGGETSIEGSLSSQFISSILIAAPLS 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G V++++ + IS PYV+MTL +ME+F V E+SD F ++ +Y+ + VEGD
Sbjct: 179 EG-VDLKVEGEFISRPYVDMTLDVMEKFSVPVEYSQGV--FSVEP-SRYRG-RTYTVEGD 233

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSASY A+ GG V +E S QGD +++ MGA V + V V+
Sbjct: 234 YSSASYLAGAVAVAGGEVRIENLFRDSRQGDRIILDIISEMGADVVDNHVVSST--- 290

Query: 314 PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L + +++ PD+ T+AV+ ADG T IR V R KET+R+ TEL K
Sbjct: 291 ----GELSGVQADLHDAPDLLPTVAVLGALADGRTEIRGVEHARYKETDRITCATELGK 346

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
LG V+E D +I + V + ++ DHR+AMAF+L E +TI D +FP
Sbjct: 347 LGVDVKELRDGMVIEGGVRRGV--VSSHGDHRLAMAFTLIGLRE-GITIMDGEVFSVSFP 403

Query: 434 DY 435
D+
Sbjct: 404 DF 405

>ref|YP_002506738.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulolyticum H10]
sp|B8I5M2.1|AROACLOCE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|ACL76758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulolyticum H10]
Length = 422

Score = 208 bits (530), Expect = 1e-51, Method: Compositional matrix adjust.
Identities = 137/400 (34%), Positives = 219/400 (54%), Gaps = 23/400 (5%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ISG++ +PGSKS + R L LA L++GT+V+ N L S D + R G + + + +
Sbjct: 9 DISGSISIPGSKSHTIRSLFLAGLAKGTSVIRNPLLSTDAVSGVNVCRAGSTYDLNNES 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+G + P E + +GN+G ++R +TAA + V G ++R+R
Sbjct: 69 YVVGNGMACPQVP-----ENVIDVGNSGTSR--LGLMTAALVDGYTVFTGDYQIRKRQ 120

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV + LG G + PV + G GG KL ++SQYLS++L+ PL
Sbjct: 121 IGPLVEAINNLGGKAFTTRGNESAPVVIKGRA--TGGYTKLD-CVTSQYLSILLNTPLL 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D +EI +L IPYVE+TL +++ G+K H +S F+I GGQ+Y+ P + GD
Sbjct: 178 EKDTHVEIT-RLNEIPYVEITLWLDKLGIKYSH-NSMKEFFIPGGQYR-PFECTIPGD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPE 313
SSA++F+ AAi+ + + + QGD ++L MGA++ + ++ + G
Sbjct: 235 FSSATFFMVQAAISERELVLTNLDMDPQGDKAVIDLADMGAEIKYDHNNIKIKG--- 290

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K LK +++MN +PD +AV A FA G T + +V R+KET+R+ + +ELTK
Sbjct: 291 ----KSLKGREIDMNSIPDALPAMAVAACFAKGETRLVNVQARLKETDRISVMCSELTK 346

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+GA + E PD +I KL+ A+ YDDHR+ M+ ++A
Sbjct: 347 MGADISELPDGLVIR-ESKLHGAAGVGYDDHRIVMSLAIA 385

>ref|YP_004262686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulophaga lytica
DSM 7489]
gb|ADY29815.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulophaga lytica
DSM 7489]
Length = 409

Score = 208 bits (530), Expect = 1e-51, Method: Compositional matrix adjust.
Identities = 152/429 (35%), Positives = 227/429 (52%), Gaps = 48/429 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ +K+ GSKS SNR+LLL AL + +NL NS+D
Sbjct: 11 KTLNSAIKITGSKSESNRLLLLQALYPNIKI-ENLSNSDD----- 49

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A+V+ G K +K EV + +AG AMR LT + G VL G RM ER
Sbjct: 50 ---AIVMQKGIKV---SKGEVDIH--HAGTAMRFLTTYFSCQDGKEV-VLTGSKRMTER 99

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV LK LGAD+ + PP+ + G + KV L +ISSQY+S+L++ AP
Sbjct: 100 PIGVLVDALKSLGADITYLENSGYPLHIKG-KKITNKVSLPANISSQYISSLVLTAPS 158

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA--YV 250
+E+E++ K+ S+PY++MTL L+ + GV+ +S++ IK K KS N V
Sbjct: 159 LDNGLELELVGKITSVPYIKMTLALLTQIGVE---NSFEGNTIKVAPK-KSVSNTTLVV 213

Query: 251 EGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
E D SSASYF + A++ G +T+ SLQGD A++ G + T+ + V +
Sbjct: 214 ESDWSSASYFYISIVAMSAVGTEITLSAYKKDSLQGDSVLADIYTDGFGVETTFDAKVVV- 272

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+ K + I +++ PD+A T+AV + + + ++KET+R+ A++
Sbjct: 273 ----KKITDKETQEITKDLNAPDIAQTIATVTFGLGLGCHLTGLHTLKIKETDRLEALK 328

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGC 427

TELTKLGAS+ I P K+N AIDTY+DH RM MAF+ A + + I D G
Sbjct: 329 TELTKLGASITVTDKTLTIKPTTKINKDIAIDTYNDHRMGMAFAPLAL-KTNLFINDAGV 387

Query: 428 TRKTFPDYF 436
K++PD++
Sbjct: 388 VSKSYPDFW 396

>ref|YP_004260363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
salanitronis DSM 18170]
gb|ADY37890.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
salanitronis DSM 18170]
Length = 421

Score = 208 bits (529), Expect = 1e-51, Method: Compositional matrix adjust.
Identities = 140/444 (31%), Positives = 224/444 (50%), Gaps = 58/444 (13%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L P I T++LP SKS+ NR L++ ALS+ + NL + +D ++ AL+ + +
Sbjct: 14 ISLVPPASIHATIQLPSSKSI CNRALIINALSQNHQALRNLSDCDDTRVLISALQDMPDT 73

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ +G AG AMR LTA ++ G T++L G
Sbjct: 74 ID-----IGAAGTAMRFLTAYLSVNEG--THLLTGT 102

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM++RPIG L L++ GA ++ PP+R+ G L ++ L G++SSQY+SAL
Sbjct: 103 PRMQQRPIGILANALREAGAHIEYAGKEGYPLRITG-SRLTHNEITLPGNVSSQYISAL 161

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM P +++ + +IS PY+++TL LM+ FG A+ SD + Y++ Y++P
Sbjct: 162 LMIGPALPDGKLTLTGTVISRPYIDLTLLEMQAFAHAQWSDE-HQLYVE-PHPYQAPA 219

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ Y+E D S+ASY+ A+ + + G SLQGD + A + +G + + V
Sbjct: 220 SYIIESDWSAASYWYEICALMPEAEIELPGLFRKSLQGDARVARLFSALGVETRYENDKV 279

Query: 306 TVTGPPPREPFGKRHLKA--IDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETER 363
+T + +K ++ + PD+A T V D P + S ++KET+R
Sbjct: 280 LLT-----KSDIKTSRMEYDFINQPDLAQTFVVTICALLDVPFRFSGLSLQSLKIKETDR 331

Query: 364 MVAIRTELTKLGASVEE-----GPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC 415
M A+ E+ KLG + E + CI P + AIDTY+DH RMAMAF+ A
Sbjct: 332 MAALIKEMKKLGYVLNETDGSILSWNGERCII--PDAR---PAIDTYEDHRMAMAFAPACI 386

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVL 439
+ I +P K++P Y+D L
Sbjct: 387 IVDNLFINNPQVVSKSYPHYWDDL 410

>ref|ZP_07978543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actG]
ref|ZP_07982994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actF]
Length = 427

Score = 207 bits (528), Expect = 2e-51, Method: Compositional matrix adjust.
Identities = 157/426 (36%), Positives = 229/426 (53%), Gaps = 27/426 (6%)

Query: 20 KLPKSKSLSNRILLALLAALSEG-TTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
++PGS+SL+NR LLL+A EG T+ + L SED AL LG V+ + A A+
Sbjct: 14 RIPGSESLTNRALLLSAAGEGATSELSYPLVSEDTIAFAEALTRLGARVQ--RPAGSALW 71

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
GG+ + +++ +AG A R L AA G + +G ++ RP+ L
Sbjct: 72 RVTGGR-----PRGAARVWCADAGTAARFLP--FFAATGTGDFTFEGSAQLTARPVAPLA 124

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L++LGA V G P +RV GL GG + + GS+SSQ+LS LLMAAPL G +
Sbjct: 125 EALRRLGARVSTAEGGRPL-LRVRS-AGLDGGDLIDGSLSSQFLSGLLMAAPLLRGPLT 182

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + +++S PY +MTL LM FG + + F ++ Y++ VE DAS+AS
Sbjct: 183 VRV-REVVSRLPYADMTLALMRHFGAEVAPSPGE-FAVRP-TGYRA-AGLRVEPDASTAS 238

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT--GPPREPFG 316
YF A AA+ GG+VTV G SLQGDV+F +VL GA+V + T +TV+ GP R F
Sbjct: 239 YFFAAAVVGGSVTVGGLSRDSLQGDVRFVDVLARAGARVEYGATGITVSGNGPLRGGF- 297

Query: 317 RKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
V+M ++ D MTLA +A AD P + + R+KE++R+ A+ L G
Sbjct: 298 -----TVDMGEISDTFMTLAAIAPLADAPVTVTGIGHARLKESDRIEAVSRNLRACGV 350

Query: 377 SVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
E G D+ I P + +I + DHR+AMAF++ +T+ DP C KTFP +
Sbjct: 351 RAETGADW-ITVHPGPVTPASIACHRDHRIAMAFVNLRTGNLTLDPAACVAKTFPGFH 409

Query: 437 DVLSTF 442
+ L F
Sbjct: 410 EELHRF 415

>gb|EFP78589.1| pentafunctional AROM polypeptide [Puccinia graminis f. sp. tritici
CRL 75-36-700-3]
Length = 1482

Score = 207 bits (527), Expect = 2e-51, Method: Compositional matrix adjust.
Identities = 168/455 (36%), Positives = 241/455 (52%), Gaps = 51/455 (11%)

Query: 12 IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEAD 70
IKEI T++ PGSKS+SNR L+LAAL GT + NLL+S+D M+ AL + G S +
Sbjct: 270 IKEI--TIRTPGSKSISNRALILAAALNGTCLKNLLHSDDTQVMINALEEMKGSFWSWE 327

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT----AAGGNATYVLDGV 126
VV G GK + V +LGNAG A R LT + ++ V+ G
Sbjct: 328 DNGATLVVSGGAGKLSSPANGKHV--YLGNAGTAARFLTTCVSLVKSQVSNQSSTVITGN 385

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVLKSGSISSQYLSAL 186
RM+ERPIG LV L+ G +D C P+R++ G PGG ++L+ S+SSQY+S++
Sbjct: 386 ARMQERPIGPLVDTLRTNGVQIDYLRNEGCLPLRISPEDGFGPGMIELAAVSSQYVSSV 445

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L++AP A V + ++ +ER A S + + I G YK+P
Sbjct: 446 LLSAPFAQAPVTLSLVG-----VERVKDPATGLPS-NTYRIPNG-TYKNPP 489

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVTWTETSV 305
+E DASSA+Y LA AA+ G ++T+E G+ SLQGD +FA +VLE MG +V TE
Sbjct: 490 VYEIESDASSATYPLAALNGLSITLETIGSGSLQGDAQFAKKVLEPMGCQVIQTERET 549

Query: 306 TVTGPPEPFGFRKHLKAI-DVNMNMPDVMATLAVVALFADGP-----TAIRDVASW 356
V GP L+ + +++M +M D +T VV A P T I +A+
Sbjct: 550 KVIGPST---VSELRQLGEIDMEEMTDAFLTACVVLGVAVQPSEKEQKMSTRIIGIANQ 605

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKL----NVTAIDTYDDHRMAMAF 410
RVKE R+ A+ EL K+G +E D + TP + L + I+ YDDHR+AMAF
Sbjct: 606 RVKECNRIAAMVAELGKMGIHAQELEDGIEVFGTPVDALAKRGDQVRINCYDDHRIAMAF 665

Query: 411 SLAACAEVP----VTIRDPGCTRKTFPDYFDVLST 441
S+ VP + + + C KT+P ++D LST
Sbjct: 666 SV--LGTVPGGKGLILNEKRCVEKTWPSWDDDLST 698

>ref|YP_003615995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
infernus ME]
gb|ADG13031.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocaldococcus
infernus ME]
Length = 425

Score = 207 bits (527), Expect = 3e-51, Method: Compositional matrix adjust.
Identities = 135/440 (30%), Positives = 237/440 (53%), Gaps = 21/440 (4%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66

++++ + + G VK P SKS ++R ++ A+L+EG +++ + LN D + R LG
Sbjct: 2 LIVRKTEHLEGGKVKAPPSKSYTHRAVISASLAEGKSLIKDPLNGRDCLASVRGCRLLGAK 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ K +++ V GGK + E+V + +GN+G +R LT+ +++ +L G

Sbjct: 62 I---KTSEKCEVEE-GGKI---ETPEDV-IDVGNSTTLRLITS-ISSLIPKGYAILTGD 112

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R+RP+ L++ L+Q+ P+ V + G KV++ G +SSQ++++L

Sbjct: 113 SSIRKRPMPEPLLLALRQINVKAYSSRLNGLAPIIVES-SKMGKNKVEIRGDVSSQFITSL 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M P D I + L S PY+++T+ ++ FGV+ E ++ + + G Q+Y+

Sbjct: 172 MMLLPFNEEDTNIILTSPLKSKPYLDITIDVLSHFVGRVEEVENG--YLVYGNQRYRCC- 228

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD SS+SY +A + + +E S QGD + E+L+ MGA + + V

Sbjct: 229 DYTVEGDYSSSYIIAAGVLINSNIVIENLFRDSKQGDKRIIEILKEMGADIKVKKDRVE 288

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G +L+ +++++N +PD+ TLAV+A FA+G T I + R KE +R+ A

Sbjct: 289 IEG-----EYNLEGVEIDVNDIPDLVPTLAVLACFAEGKTVIYNGEHVRYKECDRLRA 341

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
TEL K+GA +EE D II KL ++TY DHR+ MAF+ A AE IR

Sbjct: 342 CYTELKKMGADIEERRDGLIIRGVRKLKGAELETYHDHRLVMAFTAAGLKAEGETVIRGE 401

Query: 426 GCTRKTFPDYFDVLSTFVKN 445
+ +FP++ +V+ + N

Sbjct: 402 ESVKISFPNFVEVMKSLGAN 421

>ref|ZP_05392022.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
ref|ZP_06856903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
gb|EET87525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
gb|EFG86225.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
Length = 426

Score = 206 bits (525), Expect = 4e-51, Method: Compositional matrix adjust.
Identities = 141/441 (31%), Positives = 233/441 (52%), Gaps = 28/441 (6%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+++ P K +SG V++P SKS +R ++ A LS G + + N++ SEDV A++ LG+

Sbjct: 4 VMINPSK-LSGKVQVPTSKSACHRAVICAGLSNGISNISNVVFSSEDVEATCEAMKNLGVR 62

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ +K + + V G PV + + +G +R L G T+ G

Sbjct: 63 IKKEKDSLQ--VRGLEKLKPVNSSMD-----CSESGSTLRFLIPIGATTGEKLTf--KGK 113

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
++ ERP+ + D G P+ + G L G+ K+ G +SSQ++S L

Sbjct: 114 GKLVRLPKCYNIFDEQKLKYDNAGGK--LPLTIKG--KLKSGEYKIRGDVSSQFISGL 169

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ A PL GD +I I +L S PYV++T+ +++ +GV+ E+ + + F I+G Q YKS

Sbjct: 170 MFALPLLDGDSKIIITTELESKPYVDLTMDMLKNYGVQIENRE-YKEFIIRGNQNYKSS- 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD S A+++LA A + G + EG SLQGD ++E M K++ V

Sbjct: 228 DCEVEGDYSQAAFWLA-AGLLGNDIVCEGLDINSLQGDKAILNIIESMNGKISIEGNKVK 286

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P + K ++ ++ PD+ L +A ++G T I + A R+KE++R+ A

Sbjct: 287 AI-PSK-----TKGTIIDASQCPDLVPVLTSLAALSEGTTIIVNAARLRIKESDRLSA 338

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
I TEL +LGA +EE D II E L + +++DHR+AMA ++A+ C E PV I+D

Sbjct: 339 ISTE LNRLGADIEEKEDGLIIRGESLKGGEVQSWNDHRIAMALAVASIKCTE-PV I I K D 397

Query: 425 PGCTRKTFPDYFDVLSTFVKN 445

C +K++PD++ T N

Sbjct: 398 ASCVKKSYPDFWQHFR TLGGN 418

>ref|ZP_05417355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
finegoldii DSM 17565]
gb|EEX43369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
finegoldii DSM 17565]
Length = 410

Score = 206 bits (525), Expect = 5e-51, Method: Compositional matrix adjust.
Identities = 145/434 (33%), Positives = 225/434 (51%), Gaps = 49/434 (11%)

Query: 9 LQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68

L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 6 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPPE NLSDCDDTQVMIKALT----- 58

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

+ KE + + AG AMR LTA ++ G T + G R

Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM

Sbjct: 95 MQQRPIQILVNALRELGAIEYVRNEGYPPLRIKG-AELKGNEITLKG NVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248

P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S

Sbjct: 154 IGPALKDGLTLHLSGEII SRPYINLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307

VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +

Sbjct: 212 -VESDWSAASYWQIAALSPKAEIELGLFPNSYQGD SRGAEVFSRLGITTEFTSQGVKL 270

Query: 308 --TGPPREPFGRKHLKAIDVNMNKM PDMVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365

TG K L+ ++ + +PD+A T V + + P + S ++KET+R+

Sbjct: 271 KKTG-----KALERLEEDFVDIPDLAQTFVVTVCVLLNIPFRFTGLQSLKIKETDRIA 322

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL---NVT AIDTYDDHRMAMAFSLAACAEVPVTI 422

A+RTEL KLG +EE D ++ E+ + IDTY+DHRMAMAF+ A + I

Sbjct: 323 ALRTELKKG LVIEEENDSILMWNGERCEPEEIPVIDTYEDHRMAMAFAPAVICHPNLLI 382

Query: 423 RDPGCTRKTFPDYF 436

DP K++P Y+

Sbjct: 383 ADPQVVTKSYPGYW 396

>ref|ZP_05279686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis
3_1_12]
ref|ZP_07807445.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis
3_1_12]
gb|EFR51379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis
3_1_12]
Length = 416

Score = 206 bits (524), Expect = 5e-51, Method: Compositional matrix adjust.
Identities = 139/433 (32%), Positives = 224/433 (51%), Gaps = 51/433 (11%)

Query: 14 EISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73

I T++LP SKS+SNR L++ ALS+G V+ NL + +D M+ AL G ++

Sbjct: 10 HIKATIQLPASKSISNRALI IHALSKGNDVLSNLSDCDDTKVMVKALTEGGEVID----- 64

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

+ AG AMR LTA +++ G T+++ G RM++RP

Sbjct: 65 -----ILAAGTAMRFLTAYLSSTPG--THIIIGTERMQQRP 98

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193

I LV L++LGA ++ PP+R+ G L G ++ L G++SSQY+SALLM P+

Sbjct: 99 IQILVNALREL GASIEYTRNEGF PPLRIEG-APLAGNEITLKG NVSSQYISALLMIGPIL 157

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+++ + +++S PY+ +TL+LM+ FG A + D+ Q Y+ VE D
Sbjct: 158 KNGLQLRLTGEVVSRYINLTQLMKDFGASARWTS--DQISVPEPQPYRCVPFT-VESD 214

Query: 254 ASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
S+ASY+ A ++ + + G S QGD + AEV +G + +TE + +
Sbjct: 215 WSAASYWYQMAVLSSEADIELTGLFRHSYQGDSRGAEVFARLGIETEYTEEGERL----- 269

Query: 313 EPFGRKH---LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
RK+ +K +D + +PD+A T V D P + S ++KET+R+ A++
Sbjct: 270 ----RKNGSCVKRLDEDFVDIPDLAQTFVVTCTALLDVPFRFTGLQSLKIKETDRIEALKA 325

Query: 370 ELTKLGASVEEGPDYCIITPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIRDPG 426
E+ KLG + + D + E++ A I TY+DHRMAMAF+ AA + I +P
Sbjct: 326 EMKKLGYVLHDEDDSLYWNGERIEPQACPVIKTYEDHRMAMAFAPAAIHYPTIQIDEPQ 385

Query: 427 CTRKTFPDYFDVL 439
K++P Y+D L
Sbjct: 386 VVSKSYPGYWDDL 398

>ref|ZP_03530535.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium etli CIAT
894]
Length = 404

Score = 206 bits (524), Expect = 6e-51, Method: Compositional matrix adjust.
Identities = 154/438 (35%), Positives = 230/438 (52%), Gaps = 47/438 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ ++ P + +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIIPPGRPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMADALRAM 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++++ + VV G G P + LFLGNAG A R LTAA AA + T V+
Sbjct: 65 GVAID-EPDDTTFVVTGSGRLQP-----PKASLFLGNAGTATRFLTAA--AALVDGTVVV 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV ++ LG DV G CPPV V G G ++++ G +SSQY+
Sbjct: 117 DGDEHMRKRPIGPLVEAMRTLIGIDVTAETG--CPPVTVKGTGRFQADRIRIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A V+IE++ + I ++ Y+++T M+ FG + E +W R G
Sbjct: 175 SALLMMAAGGDRPVDIELVGEDIGALGYIDLTTAAMKAFGARVEKISPVTW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
S + VE DAS+A+Y A +TGG + + Q D + +++
Sbjct: 232 --YSAADFIVEPDASAATYLWAAEVLTTGGAILDGVPAFAFSQPDARAYDMIARF----- 283

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
P+ P +++ ++M D TLAV+A F P +A+ RVKE
Sbjct: 284 -----PQLP-----AEIDGSQMQDAVPTLAVLAAFNATPVRFVGIANLRVKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPPE---KLNVTADTYDDHRMAMAFSLAAC 415
+R+ A+ + L ++ G + EEG D + + P K IDT+ DHR+AM+F+LA
Sbjct: 326 CDRIRALSSGLNRILPGLAREEGDDLIVRSDPALAGKRLPAEIDTFADHRIAMSFALAGL 385

Query: 416 AEVPTIRDPGCTRKTFP 433
+TI DP C KT+P
Sbjct: 386 KIDGITILDPDCVGKTYP 403

>gb|AAO33155.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Oryza sativa
Japonica Group]
Length = 190

Score = 206 bits (524), Expect = 6e-51, Method: Compositional matrix adjust.
Identities = 106/117 (90%), Positives = 110/117 (94%), Gaps = 1/117 (0%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
EEIVLQPI+EISG V+LPGSKSLSNRILL+ALSEGTTVVDNLLNSEDVHYML AL+ LG

Sbjct: 74 EEIVLQPIREISGAVQLPGSKSLSNRILLLSALSEGTTVVDNLLNSEDVHYMLEALKALG 133

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LSVEADK AKRAVVVGCGGKFPVE DAKEEVQLFLGNAG AMR LTAAVTAAGGNAT

Sbjct: 134 LSVEADKAKRAVVVGCGGKFPVEKDAKEEVQLFLGNAGTAMRPLTAAVTAAGGNAT 190

>ref|YP_004120716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
aesopoeensis Aspo-2]
gb|ADU61970.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
aesopoeensis Aspo-2]
Length = 452

Score = 206 bits (524), Expect = 6e-51, Method: Compositional matrix adjust.
Identities = 161/456 (35%), Positives = 229/456 (50%), Gaps = 45/456 (9%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV P SKSLS+R L+ AAL+ G + + L+S+D+ G L G ++E

Sbjct: 7 TVVAPPSKSLSHRTLIAAALANGVSEISGALDSDITRTRGCLAACGATIEEHGDMTLVT 66

Query: 78 VVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G + D K + +LF+ +G R +TA AA G T+ + G PRM ERP

Sbjct: 67 GMEDGPRGGNADGKHKDEPPAELFMHESGTTCLRLMTA--VAAAGRGTRFRVHGAPRMHERP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCP---PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+ +L L +LG F D P P V G K++++ SSQYLS LL+ A

Sbjct: 125 MAELTDALAKLGVR---FAFEDKPGHLPF-VMTTKGYSNKKIEITLEESSQYLSGLLLGA 180

Query: 191 PLALGDVEIEIIEI-DKLISIPYVEMTLRLMERFG---VKAHSDSDW----- 232
PLA + I + +K +S PYV +TLR+ME F V+ + W

Sbjct: 181 PLADHETVISVTGNKAVSWPYVALTLRIMEDFKAGFEVEIRKDNRWQAVPWRSVKTVTPG 240

Query: 233 --RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
RF +K Y+ P + VEGD S+ASYF+A A+ V ++G SLQGD ++

Sbjct: 241 SIRFVVKP-TGYR-PAHYRVEGDWSNASYFMAAGAVGRQPVLKGLAADSLQGDRAIMDI 298

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAI 350
L MGA + + T + V P L ID++M + PD+ T+A VA FA PT I

Sbjct: 299 LSQMGATIKVSFTGILVEPGP-----LHGIDIDMGRCPLVPTVAAVAFAAATPTTI 350

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAM 408
R+VA R+KET+R+ A E+ + G + D II P + TY DHRMAM

Sbjct: 351 RNVAHLRLKETDRLEACAVEVARTGCRTDIADDSLIIRPSLLPRGKTVEFTTYGDHRMAM 410

Query: 409 AFSLAACAEVPTIRDPGCTRKTFPDYFDVLSTFVK 444
+ SL A A V V + +PGC K+FP +FD + V+

Sbjct: 411 SMSLFALAGVDVLDNPGCVGKSFPFGFFDQWNAIVE 446

>ref|YP_004087750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Asticcacaulis
excentricus CB 48]
gb|ADU13599.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Asticcacaulis
excentricus CB 48]
Length = 422

Score = 206 bits (523), Expect = 7e-51, Method: Compositional matrix adjust.
Identities = 156/438 (35%), Positives = 218/438 (49%), Gaps = 50/438 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I+G V +PGSKSL+NR L+AAL++G + + +L S+D +M AL+ +G+ +E A

Sbjct: 18 ITGAVVVPKSLTNRAFLVAALAGGESTLSGVLTSDDTVHMATAALKQMGVEIETLDATT 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ K P E LFLGNAG A R LTAAG A G V+DG MR+RPI

Sbjct: 78 VTLRSSGKLKAPAE-----PLFLGNAGTATRFLTAVALADG--AVVIDGDAHMRKRPI 129

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
LV L +LG V G CPPV V GG G V + +SSQY+SALLM A A

Sbjct: 130 QPLVEALTRLGVKVSAPTG--CPPVTVKARGGFSGDVVDIDAGLSSQYVSALLMLA--AC 185

Query: 195 GDVEIEIIDK----LISIPYVEMTLRLMERFVGK-AEHSDSWDRFYIKGGQKYKSPKNAY 249

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      G+ +E+ + + Y+++TL +M+ FG K ++ SD R G P
Sbjct: 186 GETAVEVRLRGDHGIGGRGYIDLTLGVMQAFGAKVSPSDGVWRVERTGYVAADYP---- 241

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
      +E DASS +Y A +TGG + + Q D K +++ ++W + G
Sbjct: 242 IEPDASSCTYLWAAEVLTTGGKIDFQMDTAALTQPDAKARDII-----MSWPNMPAIDG 295

Query: 310 PPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
      +++ D TLAV+A F P +A+ RVKE +R+ A+
Sbjct: 296 -----SQIQDAVPTLAVLAAFNQTPVRFVGIANLRVKECDRVSAVCD 337

Query: 370 ELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTVIRD 424
      L L G + EEG D + P T IDT++DHR+AM FSLA V I +
Sbjct: 338 GLNALRAGLAHEEGDDLIVHADPALSGATTKAVIDTHNDHRIAMCFSLAGLMMSGVVIDN 397

Query: 425 PGCTRKTFFPDYFDVLSTF 442
      P C KTFP Y+DVL +
Sbjct: 398 PKCVSKTFPTYWDVLESL 415

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>ref|YP_001108530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Saccharopolyspora
erythraea NRRL 2338]
ref|ZP_06566712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Saccharopolyspora
erythraea NRRL 2338]
sp|A4FNI0.1|AROA_SACEN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAM05605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Saccharopolyspora
erythraea NRRL 2338]
Length = 422

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Score = 205 bits (521), Expect = 1e-50, Method: Compositional matrix adjust.
Identities = 149/430 (34%), Positives = 222/430 (51%), Gaps = 26/430 (6%)

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Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + TV +PGSKS++NR L+LAAL+EG + + L S D M ALR LG ++
Sbjct: 14 VRATVPVPGSKSITNRALVLAALAEGPSTLRGPLRSRDTLMATALRALGADLQDGEPS 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      V G P+ E + G AG MR L A G T+ DG PR RERP+
Sbjct: 74 WQVAPG-----PLRGPAE---VDCGLAGTVMRFLPPVAALAEGRITF--DGDPRARERPL 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
      ++ L+ LGAD+ D P + G G L GG V + S SSQ++S LL++AP
Sbjct: 124 DAVLNALRALGADISG---DSLPLFELQGTGKLAGGAVTIDASASSQFVSGLLLSAPRFE 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      G + + S+P+++MT+ ++ GV+ + S D +++ G + VE D
Sbjct: 180 QGVTVTHTGEPVPSLPHIDMTVSMLRAAGVEVDDSKR-DVWHVAPGPIRA--LDLDVEPD 236

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
      S+A+ FLA AA+TGGTVTV G + Q ++L MGA V +TVTGP
Sbjct: 237 LSNATPFLAAAAVTGGTVPVPGWPERTDQAGDAIRDILARMGATVELGPDGLTVTGP--- 293

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      L +D++++ + ++ T+A +A FA G + +R VA R ET+R+ A++ EL+
Sbjct: 294 ----AELAPLDIDLHDVGELTPTVAALAAFASGRSRLRGVAHLRGHETDRLAALQRELSG 349

Query: 374 LGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFF 433
      LG VE+ D +I P L +Y DHRMA A ++ V + D TRKT P
Sbjct: 350 LGGDVEQTDDGLLIE-PRPLTGGNWHYSYADHRMATAGAILGLLVPGVLVEDIATTRKTIP 408

Query: 434 DYFDVLSTFV 443
      D+ + S+ +
Sbjct: 409 DFPGMWSSML 418

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>ref|ZP_05494485.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
papyrosolvens DSM 2782]
gb|EEU60455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
papyrosolvens DSM 2782]

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Length = 422

Score = 204 bits (520), Expect = 2e-50, Method: Compositional matrix adjust.
Identities = 141/425 (33%), Positives = 226/425 (53%), Gaps = 24/425 (5%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+SG++ +PGSKS + R L LA L++GT+ + N L S D R G + + + +
Sbjct: 9 ELSGSINIPGSKSHTIRSLFLAGLAKGTSKIRNPLSSDAISGADVCRAFGSTFDLKEDS 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+G + P E + +GN+G ++R +TAA V G ++R+R
Sbjct: 69 YIVNGIGACPV-----ENVIDVGNSTSLR--LGLMTAALVEGHTVFTGDYQIRKRQ 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV + LG G + PV + G GG +L S++SQYLS++L+ APL
Sbjct: 121 IGPLVKAINNLGGTAFTTRGNESAPVVIKGRA--TGGFTELD-SVTSQYLSILLNAPLL 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D I + +L IPYVE+TL +++ G+K H +S F+I G Q+YK P + GD
Sbjct: 178 EKDTHINVT-RLINEIPYVEITLWLDLKGIKYSH-NSMKEFFIPGSQQYK-PFECNIPGD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A++F+ AAI+G + + + QGD +L+ MGA + + + ++T+ G
Sbjct: 235 FSTATFFMVQAASGNELVLTNLDMSDPQGDKAVLGILQDMGADIKYDDKNITIKG---- 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K LK +++MN +PD +AV A FA G T + +V R+KET+R+ + +ELTK
Sbjct: 291 ----KSLKGREIDMNSIPDALPAMAVAACFAKGETRLVNVQPQARLKETDRISVMCSELTK 346

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEPVPTIRDPG-CTRKTf 432
+GA + E PD +I KL T++ +DDHR+ M+ ++A TI D T+
Sbjct: 347 MGADISELPDGLVIR-ESKLCGTSVKGHDDHRVMSLAIAIAGLNCQGETIITAEAMNVTY 405

Query: 433 PDYFD 437
P + +
Sbjct: 406 PGFVE 410

>ref|YP_098022.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis
YCH46]
sp|Q64YD8.1|AROABACFR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAD47488.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis
YCH46]
Length = 410

Score = 204 bits (520), Expect = 2e-50, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 223/432 (51%), Gaps = 49/432 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ ALS+G V+ NL + +D M+ AL
Sbjct: 10 QIKATIQLPASKSISNRALIIHALSKGDDVLSNLSDCDDTQVMIKAL----- 56

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ E + + AG AMR LTA +++ G + + G RM++RP
Sbjct: 57 -----TEGNEVIDIL--AAGTAMRFLTAYLSSTPG--IHTITGTERMQQR 98

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA ++ PP+R+ G L G ++ L G++SSQY+SALLM P+
Sbjct: 99 IQILVNALRELGAHIEYVRNEGFPPLRIEG-RELTGSEITLKNVSSQYISALLMIGPV 157

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW--DRFYIKGGQKYKSPKNAYVE 251
+++ + +++S PY+ +TL+LM+ FG A SW D+ + Q Y VE
Sbjct: 158 KNGLQLRLTGEIVSRPYINLTQLMKDFGASA----SWTSQSIQVDPQPYHCLPFT-VE 212

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D S+ASY+ AA++ + + G S QGD + AEV +G +TET +
Sbjct: 213 SDWSAASYWYQIAALSPQANIELTGLFRHSYQGD SRGAEVFARLGVATEYTTETGI----- 267

Query: 311 PREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370

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      R      ++ +D +   +PD+A T V   + P      + S ++KET+R+ A++TE
Sbjct: 268 -RLKKNQTCVERLDEDFVDIPDLAQTFVVTCALLNVPRFTGLQSLKIKETDRIEALKTE 326

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
      + KLG + + D +   E++ A I TY+DHRMAMAF+ AA   + I +P
Sbjct: 327 MKKLGYLHDKNDSILSWDGERVEQQACPVIKTYEDHRMAMAFAPAAIHPTIQIDEPQV 386

Query: 428 TRKTFPDYFDVL 439
      K++P Y++ L
Sbjct: 387 VSKSYPGYWNDL 398

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>ref|NP_811099.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
      thetaiotaomicron VPI-5482]
gb|AA077293.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
      thetaiotaomicron VPI-5482]
Length = 410

```

Score = 204 bits (519), Expect = 2e-50, Method: Compositional matrix adjust.
Identities = 140/429 (32%), Positives = 219/429 (51%), Gaps = 45/429 (10%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + T++LP SKS+SNR L++ AL +G   +NL + +D M+ AL
Sbjct: 12 VKATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKALT----- 58

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      + KE + +   AG AMR LTA ++A G   ++ G RM++RPI
Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSATSGER--IITGTARMQQRPI 100

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      LV L++LGA+++   PP+R+ G   L G ++ L G++SSQY+SALLM P+
Sbjct: 101 QILVNALRELGAIEYTHNEGYPPLRIKG-AELKGNEITLKGNVSSQYISALLMIGPVLK 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      + + + ++IS PY+ +TL+LM+ FG KA +   Q Y+S   VE D
Sbjct: 160 DGLTLHLTGEIISRPYINLTLQLMQDFGAKAAWTSP--SSISVAPQPYQSVPTT-VESDW 216

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
      S+ASY+ AA++   + + G   S QGD + AEV +G   +T V +   +
Sbjct: 217 SAASYWYQIAALSPEAEIELLGLFRNSYQGDSRGAEVFSRLGITTEFTPKGVKIKKTGKT 276

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      P   + ++ +   +PD+A T V   + P   + S ++KET+R+ A+RTEL K
Sbjct: 277 P-----ERLEEDFVDIPDLAQTFVVTCALLNIPRFTGLQSLKIKETDRIAALRTELKK 330

Query: 374 LGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
      LG +EE D ++   E+   V I TY+DHRMAMAF+ A   + I DP   K
Sbjct: 331 LGYLIEEENDSVLMWNGERCEPEAVPVATYEDHRMAMAFAPAVITFPKLLIADPQVVSK 390

Query: 431 TFPDYFDVL 439
      ++P Y++ L
Sbjct: 391 SYPGYWEDL 399

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>ref|YP_002872355.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas
      fluorescens SBW25]
emb|CAY49004.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas
      fluorescens SBW25]
Length = 425

```

Score = 204 bits (519), Expect = 2e-50, Method: Compositional matrix adjust.
Identities = 156/441 (35%), Positives = 225/441 (51%), Gaps = 43/441 (9%)

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Query: 8 VLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
      V P   ++G V PGSKS++NR LLLAAL++GT+ + L S+D +M ALR +G+++
Sbjct: 16 VTPPNAPLNGKVAPPKSKSITNRALLAALAKGTSRLSGALKSDDTRHMSVALRQMGVTI 75

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      D+   VV GK +   LFLGNAG AMR LTAAV G T VLDG
Sbjct: 76 --DEPDDTTFVVTGQGLQLPPQP----LFLGNAGTAMRFLTAAVATVEG--TVVLDGDD 127

```

Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
M++RPIG L+ L Q G VD G CPPV V+G+G + + ++ G +SSQY+SALL
Sbjct: 128 YMQRPIGPLELTLGQNGIQVDSPTG--CPPVTVHGVGKIKAKRFEIDGGLSSQYVSALL 185

Query: 188 MAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
M A +E+ + K I YV++TL M FG + E + GG +
Sbjct: 186 MLAACGEAPIEVALTGKDIGARGYVDLTLDICMRAFGAQVEAVNDTTWRVAPGG---YTAH 242

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +E DAS+A+Y A +TGG + + Q D K V+ + T
Sbjct: 243 DYLIEPDASAATYLWAAEVLTGGRIDIGVAAQDFTQPDAAQAVIAQ-----FPNMQAT 296

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V G ++M D TLAV+A F + P ++A+ RVKE +R+ A
Sbjct: 297 VVG-----SQMQDAIPTLAVLAAFNNTTPVRFTLANLRVKECDRVQA 338

Query: 367 IRTELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVT 421
+ L ++ G + EG D + + P + IDT+ DHR+AM F+LA V
Sbjct: 339 LHDGLNEIRPLATIEGDDLLVASDPALAGTSCALIDTHADHRIAMCFALAGLVSGVK 398

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I+DP C KT+P+Y++ L +
Sbjct: 399 IQDPDCVGKTYPEYWNALGSL 419

>ref|ZP_01053050.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polaribacter sp.
MED152]
gb|EAQ42478.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polaribacter sp.
MED152]
Length = 409

Score = 204 bits (518), Expect = 3e-50, Method: Compositional matrix adjust.
Identities = 145/432 (33%), Positives = 224/432 (51%), Gaps = 52/432 (12%)

Query: 13 KEISGTVKLPKSKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I + + GSKS SNR+L+L L T+ DNL +S+D +M AL T L V+
Sbjct: 11 RRIQEETITISGSKSESNRLLILQKLFPEITI-DNLSDSDDSVHMHHALTTEDLLVD---- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+G+AG AMR LT+ G + L G RM+ R
Sbjct: 66 -----IGHAGTAMRFLTSYFAVNRGREVF-LTGSERMQNR 99

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ LGAD+ + PP+++ G L KV+++G++SSQY+S+LL+ A
Sbjct: 100 PIEILVNALRDLGADITYAVKEGYPLKIKG-KELTKDKVQINGNVSSQYISSLLLIASK 158

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+EIE+ K+ S+PY+ MTL L+ + G+++ D+ + + K + ++ VE
Sbjct: 159 LDNGLEIELTGKITSVPYINMTLSLLSQIGIESSFEDNIIKVPKESIETQT---VVVES 215

Query: 253 DASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT-- 308
D SSASYF + A++ G +V + SLQGD AE+ + G T+ E +T+T
Sbjct: 216 DWSSASYFYISIVALSELGSSVKLSAYKKESLQGDSCLAIEYKHFGVATTFGEDCITLTKE 275

Query: 309 -GPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADG-PTAIRDVASWRVKETERMVA 366
RE R N+ PD+A T+AV FA+G + + + ++KET+R+VA
Sbjct: 276 KNTKRETLVR-----NLKDAPDIAQTIAVTC-FAEGIACNLSGLHTLKIKETDRLVA 326

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
+ ELTKLGA V + + +N AIDTY+DHRMAMAF+ A +V + I D
Sbjct: 327 LHDELTKLGAKVIITNETLQVETATSINSNVAIDTYNDHRMAMAFAPLAL-KVSIKINDA 385

Query: 426 GCTRKTFPDYFD 437
K++ +++
Sbjct: 386 EVVTKSYQKFWN 397

>ref|ZP_08123678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudonocardia sp.
P1]
Length = 434

Score = 203 bits (517), Expect = 3e-50, Method: Compositional matrix adjust.
Identities = 159/435 (36%), Positives = 218/435 (50%), Gaps = 33/435 (7%)

Query: 11 PIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P ++GTV +PGSKS++NR LLLA LS G V + D M GAL LG+ V AD
Sbjct: 9 PGAPVTGTVSPGSKSVTNRALLLAGLSGGACRVGGAPLRTDTALMTGALAALGVPSAD 68

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G ++ G AG MR A A G + DG PR R
Sbjct: 69 G---DTVTGAGHDGLRGGTGDTPAEIDCGLAGTVMRFAPPAAATASGAVRF--DGDPRAR 123

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA- 189
ERP+G ++ L+ LGA VD D P R++G G + GG+V + S SSQ++S LL++
Sbjct: 124 ERPMTGTVLSALRTLGA RV DG----DALPFRLDG-GPIAGGEVTIDASASSQFVSGLLLSG 178

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-----AEHSDSWDRFYIKGGQKYK 243
A G L S+P+++MT+ ++ GV E D+W ++ G
Sbjct: 179 ARFERGLTVRHAGRALPSLPHIDMTVGMLEAGVTVADRTTGEDPDTW---RVEPGPVAV 235

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++ +E D S+AS FLA AA+T G VTV G TS Q V VLE GA VT
Sbjct: 236 --RDWDIEPDLASNASVFLAAA VTAGRVTVRGWPATSTQPGVDVLPVLERFGATVTHDAA 293

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+TVTGP R L IDV+++ ++A T+A +A A G + +R + R ET+R
Sbjct: 294 GLTVTGPD-----LSGIDVDLHDAGELAPTVAATAALAHGTSRLRGIGHLRGHETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVT A---IDTYDDHRMAMAFSLAACAEVPV 420
+ A+ E+T LG SV E D +I P+ L A Y DHRMA A ++ V
Sbjct: 347 LAALAAEITALGGSVTETDDGLVID-PKPLTGRADRPWGAYADHRMATAGAI VGLVVPV 405

Query: 421 TIRDPGCTRKTFPDY 435
+ D GCT KT PD+
Sbjct: 406 LVDDIGCTDKTIPDF 420

>ref|ZP_07945143.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bilophila wadsworthia
3_1_6]
gb|EFV43678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bilophila wadsworthia
3_1_6]
Length = 442

Score = 203 bits (517), Expect = 3e-50, Method: Compositional matrix adjust.
Identities = 151/445 (33%), Positives = 231/445 (51%), Gaps = 38/445 (8%)

Query: 18 TVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV+ P SKS+S+R+++ AAL++G +VV +L S+D+ + LR G + + A+
Sbjct: 4 TVQAPASKSVSHRMVMGAALAQGDSVVSRLVLESKDLERTMAILRGAGAGIVRTGEGEYAI 63

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
G GG+ P + + + + +G R LTA + A G + + G PRM ERPIG+L
Sbjct: 64 S-GVGGQ-PHGGSVDPLSCDVHESGTCRLLTAVLAA--GMGRFRVHGAPRMHERPIGEL 119

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ LG F G P V GL GG+V + SSQYLS +L+AAPLA +
Sbjct: 120 TAALET LGVSF-TFEGKPGFPFVLKTCGLDGGEVGIGMDESSQYLSGVLLAAPLARAPL 178

Query: 198 EIEIII-DKLISIPYVEMTLRLMERFGV----KAEHSDSW---DRFYIK----GGQKYKSP 245
+ I K++S PYV +TL+ +E FGV + + +W D ++ G +++
Sbjct: 179 TVNIGGSKVSWPYVGLTLQALENFGVPFVSVERKEGGAWSAVDWHLEQAEPGNVRFRMV 238

Query: 246 KNAY-----VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y VEGD S ASY LA AI V +EG SLQGD ++L MGA++
Sbjct: 239 PAMYRAGRYAVEGDWSGASYLLAAGAIGPRPVRIEGLRADSLQGDVMDILRDMGARID 298

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+VTV P E L+ + +M++ PD+ T+AVVA A GPT + + A R+K
Sbjct: 299 IEPDAVTVH--PSE-----LRGVVADMSRCPDLVPTVAVVAHAHAGPTRLWNAHLRIK 350

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT AIDTYDDHRMAMAFSL 412
E +R+ EL+K+G +E D I + L+ A + DHR+AM+ +L

Sbjct: 351 ECDRIAVPAQELSKVGVRCDHDDGLTIHGDPALASRLHSLDGLAFSAHGDHRIAMSLAL 410

Query: 413 AACAEVPTTIRDPGCTRKTFPDYFD 437

+T+ DP C K+FP++++

Sbjct: 411 LELRGGRLTLDDPSCVSKSFPNFW 435

>ref|ZP_06993276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
1_1_14]

gb|EFI06182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
1_1_14]

Length = 410

Score = 203 bits (517), Expect = 3e-50, Method: Compositional matrix adjust.
Identities = 138/429 (32%), Positives = 219/429 (51%), Gaps = 45/429 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALASEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 12 VKATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKALT----- 58

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

+ KE + + AG AMR LTA ++A G ++ G RM++RPI

Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSATSGER--IITGTARMQQRPI 100

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM P+

Sbjct: 101 QILVNALRELGAIEYTHNEGYPPLRIKG-AELKGNEITLKGNVSSQYISALLMIGPVLK 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254

+ + + ++IS PY+ +TL+LM+ FG KA + Q Y+S VE D

Sbjct: 160 DGLTLHLTGEIISRPIINLTQLMQDFGAKAAWTSP--SSISVAPQPYQSVPT--VESDW 216

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313

S+ASY+ AA++ + + G S QGD + AEV +G +T + + +

Sbjct: 217 SAASYWYQIAALSPEAEIELLGLFRNSYQGDSRGAEVFSRLGITTEFTPQGIKIKKTGKT 276

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373

P + + + +PD+A T V + P + S ++KET+R+ A+RTEL K

Sbjct: 277 P-----ERLEEDFVDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAALRTELKK 330

Query: 374 LGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAEVPTTIRDPGCTRK 430

LG +EE D ++ E+ + I TY+DHRMAMAF+ A + I DP K

Sbjct: 331 LGYLIEEENDSVLMWNGERCEPEAIPVIATYEDHRMAMAFAPAVITFPKLLIADPQVVS 390

Query: 431 TFPDYFDVL 439

++P Y++ L

Sbjct: 391 SYPGYWEDL 399

>ref|YP_004043905.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paludibacter
propionicius WB4]

gb|ADQ80920.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paludibacter
propionicius WB4]

Length = 403

Score = 203 bits (516), Expect = 5e-50, Method: Compositional matrix adjust.
Identities = 141/423 (33%), Positives = 213/423 (50%), Gaps = 47/423 (11%)

Query: 19 VKLPKSGKSLSNRILLALASEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78

+KLP SKS+SNR L+L ALS + NL + +D + AL + S +

Sbjct: 17 IKLPASKSISNRALILNALSYPYDIQNLSDCDDTRVTIKALDSNDRSFD----- 66

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138

+G AG AMR LTA + G +V+ G RM++RPI LV

Sbjct: 67 -----IGAAGTAMRFLTAFLAKTVGE--WVITGSERMKQRPIKLLV 105

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198

L LGA ++ PP+R+ G L GG+++L+G +SSQY+SAL+M AP ++

Sbjct: 106 DALNSLGARIEYIENEGYPPLRILG-SALTGGEIRLNGGVSSQYISALMMIAPYMQNGLK 164

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258

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      I + +IS+PY+ MT+++M+ FGV ++ I + SP VE D S+AS
Sbjct: 165 IILEGNVISVPYIRMTMQMMKEFGVDVLFENN----TIDVKPQVYSPIQYKVESDWSAAS 220

Query: 259 YFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGR 317
      Y+ +I G G + +EG S QGD K AE+ E +G K + V +T P G
Sbjct: 221 YWFEVLISIAGKGRIMLEGLYQNSYQGD SKVAELFEQLGVKAEYKPEGVLLT-----PNG- 274

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
      ++ + + PD+A T AV + V S ++KET R+ A+ EL KLG
Sbjct: 275 NYVSKFEYDFVDQPDLAQTFQAVTCCLKGIAFHFKGVQSLKIKETNRI AALINELAKLGF I 334

Query: 378 VEEGPDYCIITPPEKLNVT A---IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
      + E + + E+ I TY+DHRMAMAF+ AA +PV+I +P K++P
Sbjct: 335 LFEP AEGELAWSGERCKQEEDIRIATYEDHRMAMAFAPAALV-MPVSIEEPQVVS KSYPS 393

Query: 435 YFD 437
      +++
Sbjct: 394 FWN 396

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>ref|YP_001404722.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Methanoregula boonei 6A8]
sp|A7I8L8.1|AROA_METB6 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABS56079.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Methanoregula boonei 6A8]
Length = 421

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Score = 203 bits (516), Expect = 5e-50, Method: Compositional matrix adjust.
Identities = 152/439 (34%), Positives = 220/439 (50%), Gaps = 28/439 (6%)

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Query: 7 IVLQPIKE-ISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      IV P + I +V P SKS ++R L+ AAL++G + + L ++D + +L LG+
Sbjct: 2 IVTLPARSGIELSVTTTPSKSYTHRALIAAALAQGRSTIVRPLMADDTKLTIASLMKLG V 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY--VL 123
      ++ AD+ ++ GC G FP L L N+G + + +A ATY L
Sbjct: 62 AIHADQ--HNIMLEGCDGSFP---NTPGTVLDDLNSG----TSLRL LASAALLATYPVTL 112

Query: 124 DGVP RMRERPIGDLVVG LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G RM+ERP+G L L LG V PPV + G L GG + GS SSQ+
Sbjct: 113 TGSARMQERPLGLAHTLNDLGGMVIFTKKEGYPPVTIGG--RLLGGTATIDGSQSSQFA 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      S+++MAAP + G V++ + S Y+++T +M FG + + RF + Y
Sbjct: 171 SSVMM AAPYSKGPVDLTVTGT PASQSYLDITAGVMTDFGAVIRR-EGYRRFLVSN CNHYT 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      + VEGD SSASYF A AAI GG VTV G S+QGD F + L+ MG +VT+
Sbjct: 230 G-RTFVVEGDYSSASYFFALAAICGGKVTVAGLAPDSVQGDRLFLDALQRMGCEV TYAHD 288

Query: 304 SVTV--TGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
      VTV GP L I +NM+ PD TL +VA A PT I + + KE+
Sbjct: 289 GVTVENQGP-----LTGITINMSSAPDTVQTL CMVA AVARTPTIITGIGHLKFKES 339

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPT 421
      +R+ L LG V D +I P L+ ID +DHR AM+F++ +T
Sbjct: 340 DRIAVTADRLRLGGIVTAERDRIVIQ-PATLHGGRIDPVNDHRTAMSF AVLGLGIGGIT 398

Query: 422 IRDPGCTRKTFPDYFDVLS 440
      I C K+FP ++++LS
Sbjct: 399 ITGAECVNKSFP GFWEILS 417

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>ref|YP_288605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobifida fusca
YX]
gb|AAZ54582.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobifida fusca
YX]
Length = 424

```

Score = 202 bits (514), Expect = 7e-50, Method: Compositional matrix adjust.
Identities = 145/427 (33%), Positives = 223/427 (52%), Gaps = 30/427 (7%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADK 71
+ + TV LKPSK++NR L+LAALSE +VV L S D M+GALR LG+ V EAD
Sbjct: 15 RVPDATVSLPGSKSMTNRALILAALSETPSVVRAPLYSRDITLMVGALRALGIGVHEAD- 73

Query: 72 AAKRAVVVGCGGKFPVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
G + V + + +GNAG MR + A G ++ DG PR
Sbjct: 74 -----GDWEVTPTTPQGPAIDVGNAGTVMRFVPLAAMARGEVSF--DGDPR 120

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RERP+G L+ L+ LGA++D G P+ + G G LPGA V L S SSQ++SALL++
Sbjct: 121 RERPVGPLLAALRTLGAIEIDDG-GRGALPMVIRGRGELPGGTVTLDASGSSQFVSALLLS 179

Query: 190 APLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
VE+ + + S P++ MT++++ GV+ + +D+ D + + G +
Sbjct: 180 GARFSKGVEVRHVGPVPSQPHLNMVQMLRDAGVEVD-TDTPDVWRVAPGPIRVT--EI 236

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSVTVT 308
VE D S+A+ FLA A +TGG VTV G + Q + MG +V +T+ +T+
Sbjct: 237 TVEPDLNAAPFLAALVTGGRVTVRGWPRHTTQPGDALRTLFAEMGGRVEFTDEGLTL- 295

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G ++ + ++ + ++ T+A VA A P+ + +A R ET+R+ A+
Sbjct: 296 -----HGTGEIRGLTADLRDVGELTPTIAAVALASTPSRLTGIAHLRRHETDRIAALV 349

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
E+ +LG EE PD +I P L+ +YDDHRMA + ++ V + + T
Sbjct: 350 REINRLGGDAEELPDGLVIR-PRPLHGGVGFHSYDDHRMATSGAVIGLVVPGVEVENIATT 408

Query: 429 RKTFFPDY 435
KT PD+
Sbjct: 409 GKTLPDF 415

>ref|ZP_03474784.1| hypothetical protein PRABACTJOHN_00439 [Parabacteroides johnsonii
DSM 18315]
gb|EEC98147.1| hypothetical protein PRABACTJOHN_00439 [Parabacteroides johnsonii
DSM 18315]
Length = 409

Score = 202 bits (514), Expect = 8e-50, Method: Compositional matrix adjust.
Identities = 144/438 (32%), Positives = 221/438 (50%), Gaps = 48/438 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+V P+ + ++KLP SKS+ NR L+L ALS + NL + +D M+ AL +
Sbjct: 4 VVKSPV-SLKASIKLPASKSICNRALILNALSYSPYEIRNLSDCDDTEVMVKALNS---- 58

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
D +++ AG AMR LTA ++ G T + G
Sbjct: 59 -----NDRDFDIKA----AGTAMRFLTAFLSKVVGWET--ITGT 91

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RM+ RPI LV L LGA V+ PP+R+ G L GG++ L+G +SSQY+SAL
Sbjct: 92 QRMKNRPILKILVDALNSLGAARVEYMEKEGYPLRIFG-SALQGEISLAGGVSSQYISAL 150

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM APL + + + +IS PY+ +TL+LME++GVKA+ W IK + P
Sbjct: 151 LMIAPLMEKGLTLHLEGAIISKPYINLTQLMEQYGVKAD----WSGQTIKVRPQDYHPI 206

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSV 305
VE D S+ASY+ + A++ + + G SLQGD A++ +G T+T+ V
Sbjct: 207 PFTVESDWSAASYWYSMMALSKNAEIELLGLFKNSLQGDAAGAKLFAQLGVGTITYTDRGV 266

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ + K ++ N PD+A T V + + P + S ++KET+R+
Sbjct: 267 ILK-----YNGNRTKLNYNFVNEPDLAQTFVVTCLLNIPFRFTGLQSLKIKETDRIE 320

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFS-LAACAEVPVT 421

A++TEL KLG + + D + E+ A I TY+DHRMAMAF+ +A +
Sbjct: 321 ALKTELCKLGYLLTDSNDSILEWNGERCEPQAHPVIATYEDHRMAMAFAPVALVVSEGIE 380
Query: 422 IRDPGCTRKTFFPDYFDVL 439
I DP RK++P +++ L
Sbjct: 381 IADPQVVRKSYPHFWEDL 398

>gb|ABV26712.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured bacterium]
Length = 444

Score = 202 bits (513), Expect = 1e-49, Method: Compositional matrix adjust.
Identities = 153/441 (34%), Positives = 223/441 (50%), Gaps = 43/441 (9%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V P ++G V PGSKS++NR LLLAAL++GT+ + L S+D +M ALR +G+++
Sbjct: 35 VTPPNFPLTGKVPAPGSKSITNRALLAALAKGTSRLSGALKSDDTRHMSVALRQMGVTI 94
Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ V + P + LFLGNAG AMR LTAAV G T VLDG
Sbjct: 95 DEPDDTTFVVTSQGSLLQPAQ-----PLFLGNAGTAMRFLTAAVATVQG--TVVLDGDE 146
Query: 128 RMRERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
M++RPIG L+ L Q G VD G CPPV V+G+G + + + G +SSQY+SALL
Sbjct: 147 YMQRPIGPLLATLQNGIQVDSPTG--CPPVTVHGMGKVQAKRFEIDGGLSSQYVSALL 204
Query: 188 MAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
M A +E+ + K I YV++TL M FG + + D D + Y +
Sbjct: 205 MLAACGEAPIEVALTGKDIGARGYVDLTDCMRAFGAQVDAVD--DTTWRVAPTGYTA-H 261
Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +E DAS+A+Y A +TGG + + Q D K V+ + T
Sbjct: 262 DYLI EPDASAATYLAEEVLTGGRIDIGVAAQDFTQPDAAQAVIAQ-----FPNMQAT 315
Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V G ++M D TLAV+A F + P ++A+ RVKE +R+ A
Sbjct: 316 VVG-----SQMQDAIPTLAVLAAFNNTPVRFTELANLRVKECDRVQA 357
Query: 367 IRTELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPT 421
+ L ++ G + EG D + + P IDT+ DHR+AM F+LA +
Sbjct: 358 LHDGLNEIRPLATIEGDDLLVASDPALAGTACTALIDTHADHRIAMCFALAGLVKSGIR 417
Query: 422 IRDPGCTRKTFFPDYFDVLSTF 442
I+DP C KT+PDY+ L++
Sbjct: 418 IQDPDCVAKTYPDYWKALASL 438

>ref|ZP_06093640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_16]
gb|EEZ26183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_16]
Length = 410

Score = 202 bits (513), Expect = 1e-49, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 221/432 (51%), Gaps = 49/432 (11%)

Query: 14 EISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ ALS+G V+ NL + +D M+ AL
Sbjct: 10 QIKATIQLPASKSISNRALIIHALSKGDDVLSNLSDCDDTQVMIKAL----- 56
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 133
+ E + + AG AMR LTA +++ G + + G RM++RP
Sbjct: 57 -----TEGNEVIDIL--AAGTAMRFLTAYLSSTPG--IHTITGTERMQQR 98
Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA ++ PP+R+ G L G ++ L G++SSQY+SALLM P+
Sbjct: 99 IQILVNALRELGAHIEYVRNEGFPLRIEG-RELTGSEITLKGNVSSQYISALLMIGPVL 157
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW--DRFYIKGGQKYKSPKNAYVE 251
+++ + +++S PY+ +TL+LM+ FG A SW D+ Q Y VE
Sbjct: 158 KNGLQLRLTGEIVSRPYINLTQLMKDFGASA----SWTSDQNIQVDPQPYHCLPFT-VE 212

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+ASY+ AA++ + + G S QGD + AEV +G +TET +
Sbjct: 213 SDWSAASYWYQIAALSPQADIELTGLFRHSYQGDSRGAEVFARLGVATEYTETGI----- 267

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R ++ +D + +PD+A T V + P + S ++KET+R+ A++TE
Sbjct: 268 -RLKKNGTCTVERLDEDFVDIPDLAQTFVVTCALLNVPRFTGLQSLKIKETDRIEALKTE 326

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
+ KLG + + D + E++ I TY+DHRMAMAF+ AA + I +P
Sbjct: 327 MKKLGYYILHDENDSILSWDGERVEQQTCPVIKTYEDHRMAMAFAPAAIHYPTIQIDEPQV 386

Query: 428 TRKTFPDYFDVL 439
K++P Y+D L
Sbjct: 387 VSKSYPGYWDDL 398

>ref|ZP_02030211.1| hypothetical protein PARMER_00179 [Parabacteroides merdae ATCC 43184]
gb|EDN88436.1| hypothetical protein PARMER_00179 [Parabacteroides merdae ATCC 43184]
Length = 410

Score = 201 bits (510), Expect = 2e-49, Method: Compositional matrix adjust.
Identities = 146/433 (33%), Positives = 218/433 (50%), Gaps = 49/433 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ +VKLP SKS+ NR L+L ALS + NL + +D M+ AL +
Sbjct: 11 LKASVKLPASKSICNRALILNALSYSYPYAIRNLSDCDDTEVMVKALNS----- 58

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
D +++ AG AMR LTA ++ G T + G RM+ RPI
Sbjct: 59 -----NDRDFDIKA---AGTAMRFLTAFLSKVVGWEW--ITGTERMKNRPI 99

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
LV L LGA V+ PP+R+ G L GG++ L+G +SSQY+SALLM APL
Sbjct: 100 KILVDALNALGARVEYMEKEGYPLRIFG-SALQGGEISLAGGVSSQYISALLMIAPLME 158

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ + + +IS PY+ +TL+LME++GVKAE W+ IK + P VE D
Sbjct: 159 NGLTLHLEGVVISKPYINLTQLMEQVGVKAE---WNGQTIKVRPQDYHPIPTVESDW 214

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+ASY+ + A++ + + G SLQGD A++ +G T+T+ V +
Sbjct: 215 SAASYWYSMMALSKNAEIELLGLFKNSLQGDAAAGAKLFAQLGVGTTTYTDRGVVLK----- 269

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K ++ N PD+A T V + + P + S ++KET+R+ A++TEL K
Sbjct: 270 -HNGNRTKKLNYNFVNPDLAQTFVVTCLLNIPFRFTGLQSLKIKETDRIEALKTELK 328

Query: 374 LGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEV--VTIRDPGCT 428
LG + + + + E+ A I TY+DHRMAMAF+ AA +P + I DP
Sbjct: 329 LGYLLTDSNNSILEWNGERCEPQAHQVITTYEDHRMAMAFAPAALV-LPEGIEIADPQVV 387

Query: 429 RKTTFPDYFDVLST 441
K++P Y+ L T
Sbjct: 388 SKSYPHYWRDLRT 400

>ref|YP_210369.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis NCTC 9343]
sp|Q5LHG9.1|AROABACFN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH06411.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis NCTC 9343]
Length = 410

Score = 201 bits (510), Expect = 2e-49, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 220/432 (50%), Gaps = 49/432 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ ALS+G V NL + +D M+ AL
Sbjct: 10 QIKATIQLPASKSISNRALIIHALSKGDDVPSNLSDCDDTQVMIKAL----- 56

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ E + + AG AMR LTA +++ G + + G RM++RP
Sbjct: 57 -----TEGNEVIDIL--AAGTAMRFLTAYLSSTPG--IHTITGTERMQORP 98

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA ++ PP+R+ G L G ++ L G++SSQY+SALLM P+
Sbjct: 99 IQILVNALRELGAHIEYVRNEGFPPLRIEG-RELTGSEITLKGNVSSQYISALLMIGPVL 157

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW--DRFYIKGGQKYKSPKNAYVE 251
+++ + ++S PY+ +TL+LM+ FG A SW D+ Q Y VE
Sbjct: 158 KNGLQLRLTGEIVSRPYINLTQLMKDFGASA----SWTSDQNIQVDPQPYHCLPFT-VE 212

Query: 252 GDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+ASY+ AA++ + + G S QGD + AEV +G +TET +
Sbjct: 213 SDWSAASYWYQIAALSPQADIELTGLFRHSYQGDSRGAIEVFARLGVATEYTETGI----- 267

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R ++ +D + +PD+A T V + P + S ++KET+R+ A++TE
Sbjct: 268 -RLKKNGTCTVERLDEDFVDIPDLAQTFVVTCALLNVPRFTGLQSLKIKETDRIEALKTE 326

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
+ KLG + + D + E++ I TY+DHRMAMAF+ AA + I +P
Sbjct: 327 MKKLGYYILHDKNDSILSWDGERVEQQTCPVIKTYEDHRMAMAFAPAAIHYPYTIQIDEPQV 386

Query: 428 TRKTFPDYFDVL 439
K++P Y+D L
Sbjct: 387 VSKSYPGYWDDL 398

>ref|YP_001832750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beijerinckia indica
subsp. indica ATCC 9039]
gb|ACB95261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beijerinckia indica
subsp. indica ATCC 9039]
Length = 424

Score = 201 bits (510), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 152/440 (34%), Positives = 224/440 (50%), Gaps = 47/440 (10%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + + G ++ PGSKS++NR LLLAAL++G + + L S+D YM AL+ +G+ +E+
Sbjct: 16 PQQPLQGHIRPPGSKSITNRALLAALAKGESRLTGALASDDTAYMAKALKAMGVGIESP 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A V P E LFLGNAG A R LTAA A G V+DG MR
Sbjct: 76 DATTFHVKGTHLHAPGE-----TLFLGNAGTATRFLTAAALADGRV--VIDGDANMR 127

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RPI LV L+ LG ++ G CPPV ++G G + G V + +SSQY+SALLM A
Sbjct: 128 KRPIAPLVLTALQSLGVSIEAPTG--CPPVTIDGRGRVAAGDVSIDAGLSSQYVSALLMLA 185

Query: 191 PLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSD--SWDRFYIKGGQKYKSPKN 247
P G + I + I YV++TL M FG + D SW Y++ ++
Sbjct: 186 PCGEGPIRIVLQGTGIGARGYVDLTAAAMHHFGAEVLQKDEVSW----TLAPTGYRA-RD 240

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E DAS+A+Y A A +T GT+ + + Q D K ++
Sbjct: 241 FVIEPDASAATYLAWAAVLTQGTIDLGVPSAFTQPDAKAYSLITSF----- 287

Query: 308 TGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
H+ A+ + +++ D TLAV+A F P D+A+ RVKE +R+ A+
Sbjct: 288 -----PHMPAV-IEGSIQDAVPTLAVMAAFNKTPVRFTDIANLRVKECDRIHAL 336

Query: 368 RTELTKLGASV--EEGPDYCIITPPE---KLNVTIADTYDDHRMAMAFSLAACAEVPVTI 422
TEL ++ + EEG D + P + I+TYDDHR+AM+F+LA +TI
Sbjct: 337 ATELARITPDLAREEGDDLIVTGDPALIGRRTDIIETDYDDHRIAMSFALAGLMDGLTI 396

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
DP C KT+P +++ L +
Sbjct: 397 LDPDCVAKTYPGFWN DLGSL 416

>ref|YP_003736795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halalkalicoccus
jeotgali B3]
gb|ADJ15003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halalkalicoccus
jeotgali B3]
Length = 439

Score = 201 bits (510), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 155/444 (34%), Positives = 217/444 (48%), Gaps = 43/444 (9%)

Query: 15 ISGTVKLPKSGKSLNRI LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT + P SKS ++R +L A + G TV D L +S D H A+ G V A
Sbjct: 10 LRGTAAQAPPSKSYTHRAILAAGYASGATVVDPL-DSADPHATARAIEAFGGDVSA----- 63

Query: 75 RAVVVGCGGKFPVE-----DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
G F VE D V + GN+G MR +T TAA + VL G
Sbjct: 64 -----VDGGFAVEGFAGVPDPVANV-IDCGNSGTTMRLVTG--TAALADGITVLTGDDS 114

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP G L+ ++ LG + G P+ + G + GG+V + G +SSQY++ALLM
Sbjct: 115 LRSRPQGPLLDAIEGLGGAESTRGNGQAPLVIEGP--VSGGRVSIPGDVSSQYITALLM 172

Query: 189 AAPALALGDVEIEIIDLKISIPYVEMTLRLMERFGVKA-----HSDSWDRFYIKGG 239
A + +EI++ +L S PYV++TL ++ FGV+AE S F + GG
Sbjct: 173 AGAVTEEGIEIDLETELKSAPYVDITLEVLSAFGVEAEPVGADGGEVRSAGASGFRVPGG 232

Query: 240 QKYKSPKNAY-VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAK 297
Q Y+ Y V GD SS SY LA + +TV G S QGD + E MG
Sbjct: 233 QTYEPEGGEYHVPDFSSISYLLAAGVLADEGLTVRGA-QPSAQGDTAIVGIAERMGGD 291

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
V W + + + L I V++ PD+ T+A + ADG T I + R
Sbjct: 292 VQWDREAGEIE-----VSKSELGITVDVGDTPDLLPTIATLGAVADGETRITNCEHVR 345

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAA-C 415
KET+R+ A+ TEL KLGASV E D ++ + +L+ +D YDDHR+ MA SLA
Sbjct: 346 YKETDRVSAMATELGLKLGASVTEYEDELVVHGEDSELGAIVDGYDDHRIVMALSLAGLV 405

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVL 439
AE +R +FPD+FDVL
Sbjct: 406 AEGETTVRGAEHVDVSFPDFFDVL 429

>gb|ABM21481.1| 5'-enolpyruvylshikimate 3-phosphate synthase [Pseudomonas
fluorescens]
Length = 444

Score = 201 bits (510), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 153/435 (35%), Positives = 220/435 (50%), Gaps = 43/435 (9%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRI LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V P ++G V PGSKS++NR LLLAAL++GT+ + L S+D +M ALR +G+++
Sbjct: 35 VTPPNFPLTGKVPAPPGSKSITNRALLAALAKGTSRLSGALKSDDTRHMSVALRQMGVTI 94

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ V + P + LFLGNAG AMR LTAAG G T VLDG
Sbjct: 95 DEPDDTTFVVTSGSLQLPAQ-----PLFLGNAGTAMRFLTAAGVATVQG--TVVLDGDE 146

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
M++RPIG L+ L Q G VD G CPPV V+G+G + ++ G +SSQY+SALL
Sbjct: 147 YMQKRPIGPLLATLQNGIQVDSPTG--CPPVTVHGMKVKQAKRFEIDGGLSSQYVSALL 204

Query: 188 MAAPALALGDVEIEIIDLKISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
M A +E+ + K I YV++TL M FG + + D D + Y +
Sbjct: 205 MLAACGEAPIEVALTGKDIGARGYVDLTDCMRAFGAQVDAVD--DTTWRVAPTGYTA-H 261

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306

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      + +E DAS+A+Y A +TGG + + Q D K V+ + T
Sbjct: 262 DYLI EPDASAATYLWAAEVL TGGRIDIGVAAQDFTQPDAKAQAVIAQ-----FPNMQAT 315

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKM P D VAMT L A V V A L F A D G P T A I R D V A S W R V K E T E R M V A 366
      V G ++M D T L A V + A F + P ++A+ R V K E + R + A
Sbjct: 316 VVG-----SQMQDAIPT L A V L A A F N N T P V R F T E L A N L R V K E C D R V Q A 357

Query: 367 I R T E L T K L --G A S V E E G P D Y C I I T P P E K L N V T A ---I D T Y D D H R M A M A F S L A A C A E V P V T 421
      + L ++ G + E G D + + P I D T + D H R + A M F + L A V
Sbjct: 358 L H D G L N E I R P G L A T I E G D D L L V A S D P A L A G T A C T A L I D T H A D H R I A M C F A L A G L K V S G V R 417

Query: 422 I R D P G C T R K T F P D Y F 436
      I + D P C K T + P D Y +
Sbjct: 418 I Q D P D C V A K T Y P D Y W 432

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>emb|CBW21292.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides fragilis 638R]
Length = 410

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 220/432 (50%), Gaps = 49/432 (11%)

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Query: 14 E I S G T V K L P G S K S L S N R I L L L A A L S E G T T V V D N L L N S E D V H Y M L G A L R T L G L S V E A D K A A 73
      + I T ++L P S K S + S N R L ++ A L S + G V N L + + D M A L
Sbjct: 10 Q I K A T I Q L P A S K S I S N R A L I I H A L S K G D D V P S N L S D C D D T Q V M T K A L ----- 56

Query: 74 K R A V V V G C G G K F P V E D A K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P 133
      + E + + A G A M R L T A +++ G + + G R M ++R P
Sbjct: 57 -----T E G N E V I N I L A --A G T A M R F L T A Y L S S T P G --I H T I T G T E R M Q Q R P 98

Query: 134 I G D L V V G L K Q L G A D V D C F L G T D C P P V R V N G I G G L P G G K V K L S G S I S S Q Y L S A L L M A A P L A 193
      I L V L ++L G A ++ P P + R + G L G ++ L G ++ S S Q Y + S A L L M P +
Sbjct: 99 I Q I L V N A L R E L G A H I E Y V R N E G F P P L R I E G - R E L T G S E I T L K G N V S S Q Y I S A L L M I G P V L 157

Query: 194 L G D V E I E I I D K L I S I P Y V E M T L R L M E R F G V K A E H S D S W --D R F Y I K G G Q K Y K S P K N A Y V E 251
      +++ + ++S P Y + + T L + L M + F G A S W D + Q Y V E
Sbjct: 158 K N G L Q L R L T G E I V S R P Y I N L T L Q L M K D F G A S A ----S W T S D Q N I Q V D P Q P Y H C L P F T - V E 212

Query: 252 G D A S S A S Y F L A G A A I T - G G T V T V E G C G T T S L Q G D V K F A E V L E M M G A K V T W T E T S V T V T G P 310
      D S + A S Y + A A ++ + + G S Q G D + A E V + G + T E T +
Sbjct: 213 S D W S A A S Y W Y Q I A A L S P Q A N I E L T G L F R H S Y Q G D S R G A E V F A R L G V A T E Y T E T G I ----- 267

Query: 311 P R E P F G R K H L K A I D V N M N K M P D V A M T L A V V A L F A D G P T A I R D V A S W R V K E T E R M V A I R T E 370
      R ++ + D + + P D + A T V + P + S ++K E T + R + A ++T E
Sbjct: 268 - R L K N G T C V E R L D E D F V D I P D L A Q T F V V T C A L L N V P F R F T G L Q S L K I K E T D R I E A L K T E 326

Query: 371 L T K L G A S V E E G P D Y C I I T P P E K L N V T A ---I D T Y D D H R M A M A F S L A A C A E V P V T I R D P G C 427
      + K L G + + D + E ++ A I T Y + D H R M A M A F + A A + I + P
Sbjct: 327 M K K L G Y I L H D K N D S I L S W D G E R V E Q Q A C P V I K T Y E D H R M A M A F A P A A I H Y P T I Q I D E P Q V 386

Query: 428 T R K T F P D Y F D V L 439
      K ++P Y ++ L
Sbjct: 387 V S K S Y P G Y W N D L 398

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>ref|ZP_07334199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio fructosovorans JJ]
gb|EFL50559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio fructosovorans JJ]
Length = 439

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 155/450 (34%), Positives = 232/450 (51%), Gaps = 40/450 (8%)

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Query: 18 T V K L P G S K S L S N R I L L L A A L S E G T T V V D N L L N S E D V H Y M L G A L R T L G L S V E A D K A A K R A V 77
      T V P S K S + S + R ++ A + L + G T + V L L + S + D + + + G ++ +
Sbjct: 3 T V A A P P S K S V S H R A V I A A S L A A G T S R V S G L L D S Q D I T R T R D C M A A M G A D F H P - Q S D G S V I 61

Query: 78 V V G C G G K F P V E D A K - E E V Q L F - L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P I G 135
      V G G D + + E Q + + G + G R L T A A A G + + G R M + R P I G

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Sbjct: 62 VSGTAGHPQGGDVEHDEPQILDVGESGTTTCRLTA--VAAAGRGVFEIRGEGRMHDRPIG 119

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+LV L LG ++ + CPP+ + GL GG +S SSQYLS LL+AAPLA

Sbjct: 120 ELVNALLPLGVEILYLEKSGCPPLHMAS--NGLSGGTASISLEDSSQYLSGLLLAAPLAAA 178

Query: 196 DVEIEII-DKLISIPYVEMTLRLMERF----GVKAEHSDSWDRF-----YIKGGQKYK 243
+ +EI +K +S PYV +TL + F V+ D+W+R I G ++

Sbjct: 179 PLTVEITGNKTVSWPYVAITLSTLADFSVPFAVETR DGD AWERVDWRTLTDVIPGQVRFA 238

Query: 244 -----SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGAK 297
P++ VEGD SSASYFLA A+ VTV G SLQGD ++L MGA+

Sbjct: 239 MRPALYKPRDYAVEGDWSSASYFLAAGAVGKAPVTVTGLRPDSLQGDRAICDILARMGAR 298

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
+ +TV L D++M + PD+ T+A A FA G T IR+VA R

Sbjct: 299 IEAGPDGITVL-----PGSLTGQDLMGRCPDLVPTVATAACFAKGETTIRNVHLR 350

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPP----EKLNVTAIDTYDDHRMAMAFSL 412
+KE++R+ A+ T+ GA V PD I P E++ +A + DHR+AM+ ++

Sbjct: 351 LKESDRIEAVAENCTQAGAVVTTTPDGMRIKPRPLTGERVEFSA---FGDHLAMSAAI 407

Query: 413 AACAEVPTTIRDPGCTRKTFPDYFDVLSTF 442
A + V + +P C K+FP +++ T

Sbjct: 408 FEMAGIEVALDNPACVAKSFPTFWKWRTL 437

>gb|ADX68016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Weeksella virosa DSM
16922]
Length = 414

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 139/433 (32%), Positives = 227/433 (52%), Gaps = 46/433 (10%)

Query: 10 QPIKEISGTVKVLPGSKSLSNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++S VK+ GSKS SNR+LLL AL + + NL N+ED M AL+

Sbjct: 7 QPKNKLSP-VKITGSKSESRLLLLNALFDDALDLQNLNAEDTQLMQNALK----- 57

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ KE V + +AG AMR LTA A T++L G RM

Sbjct: 58 -----EKKEVVDI--HHAGTAMRFLTAYF-AIQNKETHILTGSQRM 95

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+ERPI LV LK+LGA+++ PP+++ G L + + +ISSQY++ALL+

Sbjct: 96 KERPIKILVDALKELGAEIEYLENDGFPLKITG-TELTQPTIDIPANISSQYITALLLI 154

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY 249
+ + I +I K+ S+PY+ M++ L++ G++ E +++ + K P+

Sbjct: 155 GTKLVNGLTINLIGKITSPLYLMSVELLKNVGIEVEFTNNQ---LVVAYSKNILPQVFE 211

Query: 250 VEGDASSASYFLAGAAITG--GTVTVEGCGTTSLQGDVKFAEVL-EMMGAKVTWTETSVT 306
+E D SSASYF + A++ T+T++ SLQGD + E G + ++ + +T

Sbjct: 212 IESDWSSASYFYFIALSEPETTITIQNYRAKSLQGDAAALQTIYRENFGEVSEFEKNCLT 271

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ K I +++N+ PD+A TLAV L + P + + ++KET+R+VA

Sbjct: 272 LKKIKDFSLPTK----ILLDLNQTPDIAQTLAVTCLGLEIPCHFTGLETLKIKETDRLVA 327

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPTIR 423
++ EL+K GA V IT + N++ ++TY+DHRMAMAF+ A +I+

Sbjct: 328 LQNELSKFGAKVNITQQLSITAYNENNLRELIVETYNDRMAMAFAPLAILH-SFSIK 386

Query: 424 DPGCTRKTFPDYF 436
DP +K++P+++

Sbjct: 387 DPDVVVKSYPNFW 399

>ref|ZP_02329207.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus larvae
subsp. larvae BRL-230010]
ref|ZP_08055388.1| 3-phosphoshikimate 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]

gb|EFX46929.1| 3-phosphoshikimate 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
Length = 430

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 148/438 (33%), Positives = 229/438 (52%), Gaps = 22/438 (5%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ P +SG ++ SK+ + R LL AALSEG+ + SED M +R LG +
Sbjct: 4 IVHPTPRLSGDIQALSSKNYTRFLLAAALSEGTSIIYPAQSEDGEAMRRICIRDLGARI 63

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E D + +++ GK+P + KE L +GNAG +R L + V A T+V
Sbjct: 64 EEDD---QKIIITGFGKYP-QQVKE---LNVGNAGAVLRFLMS-VAAFCQEVTFVNAYPE 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP DL+ L+Q+G +V G P+ + G G GG++++SG++SSQ+LS++L
Sbjct: 116 SLGKRPHDDLHLEQMGVEVVNQDGR--LPITIRG-GEPRGGRIQVSGNVSSQFLSSIL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
APL D EIE++ L S + TL +++ G++ E S + I G Q Y+ P+
Sbjct: 173 FIAPLLKEDSEIEVLHDLKSKIVIGQTLQAGIRVEASKDLMHYRIPGNQTYQ-PRE 231

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V+GD ++ LA AA+T VTV SLQG+ +VL MG +T + V V
Sbjct: 232 YVVQGDYPGSAAILAAAVTESDVTNNLEENSLQGERACIDVLRQMGVLLTHKDRQVQV 291

Query: 308 TGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G R LK ++ + ++ D + + A+FADG T +V + R KE +R+
Sbjct: 292 KGNR-----LKPVEFDGDEFTDAVLAMVATAVFADGTRFYNNENLRYKECDRITDF 344

Query: 368 RTELTKLASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIRD 424
TEL K GASVEE I+ PE + ID + DHR+ MA S+ + +TIRD
Sbjct: 345 LTELKAGASVEERQSEIIVHGKPEGVEGGVEIDAHDHVRVIMALSVVGLRSRKGTLIRD 404

Query: 425 PGCTRKTFPDYFDVLSTF 442
K++P +F+ L
Sbjct: 405 AQHVAKSYPHFFNHLQAL 422

>ref|NP_613913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanopyrus kandleri
AV19]
sp|Q8TXN4.1|AROAMETKA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAM01843.1| 5-enolpyruvylshikimate-3-phosphate synthase [Methanopyrus kandleri
AV19]
Length = 428

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 151/441 (34%), Positives = 231/441 (52%), Gaps = 26/441 (5%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+ + L+ I E+ GTV P SKS S+R L+ A+L +G+T + N+L++EDV L R LG
Sbjct: 2 KRVELEGIPEVRGTVCPPPSKSGSHRALIAASLCDGSTELWNVLDAEDVRATLRLCRMLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V+ D + V G P A E+V + GN+G +R AA T +L
Sbjct: 62 AEVDVDGEERLEATVSGFGDSP--RAPEDV-VDCGNSGTTLR--LGCGLAALVEGTTILT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQ 181
G +R RP+GDL+ L+ LG D G + PPV ++G P +V + G +SSQ
Sbjct: 117 GDDSLRSRPVGDLLAALRSLGVDARGRVVGEYPPVVISG--RPLRERVAVYGDVSSQ 173

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++SALL LG + +++ L S PYV+MT+ +ERFGV S F ++G +
Sbjct: 174 FVSALLFLGA-GLGALRVVDVGLDLRSRPYVDMTVETLERFGVSVVREGS--SFEVEG--R 228

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTSLQGDVKFAEVLEMMGAKVTWT 301
+SP VE D SSA YF+A AI GG + +EG S D + E+ MGA+V

Sbjct: 229 PRSPGKLRVENDWSSAGYFVALGAI-GGEMRIEGVDLDSSHPDRRIVEITREMGAEVVRI 287

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + V R L+ ++V+++ PD+ T+A +A FA+G T I +V R KE

Sbjct: 288 DGGIVVRSTGR-----LEGVEVDLSDSPDLVPTVAAMACFAEGVTRIENVGHLRYKEV 340

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS-LAACAEVPV 420
+R+ A+ EL K G V EG D+ I E + +D+ DHRMAMA + + A A

Sbjct: 341 DRLRALAAELPKFGVEVREGKDWLEIVGGEPVGAR-VDSRGDHRMAMALAVVGAFARGKT 399

Query: 421 TIRDPGCTRKTFFPDYFDVLST 441
+ ++P +++ L++

Sbjct: 400 VVERADAVSISYPRFWEDLAS 420

>ref|ZP_08075517.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phascolarctobacterium
sp. YIT 12067]
gb|EFY05739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phascolarctobacterium
sp. YIT 12067]
Length = 433

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 147/442 (33%), Positives = 233/442 (52%), Gaps = 34/442 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ + P K ++GTV++P SKS+ +R ++ A L+ GT++VDN+ S+D+ + LR +

Sbjct: 2 EKVKIYPAK-LAGTVQVPSSKSMGHRHREICAGLAGGTSIVDNISMSQDIEATMRVLRAMN 60

Query: 65 LSVEAD---KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
+SV+ + K + G G D + G +G +R G T

Sbjct: 61 VSVDEIPSMIEGRKALQITGTGHPAAAD----NVDCGESGSTLRFFIPLGANLGCPLT 115

Query: 121 YVLDGVPRMRERPIGDLVVGL-KQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
++ G ++ RP+ L KQ V F P+ VNG L GK +L G +S

Sbjct: 116 FIGHG--KLVSRLQAYYDILDKQF--VQYFNDNGNLPLTVNG--HLMGPKFELPGDVS 168

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ++S LL A PL GD EI I L S YV+MTL + ++GVK E+ D R Y+ G

Sbjct: 169 SQFVSGLLFALPLLKGDSEIIITSPLASASYVDMTLNCLAKYGVKIENVDAHRHYLVPG 228

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
++ +++ VEGD S A+++ G A+ G +T G SLQGD E+++ MGA +

Sbjct: 229 KQRFKAQDSKVEGDSQAAFWTVGGAL-GAGITASGIDFASLQGDKAVVEIMQRMGADIA 287

Query: 300 WTETSVTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
SVTV + A ++ + PD+ L V+A ++G T I + R+K

Sbjct: 288 QNADSVTVNSSTTQ-----ATVIDASNCPIIPVLTVLAADVSEGTTKIINAGRLRIK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIIT-PPEKLN--VTAIDTYDDHRMAMAFSLAA-- 414
E +R+ A+ +EL K+GA++ E + IT PE L V A D ++DHR+AM+ ++AA

Sbjct: 340 ECDRLAAMTSELNKMGAATELEGLTITGKPEGLRGVEA-DAWNDRHIAAMSLAIAAQ 398

Query: 415 CAEVPVTIRDPGCTRKTFFPDYF 436
CAE P+T+ G K++PD++

Sbjct: 399 CAE-PITLTGAGSVSKSYPDFW 419

>ref|ZP_01691566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microscilla marina
ATCC 23134]
gb|EAY27343.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microscilla marina
ATCC 23134]
Length = 421

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 147/438 (33%), Positives = 226/438 (51%), Gaps = 52/438 (11%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I V+LP SKS SNR L++ AL++ N+ L EA

Sbjct: 15 IQTAVQLPSSKSESNRALIIQALAKYQAAANI-----KLSNISEARDTQT 60

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

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      ++G GK          L + +AG MR LTA +      + +L G RM+ RPI
Sbjct: 61 LQRLLGEEGKI-----LDVLDAGTTMRFLTAFIAVTQQHK--ILTGTARMQSRPI 108

Query: 135 GDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      G L LK LGA ++      PP+ ++      L G +++ G ISSQY+SALLM APL
Sbjct: 109 GILAEALKSLGASIEFLKHAGYPPIEIHPKHPLQGKAIQMRGDISSQYISALLMIAPLLP 168

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPKNAYVEGD 253
      ++IE+ K+ S PY+EMTL+LM FG+++ S++ +IK Q Y++ + A +E D
Sbjct: 169 EGLDIELTGKINSRPYIEMTLQLMMHFGIQS----SFEGNHKVAHQTYQANQYA-IESD 223

Query: 254 ASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--- 307
      S ASY+ A A++ T +T++G SLQGD E+++ G K T+ V +
Sbjct: 224 WSGASYWYAIVALSSENTTKITLKGRLADSLQGDRVIVELMQHFGVKSTFVADGVVLEKV 283

Query: 308 -TGPPREPFPGRKHLKAI DVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
      P P      +++N + PD+A T+AVVA P ++ + S ++KET+R+ A
Sbjct: 284 AIAPESTP-----LELNFAQCPLAQTVAVVAAGMPLQMKGLESKIKETDRVNA 335

Query: 367 IRTELTKLGASVEEGPDYC--IITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPVTI 422
      ++ EL K+G+ +EE ++ P +L I TY+DHRMAMAF+ AC + + I
Sbjct: 336 LQQELKLVGSHLEEKESQAEWLLHPGAELPTVPITITQTYEDHRMAMAFAPLACL-LNLNI 394

Query: 423 RDPGCTRKTFPDYFDVLS 440
      DP K++P ++D L
Sbjct: 395 EDPEVVAKSYPRFWDDLQ 412

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>ref|ZP_07721584.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Algoriphagus sp. PR1]
gb|EAZ80100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Algoriphagus sp. PR1]
Length = 413

Score = 200 bits (509), Expect = 3e-49, Method: Compositional matrix adjust.
Identities = 142/427 (33%), Positives = 220/427 (51%), Gaps = 56/427 (13%)

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Query: 18 TVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
      T+ L SKS SNR+L++ AL+E + + NL + D M+ L+T
Sbjct: 21 TIPLSASKSESNRVLIIDALTEVSNIKISNLAEARDTQTMIRLLQT----- 65

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
      PV D      + +AG MR LTA AA N V+ G PRM ERPIG L
Sbjct: 66 -----NPPVFD-----VLDAGTTMRFLTAF--AAATNQNKVMTGTPRMCERPIGIL 109

Query: 138 VVGLKQLGADVDCFLGTD-CPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
      V L+ +GA++ ++G + PP+ ++G+ +VK+ G +SSQY+SA+LM AP
Sbjct: 110 VDALRTVGAEIH-YMGVEGYPLAIHGLSEQTTNQVKIRGDVSSQYISAMLMIAPTLPKG 168

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
      +E+E+ K+ S Y+EMTL LM +FG+K E W I + P VE D S
Sbjct: 169 LELELEKGVGSRTYIEMTLELMAQFGIKYE----WKGNKISVDSQQYQPTTFVESDWSG 224

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFP 315
      ASY+ + A G++ +EG SLQGD K E+++++G K T+ E V +
Sbjct: 225 ASYWFSLLACADSGSLFLEGLKENSQGDGSKIVEIMDLLGIKSTFKEGGVLLQ----- 277

Query: 316 GRKHLKAI-DVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
      ++ +K + + + PD+A T+AV + S ++KET+R++A++ EL K
Sbjct: 278 -KQEVKGLKEWDFTHCPDLAQTVAVTCAILGQNAIFTGLESKIKETDRILALQQLAKF 336

Query: 375 GASVEEGPD--YCII---TPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
      A ++E Y +I T P+++ I TY+DHRMAMAF + + V DP
Sbjct: 337 NAELKEIETEYVQVIPSVTMPQEVK---IHTYEDHRMAMAF-MPLVTKTQVVFDDPEVVN 392

Query: 430 KTFPDYF 436
      K++P ++
Sbjct: 393 KSYPSFW 399

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>ref|ZP_08155395.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus equi ATCC 33707]
gb|EGD23360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus equi ATCC

33707]
Length = 428

Score = 200 bits (508), Expect = 4e-49, Method: Compositional matrix adjust.
Identities = 153/439 (34%), Positives = 230/439 (52%), Gaps = 39/439 (8%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA--DKAAKR 75
+V LPGSKS++NR L+LAAL+ G + + L S D M+ LR LG+++ A D A
Sbjct: 4 SVTLPGSKSITNRALILAALASGPSTITGALRSRDTDLMIQGLRALGVAITATPDPATGT 63

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ V G P+ A + L AG MR L A A G T +DG + R RP+G
Sbjct: 64 TLHVVPG---PMTGAAVDCGL----AGTVMRFLPPAAALAEG--TVAVDGDGEQARTRPLG 114

Query: 136 DLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ L+ LGAD+D D P V+G GGL GG V + S SSQ++S LL++A A
Sbjct: 115 TILDALRGLGADIDG----DALPFTVHGHGGLRGGTVTIDASGSSQFVSGLLLSA--ARF 168

Query: 196 DVEIEIIDK---LISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYIKGGQKYKSPK 246
D + + + L S+P+++MT+ ++ GV ++ +D+W K P
Sbjct: 169 DEGVTVRHQGGLSPMPHIDMTVEMLREAGVTVHTPGESGDADTWKVLPGK-----IDPV 223

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VE D S+A+ FLA AA+TGGTV V + + Q +L MGA V E ++
Sbjct: 224 DWVVEPDLNATPFLAAAVTGGTVRVLWPSRTTQPGDAIRGILAEMGADVRLGEEVLS 283

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
VTGP K L+ ID++++ + ++ T+A +A ADGP+ +R +A R ET+R+ A
Sbjct: 284 VTGP-----KTLRGIDIDLHDIGELTPTVAALALADGPSVLRGIAHLRGHETDRLAA 336

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTTIRDPG 426
+ TE+ KLG + E D I P L+ +Y DHRMA A ++ V I D G
Sbjct: 337 LATEIGKLGAATETADGLRIE-PRPLHGAQWHSYADHRMATAGAILGLVVDGVDIEDVG 395

Query: 427 CTRKTFPDYFDVLSTFVKN 445
T KT P + ++ + +
Sbjct: 396 TTAKTLPGFENLWTAMLDE 414

>ref|YP_003146820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kangiella koreensis
DSM 16069]
gb|ACV27052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kangiella koreensis
DSM 16069]
Length = 442

Score = 200 bits (508), Expect = 4e-49, Method: Compositional matrix adjust.
Identities = 147/426 (34%), Positives = 225/426 (52%), Gaps = 26/426 (6%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
++LPGSK L+NR ++LAA+S+GTT + N+ ++D+ LGA++ LG VE + +V
Sbjct: 16 LRLPGSKYLANRYVVLAAISDGTTRLNPNRNDLILAAALGAIQALGAKVEW--LDQTSVE 73

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV----TAAGGNATYVLDGVPRMRERPI 134
+ F + D +V + ++G R +TA ++ G T + G +MR RP+
Sbjct: 74 IKGIESFELAD---DVVIDCHDSGTLARFITALTGLFYSSVGHQIT--ITGSQQMRSRPM 128

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ V L+ LG ++ G P++++G + GG +L S SSQ+LS LL+A A
Sbjct: 129 QESVASLETGLVSEIESEKGF--LPIKISG--PITGGSCELDASRSSQFLSGLLIACLKAE 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D I + +S YVE+TLR +E FG + + + + F+I G Q + K+ +V GD
Sbjct: 185 KDTLIHLSSDAVSESYVELTLRAIELFGGEVKRINCRE-FFIPGQQALVA-KDIHVAGDV 242

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT-GPPRE 313
S+SYFLA + + TV S QG+ KF +VLE MGAKV + + V P
Sbjct: 243 VSSSYFLAAGLLAESSCTVLNYHFDSPQGESKFPQVLERMGAKVYLKQDDLKVEYDSP-- 300

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L+ IDV+M MPDV TLA +A FA G T I ++A KE+ R+V + +L K
Sbjct: 301 -----LQGIDVDMGNMPDVVPTLAALACFAQGETRITNIAHLAFKESNRIVDLCEQLKK 354

Query: 374 LGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
LGA E I ++L + + DHR+AM+ +L +TI K+FP
Sbjct: 355 LGADCEYDESSITIRGGKQLIADKVVSSCHDHRSLALIGIKLGLTIESSEAVAKSFP 414

Query: 434 DYFDVL 439
DY+ L
Sbjct: 415 DYQYL 420

>ref|ZP_04841395.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_2_5]
gb|EES87996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
3_2_5]
Length = 412

Score = 200 bits (508), Expect = 4e-49, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 220/432 (50%), Gaps = 49/432 (11%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ ALS+G V+ NL + +D M+ AL
Sbjct: 10 QIKATIQLPASKSISNRALIIHALSKGDDVLSNLSDCDDTQVMIKAL----- 56

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ E + + AG AMR LTA +++ G + + G RM++RP
Sbjct: 57 -----TEGNEVIDIL--AAGTAMRFLTAYLSSTPG--IHTITGTERMQQRP 98

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGA ++ PP+R+ G L G ++ L G++SSQY+SALLM P+
Sbjct: 99 IQILVNALRELGAHIEYVRNEGFPPRIEGTE-LTGSEITLKGNVSSQYISALLMIGPVL 157

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW--DRFYIKGGQKYKSPKNAYVE 251
+ + + +++S PY+ +TL+LM+ FG A SW D+ Q Y VE
Sbjct: 158 KNGLLLRLTGEIVSRPYINLTQLMKDFGASA----SWTSDQNIQVDPQPYHCLPFT-VE 212

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+ASY+ AA++ + + G S QGD + AEV +G +TET +
Sbjct: 213 SDWSAASYWYQIAALSPQADIELTGLFRHSYQGDSRGAEVFARLGVATEYTETGI----- 267

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R ++ +D + +PD+A T V + P + S ++KET+R+ A++TE
Sbjct: 268 -RLKNGTCVERLDEDFVDIPDLAQTFVVTCALLNVFPFRFTGLQSLKIKETDRIEALKTE 326

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
+ KLG + + D + E++ I TY+DHRMAMAF+ AA + I +P
Sbjct: 327 MKKLGYLHDKNDSILSWDGERVEQQTCPVIKTYEDHRMAMAFAPAAIHYPYTIQIDEPQV 386

Query: 428 TRKTFPDYFDVL 439
K++P Y+D L
Sbjct: 387 VSKSYPGYWDDL 398

>ref|ZP_07961875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella salivae
DSM 15606]
gb|EFV04680.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella salivae
DSM 15606]
Length = 412

Score = 200 bits (508), Expect = 4e-49, Method: Compositional matrix adjust.
Identities = 137/437 (31%), Positives = 231/437 (52%), Gaps = 46/437 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I T++LP SKS+SNR L++ AL+ G V +L + +D ++ AL+T +++
Sbjct: 9 QHIDTTIQLPPSKSISNRALIIQALANGNLVPRHLSDCDDTKVIVEALKTKSETID---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ AG AMR LTA ++ G +VL G RM++R
Sbjct: 65 -----IKAAGTAMRFLTAYLSVREGE--HVLGTDRMKQR 97

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+ LGAD+ PP+R+ G L GG +++ G++SSQ++SALL+ P+
Sbjct: 100 PIGLV L+ LGAD+ PP+R+ G L GG +++ G++SSQ++SALL+ P+ 157

Sbjct: 98 PIGVLVDALRYLGADIQYEGEAGYPPLRIKG-HPLAGGFIEIPGNVSSQFISALLLIGPM 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+++ D++IS PY+++TL +M FG A+ +D I+ K S ++ Y+E

Sbjct: 157 LEKGLLELKLTDDEIISRPYIDLTLMMRDGFAIADWTDV---DTIRVAAKAYSARDYYIES 213

Query: 253 DASSASYF---LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D +++SY+ +A A + V +EG S QGD + ++G K T T G

Sbjct: 214 DWTASSYWEIMALADDSEAVVRLEGLMDGSKQGDSVVKYIFSLLGIK---TSFETTA PG 270

Query: 310 PPREFPGRKH---LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P +H L ++ + PD+A T+ V + + ++ +++ R+KET+R+ A

Sbjct: 271 VPNIIVTLHRHKCLLPRLLEYDTGSPDLAQTVVVTCVNMNIKFHLKGLSTLRIKETDRIEA 330

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
++TEL KLG ++ D ++ E+ + I+TY+DHRMA+AF+ A + I +

Sbjct: 331 LKTELRLKGLFVLQSVGDELWDGERCQPSDEPIETYEDHRMALAFAPVALKRQGLQINN 390

Query: 425 PGCTRKTFFPDYFDVLST 441
P K++PDY+ L T

Sbjct: 391 PEVVSKSYPDYWKDLQT 407

>ref|ZP_05618982.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enhydrobacter
aerosaccus SK60]
gb|EEV23836.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enhydrobacter
aerosaccus SK60]
Length = 422

Score = 199 bits (507), Expect = 6e-49, Method: Compositional matrix adjust.
Identities = 143/438 (32%), Positives = 225/438 (51%), Gaps = 47/438 (10%)

Query: 13 KEISGTVKLPGSKSLNRILLALAESEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G + +PGSKSL+NR L+LA+++ G + + N+L S+D M+ LR +G+S+ +

Sbjct: 17 KPVEGVISVPGSKSLNRLILASVANGQSTLSNVLSDDTEVMINGLRQMGVSISFVEP 76

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K ++V GK ++ + +FLGNAG A R LTA G ++DG MR R

Sbjct: 77 NK--ILVNSNGKL----SEPKQPIFLGNAGTATRFLTAMSCLVKGEV--IIDGDEYMRTR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV LK +G D+ T CPPV + G L +V + ++SSQY+SALLM +P

Sbjct: 129 PILPLVNALKSIGIDIQS--DTGCPPVTIKSKGVLSSSEVTIDANLSSQYVSALLMLSPF 186

Query: 193 ALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L + +I + D I Y+++TL +M+ FG+ E + + ++ Q YK+ N ++E

Sbjct: 187 NLKEFKIILKDSNIGGKGYIDLTLNIMKEFGITIE---TIENGWLIRRQSYKA-TNYFIE 242

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D+SSA+Y A +T G + + Q D K +++ P

Sbjct: 243 PDSSSATYIWAIEKLTNGKIDIGFEAKKMTQPDAKVYDLINSF-----P 286

Query: 312 REPFGRLKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
P ID ++ D TLAV+A F++ + + RVKE +R+ AI+ L

Sbjct: 287 NFP-----DLID--GSQFQDAIPTLAVMAAFSNKKVLFRTGIENLRVKECDRIKAIKEGL 338

Query: 372 TKLGA--SVEEGPDYCI-----ITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
K+ ++E G + I + LNV ID+YDHR+AM+FSLA ++I +

Sbjct: 339 CKIHPELAIEIGDQLLVNGEIDIYNIKNLNV-LIDSYYDHRIAMSFSLAGILIDGISISN 397

Query: 425 PGCTRKTFFPDYFDVLSTF 442
C KT+P Y+ L +

Sbjct: 398 YNCVSKTYPYWKSLQSL 415

>ref|ZP_07366540.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella marshalli
DSM 16973]
gb|EFM01078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella marshalli
DSM 16973]
Length = 416

Score = 199 bits (506), Expect = 6e-49, Method: Compositional matrix adjust.
Identities = 143/442 (32%), Positives = 225/442 (50%), Gaps = 59/442 (13%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+E+ T+ LP SKS+SNR+L++ ALSEG+ NL +D M+ ALR + ++
Sbjct: 9 RELDATIDLPASKSISNRVLIIHALSEGSIPPSNLSRCDDTEVMVAALRDMPEID---- 64

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
+ AG AMR +TA + G +V+ G RM R
Sbjct: 65 -----IKAAGTAMRFMTAYLAVTRGE--HVITGTERMCHR 97

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ +GAD++ PP+R+ G L GG + +SG +SSQY+SALLM +
Sbjct: 98 PIKVLVDALRYMGADIEYMGEEGYPPLRIRG-KQLEGGLSISGHVSSQYISALLMIGAV 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G +++++ ++S PY+++TL M +G K + +D D I+ Q Y S + +E
Sbjct: 157 LEGGLQLQLTGEIVSRPYIDLTLCTMREYGAKVDWTDK-DTISIQ-PQSYVS-RPYLIEN 213

Query: 253 DASSASYFLAGAAITG---GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-----ET 303
D S+ASY+ A++G +V + G S QGD + ++G K + +T
Sbjct: 214 DWSAASYWYEIMALSGVREASVRMTGLRDGSRQGDVVRYLFSLLGVKSAFASKEPKD 273

Query: 304 SVTVTGPPREPFGKRLKAI---DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+VT++ HL A+ D + PD+ TLAV P + + R+KE
Sbjct: 274 TVTLS-----NHLNALPRMDYDFINQPDLTQTLAVSCCLRGIPFHTGLGNLRIKE 324

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAFSLAACAE 417
T+R+ A++TEL KLG V+E +I E+ + IDTY+DHRMAMAF+ A+
Sbjct: 325 TDRIEALQTELRLKLGFFVKE+TNGNELIWDGERCETMPCPVIDTYEDHRMAMAFAPASFLV 384

Query: 418 VPVTIRDPGCTRKTFPDYFDVL 439
+ I DP K++P ++D L
Sbjct: 385 PGLRINDPAVVTKSYPHFWDDL 406

>ref|YP_003997622.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leadbetterella
byssophila DSM 17132]
gb|ADQ17269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leadbetterella
byssophila DSM 17132]
Length = 409

Score = 199 bits (506), Expect = 6e-49, Method: Compositional matrix adjust.
Identities = 142/427 (33%), Positives = 215/427 (50%), Gaps = 51/427 (11%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ L SKS SNR L+L AL+ + + NL ++ D M+ L+
Sbjct: 17 IALASSKSESNRALILNALTGFKSELKNLSSARDTQTMIRLLQ----- 59

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPIGDLV 138
+ EE L +AG MR LTA TA N ++ G PRM ERPIG L+
Sbjct: 60 -----STEETADVL-DAGTTMRFLTAFFTAT--NTPKIMTGTPRMCERPIGILI 105

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
LK LGA+++ PP +++G ++++ G +SSQY+SALLM AP +E
Sbjct: 106 DALKTLGAIEIYLEKPGYPHKIHGFTDQKTNQLEIRGDVSSQYISALLMIAPTLPQGLE 165

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I++ ++ SIPY+ MT+R ME FGK E W +K + +P +E D S AS
Sbjct: 166 IQLTGEIGSIPYITMTIRQMEAFGVKVEA--DWKAKTLKVKPQTYTPVTYQIESDWSGAS 223

Query: 259 YFLAGAAITGG---TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
Y+ + A+ + + G SLQGD A+++ +G K T+T+ V + P
Sbjct: 224 YWYSMVALASHPETKIELLGLKLSLQGDSSAIADIMVHLGVKSTFTKDGVLLEKIPAA-- 281

Query: 316 GRKHLKAIDVNMNMKMPDVAMTLAVV--ALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K N + PD+ T+AV+ AL +G + + S ++KET+R++A++ EL K
Sbjct: 282 -----KDFRWNFSDCPDLTQTVAVILAALRIEG--ELTGIESLKIKETDRVLALQNELKK 334

Query: 374 LGA---SVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
+GA VE+ Y + + I TYDDHRMAMAF+ C V I +PG K

Sbjct: 335 IGAE LVEVEKNLKYKVTNFKAYTEIPQIATYDDHRMAMAF-PLCQLG DVIIEEPGVVAK 393

Query: 431 TFPDYFD 437

++P ++D

Sbjct: 394 SYPSFWD 400

>ref|YP_004253987.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Odoribacter
splanchnicus DSM 20712]
gb|ADY33807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Odoribacter
splanchnicus DSM 20712]
Length = 411

Score = 199 bits (506), Expect = 6e-49, Method: Compositional matrix adjust.
Identities = 141/432 (32%), Positives = 212/432 (49%), Gaps = 46/432 (10%)

Query: 13 KEISGTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GTV LP SKS+SNR+L++ AL++ ++NL + +D M+ L

Sbjct: 10 KRVQGTVTLPASKSISNRVLIVNALADSELP IENLADCDTQSMVRIL----- 57

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
E +G+AG AMR LTA ++ G +VL G RM++R

Sbjct: 58 -----CSENSYFDVGHAGTAMRFLTAYLSRIIGK--WVLTGSERMKQR 98

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L +LGA + PP+ + G L GG + + S+SSQY+SALLM AP

Sbjct: 99 PIRVLVEALNRLGARIGYLENEGFPPL E IYG-SRLVGGSIDIPASVSSQYISALLMIAPY 157

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+EI + K++S Y++MTL++M FG + D+ +K G+ P VE

Sbjct: 158 MEKGLEIRLTGKVVSSSYIDMTLQIMREFGAEVGREDT--VIGVKPEYRSVPYR--VES 213

Query: 253 DASSASYFLAGAAITG-GT V TVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S+ASYF AI G G + + G S+QGD + V +G + + V ++

Sbjct: 214 DWSAASYFYELLAIAAGEGEIILTGLKEKSMQGDSRQTVVWRKLGVRTCYEGDLVRLSA-- 271

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ + +D + +MPD+ + AV P R V + R+KET+R+ A+ EL

Sbjct: 272 ----AKPEIDRLDYDFVEMPD LVQSFVACCMRRIPFLFRGVETLRIKETDRIQALIEEL 327

Query: 372 TKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
KLG ++ D +I E+ I TY DHRMAMAF+ AA + I D

Sbjct: 328 GKLGYLLKAEGD GALIWEGERTGGQPCPRIATYHDHRMAMAFAPAALKHPGLVIVDKEVV 387

Query: 429 RKTFPDYFDVLS 440

K+FP Y++ L+

Sbjct: 388 SKSFPRYWEALA 399

>ref|ZP_02066162.1| hypothetical protein BACOVA_03157 [Bacteroides ovatus ATCC 8483]
gb|ED011254.1| hypothetical protein BACOVA_03157 [Bacteroides ovatus ATCC 8483]
Length = 410

Score = 199 bits (506), Expect = 7e-49, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 219/435 (50%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 6 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPPE NLSDCDDTQVMIKALT----- 58

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R

Sbjct: 59 -----EEKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM

Sbjct: 95 MQQRPIQILVNALRELGAIEFYTRNEGYPPLRIKG-AELKGNEITLKG NVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + Q Y+S

Sbjct: 154 IGPALKDGLTLHLSGEIISRPYINLTQLMQDFGAKAAWTSP--SSISVAPQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 212 -VENDWSAASYWYQIAALSPKAEIELLGLFHNSYQGDSRGAEVFSRLGITTEFTSQGVKL 270

Query: 308 TGPPREPFGRKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271 KKTGKAP-----ERLEEDFIDIPDLAQTFVVTALLNIPFRFTGLQSLKIKETDRIAAL 324

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
R EL KLG +EE D ++ E+ I+TY+DHRMAMAF+ A + I D
Sbjct: 325 RAE LKKLGYVIEEENDSILMWNGERCPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAD 384

Query: 425 PGCTRKTFPDYFDVL 439
P K++P Y++ L
Sbjct: 385 PQVVTKSYPGYWEDL 399

>ref|YP_004007995.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Rhodococcus equi
103S]
emb|CBH49316.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Rhodococcus equi
103S]
Length = 443

Score = 199 bits (505), Expect = 8e-49, Method: Compositional matrix adjust.
Identities = 155/439 (35%), Positives = 231/439 (52%), Gaps = 33/439 (7%)

Query: 15 ISGTVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA--DKA 72
+ +V LPGSKS++NR L+LAAL+ G + + L S D M+ LR LG+++ A D A
Sbjct: 16 VDASVTLPGSKSITNRALILAALASGPSTITGALRSRDTDLMIQGLRALGVAITATPDAA 75

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G P+ A + L AG MR L A AG T +DG + R R
Sbjct: 76 TGTTLHVVPG---PMTGAAVDCGL----AGTVMRFLPPAAALAEG--TVAVDGDEQARTR 126

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G ++ L+ LGAD+D D P V+G GGL GG V + S SSQ++S LL++A
Sbjct: 127 PLGTILDALRALGADIDG----DALPFTVHGHGGLRGGT VTIDASGSSQFVSGLLLSA-- 180

Query: 193 ALGDVEIEIIDK---LISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGQKYKSPK 246
A D + + + L S+P+++MT+ ++ GV S D + + G K S
Sbjct: 181 ARFDEGVTVRHQGGSLPSMPHIDMTVEMLREAGVTVHTPGESGDADTWKVLPG-KIDS-V 238

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VE D S+A+ FLA AA+TGGTV V + + Q +L MGA V E ++
Sbjct: 239 DWVVEPDLSNATPFLAAA AVTGGTVRVPLWPSRTTQPGDAIRGILAEMGADVRL EEGVLS 298

Query: 307 VTGPPREPFGRKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
VTGP K L+ ID++++ + ++ T+A +A ADGP+ +R +A R ET+R+ A
Sbjct: 299 VTGP-----KTLRGIDIDLHDIGELTPTVAALADGPSVLRGIAHLRGHETDRLAA 351

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
+ TE+ KLG +V E D I P L+ +Y DHRMA A ++ V I D G
Sbjct: 352 LATEIGKLGGAVTETADGLRIE-PRPLHGAQWHSYADHRMATAGAILGLVVDGVDIEDVG 410

Query: 427 CTRKTFPDYFDVLSTFVKN 445
T KT P + ++ + +
Sbjct: 411 TTAKTLPGFENLWTAMLDE 429

>ref|ZP_06408448.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
melaninogenica D18]
gb|EFC72968.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
melaninogenica D18]
Length = 417

Score = 198 bits (504), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 142/436 (32%), Positives = 225/436 (51%), Gaps = 47/436 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K I ++ LP SKS+SNR L++ AL++G + +NL + +D ++ GLS ++D

Sbjct: 9 KPIDTSITLPASKSISNRALIIQALTKGGMPENLSDCDDTEVIIR-----GLSKQSDVI 63

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+A AG AMR +TA ++A G Y + G RM+ R

Sbjct: 64 DIKA-----AGTAMRFMTAYLSATDGE--YTITGTERMKHR 97

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+ LGA+++ PP+ + G L GG +++ G++SSQY+SALLM AP+

Sbjct: 98 PIGILVDALRYLGAIEYVGEEGYPPLHIRG-RQLEGGSLQIPGNVSSQYISALLMIAPI 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
+E+++ +IS PY+++TL LM FGV AE SD +D +K Q Y+ + AY +E

Sbjct: 157 LTKGLELKLGTNIISRPIYIDLTLHLMHEFGVSAEWSDFDTISVK-SQAYQ--QRAYTIE 212

Query: 252 GDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
D S+ASY+ A+T T V ++G S QGD + ++G K ++ +

Sbjct: 213 SDWSAASYWYEIALTDDTRSKVALQGLKDGSRQGSASVRYIFSLLGIKTSFKDKD--SN 270

Query: 309 GPPREPFGR--KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
G P R + L ++ + PD+A TL V P + + ++KET+R+ A

Sbjct: 271 GLPEAILTRHSRMLNRMEDFTNQPDLAQTLIAVCPILGIPHFHTGLGLTKIKETDRIEA 330

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIR 423
+ E+ KLG + + + E+ A I+TY+DHRMAM+F+ A + I

Sbjct: 331 MTREMEKLGYYILYSENETELSWNGERCEPMAEPIIETIEDHRMAMSFAPLAIKLGEIRIN 390

Query: 424 DPGCTRKTFFPDYFDVL 439
P K++P Y+D L

Sbjct: 391 HPEVVSXSYPHYWDDL 406

>ref|YP_003313731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sanguibacter keddieii
DSM 10542]
gb|ACZ20897.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sanguibacter keddieii
DSM 10542]
Length = 448

Score = 198 bits (504), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 152/440 (34%), Positives = 222/440 (50%), Gaps = 35/440 (7%)

Query: 9 LQPIK-EISGTVKLPGSKSLNRILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSV 67
L P+ ++ TV++PGSKSL+NR L+LAAL++G + L S D M+ ALR+LG +V

Sbjct: 24 LAPVAGQLDATVEVPGSKSLTNRYLVLAALADGPGTLRGALRSRDTLMDVALRSLGATV 83

Query: 68 -EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E + ++ + G +V + G AG MR + A +G T LDG

Sbjct: 84 TEGESPSEWHITPGT-----VSGDVTVDCLAGTVMRFVPAVAALSGARVT--LDGD 133

Query: 127 PRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
R RP+G ++ GL+ LG VD G P + G G + GG V + S SSQ++S L

Sbjct: 134 EGARVRPMGPILDGLRGLGVRVDDG-GRGLLPFTIQAGSVRGGSDVDASASSQFVSGL 192

Query: 187 LMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS--WDRFYIKGGQKYK 243
L+AA G L SIP+++MT+ L+ GV + S W Q

Sbjct: 193 LLAAARFEQGLTLRHTGATLPSIPHIDMTVELLREAGVTVDASRPAAIW-----QVSP 244

Query: 244 SP---KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
P ++ VE D S+A FLA A + GGTV V G TT+ Q E+L MG

Sbjct: 245 GPVAARDVRVEPDLSNAGPFLAAALVAGGTVRVPGWPTTTTQPGAMPELLTRMGSAHL 304

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+TVTG + IDV+++ ++A T+A +A A P+ +R +A R E

Sbjct: 305 DGDVLTVTG-----TGEIHGIDVDLHAAGELAPTIAALAAIAGSPSRLRGIAHLRGHE 357

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ TE+T+LG E+ D +IT P L+ +TY DHRMA A ++ V

Sbjct: 358 TDLAALATEITRLGGQAEQTSGLVIT-PRPLHGGVFETYHDHRMATAGAIIGLRVPGV 416

Query: 421 TIRDPGCTRKTFFPDYFDVLS 440
++D G T KT P + D+ S

Sbjct: 417 QVQDVGTAKTLPGFDTLWS 436

>ref|ZP_08112518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
ND132]
gb|EGB16403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
ND132]
Length = 446

Score = 198 bits (504), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 158/444 (35%), Positives = 219/444 (49%), Gaps = 37/444 (8%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V P SKSLS+R L+ AAL+ G + + ++L S+D+ L G S+
Sbjct: 8 VNAPASKSLSHRTLIAAALAGGVSNISSVLESDDITRTRDCLTACGASIVEKDGVLVVTG 67

Query: 79 VCGCGKFPVEDAKEE----VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G K D K + +LF+ +G R +TA AA G T+ + G PRM ERP+
Sbjct: 68 MSDGPKGGNADGKHKDETPHELFMHESGTTCLMTA--VAAAGKGTFRVHGAPRMHERPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+L L LGA F G + V G V+++ SSQYLS LL+ APLA
Sbjct: 126 AELTTALAALGAKF-AFEGQEGYLPFMTANGYKKKSVEITLEEESQYLSGLLLGAPLAD 184

Query: 195 GDVEIEII-DKLISIPYVEMTLRLMERF--GVKAEHSD--SWDRFYIKGGQKYKSPKNAY 249
+ I +I +K +S PYV +TLR+ME F G E D W + + K K +
Sbjct: 185 HETTISVIGEKAWSWPYVALTLRIMEDFKAGFAVEILDGREWKAVPWRSVKGKPGKVRF 244

Query: 250 -----VEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGA 296
VEGD S+ASYFLA A+ V ++G SLQGD ++L MGA
Sbjct: 245 IVQPMGYENTGYQVEGDWSNASYFLAAGAVGTRPVLLKGLAADSLQGDRAIMDILSQMGA 304

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPATAIRDVASW 356
+ + V P L+ I+VNM + PD+ T+A VA FA PT I +VA
Sbjct: 305 SIKVNF DGILVEPGP-----LRGINVNMGRCPDLVPTVAAVAFAATPTTIGNVAHL 356

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITP---PEKLNVTADITYDDHRMAMAFSLA 413
R+KET+R+ A EL ++G E D II P P V TY+DHRMAM+ SL
Sbjct: 357 RLKETDRLAACANELARVCGGTEATVDSLII RPAPLPRDSEVN-FTTYNDHRMAMMSMLF 415

Query: 414 ACAEVPVTIRDPGCTRTFPDYFD 437
A + V + +P C K+FP +F+
Sbjct: 416 ELAGIKVNLDNPACVGKSFPGFGE 439

>dbj|BAJ27727.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Kitasatospora setae KM-6054]
Length = 410

Score = 198 bits (504), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 156/430 (36%), Positives = 215/430 (50%), Gaps = 35/430 (8%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V++PGSKS++ R L LAA ++G T + L S+D LR LG VE +A + +
Sbjct: 4 VEIPGSKSVTARALFLAAAADGVTTLVRLPLASDDTEGFTTEGLRALGYQVE--RAEREWRI 61

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G P + +F + R L AA G+ T+ D +MR RP+G L
Sbjct: 62 TGR----PQGPVGVDGASVFCRDGATTARFL--PTLAAAGHGTFFHFDASEQMRRRPLGPLT 115

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LG ++ P+ + G+ GG+V L +SSQYL+ALL+ PL +
Sbjct: 116 TALRDLGVRLEHRGAEGHHPLSIEA-SGVEGGEVTL DAGLSSQYL TALLLLGPLTRTGLR 174

Query: 199 IEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY-----VEG 252
I + D L+S PY+E+TL +M FGV+ + G + P Y VE
Sbjct: 175 IHVTD-LVSAPYIEITLAMMRSFGEV-----AREGNVFDVPAGGYTAARYPVEP 223

Query: 253 DASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
DAS+ASYF A AA+TG VTV G G +LQGD+KF EVLE +GAKV G
Sbjct: 224 DASTASYFFAAAAALTGREVTVPGLGRGALQGD LKFVEVLERLGAKVE-----IGTDA 275

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
L VNM + D TLA +A FA GP I DV + RVKE +R+ A L
Sbjct: 276 TTVTGGTLTGGTVNMNRDISDTMPTLAAIAPFASGPIRIEDVYNTRVKECDRLDACADNLR 335

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 432
+ G V G D+ I P V I+T+ DHR+ M+F++A + DPGC RKT
Sbjct: 336 RQGIDVATGRDWIEIRPGSPKPE-IETHGDHRIVMSFAVAGLRTPGTSYDDPGCVKRT 394

Query: 433 PDYFDVLSTF 442
P + D + +
Sbjct: 395 PGFHDAFAAW 404

>ref|ZP_07213686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. 20_3]
gb|EFK65016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. 20_3]
Length = 411

Score = 198 bits (504), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 149/441 (33%), Positives = 220/441 (49%), Gaps = 61/441 (13%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P I TVKLP SKS+SNR L+L ALS V+NL + +D + M+ AL +
Sbjct: 8 PGSAIRTTVKLPASKSISNRALILNALSYSAYDVENLSDCDDTNLMVKALNS----- 59

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +G AG MR LTA ++ G T + G RM+
Sbjct: 60 -----NDRDFNVGAAGTTMRFLTAFLSKVVGWET--ITGTERMK 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L LGA ++ PP+R+ G L GG++ L G++SSQY+SA+LM A
Sbjct: 97 NRPIKVLVDALNALGARIEYMEKEGYPLRIFG-SALQGGEISLPGNVSSQYISAILMIA 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKG-GQKYKSPKNAY 249
PL V + + +IS PY+ +TL+LME++GV+A SW IK Q+YK P +
Sbjct: 156 PLTENGVTLHLEGAIISRPYIHITLQLMEQYGVRA----SWTENMIKVLQPQYK-PIHFT 210

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VE D S+ASY+ A++ + + G SLQGD A++ +G T+T+ V +
Sbjct: 211 VESDWSAASYWYEIMALSKNAEIELLGLFKNSLQGDAAAGAKLFAQLGVGTTYTKRGVVL- 269

Query: 309 GPPREPFGFRKH----LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
KH + + N PD+A T V + + P + S ++KET+R+
Sbjct: 270 -----KHTGNICEKLVNFVNEPDLAQTFVVTCVLLNIPFRFMGLQSLKIKETDRI 320

Query: 365 VAIRTELTKLGASVEEGPDYCI-----ITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP 419
A++TEL KLG + + D + PE V A TY+DHRMA++F+ AA
Sbjct: 321 EALKTELRLKLGVLTDNRDSILEWNGERKEPESHPIA--TYEDHRMALSFAPAALVRPE 378

Query: 420 -VTIRDPGCTRKTFFDYFDVL 439
+ I P K++P Y++ L
Sbjct: 379 GIEIAHPQVVSXSYPHYWEDL 399

>ref|ZP_01961379.1| hypothetical protein BACCAC_03010 [Bacteroides caccae ATCC 43185]
gb|EDM19755.1| hypothetical protein BACCAC_03010 [Bacteroides caccae ATCC 43185]
Length = 410

Score = 198 bits (503), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 220/435 (50%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P + T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 6 LIPPPSVKATIQLPASKSISNRALIINALGKGIYSPENLSDCDDTQVMIKALT----- 58

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ +E + + AG AMR LTA ++ G V+ G R
Sbjct: 59 -----EGQETIDIM--AAGTAMRFLTAYLSVTPGER--VITGTAR 94

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM
Sbjct: 95 MQQRPIQILVNALRELGAIEYVHKEGYPLRIKG-SVLKGNITLKNVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG +A + S + + Q YKS
Sbjct: 154 IGPTLKDGLTLHLSGEIISRPYINLTQLMQDFGARAVWT-SPNSISV-APQSYKSVPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ A ++ + + G S QGD + AEV +G +T V +
Sbjct: 212 -VESDWSAASYWYQIATLSPEAEIELVGLFHNSYQGDSRGAEVFSRLGITTEFTPQGVKL 270

Query: 308 TGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271 KKTGKAP-----EKLEEDFVDIPDLAQTFVVTICALNIPFRFTGLQSLKIKETDRIAAL 324

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
RTEL KLG +EE D ++ E+ I TY+DHRMAMAF+ A + I D
Sbjct: 325 RTELKLGIVYVIEEENDSILMWNGERCPEETPVITTYEDHRMAMAFAPAVICHPNMLIAD 384

Query: 425 PGCTRKTFFPDYFDVL 439
P K++P Y++ L
Sbjct: 385 PQVVTKSYPGYWEDL 399

>ref|ZP_06275683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACTE]
gb|EFB64103.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACTE]
Length = 459

Score = 198 bits (503), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 151/446 (33%), Positives = 223/446 (50%), Gaps = 42/446 (9%)

Query: 15 ISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----- 68
+ TV +PGSKS++NR L+LAALS + L S D M ALRT+G+ +E
Sbjct: 20 VDATVTVPKSKSVTNRALVLAALSSEPGWLRRLRSRDTLLMAQALRTMGVIEEGVGP 79

Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A R + G G V+ +GNAG MR L A G + DG PR
Sbjct: 80 GSGEAWRVIPAGLHGPAITVD-----VGNAGTVMRFLPPVACLADGPVHF--DGDPR 128

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLM 188
ERP+ ++ L+ LGA +D G P+ V+G G L GG V + S SSQ++SALL+
Sbjct: 129 SYERPLHGVIDALRALGARIDDD-GRGALPLTVHGAGALDGGTVAIDASSSSQFVSALLL 187

Query: 189 AAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK---YKS 244
+ P VE+ L S+P++ MT+ ++ G + + ++ GG++ S
Sbjct: 188 SGPRFNQGVQVEVRHTGSTLPSMPHIRMVTDMLRAVGARVDEPET-----GGERNVWRVS 240

Query: 245 P-----KNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
P ++ VE D S+A FLA A +TGG VTV T + Q E+ MG
Sbjct: 241 PSALLGRDLTVEPDLNAQPFLAAALVTGGRVTVDPWPTRTTQPGDALREIFTAMGGSCE 300

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
TE +T TG GR H IDV++++ ++ +A +A AD P+ + VA R+
Sbjct: 301 LTEHGLTFTG----SGRIH--GIDVDLSEVGELTPGIAALADSPSTLSGVVHLRLH 353

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVP 419
ET+R+ A+ E+ LG V+E D +I P L TYDDHRMA A ++ A
Sbjct: 354 ETDRLAALTEEINGLGGDVKETDDGLMIR-PRPLQGGVFRITYDDHRMATAAAIIGLAVPG 412

Query: 420 VTIRDPGCTRKTFFPDYFDVLSTFVKN 445
V + + G T KT PD+ D+ + + +
Sbjct: 413 VEVENVGTTAKTLPDFPDLWTGMLDS 438

>ref|YP_001689222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halobacterium
salinarum R1]
sp|B0R558.1|AROHAHALS3 RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAP13874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halobacterium

salinarum R1]
Length = 430

Score = 198 bits (503), Expect = 1e-48, Method: Compositional matrix adjust.
Identities = 156/434 (35%), Positives = 224/434 (51%), Gaps = 25/434 (5%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ G + P SKS ++R LL A ++G TVV + L S D A+ LG + A +
Sbjct: 8 SRVGRARAPPKSYTHRALLAAGYADGETVVRDPLVSADTRATARAVELLGGA--AARE 65

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G G + + DA + N+G MR +TAA A G T VL G +R R
Sbjct: 66 NGDWVVTGFGSRPAIPDAV----IDCANS GTTMR LVTAAALADG--TTVLTGDESLRAR 119

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P G L+ L LG G P+ V+G + GG V L G +SSQ+++ALLMA +
Sbjct: 120 PHGPLLDALSGLGGTARSTRGNGQAPLVVDGP--VSGGSVALPGDVSSQFVTALLMAGAV 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
+E ++ +L S PYV++TL +++ FGV A S++ + ++GGQ Y Y V
Sbjct: 178 TETGIETDLTTELKSAPYVDITLDVLDAGVGA--SETAAGYRVRGQYAPSGAEYAVP 235

Query: 252 GDASSASYFLAGAAITGGTVTV---EGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SSASY LA A+ EG S QGD +VLE MGA + W S +T
Sbjct: 236 GDFSSASYLLAAGALAAADGAVVVEGM-HPSAQGDAAIVDVLERMADIDWDTESGVIT 294

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L ++V + PD+ T+AV+ ADG T I D R KET+R+ A+
Sbjct: 295 -----VQRSELSGVEGVADTPDLLPTIAVLGAAADGTTTRITDAEHVRYKETDRVAAMA 348

Query: 369 TELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
L+KLGASVEE PD ++ + +L+ ++D DHR+ MA ++A A+ TI
Sbjct: 349 ESLSKLGASVEERPDELVVRRGGDELTSGLSASVDGRGDHRLVMALAVAGLVADGETTIAGSE 408

Query: 427 CTRKTFPDYFDVLS 440
+FPD+F+VL+
Sbjct: 409 HVDVSFPDFFEVLA 422

>emb|CBL15191.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus bromii
L2-63]
Length = 432

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 143/429 (33%), Positives = 220/429 (51%), Gaps = 41/429 (9%)

Query: 16 SGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+G V +P SKS +R ++ AAL+ G + + S D+ +G + +G + + K
Sbjct: 21 NGEVNIIPPSKSDVHRAIICAALTRGKCTIAPVALSNDIKATIGVIEDMGCTA----SIKD 76

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
V+ G D V L G +G A+R A G NAT+V G ++ ERPIG
Sbjct: 77 GVLTVDGNTNIFKTD---NVTLDCEGSGSALRFFIPVAAAGGINATFVGHG--KLPERPIG 131

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
L + G + G P++++G L G ++ G++SSQ+++ LL+A PL G
Sbjct: 132 IFTEALPKAGVKCETEGGL---PLKISG--RLESGTFEIPGNVSSQFITGLLLALPLVEG 186

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
D +I + + S+ Y+ MT+ M +FGV+ E +D + ++IKGGQ Y P + +GD S
Sbjct: 187 DSDIVLTSPIESVGYINMTIHTMAQFGVEIETD--NGWHIKGGQSY-IPHDYTTDGDWS 243

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
A++F+ A+ GG VTV G S QGD K AE+L GAKVT T+TSVTV
Sbjct: 244 QAFFMVAGAL-GGKVTVNGVNRNSAQGDRKIAELLARFGAKVTQTDTSVTVE----- 295

Query: 316 GRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
+ L AID++ +++PD+ L V A FA G T I + R+KE +R+ A + LG
Sbjct: 296 -KGELNAIDIDASQIPDLVPVLTVCAAFAGTTRIYNAERLRIKECDRLTATAKLINDLG 354

Query: 376 ASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPG-----C 427

V E PD +I + L + ++DHR+ M S CA +R G
Sbjct: 355 GKVTLPDGLVIEGIDTLKGGFCEGFNDHRIVM--SAGVCA-----VRLGGEIESSYALS 407
Query: 428 TRKTFPDYF 436
K++PD++
Sbjct: 408 INKSYPDFY 416

>pir||S41329 5-enolpyruvylshikimate-3-phosphate synthase - Pseudomonas
pseudoalcaligenes
Length = 409

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 137/331 (41%), Positives = 182/331 (54%), Gaps = 35/331 (10%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQP + ++G ++LPG KS+SNR LLL AL+EG T V LL+S+D ML ALR LG+ +E
Sbjct: 10 LQPWRHVTGHLRLPGDKSISNRSLLLGALAEGVTEVTGLLDSDDARAMLNALRDLGVVIE 69
Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEV-QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R V G G + K LFLGNAG AMR L+AA+ + T L G P
Sbjct: 70 GPHQG-RCTVHGVG----LHGLKAPPGLFLGNAGTAMRPLSAALALQPFDDT--LTGDP 122
Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM ERPI LV L+++GA ++ PP+ + G GS+SSQ+L+ALL
Sbjct: 123 RMSERPINRLVDALREMGAVIEYLAQEGYPPLTIRG-----GGSVSSQFLTALL 171
Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
M AP+A ++ + L+S PY+++TL +M FGV D +R + +Y SP
Sbjct: 172 MTAPMASAQIKSGL---LLSKPYIDITLNVMP-FGVPTR--DHTERIFAVSAIRYPSPAV 225
Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+EGDA+SASYFLA A I G V V G G S+QGD FA L MGA+ + V
Sbjct: 226 LRLEGDATSASYFLAAAGIKG--VPVTGIGRHSMQGDSWFAALRRMGARSCGSSMIVCP 283
Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLA 338
G R A+ + N +PD AMTLA
Sbjct: 284 RGELR-----AAVRSDSNSIPDAAMTLA 306

>ref|YP_004164981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulophaga algicola
DSM 14237]
gb|ADV49483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulophaga algicola
DSM 14237]
Length = 409

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 147/439 (33%), Positives = 219/439 (49%), Gaps = 56/439 (12%)

Query: 13 KEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
I +K+ GSKS SNRILL AL + +N+ NS+D M L
Sbjct: 11 NHILANIKVTGSKSESNRILLLQALYSNIKI-ENVSNSDDAQVMAKGL----- 57
Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
A+V G + + +AG AMR LTA G VL G RM ER
Sbjct: 58 ---AMVDGV-----VDIHAGTAMRFLTAYFATQEGKDV-VLTGSQRMTER 99
Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV LK+LGA++ PP+++ G + KV L +ISSQY+SALL+ AP
Sbjct: 100 PIKVLVAALKELGAEISYVKNEGYPPKITG-KKITKNKVS L PANISSQYISALLLTAPS 158
Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA---- 248
+ +E+I K+ S+PY++MTL L+ + G++ +S++ IK SPK A
Sbjct: 159 LENGIALELIGKITSVPYIKMTLALLTQLGIE---NSFEGNSIK-----VSPKKAVENQ 209
Query: 249 --YVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
VE D SSASYF + AA++ G + + SLQGD AEV + G +
Sbjct: 210 TLIVESDWSSASYFYISIAALSEIGSKIGLSSYKHDSLQGDSVLAEVYKEFGVDTVFINN 269
Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + +EP +K ++ ++ PD+A T+AV + + + +KET+R+

Sbjct: 270 IEL-HKVKEP----QIKTLEWDLANAPDIAQTIAVTCFGLQMSCHLTGLHTLKIKETDRL 324

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTIR 423
A+ EL+KLGAS+ + +N AI TY+DHRMAMAF+ A + + I

Sbjct: 325 EALDVELSKLGASISVTDKTLTLNAATSINADVAIATYNDHRMAMAFAPLAL-KTTIYIN 383

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
D K+FPD++ ++T

Sbjct: 384 DAEVVSFSFPDFWTDMATL 402

>ref|ZP_05760597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D2]
Length = 409

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 142/437 (32%), Positives = 222/437 (50%), Gaps = 49/437 (11%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P ++ ++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 5 LIPPSTVTTAIQLPASKSISNRALIINALGKGMYPENLSDCDDTQVMIKAL----- 56

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
GK ++ + AG AMR LTA ++ G T + G R

Sbjct: 57 -----TEGKGTID-----IMAGTAMRFLTAYLSVTPGERT--ITGTAR 93

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+ + G L G ++ L G++SSQY+SALLM

Sbjct: 94 MQQRPIQILVNALRELGAIEFYTHNEGYPPLCIKG-AELKGNEITLKGNVSSQYISALLM 152

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P+ + + + ++IS PY+ +TL+LM+ FG KA + Q Y+S

Sbjct: 153 IGPVLKDGLTLHLSGEIISRPIYNLTQLMQDFGAKAAWTSP--SSISVAPQLYQSIPFK 210

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKAFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +

Sbjct: 211 -VESDWSAASYWYQIAALSPKAEIELLGLFRNSYQGDSEVFSRLGITTEFTSQGVKL 269

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+

Sbjct: 270 KKTGKAP-----ERLEEDFVDIPDLAQTFVVTALLNIPFRFTGLQSLKIKETDRIAAL 323

Query: 368 RTELTCLKGASVEEGPDYCI-----TPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTI 422
RTEL KLG +EE D ++ PE++ V IDTY+DHRMAMAF+ A + I

Sbjct: 324 RTELKKLGYVIEEENDSILMWNGKRCPEEIPV--IDTYEDHRMAMAFAPAVICHPNLLI 381

Query: 423 RDPGCTRKTFFPDYFDVL 439
DP K++P Y++ L

Sbjct: 382 ADPQVVTKSYPGYWEDL 398

>ref|NP_280114.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halobacterium sp.
NRC-1]
sp|Q9HQC1.1|AROHA_HALSA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAG19594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halobacterium sp.
NRC-1]
Length = 439

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 156/434 (35%), Positives = 224/434 (51%), Gaps = 25/434 (5%)

Query: 13 KEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ G + P SKS ++R LL A ++G TVV + L S D A+ LG + A +

Sbjct: 17 SRVRGRARAPPKSYTHRALLAAGYADGETVVRDPLVSADTRATARAVELLGGA--AARE 74

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G G + + DA + N+G MR +TAA A G T VL G +R R

Sbjct: 75 NGDWVVTGFGSRPAIPDAV----IDCANS GTTMRRLVTAALADG--TTVLTGDESLRAR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P G L+ L LG G P+ V+G + GG V L G +SSQ+++ALLMA +
Sbjct: 129 PHGPLLDALSGLGGTARSTRGNGQAPLVVDGP--VSGGSVALPGDVSSQFVTALLMAGAV 186

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
+E ++ +L S PYV++TL +++ FGV A S++ + ++GGQ Y Y V
Sbjct: 187 TETGIETDLTTELKSAPYVDITLDVLDAGVGA--SETAAGYRVRGQAYAPSGAEYAVP 244

Query: 252 GDASSASYFLAGAAITGGTVTV--EGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SSASY LA A+ EG S QGD +VLE MGA + W S +T
Sbjct: 245 GDFSSASYLLAAGALAAADGAADVVEGM-HPSAQGDAAIVDLERMGADIDWDTESGVIT 303

Query: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
R L ++V + PD+ T+AV+ ADG T I D R KET+R+ A+
Sbjct: 304 -----VQRSELSGVEVGADTPDLLPTIAVLGAAADGTTTRITDAEHVRYKETDRVAAMA 357

Query: 369 TELTKLGASVEEGPDYCIITPPE-KLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
L+KLGASVEE PD ++ + +L+ ++D DHR+ MA ++A A+ TI
Sbjct: 358 ESLSKLGASVEERPDELVVRRGGDTLSGASVDGRGDHRLVMALAVAGLVADGETTIAGSE 417

Query: 427 CTRKTFPDYFDVLS 440
+FPD+F+VL+
Sbjct: 418 HVDVSFPDFFEVLA 431

>ref|ZP_07918691.1| conserved hypothetical protein [Bacteroides sp. D2]
gb|EFS33161.1| conserved hypothetical protein [Bacteroides sp. D2]
Length = 410

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 142/437 (32%), Positives = 222/437 (50%), Gaps = 49/437 (11%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P ++ ++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 6 LIPPSTVTTAIQLPASKSISNRALIINALGKGMYPENLSDCDDTQVMIKAL----- 57

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
GK ++ + AG AMR LTA ++ G T + G R
Sbjct: 58 -----TEGKGTTID-----IMAAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+ + G L G ++ L G++SSQY+SALLM
Sbjct: 95 MQQRPIQILVNALRELGAIEYTHNEGYPPLCIKG-AELKGNEITLKNVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P+ + + + ++IS PY+ +TL+LM+ FG KA + Q Y+S
Sbjct: 154 IGPVLKDGLTLHLSGEIISRPYINLTQLMQDFGAKAAWTSP--SSISVAPQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 212 -VESDWSAASYWYQIAALSPKAEIELLGLFRNSYQGDSEVFSRLGITTEFTSQGVKL 270

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271 KKTGKAP-----ERLEEDFVDIPDLAQTFVVTALLNIPFRFTGLQSLKIKETDRIAL 324

Query: 368 RTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
RTEL KLG +EE D ++ PE++ V IDTY+DHRMAMAF+ A + I
Sbjct: 325 RTELKKLGYVIEEENDSILMWNGKRCEPEEIPV--IDTYEDHRMAMAFAPAVICHPNLLI 382

Query: 423 RDPGCTRKTFPDYFDVL 439
DP K++P Y++ L
Sbjct: 383 ADPQVVTKSYPGYWEDL 399

>ref|YP_003586028.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zunongwangia profunda
SM-A87]
gb|ADF53832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zunongwangia profunda
SM-A87]
Length = 407

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 144/430 (33%), Positives = 219/430 (50%), Gaps = 49/430 (11%)

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Query: 15  ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G +++ GSKS SNR+L++ +L + + NL NS+D M AL +
Sbjct: 12  VKGALQITGSKSESNRLLIIESLFFKNLEI-SNLSNSDDTQVMKKALTS----- 58

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      EV++ + +AG AMR LTA G T VL G PRM+ERP+
Sbjct: 59  -----NEVEVDIHAGTAMRFLTAYFAVQEGRET-VLTGSPRMQERP 100

Query: 135  GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL-LMAAPLA 193
      LV L+ +GAD+ PP+R+ G L V L +ISSQY+SAL L+ A L
Sbjct: 101  KLLVEALRSMGADISYERNEGYPPIRIQG-KKLQANAVSLQANISSQYISALMLIGASLP 159

Query: 194  LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      G + I + ++ S PY+ MTL +++R G++ D+ R SPK VE D
Sbjct: 160  EG-LTINLEGQVTSTPYILMTLEMLQRSIGQSFEDNIIRIEACAA---VSPKTIPVESD 215

Query: 254  ASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP- 311
      SSASYF + AA+ + + SLQGD A + + G + ++ E S+T+
Sbjct: 216  WSSASYFYISIAALAEAEIRLSNRYKESLQGDSCSLATYQQFGVETSFEENSITLKKSKC 275

Query: 312  REPFFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
      +P +I ++ PD+A T+AV L + + + ++KET+R+VA++ E+
Sbjct: 276  SKP-----ASISEDLRNSPDIAQTIAVTCLGLGTACKLTGLHTLKIKETDRLVALKNEI 329

Query: 372  TKLGASVEEGPDYCIITPPE--KLNVTADTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
      KLG V ++ + P K NV I+TY+DHRMAMAF+ A +VPV I D
Sbjct: 330  EKLGGEVVISDEHLELKPSAILKENV-EIETYNDHRMAMAFAPIAL-KVPVLIADAMVVS 387

Query: 430  KTFPDYFDVL 439
      K++PD++ L
Sbjct: 388  KSYPDFYSDL 397

```

>emb|CBK66251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
xylanisolvens XB1A]
Length = 410

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 222/435 (51%), Gaps = 45/435 (10%)

```

Query: 9  LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 6  LIPPSVVTATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKALT----- 58

Query: 69  ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
      + KE + + AG AMR LTA ++ G T + G R
Sbjct: 59  -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129  MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM
Sbjct: 95  MQQRPIQILVNALRELGAIEYTRNEGYPPLRIK-AELKGNEITLGNVSSQYISALLM 153

Query: 189  AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S
Sbjct: 154  IGPALKDGLTLHLSGEIISRPIINLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 211

Query: 249  YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 212  -VESDWSAASYWQIAALSPKAEIELLGLFPNSYQGDSRGAEVFSRLGITTEFTSQGVKL 270

Query: 308  TGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
      + P + + + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271  KKTGKAP-----ERLEEDFVDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAAL 324

Query: 368  RTELTKLGASVEEGPDYCIITPPEKL---NVTADTYDDHRMAMAFSLAACAEVPTIRD 424
      R EL KLG ++E D ++ E+ I+TY+DHRMAMAF+ A + I D
Sbjct: 325  RAEKKGKGYMIKEENDSILMWNGERCEPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAD 384

```

Query: 425 PGCTRKTFPDYFDVL 439
P K++P Y++ L
Sbjct: 385 PQVVTKSYPGYWEDL 399

>ref|ZP_06917240.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus
ATCC 29083]
gb|EDY54343.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus
ATCC 29083]
Length = 415

Score = 198 bits (503), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 157/428 (36%), Positives = 218/428 (50%), Gaps = 23/428 (5%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ LPGSKS++ R L LAA ++G T + L S+D L LG V +
Sbjct: 7 LSLPGSKSITARALFLAAAADGVTTLVRPLRSDDTEGFAEGLVRLGYRV----GRTPDT 61

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G+ P A E ++ + R L AA G+ TY D P+MR RP+ L
Sbjct: 62 WQVDGR-PQGPAAVEADVYCRDGATTARFL--PTLAAAGHGTYRFDASPMRRRPLPLS 118

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LG D+ P+ V G+ GG+V L SSQYL+ALL+ PL +
Sbjct: 119 RALRDLGVDLRHEEAEGHHPLTVRA-AGVEGGEVTLTAGQSSQYLTALLLLGPLTRQGLR 177

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I + D L+S PYVE+TL +M FGV E + D F + G Y++ A +E DAS+AS
Sbjct: 178 IRVTD-LVSAPYVEITLMMRAFGV--EVAREGDVFPVPPG-GYRATTYA-IEPDASTAS 232

Query: 259 YFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
YF A AA+T G VTV G GT +LQGD+ F +VL MGA+V+ + TV G
Sbjct: 233 YFFAAAALTPGAEVTVPLGTGALQGDVGFDVLRMGAEVSVGADATTVRG-----T 285

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
L+ + NM + D TLA +A FA P I DVA+ RVKE +R+ A L +LG
Sbjct: 286 GELRGLTANMRDISDTMPTLAAIAPFASAPVRIEDVANTRVKECDRLEACAENLRLGVR 345

Query: 378 VEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTFFPDYFD 437
V GPD+ I P + +Y DHR+ M+F++ ++ DPGC RKTFF + +
Sbjct: 346 VATGPDWIEIHGPGATGAQ-VTSYGDHRIVMSFAVTGLRVPGISFDDPGCVRKTFPGFHE 404

Query: 438 VLSTFVK 445
+ +
Sbjct: 405 AFAELRRG 412

>ref|ZP_07775185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas
fluorescens WH6]
gb|EFQ63780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas
fluorescens WH6]
Length = 441

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 157/442 (35%), Positives = 221/442 (50%), Gaps = 45/442 (10%)

Query: 8 VLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
V P ++G V PGSKS++NR LLLAAL++GT+ + L S+D +M ALR +G+++
Sbjct: 32 VTPPNFPLNGKVAPPGSKSITNRALLAALAKGTSRLSGALKSDDTRHMSVALRQMGVTI 91

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D+ VV GK + LFLGNAG AMR LTAAG G T VLDG
Sbjct: 92 --DEPDPTTFVVTVSGKLQLPTQP----LFLGNAGTAMRFLTAAGVATVDG--TVVLDGDD 143

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
MR+RPIG L+ L Q G VD G CPPV V+G G + + ++ G +SSQY+SALL
Sbjct: 144 YMRKRPIGPLLATLSQNGIQVDSPTG--CPPVTVHGAGKVQATRFEIDGGLSSQYVSALL 201

Query: 188 MAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKA-EHSDSWDRFYIKGGQKYKSP 245
M A +E+ + K I YV++TL M FG + E +D+ R G +
Sbjct: 202 MLAACGEAPIEVALTGKDIGARGYVDLTLCMRAFGAQVDEVNDTTWRVAPTGYTAH--- 258

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ +E DAS+A+Y A +TGG + + Q D K V+ +
Sbjct: 259 -DYLIEPDASAATYLAEEVLTGGHIDIGVAAQDFTQPDAAQAVIAQ-----FPMQA 311

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G ++M D TLAV+A F P ++A+ RVKE +R+
Sbjct: 312 TVVG-----SQMQDAIPTLAVLAAFNTTPVRFTELANLRVKECDRVQ 353

Query: 366 AIRTELTKL--GASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPV 420
A+ L + G + EG D + P + IDT+ DHR+AM F+LA +
Sbjct: 354 ALHDGLNAIRPLATIEGDDLVAADPALAGTSCNALIDTHADHRIAMCFALAGLVSGI 413

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I+DP C KT+P Y+ L +
Sbjct: 414 RIQDPDCVAKTYPGYWKALGSL 435

>ref|ZP_04548784.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_2_4]
ref|ZP_06615418.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides ovatus SD
CMC 3f]
gb|EEO58278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_2_4]
gb|EFF54607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides ovatus SD
CMC 3f]
Length = 409

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 222/435 (51%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVE 68
L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 5 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKALT----- 57

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R
Sbjct: 58 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 93

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM
Sbjct: 94 MQQRPIQILVNALRELGAIEYTRNEGYPLRIKG-AELKGNEITLKGNVSSQYISALLM 152

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S
Sbjct: 153 IGPALKDGLTLHLSGEIISRPYINLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 210

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 211 -VESDWSAASYWYQIAALSPKAEIELLGLFPNSYQGDSRGAEVFSRLGITTEFTSQGVKL 269

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 270 KKTGKAP-----ERLEEDFVDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAAL 323

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
R EL KLG +EE D ++ E+ I+TY+DHRMAMAF+ A + I +
Sbjct: 324 RAEKLLKGYVIEEENDSILMWNGERCPEETPVIETEDHRMAMAFAPAIIRHPNLLIAN 383

Query: 425 PGCTRKTFPDYFDVL 439
P K++P Y++ L
Sbjct: 384 PQVVTKSYPGYWEDL 398

>ref|ZP_06268360.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
bivia JCVIIMP010]
gb|EFB93156.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
bivia JCVIIMP010]
Length = 418

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.

Identities = 132/440 (30%), Positives = 225/440 (51%), Gaps = 47/440 (10%)

```
Query: 11 PIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + I ++ LP SKS+SNR L++ LS+ +NL + +D + ++ AL+ + ++
Sbjct: 8 PTEPIDASINLPSSKSLNRSLIINVLSKSKITPNNLSDCDDTNVIAKALKDMPKVID-- 65

Query: 71 KAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+G AG AMR +TA ++ G +++ G RM+
Sbjct: 66 -----VGAAGTAMRFMTAFLSVTAGE--HIITGSERMK 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPIG LV L+ LGA + PP+ + G L GG + ++G++SSQY+SALLM
Sbjct: 97 HRPVIGLVLSALRSLGASITYEGEEGFPPLCIQG-QRLKGGHLDIAGNVSSQYISALLMVG 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P+ +E+ +I ++S PY+++TL +M +GV+ E +D D + Q Y++ N Y+
Sbjct: 156 PIFEGLLELRILIGNIVSRPYIDLTLHIMHEYGVREWTDV-DTITVP-AQDYQA-DNYII 212

Query: 251 EGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTV 307
E D ++++Y+ A+ GT +T+ G S QGD + ++G K +
Sbjct: 213 ENDWTASNYWYEILALHKGTEAKLTLPGLRDGSRQGDSSVRYIFSLGIKTAFVNNG--- 269

Query: 308 TGPPREPFGKRKH--LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
G KH LK ++ + PD+A T + + P +AS ++KET+R+
Sbjct: 270 DGDQSAVKLSKHACMLKRLEYDFINQPDLAQTFIALCPLLNMFFHFTGLASLKIKETDRI 329

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFSLAACAEVPVT 421
+A++TE+ KLG + + D + E+ N I+TY+DHRMAMAF+ A +T
Sbjct: 330 MAMKTEMRKLGVLHDKNDAELYWDGERCEAENDPVIETYEDHRMAMAFAPLALKLGKIT 389

Query: 422 IRDPGCTRKTFFPDYFDVLST 441
I DP K++P +++ L +
Sbjct: 390 INDPLVVTKSYPHFWEDLKS 409
```

>emb|CBI32963.3| unnamed protein product [Vitis vinifera]
Length = 622

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 104/187 (55%), Positives = 122/187 (65%), Gaps = 36/187 (19%)

```
Query: 100 NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPV 159
NAG MR L AAVTAAGG+A+YV+DGV RMRE IGDLV GLKQLGADV+ FLGT+C PV
Sbjct: 372 NAGTVMRPLIAAVTAAGGDASYVIDGVLRMRETSIGDLVTGLKQLGADVNGFLGTNCSPV 431

Query: 160 RVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLME 219
R+ + ++ SIPYVE TL+LME
Sbjct: 432 RI-----WRLRLINSFSIPYVETTLKLME 456

Query: 220 RFGVKAHSDSWDRFYIKGGQK-YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
RFGV EHS +WD+F I+GG+K YKSP NA+VE DASSASYFLA AA+TG T+ VE CGT
Sbjct: 457 RFGVSVEHSSWDQFLIQGGKKKYKSPGNAFVEDDASSASYFLASAAVTGETIIVEDCGT 516

Query: 279 TSLQGDV 285
SLQG+V
Sbjct: 517 NSLQGNV 523
```

>ref|ZP_06288831.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella timonensis CRIS 5C-B1]
gb|EFA98024.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella timonensis CRIS 5C-B1]
Length = 417

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 139/430 (32%), Positives = 224/430 (52%), Gaps = 42/430 (9%)

```
Query: 18 TVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV+LP SKS+SNR L++ ALS G +L + +D ++ A+ +
Sbjct: 15 TVQLPSSKSVSNRALIIHALSGGKVQPHHLSDCDDTQVIMNAIMHMP----- 61
```

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
PV D K AG AMR LTA ++ + G +VL G RM+ RPIG L
Sbjct: 62 -----PVIDIKA-----AGTAMRFLTAFLSISEGE--HVLGTGTERMQHRPIGPL 103

Query: 138 VVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
V L+ LGAD++ ++G D PP+R++G L GG +++ G++SSQY+SALLM P+
Sbjct: 104 VDALRYLGADIE-YMGEDGYPLRIHG-KQLTGGNIEMPGNVSSQYVSALLMLGPVLPKG 161

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I++ + +IS PY+++TL +M++FG + E +D D ++ K +P Y+E D S+
Sbjct: 162 LNIKLNTGMISRPIYIDLTLWVMQQFGAEVEWTDI-DTIAVR--PKPYAPCTYYIESDWSA 218

Query: 257 ASYF---LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTGTGPPRE 313
ASY+ LA + T + G S QGD + ++ K E T + R
Sbjct: 219 ASYWYELALSTHRDNTFFLPGLLDGSKQGDVSLRYLFSLLSVKTEVEEADDTHSAGMRI 278

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++L ++ + PD+A T V D P +++ +KET R+ A++ E+ K
Sbjct: 279 TRHERNLPRLEYDFVNCPLDAQTFVCCAVLDIPFLFTGLSTLLIKETNRLEALKVEMRK 338

Query: 374 LGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
LG ++E ++ E+ + IDTY+DHRMAMAF+ AA + I P K+
Sbjct: 339 LGYVIKEQNKSELVWNGERCEPSFEPIDTYEDHRMAMAFAPAAIKFPLRINHPEVVSXS 398

Query: 432 FPDYFDVLST 441
+P +++ L +
Sbjct: 399 YPQFWDNLR 408

>ref|YP_003813565.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
melaninogenica ATCC 25845]
gb|ADK95755.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
melaninogenica ATCC 25845]
Length = 417

Score = 197 bits (502), Expect = 2e-48, Method: Compositional matrix adjust.
Identities = 141/436 (32%), Positives = 224/436 (51%), Gaps = 47/436 (10%)

Query: 13 KEISGTVKLPGSKSLNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I ++ LP SKS+SNR L++ AL++G + +NL + +D ++ GLS ++D
Sbjct: 9 EHIDTSITLPASKSISNRALIIQALTKGGMMPENLSDCDDTEVIIR-----GLSKQSDVI 63

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+A AG AMR +TA ++A G Y + G RM+ R
Sbjct: 64 DIKA-----AGTAMRFMTAYLSATDGE--YTITGTERMKHR 97

Query: 133 PIGDLVVLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+ LGA+++ PP+ + G L GG +++ G++SSQY+SALLM AP+
Sbjct: 98 PIGILVDALRYLGAEIEYVGEEGYPPLHIRG-RQLEGGSLQIPGNVSSQYISALLMIAPI 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
+E+++ +IS PY+++TL LM FGV AE SD +D +K Q Y+ + AY +E
Sbjct: 157 LTKGLELKLGTGNIISRPYIDLTLHLHMEFGVSAEWSDFDTISVK-SQAYQ--QRAYTIE 212

Query: 252 GDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
D S+ASY+ A+T T V ++G S QGD + ++G K ++ +
Sbjct: 213 SDWSAASYWYEILALTDTRSKVALQGLKDGSRQGDASVRYIFSLLGIKTSFKDKD--SN 270

Query: 309 GPPREPFGR--KHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
G P R + L ++ + PD+A TL V P + + ++KET R+ A
Sbjct: 271 GLPEAILTRHSRMLNRMEDFTNQPDLAQTLIAVCPILGIPFHTGLGTLKIKETNRIEA 330

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIR 423
+ E+ KLG + + + E+ A I+TY+DHRMAM+F+ A + I
Sbjct: 331 MTREMEKLGILYSENETELSWNGERCEPMAEPIIETEDHRMAMSFAPLAIKLGEIRIN 390

Query: 424 DPGCTRKTFFPDYFDVL 439
P K++P Y+D L
Sbjct: 391 HPEVVSXSYPHYWDDL 406

>ref|YP_001304474.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parabacteroides distasonis ATCC 8503]
ref|ZP_05285105.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. 2_1_7]
gb|ABR44852.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parabacteroides distasonis ATCC 8503]
Length = 411

Score = 197 bits (501), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 147/439 (33%), Positives = 219/439 (49%), Gaps = 57/439 (12%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P I TVKLP SKS+SNR L+L ALS V+NL + +D + M+ AL +
Sbjct: 8 PGSAIRTTVKLPASKSISNRALILNALSYSAYDVENLSDCDDTNLMVKALNS----- 59

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +G AG MR LTA ++ G T + G RM+
Sbjct: 60 -----NDRDFNVGAAGTTMRFLTAFLSKVVGWET--ITGTERM 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L LGA ++ PP+R+ G L GG++ L G++SSQY+SA+LM A
Sbjct: 97 NRPIKVLVDALNALGARIEYMEKEGYPLRIFG-SALQGGEISLPGNVSSQYISAILMIA 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKG-GQKYKSPKNAY 249
PL V + + +IS PY+ +TL+LME++GV+A SW IK Q+YK P
Sbjct: 156 PLTENGVTLHLEGAIISRPIYHITLQLMEQYGVRA----SWTENTIKVLPQEYK-PIRFT 210

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
VE D S+ASY+ A++ + + G SLQGD A++ +G T+T+ V +
Sbjct: 211 VESDWSAASYWYEMALSKNAEIELLGLFKNSLQGDAAAGAKLFAQLGVGTTYTKRGVVL- 269

Query: 309 GPPREPFGRKH----LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
KH + + N PD+A T V + + P + S ++KET+R+
Sbjct: 270 -----KHTGNICEKLVYNFVNEPDLAQTFVVTCVLLNIPFRFTGLQSLKIKETDRI 320

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVP-V 420
A++TEL KLG + + D + E+ + I TY+DHRMA++F+ AA +
Sbjct: 321 EALKTELKRLKGYVLTDRNDSILEWNGERREPESHPIATYEDHRMALSFAPAALVRPEGI 380

Query: 421 TIRDPGCTRKTFPDYFDVL 439
I P K++P Y++ L
Sbjct: 381 EIAHPQVVSKSYPHYWEDL 399

>ref|ZP_03968049.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase
[Sphingobacterium spiritivorum ATCC 33300]
gb|EEI92091.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase
[Sphingobacterium spiritivorum ATCC 33300]
Length = 416

Score = 197 bits (501), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 142/443 (32%), Positives = 221/443 (49%), Gaps = 58/443 (13%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P K I GTV+L GSKS SNR L++ ALS+G ++NL N++D M AL
Sbjct: 10 HPGKTIKGTVQLTGSKSESNRALIIQALSKGNVRIENLSNADDTVIMQRAL----- 60

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
K E E + +G AG AMR LT+ + GN ++L G RM
Sbjct: 61 -----KIAAEPQSETQTINIGPAGTAMRFLTSYLNLVKGN--FILTGTERM 104

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
++RPIG LV LK LGAD+ PP+++ G +V + G+ISSQY+S+LL+
Sbjct: 105 QQRPIGILVDALKTLGADIHYEKKAGYPLKIEGGMFQNKNEVSISKNISSQYISSLLLI 164

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY 249
A + + I +L S PYV MTL +++ G+ S +W I+ + Y
Sbjct: 165 AAALKKGLTLHIEGELTSRPYVSMTLDMLKEAGI---SHTWSENAIEIAPQETKEATLY 220

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
+E D S+ASY+ A A++ G + + G SLQGD +++ G + ++ + +
Sbjct: 211 VESDWSAASYWYEMALSKNAEIELLGLFKNSLQGDAAAGAKLFAQLGVGTTYTKRGVVL- 269

Sbjct: 221 IEPDWSAASYWYAIVALSKDGHIVLPGLKQNSLQGD SAIVDIMTHFGVRSSFEQDGL--- 277

Query: 309 GPPREPFGKRHLK--AID-----VNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
HL+ A+D + + PD+A T+ V A + + + ++KET

Sbjct: 278 -----HLRKS AVDSQTLFDFKECPDLAQTVIVCAAALKRDISFTGLET LKIKET 327

Query: 362 ERMVAIRTELTKLGA-SVEEGPDYCIITP----PEKLNVT AIDTYDDHRMAMAFSLAACA 416
+R+ A++ E+ K GA +E+ Y + T PE + AI TY+DHRMAMAF+ A

Sbjct: 328 DRIAALQNEIGKFGALLLEDNGVYHLKTSNVFKPENI---AISTYEDHRMAMAFAPLALV 384

Query: 417 EVPVTIRDPGCTRKTFPDYFDVL 439
+ I D K++P+++D L

Sbjct: 385 FDQIHIEDH MVVEKSYPEFWDHL 407

>ref|ZP_07402495.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
matruchotii ATCC 14266]
gb|EFM49802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
matruchotii ATCC 14266]
Length = 441

Score = 197 bits (500), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 144/450 (32%), Positives = 227/450 (50%), Gaps = 50/450 (11%)

Query: 13 KEISGTVKLP GSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K TV++PGSKS++NR L+LAA++E T + L S D M AL+ +G+ V+A+

Sbjct: 21 KPFKATVRVPGSKSITNRALVLA AIAENPTTITGALWSRDTQLMAQALKRIGVDVQAE-- 78

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFL-----GNAGIAMRSLTA AVTAAGGNAT 120
P D+ +F+ G AG MR + A G+

Sbjct: 79 -----PDPSPANATIFVEPTGFTGGTVDCGLAGTVMRFVPPLAALADGDVF 125

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ DG R+RP+ ++ GL+ LG V D P +V+G G GG V++ S SS

Sbjct: 126 F--DGDEHARQRP MKGILDGLRALGISVQG---DSL PFKVSGNGSPMGMVEIDASASS 179

Query: 181 QYLSALLMAAP-LALGDVEIEIIDKLISIPYEMTLRLMERFGVKA EHSDSWDRFY---- 235
Q++S LL+AAP A G I + L S+P++EMT+ ++ + G + + ++

Sbjct: 180 QFVSGLLLAAPRFAQGITVRHIGETLPSMPHIEMTVHMLRQAGASVDTTTAYQWSVAPGP 239

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMG 295
I+GG VE D S+A+ FLA AA+TG TV V+ TT+ Q +LE MG

Sbjct: 240 IRGGV-----VRVEPDL SNATPFLAAA AVTGSTVQVKDWPTTTTQPGDAIRNILERMG 292

Query: 296 AKVTWTETS VTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVAS 355
V+ T+ +TVTGP +P L+ I+++M+ + ++ T+A +A A+ P+A+ +A

Sbjct: 293 CTVSLTDGDLTVTGP--KP---GSLQGIEIDMSDIGELTPTVAAMATVANS PSALTGIAH 347

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC 415
ET+R+ A+ TE+TK+G E PD I P L+ TYDDHRMA ++

Sbjct: 348 LHGHETDRLQALATEITKIGGCSEL PDGLAIKPSGLHGAHWSTYDDHRMATTGAIIGL 407

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
+ + + T KT P + + + V+

Sbjct: 408 VAPGIKVENIETTAKTLPGFDRMWADMVQE 437

>ref|ZP_07082504.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobacterium
spiritivorum ATCC 33861]
gb|EFK57763.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobacterium
spiritivorum ATCC 33861]
Length = 416

Score = 197 bits (500), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 140/441 (31%), Positives = 219/441 (49%), Gaps = 54/441 (12%)

Query: 10 QPIKEISGTVKLP GSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P K I GTV+L GSKS SNR L++ ALS+G ++NL N++D M AL

Sbjct: 10 HPGKTIKGT VQLTGSKSES NRALIIQALSKGNVHIENLSNADDTVIMQRAL----- 60

Query: 70 DKA AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA AVTAAGGNATYVLDGVPRM 129

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      K   E   E   + +G AG AMR LT+ +   GN  ++L G  RM
Sbjct: 61  -----KIAAEPQPETQTINIGPAGTAMRFLTSYLNLVKGN--FILTGTTERM 104

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
      ++RPIG LV  LK LGAD+      PP+++ G      +V + G+ISSQY+S+LL+
Sbjct: 105 QQRPIGILVDALKTLGADIHYEKKAGYPPLKIEGGMFQNKNEVSIKGNISSQYISSLLLI 164

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
      A      + + I  +L S PYV MTL +++ G+   S +W   I+   +      Y
Sbjct: 165 AAALKKGLTLHIEGELTSRPYVSMTLMDLKEAGI----SHTWSENAIEIAPQETKEATLY 220

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      +E D S+ASY+ A  A++ G + + G   SLQGD   +++ G + ++ + + +
Sbjct: 221 IEPDWSAASYWYAIVALSEDGHIVLPLGLKQNSLQGD SAIVDIMTHFGVRSFFEQDGLHL- 279

Query: 309 GPPREPFGKRHLKAID-----VNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      H  A+D      + + PD+A T+ V A      +   + + ++KET+R
Sbjct: 280 -----HKSAVDSQTLFDFKECPDLAQTVIVCAAALKRDISFTGLETLKIKETDR 329

Query: 364 MVAIRTELTKLGA-SVEEGPDYCIITP----PEKLNVTADITYDDHRMAMAFSLAACAEV 418
      + A++ E+ K GA  +E+   Y + T      PE +   I TY+DHRMAMAF+ A
Sbjct: 330 IAALQNEIGKFGALLLEDNGIYHLKTSNVFKPEHI---TIRTYEDHRMAMAFAPLALVFD 386

Query: 419 PVTIRDPGCTRKTFFPDYFDVL 439
      + I D      K++P+++D L
Sbjct: 387 QIHIEDHMMVVEKSYPEFWDHL 407

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>ref|ZP_05544099.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parabacteroides sp.
      D13]
ref|ZP_06984088.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
      3_1_19]
gb|EEU52832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parabacteroides sp.
      D13]
gb|EFI10153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
      3_1_19]
Length = 411

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Score = 197 bits (500), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 147/439 (33%), Positives = 219/439 (49%), Gaps = 57/439 (12%)

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Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P   I   TVKLP SKS+SNR L+L ALS      V+NL + +D + M+ AL +
Sbjct: 8   PGSAIRTTVKLPASKSISNRALILNALSYSAYDVENLSDCDDTNLMVKALNS----- 59

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
      +      +G AG MR LTA ++   G T + G RM+
Sbjct: 60 -----NDRDFNVGAAGTTMRFLTAFLSKVVGEWT--ITGTERMK 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      RPI LV  L  LGA ++      PP+R+ G   L GG++ L G++SSQY+SA+LM A
Sbjct: 97 NRPIKVLVDALNALGARIEYMEKEGYPLRIFG-SALQGGEISLPGNVSSQYISAILMIA 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQKYKSPKNAY 249
      PL   V + +   +IS PY+ +TL+LME++GV+A   SW   IK   Q+YK P
Sbjct: 156 PLTENGVMHLLEGAIISRPIYHITLQLMEQYGVRA----SWTENTIKVLPQYK-PIRFT 210

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      VE D S+ASY+   A++   + + G   SLQGD   A++ +G T+T+ V +
Sbjct: 211 VESDWSAASYWYEIMALSKNAEIELLGLFKNSLQGDAAGAKLFAQLGVGTTYTKRGVVL- 269

Query: 309 GPPREPFGKRKH----LK AIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      KH      + + N   PD+A T V + + P      + S ++KET+R+
Sbjct: 270 -----KHTGNICEKLVYNFVNEDPLAQTFVVTVCVLLNIPFRFTGLQSLKIKETDRI 320

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT A---IDTYDDHRMAMAFSLAACAEV-P 420
      A++TEL KLG + + D +   E+   +   I TY+DHRMA++F+ AA      +
Sbjct: 321 EALKTELKRLKGYVLTDRNDSILEWNGERREPESHPIATYEDHRMALSFAPAALVRPEGI 380

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
      I P      K++P Y++ L

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Sbjct: 381 EIAHPQVVSKSYPHYWEDL 399

>ref|ZP_06076094.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_33B]
gb|EEY83766.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_33B]
Length = 411

Score = 197 bits (500), Expect = 4e-48, Method: Compositional matrix adjust.
Identities = 149/441 (33%), Positives = 219/441 (49%), Gaps = 61/441 (13%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P I TVKLP SKS+SNR L+L ALS V+NL + +D + M+ AL +
Sbjct: 8 PGSAIRTTVKLPASKSISNRALILNALSYSAYDVENLSDCDDTNLMVKALNS----- 59

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +G AG MR LTA ++ G T + G RM+
Sbjct: 60 -----NDRDFNVGAAGTTMRFLTAFLSKVVGEWT--ITGTERMK 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L LGA ++ PP+R+ G L GG++ L G++SSQY+SA+LM A
Sbjct: 97 NRPIKVLVDALNALGARIEYMEKEGYPLRIFG-SALQGGEISLPGNVSSQYISAILMIA 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQKYKSPKNAY 249
PL V + + +IS PY+ +TL+LME++GV+A SW IK Q+YK P
Sbjct: 156 PLTENGVTLHLEGAIISRPYIHITLQLMEQYGVRA----SWTENTIKVLPQEYK-PIRFT 210

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVT 308
VE D S+ASY+ A++ + + G SLQGD A++ +G T+T+ V +
Sbjct: 211 VESDWSAASYWYEIMALKNAEIELLGLFKNSLQGDAAAGAKLFAQLGVGTTYTKRGVVL- 269

Query: 309 GPPREPFGFRKH---LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
KH + + N PD+A T V + + P + S ++KET+R+
Sbjct: 270 -----KHTGNICEKLVYNFVNEDPLAQTFVVTVCVLLNIPFRFTGLQSLKIKETDRI 320

Query: 365 VAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP 419
A++TEL KLG + + D + PE V A TY+DHRMA++F+ AA
Sbjct: 321 EALKTELRLKGLYVLTDRNDSILEWNGERGEPESEHPVIA--TYEDHRMALSFAPAALVRPE 378

Query: 420 -VTIRDPGCTRKTFPDYFDVL 439
+ I P K++P Y++ L
Sbjct: 379 GIEIAHPQVVSKSYPHYWEDL 399

>ref|YP_004266660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophobotulus
glycolicus DSM 8271]
gb|ADY56659.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophobotulus
glycolicus DSM 8271]
Length = 438

Score = 196 bits (498), Expect = 6e-48, Method: Compositional matrix adjust.
Identities = 137/434 (31%), Positives = 227/434 (52%), Gaps = 28/434 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V +P SKS+S+R L+ AAL+EGT+ + N + S+D+ + LR LG +EA++
Sbjct: 11 LKGSVIVPPSKSISHRALICAALAEGTSNIGNFMISDDMMATMNGLRALGAGIEAEQGA 70

Query: 75 RAV----VVGCGGKFPVEDAK----EEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + G G E + EE +L +G +R L A N+ G
Sbjct: 71 EGIHLLRITGIGANLFGEGEKNHLEDRLIDCQESGSTLRFLP--LAGLKNSWVTFTG 128

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
R+ RP+ + G + G P++VNG+ L G+ ++ G ISSQ++S
Sbjct: 129 RGRLVSRPLDVYFRLFDEHGVSEK-QGNSSLPLKVNL--LQPGEYRVEGDISSQFISG 185

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ PL D I I KL S Y+++T+ ++ RF +K E++ F IKG Q+Y+
Sbjct: 186 LMFLLPLLASDSRIVITSKLESGYLDLTMDMLSRFSIKIENNHD-KEFIIKGNQRYQK- 243

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 305

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      ++ +EGD S +++LA A + GG +      + SLQGD +      +L+ MG ++T + S+
Sbjct: 244 QDTEIDGYSQVAFWLA-AGLLGGEIDCLNMNSQSLQGDREIVNQLQGMGGRITAGQKSI 302

Query: 306 TVTGGPPREPFGKRHL-KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      R L K ++ ++ PD+ LA +A ++G T I +      R+KE++R+
Sbjct: 303 RA-----RASLTGKTVIDGSQCPIIPVLAALAAVSEGETRIINAERLRIKESDRL 353

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
      AI TEL KLGA VEE D I + L+ + +++DHR+AMA ++AAC PV I
Sbjct: 354 KAISTELNKLGAKEETADGLDILGCKNLHGPGVSSWNDHRIAMALAVAACRCTEPLVIE 413

Query: 424 DPGCTRKTFFPDYFD 437
      K++P +++
Sbjct: 414 GSDAVSKSYPHFWE 427

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>ref|ZP_07627942.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
      amnii CRIS 21A-A]
gb|EFN91251.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
      amnii CRIS 21A-A]
Length = 418

```

Score = 196 bits (498), Expect = 6e-48, Method: Compositional matrix adjust.
Identities = 135/438 (30%), Positives = 222/438 (50%), Gaps = 47/438 (10%)

```

Query: 8 VLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
      + P I+ + LP SKS+SNR L++ ALS+ + DNL + +D ++ AL+ + +
Sbjct: 5 ITSPANPINACIYLPASKSVSNRSLIINALSKSIIIPDNLSDCDDTKVIIDALKNMPYQI 64

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      D A G AMR +TA ++ G +V+ G
Sbjct: 65 NVDA-----GTAMRFMTALLSVTEGE--HVITGNE 93

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      RM+ RPIG LV L+ +GA++ PP+R+ G L GG +++G+ISSQY+SALL
Sbjct: 94 RMKHRPIGVLVDALRSIGANITYEEEEGFPLRIIG-KKLKGGHIEMAGNISSQYISALL 152

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      M AP+ +E+ + + +IS PY+++TL +M +GVKAE +D D + QKYK+ ++
Sbjct: 153 MVAPVFEEGLEHLKNNIISRPYIDLTLHVMHEYGVKAETDV-DTITVP-VQKYKA-RH 209

Query: 248 AYVEGDASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET- 303
      YVE D S++SY+ A+ + + G S QGD + ++G K +
Sbjct: 210 YVENDWSASSYWYEMIALHKSNNVVELLLPGLMDCSRQGSALRYIFSLLGVKTFFERKK 269

Query: 304 --SVTVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
      S+ V + KHL D N PD+A T + + +AS ++KET
Sbjct: 270 NDSLFPVKLSKHTCMLKHL---DYNFINQPDIAPTFIALCPLLNMSFHTGLASLKIKET 326

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAAA-IDTYDDHRMAMAFSLAACAEV 418
      +R+ A++ E+ KLG + D + ++ ++ + I+TY DHR+AMAF+ A
Sbjct: 327 DRIEAMKCEMRKLGVLVLYNNNDDELWDGKRCDIESEPIINTYGDHRIAMAFAPLALRLG 386

Query: 419 PVTIRDPGCTRKTFFPDYF 436
      + I DP K++P ++
Sbjct: 387 RIIISDPNVVTKSYPLFW 404

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>ref|ZP_07040911.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
      3_1_23]
gb|EFI37917.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
      3_1_23]
Length = 410

```

Score = 196 bits (498), Expect = 6e-48, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 221/435 (50%), Gaps = 45/435 (10%)

```

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 6 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPPENLSDCDDTQVMIKALT----- 58

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Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R
Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+ + G L G ++ L G++SSQY+SALLM
Sbjct: 95 MQQRPIQILVNALRELGAIEYVHHEGYPLCIKG-AELKGNEITLKGNVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S
Sbjct: 154 IGPALKDGLTLHLSGEIISRPIYNLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 212 -VESDWSAASYWYQIAALSPKAEIELLGLFHNSYQGDSRGAEVFSRLGITTEFTSQGVKL 270

Query: 308 TGPPREPFGGRKHLKVIDNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271 KKTGKAP-----ERLEEDFVDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAL 324

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVTATIDTYDDHRMAMAFSLAACAEVPVTIRD 424
R EL KLG +EE D ++ E+ I+TY+DHRMAMAF+ A + I D
Sbjct: 325 RAEKKGKLVIEEENDSILMWNGERCEPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAD 384

Query: 425 PGCTRKTFFPDYFDVL 439
P K++P Y++ L
Sbjct: 385 PQVVTKSYPGYWEDL 399

>ref|YP_001854793.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kocuria rhizophila
DC2201]
sp|B2GLU6.1|ARO_A_KOCR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAG29287.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kocuria rhizophila
DC2201]
Length = 445

Score = 196 bits (498), Expect = 6e-48, Method: Compositional matrix adjust.
Identities = 154/436 (35%), Positives = 221/436 (50%), Gaps = 41/436 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV +PGSKSL+NR L+LAAL+ ++V L+S D M+ AL+TLG +V
Sbjct: 24 VSGTVAVPGSKSLTNRYLVLAALASEPSLVRRLPHSRDSALMVAAQLTGAAVTP----- 78

Query: 75 RAVVVGCGGKF-----PVE---DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ G F PV A + V++ G AG MR + G + D
Sbjct: 79 ----LPDPGPGFGLRIDPVRRSAPADPVRIDCGLAGTVMRFVPLAALHTGQVDF--D 132

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G R RP+G ++ GL+QLG V G P RV G G +PGG V + S SSQ++S
Sbjct: 133 GDDAARVRPMGPVLDGLRQLGVHV-VDQGRAALPFRVLGTGSPGGTVTIDASGSSQFVS 191

Query: 185 ALLMAA-----PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
ALL+AA PL L + + S+P+VEMTL+++ GV A D + G
Sbjct: 192 ALLLAARVFDSPVL---RHDAPGGVPSLPHVEMTLQVLRDAGVDARRVDESRVVPD 248

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + VE D S+A FLA A TGGTV++ + QG + +L GA VT
Sbjct: 249 ---VAGLDVTVEPDLSNAGPFLAAAVATGGTVSIPDWPQHTTQGGDHWRHILPRFGADVT 305

Query: 300 WTETSVITVTGPPREPFGGRKHLKVIDNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
E TVTGP + L+ +D++++ ++A T+A + A GP+ +R +A R
Sbjct: 306 LREGVFTVTGP-----RELRGVLDLSEAGELAPTVAALCALASGPSRLRGIAHLRGH 358

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIDTYDDHRMAMAFSLAACAEVP 419
ET+R+ A+ TEL LG +V E D I P L+ TY DHRMA A ++
Sbjct: 359 ETDRLAALSTELNGLGAVTETLDGLAIE-PTALHGGVFHTYQDHRMATAGAILGLRVPG 417

Query: 420 VTIRDPGCTRKTFFDY 435
V + D T KT P++

Sbjct: 418 VQVADIATTAKTLPEF 433

>ref|ZP_07001809.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D22]
gb|EF11790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D22]
Length = 410

Score = 196 bits (498), Expect = 7e-48, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 219/435 (50%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 6 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPPENLSDCDDTQVMIKALT----- 58

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R
Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM
Sbjct: 95 MQQRPIQILVNALRELGAIEYTRNEGYPPLRIKG-AELKGNEITLKNVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + Q Y+S
Sbjct: 154 IGPALKDGLTLHLSGEIIISRPYINLTQLMQDFGAKAAWTSP--SSISVAPQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 212 -VENDWSAASYWYQIAALS PKAEIELLGLFHNSYQGD SRGA EVFSRLGITTEFTSQGVKL 270

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + + + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 271 KKTGKAP-----ERLEEDFIDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAL 324

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
R EL KLG ++E D ++ E+ I+TY+DHRMAMAF+ A + I +
Sbjct: 325 RAELKKLGYMIKEENDSILMWNGERCPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAN 384

Query: 425 PGCTRKTFPDYFDVL 439
P K++P Y++ L
Sbjct: 385 PQVVTKSYPGYWEDL 399

>emb|CAA54317.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
pseudomallei]
Length = 409

Score = 196 bits (498), Expect = 7e-48, Method: Compositional matrix adjust.
Identities = 136/331 (41%), Positives = 181/331 (54%), Gaps = 35/331 (10%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQP + ++G ++LPG KS+SNR LLL AL+EG T V LL+S+D ML ALR LG+ +E
Sbjct: 10 LQPWRHVTGHLRLPGDKSISNRSLLLGALAEGVTEVTGLLDSDDARAMLNALRDLGVVIE 69

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEV-QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R V G G + K LFLGNAG AMR L+AA+ + T L G P
Sbjct: 70 GPHQG-RCTVHGVG----LHGLKAPPGLFLGNAGTAMRPLSAALALQPFDTT--LTGDP 122

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM ERPI LV L+++GA ++ PP+ + G GS+SSQ+L+ALL
Sbjct: 123 RMSERPINRLVDALREMGAVIEYLAQEGYPPLTIRG-----GGSVSSQFLTALL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
M AP+A ++ + L+S PY+++TL +M FGV D +R + +Y SP
Sbjct: 172 MTAPMASAQIKSGL---LLSKPYIDITLNVMP-FGVPTR--DHTERIFAVSAIRYPSPAV 225

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+EGDA+SASYFLA A I G V V G G S+QGD F L MGA+ + V
Sbjct: 226 LRLEGDATSASYFLAAGIKG--VPVTGIGRHSMQGDSWFPRALRRMGARSCGSSMIVCP 283

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLA 338

G R A+ + N +PD AMTLA
Sbjct: 284 RGELR-----AAVRSDSNSIPDAAMTLA 306

>ref|YP_120804.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nocardia farcinica IFM 10152]
dbj|BAD59440.1| putative 5-enolpyruvylshikimate-3-phosphate synthetase [Nocardia farcinica IFM 10152]
Length = 437

Score = 196 bits (498), Expect = 7e-48, Method: Compositional matrix adjust.
Identities = 148/430 (34%), Positives = 228/430 (53%), Gaps = 34/430 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
+ TV LPKSGKSLNR L+LAAL++G + + L S D M+ LR LG + EAD
Sbjct: 21 VHATVTLPGSKSITNRALILAAALADGPSTITGALRSRDTDLMIAGLRALGTEITGEADTL 80

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+G G + G AG MR L T A G+ + DG + R R
Sbjct: 81 TVTPAALGGG-----TVDCGLAGTVMRFLPPVATLATGSAF--DGDQLARLR 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-AAP 191
P+ ++ L+ LGAD+D D P V+G GGL GG V + S SSQ++S LL+ AA
Sbjct: 127 PLRTILDLRGLGADIDG----DTLPFTVHGKGLRGTTVIDASGSSQFVSGLLLSAAR 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS--WDRFYIKGGQKYKSPKNAY 249
A G + L S+P++EMT+ ++ R V+ E ++ ++ ++ + ++ +
Sbjct: 183 FADGLTVHGEGNPLPSLPHIEMTVEMLRADVRVEAPENPRAEQTWVHPGEIRA-VDWE 241

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQ-GDVKFAEVLEMMGAKVWTETSVTVT 308
VE D S+A+ FLA AA+TGG+V++ + Q GDV E+L MGA+ + +TV
Sbjct: 242 VEPDLNATPFLAAAVTGGSVSIPHWRLTTPQGDV-IREILVRMGAEARIFDGLVTVH 300

Query: 309 GPPREPFGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
GP R L ID++++ + ++ T+A +A AD P+ +R +A R ET+R+ A+
Sbjct: 301 GPDR-----LAGIDIDLHDVGELTPTVAALAAALADSPSRIRGIAHLRGHETDRLAALS 353

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
TE+ +LG V E D I P L+ +Y DHRMA A ++ A + I D G T
Sbjct: 354 TEINRLGGKVTEDEDGLEIV-PAPLHGGTWHYSYADHRMATAGAILGLAVEGIEIEDIGTT 412

Query: 429 RKTFFPDYFDV 438
KT P++ ++
Sbjct: 413 AKTLPNFVEL 422

>gb|ADZ09189.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanobacterium sp. AL-21]
Length = 420

Score = 196 bits (497), Expect = 8e-48, Method: Compositional matrix adjust.
Identities = 151/442 (34%), Positives = 228/442 (51%), Gaps = 37/442 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
++ +Q EI+GTVK P SKS S+R L+A L++G + + + L SED L +L
Sbjct: 2 DLTVQAANEITGTVKAPPSKSYSHRAFLMAFLADGESTLRDPLYSED-----TLASLNT 55

Query: 66 SVEADKAAKRA---VVVGCGGK---FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG 117
+E KR + G GK + V D K N+G +R +T+ + A G
Sbjct: 56 GIEMGSTVKRTESLCSIQGVAGKPKTPYDVLDLK-----NSGTTLRIMTSLASLADG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
VL G ++ RP+ DL+ LK LG P+ V G G GG+ + G
Sbjct: 108 FT--VLTGDNLSLKTTPMDLLDALKPLGVTTACSTRNDGKAPIIVKG--GFYGGETSIKGD 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+SSQ++S+++MAAPLA V++++ + IS PYV MTL LM +FGVK + + + F+I+
Sbjct: 164 VSSQFISSIIMAAPLAKKPVDLKVKGEFISQPYVMMTLELMNKFVKVDFDKTENSFHIE 223

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
Q YK P + VEGD SSASY +A AA V ++ S QGD +++ MG +

Sbjct: 224 -PQSYK-PADYTVGEDYSSASYIIAAAAALKSDVKIKNLMKDSKQGDKIILDIVRDMGCE 281

Query: 298 VTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
V + G+ L +DVN+ PD+ T+A + ADG T I V R

Sbjct: 282 VKVKNEVEIK-----GQMLNGVDVNLQNAPDLLPTVAALGAMADGTTNIYGVEHAR 334

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
KET+R+ TEL+KLG S+ E D I ++ + ++ DHR+AMAF +

Sbjct: 335 FKETDRIHTCSTELSKLGVSLIEKRDIQING--GVHGGVVKSHMDHRLAMAFYIVGLKV 392

Query: 418 VPTVIRDPGCTRKTFPDYFDVL 439
+ I+D + +FPD+ D++

Sbjct: 393 GGICIKDASVYKVSFPDFPDIM 414

>ref|NP_275908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermobacter
thermautotrophicus str. Delta H]
sp|O26860.1|AROAMETTH RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAB85269.1| 5-enolpyruvylshikimate 3-phosphate synthase [Methanothermobacter
thermautotrophicus str. Delta H]
Length = 419

Score = 195 bits (495), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 152/432 (35%), Positives = 222/432 (51%), Gaps = 30/432 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ ++ + GTVK P SKS ++R +++AAL+EG + + + L +ED L A R G+

Sbjct: 2 DLTVEKSGNLEGTVKAPPSKSYTHRAVIAAALAEVSEIRDPLIAEDTLSSLNACRAFGI 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V+ A V G GG+ D ++LGN+G +R +T+ V N T VL G

Sbjct: 62 RVDEGDW---TVHSGSGELETPDDV---IYLGNSGTTLRMTS-VAGLAENYT-VLTG 112

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R RP+ L+ L+ LG + PP+ V G GL GG + G +SSQ++S+

Sbjct: 113 DESLRTRPMQPLLDALRPLGVEALSSRMNGLPPIIVRG--GLRGGSTSIRGDVSSQFISS 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY--IKGGQKYK 243
+L+AAPL G VE+ + IS PYV+MT+ +MERF V ++S+ R + G Y

Sbjct: 171 ILIAAPLTEG-VEVMVEGDFISRPYVDMTVDMERFSVPVDYSEGTFRVEPAVYRGLDYT 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTET 303
VEGD SSASY A GG V +E S QGD +++ MGA+V E

Sbjct: 230 -----VEGDYSSASYLAGAVAAAGGDVLNLFDRSRQGDRIILDIISDMGAEVRRGED 283

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
V + L + VN++ PD+ T+AV+ A G T I V R KET+R

Sbjct: 284 HVRIAST-----GELSGVSVNLHDAPDLLPTVAVLGALATGRTEIGGVEHARYKETDR 336

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ EL +LG V E PD II + + ++ DHR+AMAF+L E +TIR

Sbjct: 337 ISTCAELRLRLGVDVTELPDGMIEG--GASGGTVVWSHGDHRLAMAFTLIGLRE-GITIR 393

Query: 424 DPGCTRKTFPDY 435
D +FPD+

Sbjct: 394 DAEVFSVSFPDF 405

>ref|ZP_03312373.1| hypothetical protein DESPIG_02300 [Desulfovibrio piger ATCC 29098]
gb|EEB32808.1| hypothetical protein DESPIG_02300 [Desulfovibrio piger ATCC 29098]
Length = 456

Score = 195 bits (495), Expect = 1e-47, Method: Compositional matrix adjust.
Identities = 154/462 (33%), Positives = 228/462 (49%), Gaps = 45/462 (9%)

Query: 16 SGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+ V+ P SKS+S+R + AAL+ GT+ + ++L+S D+ L G +EA A +

Sbjct: 6 TACVRAPASKSISHRYCIGAAAHGTSSELHHVLDSDRLECTRAILCAAGARMEALPAEEG 65

Query: 76 AV-VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G G+ P + + +G R LTA + A G+ + + G PRM ERPI
Sbjct: 66 GWRVTGMDGR-PRGGTDTPLSCDVHESGTTTCLLLTAVLAA--GHGLFRIHGAPRMHERPI 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLP---GGKVKLSGSISSQYLSALLMAAP 191
+L L+ LG DV DCP+ + G P GG+V+L SSQY S LL+AAP
Sbjct: 123 DELTRALEALGTDVRFQRPDCPPLLLRAAGLDPARNGGRVRLGMDASSQYFSGLLLAAP 182

Query: 192 LALGDVEIEIII-DKLISIPYVEMTLRLMERFGVK-----AEHSDSWDRFYIKGGQKYKSP 245
LA + +E+ K +S PYV +TL +E FG++ E W G + ++
Sbjct: 183 LAPAPLCVELGGQKAVSWPYVGLTLHCLEDFGIRFCVETREPDGPWQVLPDGGWRALRTA 242

Query: 246 K-----NAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAE 289
+ + + VEGD S ASY LA A+ V V+G SLQGD +
Sbjct: 243 RPDGLRITVQPQTYRAGSYQVEGDWSGASYLLAAGALGKRVPVRVDGLRADSLQGDRAMLD 302

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTA 349
+L MGA+ TS+TV P L+ +DV+M PD+ T+AV+A FA GPT
Sbjct: 303 ILRAMGARAEVEGTSITV-----HPSA---LRGVDVDMGHCPDLVPTVAVLAFAAQGPTR 354

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVT AIDTYDDH 404
+R+VA R+KE++R+ A TEL +LG V+E D + P ++DH
Sbjct: 355 VRNVAHLRIKESDRITAPATELARLGVRVDEHDDGLTVHGLGPDGPAWDEAARFSAHNDH 414

Query: 405 RMAMAFSLAAC---AEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
R+AM+ +L + + DP RK+FP ++ V +
Sbjct: 415 RIAMSLALLGLPYGKRMDALLDDPLVVRKSFPFVWKVWEPLL 456

>ref|ZP_05916273.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 472 str. F0295]
gb|EEX54295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 472 str. F0295]
Length = 415

Score = 194 bits (494), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 142/436 (32%), Positives = 216/436 (49%), Gaps = 60/436 (13%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V LP SKS+SNR L++ ALS + NL N +D M+ AL + +++ RA
Sbjct: 15 VTLPASKSISNRALIMHALSGRPILPQNLSNCDDTRVMVRALTDMPKNIDV-----RA-- 67

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
AG AMR +TA ++ G T L G RMR+RPI LV
Sbjct: 68 -----AGTAMRFMTAYLSCKRGEHT--LTGTQRMQRPIKPLV 103

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LGA ++ PP+R+ G L GG V++ G ISSQ++SALLM P +E
Sbjct: 104 EALRYLGAKIEYEAKDGYPPIRIYG-KPLEGNNVEMPGGISSQFISALLMIGPSLKKGLE 162

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+++ ++ S PY+++TL +M +G KAE +D D +K GQ + +E D S+AS
Sbjct: 163 LKMTGQIASRPYIDLTLMMREYGAKAEWTDI-DAISVKPGQ--YNIGQYTIESDWSAAS 219

Query: 259 YFLAGAAITG---GTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTVTG 309
Y+ A++ T+ +EG S QGD + ++G K +++ T VT+
Sbjct: 220 YWYEMVALSNDPDATIELEGLSENSKQGDSVVRHIFSLLGVKTVFSKHPAGQLTKVTLKK 279

Query: 310 PPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
R L ++ + PD+A TL V P + ++S R+KET+R+ A++
Sbjct: 280 -----LRTRLPKLEYDFVNSPDLAQLVVTCAAMGVFFYFKGLSSLRKETDRIEALKK 333

Query: 370 ELTKLGASVEE-----GPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR 423
E+ KLG + E D P ++ AIDTY+DHRMA+AF+ A V I
Sbjct: 334 EMAKLGFI LREMGEGLAWDMRCRPSDE---AIDTYEDHRMALAFAPVALVNKEVKIN 389

Query: 424 DPGCTRKTFPDYFDVL 439
PG K++P ++ L
Sbjct: 390 QPGVVSXSYPQFWSDL 405

>ref|ZP_06287745.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
buccalis ATCC 35310]
gb|EFA91385.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
buccalis ATCC 35310]
Length = 422

Score = 194 bits (494), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 141/428 (32%), Positives = 214/428 (50%), Gaps = 40/428 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ T+KLP SKS+SNR L++ ALS G +NL + +D ++ AL+ +
Sbjct: 12 FNHTIKLPASKSVSNRALIINALSGGKISPENLSDCDDTQVVIDALKNM-----P 61

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + V AG AMR LTA + GG +V+ G RM+ RPI
Sbjct: 62 RVIDVKA-----AGTAMRFLTAYLAVRGGE--HVITGTERMKHRPI 100

Query: 135 GDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G LV L+ GAD++ PP+R+ G L GG +++ G +SSQY+SALLM +
Sbjct: 101 GPLVDALRYFGADIEYTEQEGFPPLRIKG-KPLKGGYLEMPGDVSSQYISALLMIGSVLK 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+E+++ L S Y+++TL +M++FG +AE SD D +K P Y+E D
Sbjct: 160 DGLELKLTLGTLASRSYIDLTLWVMQQFGAAEWSDI-DTLAVKPTP--YQPHEYYIESDW 216

Query: 255 SSASYF---LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
S+ASY+ LA ++ T ++G S QGD + ++ K + TG
Sbjct: 217 SAASYWYEILALSSHRDNTFMLKGLTDGSKQGDSVARYLFSLLSVKTVVVDGDDPRTGGI 276

Query: 312 REPFGGRKHLKADIVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R + L ++ + PD+A T AV D P ++S +KET R+ A++TEL
Sbjct: 277 RITRHRVTLPLKLEYDFINSPDLAQTFVCCAVLDIPFLTGLSSLLIKETNRIEALKTEL 336

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
KLG +++ + EK T IDTY+DHRMAMAF+ AA + I P
Sbjct: 337 RKLGYVIKDQNGSELFDWGEKCEPTFEPIDTYEDHRMAMAFAPAAINFPLGRINHPEVVS 396

Query: 430 KTFPDYFD 437
K++P ++D
Sbjct: 397 KSYPHFWD 404

>ref|ZP_03644102.1| hypothetical protein BACCOPRO_02477 [Bacteroides coprophilus DSM
18228]
gb|EEF76970.1| hypothetical protein BACCOPRO_02477 [Bacteroides coprophilus DSM
18228]
Length = 434

Score = 194 bits (494), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 140/444 (31%), Positives = 222/444 (50%), Gaps = 51/444 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGL 64
+ I L +I T++LP SKS+ NR L++ AL++ ++NL + +D M+ AL+ +
Sbjct: 27 KRIQLTAPNQIQTATILPSSKSICNRALIIIRALAQSHAPIENLSDCDDTRVMVKALQEMK 86

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
PV D + AG AMR LTA ++ G +++
Sbjct: 87 -----PVID-----IMAAGTAMRFLTAYLSVTEG--SHLIT 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM++RPI LV L+ LGA ++ PP+++ G L ++ L G++SSQY+S
Sbjct: 116 GTERMQRPIRILVDALRSLGAQIEYAGNEGFPLKITGTE-LTQSEISLPGNVSSQYIS 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW--DRFYIKGGQK 241
ALLM P+ + + + ++IS PY+++TL+LM R G A W + +K Q
Sbjct: 175 ALLMIGPVLKKGLRLTLTGEIISRPIYIDLTLQLMNRNGADA----GWTGPNILEVK-PQP 229

Query: 242 YKSPKNAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y+ P Y+E D S+ASY+ A AA+T T+ + SLQGD + AE+ +G T+
Sbjct: 230 YQ-PTPYIESDWSAASYWYAFALTTPRATLRLPDLYQDSLQGDARVAELFSRLGVSTTY 288

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E V +T ++ + + PD+A T V + S ++KE
Sbjct: 289 HEKYVELTR-----TSACVEELTNDFTNQPDLAQTFVVTCALLGIRFRFSGLSLKIKE 342

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAE 417
T+RM A+ E+ KLG + E +I E+ AIDTY+DHRMAMAF+ A
Sbjct: 343 TDRMAALIKEMKKLGYLLREEAGSVLIWDGERCEPDACPAIDTYEDHRMAMAFAPACFKF 402

Query: 418 VPVTIRDPGCTRKTFPDYFDVLST 441
+ I +P K++PD++ L T
Sbjct: 403 KGLQINEPQVVSKSYPDFWKDLQT 426

>ref|ZP_02160130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kordia algicida OT-1]
gb|EDP98063.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kordia algicida OT-1]
Length = 409

Score = 194 bits (493), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 143/421 (33%), Positives = 209/421 (49%), Gaps = 43/421 (10%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ + GSKS SNR+LLL AL ++ N+ NS+D M AL++ AD
Sbjct: 16 IAITGSKSESNRILLALLQALYPNISI-KNISNSDDATLMQKALQS-----AD----- 60

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
V+D + +AG AMR LTA G L G RM+ERPI LV
Sbjct: 61 -----SVKD-----IHHAGTAMRFLTAYYATRNGQEI-TLTGSSRMQERPIKILV 104

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L QLGAD+ PP+++ G L G V L +ISSQY+SALL+ AP +
Sbjct: 105 EALGQLGADIQYTNNEGYPPLQIKG-QQLQGNLVTLDANISSQYISALLLIAPTLKNGLT 163

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + K+ S+PY+ MTL L+ GV E + + + + K VE D SSAS
Sbjct: 164 LTLNGKITSVPIYINMTLSLLNELGV--ETNFEGNTITVAKFEATNEAKTFTVESDWSAS 221

Query: 259 YFLAGAAITGGTVTVE--GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
YF + A++G ++E SLQGD AE+ G + T+ ++T+T
Sbjct: 222 YFYSLIAISGIGTSIELSSYKQDSLQGDSCLAIEYTKFGVETTFKNNITITLKTHEAT-- 279

Query: 317 RKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
+ I +++ PD+A T+AV A + + + ++KET+R+VA++ EL KLGA
Sbjct: 280 ---QETITLDDLKNAPDIAQTIAVTAFLGLQLSCEMIGLHTLKIKETDRLVALKVELEKLGA 336

Query: 377 SVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
SV+ + +N +I TY DHRMAMAF+ A VP+ I K+FPD+
Sbjct: 337 SVDITDASLYLHKASTINKNISIATYKDHARMAMAFPLAL-RVPLQIEKADVVSFSFPDF 395

Query: 436 F 436
+
Sbjct: 396 W 396

>ref|ZP_07322655.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
disiens FB035-09AN]
gb|EFL46917.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
disiens FB035-09AN]
Length = 417

Score = 194 bits (492), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 134/443 (30%), Positives = 226/443 (51%), Gaps = 53/443 (11%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P I + LP SKS+SNR L++ AL+ +N+ +D + A +
Sbjct: 5 IKPPHHIEANIDLPAKSSISNRALIINALTGSNKWPENISTCDDTKVICKAFK----- 57

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ ++ + AG AMR +TA + A+ G +V+ G R
Sbjct: 58 -----QQPYEIDIMAAGTAMRFMTAFLAASEGE--HVITGTER 93

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L+ LGA+V+ PP+R+ G L GG+V++ G++SSQY+SAL+M
Sbjct: 94 MKQRPIKILVDALRFLGAEVEYTEKEGFPPLRIKG-KKLMGGRVEIEGNVSSQYISALMM 152

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AP +E++++ +IS PY+++TL LM +G AE +D D I+ KYK ++
Sbjct: 153 IAPTLKKGLELKLGNIIISRPYIDLTLHLMHEYGADAEWTDV-DTITIR-PTKYKE-RSY 209

Query: 249 YVEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE--- 302
+E D ++ASY+ A + T +T +G S QGD + ++G K ++ +
Sbjct: 210 TIENDWTAASYWYAIITLLNDTDSYITFKGLKNGSRQGDSAVKYIFSLGIKTSFADKEK 269

Query: 303 ---TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
T VT+ R L ++ + PD+A T+ + P ++S ++K
Sbjct: 270 DELTEVTICKQQR-----MLPRLEYDFKNQPDLAQTMATCCVMNIPFKFMGLSSSLKLK 323

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN---TAIDTYDDHRMAMAFSLAACA 416
ET+R+ A++ E+TKLG + + D II E+ IDTY DHRMAMAF+ +
Sbjct: 324 ETDRIEAMKVEMTKLGYVLHDSNDSEIWDGERCEAEKSIVIDTYKDHRMAMAFAPLSVK 383

Query: 417 EVPVTIRDPGCTRKTFFPDYFDVL 439
+TI +P K++P++++ L
Sbjct: 384 LGELTINNPEVVSYSYPNFWNEL 406

>ref|YP_698016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens SM101]
sp|Q0SV34.1|ARO_A_CLOPS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG85908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens SM101]
Length = 424

Score = 194 bits (492), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 134/438 (30%), Positives = 236/438 (53%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LRGSVKIPPSKSMARAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61 ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRLVLPISLIKDNKVNFI 112

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLKGKRLKTY---EIFEEQEIKYSYEEENLDLNIIEGSLKGGEFKVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLKDDSKIIITTELESKGYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK-VTWT 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA+ +
Sbjct: 226 K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIKNQ 283

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T+I + R+KE
Sbjct: 284 EESLSII-----HGDNLGTIIDASQCPDIIPVLTVVAALSKGETSIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II ++L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNKLKADIKELKDGLIINGVKELIGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFFPDYFD 437
V IR+P C +K++P +++
Sbjct: 395 VIIREPDCVKKSYPGFWE 412

>ref|ZP_03016982.1| hypothetical protein BACINT_04593 [Bacteroides intestinalis DSM

17393]
gb|EDV05446.1| hypothetical protein BACINT_04593 [Bacteroides intestinalis DSM
17393]
Length = 416

Score = 194 bits (492), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 144/435 (33%), Positives = 217/435 (49%), Gaps = 56/435 (12%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV+LP SKS+SNR L+L AL++G NL + +D M+ AL
Sbjct: 14 TVQLPASKSISNRALILHALAQGHITPTNLSDCDDTCVMIKAL----- 56

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+ E + + AG AMR LTA ++ G T ++ G RM++RPI L
Sbjct: 57 -----DGNPEHIDIL--AAGTAMRFLTAYLSVTPG--TRIITGTERMQQRPIL 102

Query: 138 VVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L++LGA ++ PP+R+ G L G ++ L+G++SSQY+SALLM P+ +
Sbjct: 103 VDALRELGAQIEYAGNEGFPPLRITGTI-LTGEEINLAGNVSSQYISALLMIGPILKNGL 161

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ + ++IS PY+ +TL+LM+ FG A S S + GQ P VE D S A
Sbjct: 162 RLNLTEIISRPIYINLTQLMKEFGADAAWS-SESSISVHPGQYEDIPFT--VESDWWSGA 218

Query: 258 SYFLAGAAITGGT-----VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSV--TV 307
SY+ A++ + V + G S QGD + E+ +G + T+T+ V T
Sbjct: 219 SYWYQMVALSQDSKEEPAKTEVELLGLFPRSYQGDSRGTEIFAKLGVRTTYTDRGVVLTK 278

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
TG P + ++ ++ +PD+A T V + P + S ++KET+R+ A+
Sbjct: 279 TGTP-----VARLEEDLDIPDLAQTFVVTCCCLMNIPFRFSGLSLQSLKIKETDRIQAL 330

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTVIRD 424
TEL KLG V D +I E+ A I TY+DHRMAMAF+ AA V I +
Sbjct: 331 ITELHKLGYVVRSEQDSILIWNGERCEPEASPVIATYEDHRMAMAFAPAALLVPSVQIAE 390

Query: 425 PGCTRKTFFPDYFDVL 439
P K++P Y+ L
Sbjct: 391 PQVVSXSYPGYWKDL 405

>ref|ZP_07060276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella bryantii
B14]
gb|EFI72539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella bryantii
B14]
Length = 416

Score = 194 bits (492), Expect = 3e-47, Method: Compositional matrix adjust.
Identities = 134/432 (31%), Positives = 215/432 (49%), Gaps = 42/432 (9%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I T++LP SKS+SNR L++ ALS G + NL + +D ++ AL+ D
Sbjct: 11 QIDATIELPASKSISNRALIIYALSHGGILPKNLSDCDDTEVIIAALKN-----SPDIID 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+A AG AMR +TA +++ G+ T + G RM+ RP
Sbjct: 66 IKA-----AGTAMRFMTAFLSSTLGSH--ITGTERMQHRP 99

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV LK LGA++ PP+ + G L GG +++ G+ISSQY+SALLM P+
Sbjct: 100 IKILVDALKSLGANISYIKEDGFPLHITG-KQLTGHLQIPGNISSQYISALLMIGPIL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
+E+E+ +++S PY+ MTL++M FG +A+ W+ IK K K VE
Sbjct: 159 KQGLELELSGEIVSRPIYINMTLKIMAYFGAEAQ----WESENIKVSPPKYINKAYLVEN 214

Query: 253 DASSASYFLAGAAIT---GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S +SY+ A+ + + G SLQGD ++ +G + + E+ T
Sbjct: 215 DWSSSYWYEIMALCKDDQAKIHLTGLFRNSLQGDSDVIQDIFAKLGVRTVFEESGTDATT 274

Query: 310 PPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369

HL++ + K PD+A T+ V +AS ++KET+R+ A++
Sbjct: 275 TVTLTKTPYHLESFTYDFTKCPDLAQTVVVTCCELGIKFHFTGLASLKIKETDRIEALKI 334
Query: 370 ELTKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
EL KLG + + D +I ++ ++ IDTY+DHRMAMAF+ + + +P
Sbjct: 335 ELRKLGFIHDEHDDTLIWNDRCEASMAPIDTYEDHRMAMAFAPTFCVHKDLLMNNPQV 394
Query: 428 TRKTFPDYFDVL 439
K++P ++D L
Sbjct: 395 VSKSYPHFWDDL 406

>ref|NP_619403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina
acetivorans C2A]
sp|Q8THH3.1|AROA_METAC RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAM07883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina
acetivorans C2A]
Length = 430
Score = 193 bits (491), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 166/433 (38%), Positives = 230/433 (53%), Gaps = 27/433 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V P SKS ++R + LAALS + V LL S D + A G SV+ ++ +
Sbjct: 10 VKGEVFAPSSKSYTHRAITLAALSNEISIVRRPLL-SADTLATIRASEMFGASVKREE--E 66
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G GK V D + N+G +R +TA G VL G +R RP
Sbjct: 67 NLIHGFNGKPNVPDD---VIDAANS GTTLRLMTA IAGLTDG--ITVLTGDSSLRTRPN 120
Query: 135 GDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ L QLGA G + P+ V G GL G KV + GSISSQ++SALL+A PLA
Sbjct: 121 GPLLKTNLQLGASACSTRGNEKAPLVVKG--GLEGKKVSIIEGSISSQFISALLIACPLAE 178
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKYKSPKNAYVEG 252
+ II KL S PYV++T+ ++E GVK H+D + +F I G QKY K + G
Sbjct: 179 NSTTSLIIGKLSRPYVDVTIEMLELAGVKI-HTDENNGTKFIIPGKQKY-DLKEYTIPG 236
Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS--VTVTG 309
D SSASY LA AA+T G+ +TV+ S QGD E L+ MGA +TW + VTV G
Sbjct: 237 DFSSASYLLAAAAMTEGSEITVKNL-FPSKQGD KLI IETLQMGADITWDREAGIVTVRG 295
Query: 310 PPREFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
GRK LKA+ + PD+ T+AV+A A+G + I + R KET+R+ A+ T
Sbjct: 296 -----GRK-LKAVTFDAGATPDLVPTVAVLA AEAEGTSRIENAEHVRYKETDRLSALAT 348
Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
EL KLG ++E D IT E L + +DDHR+ M+ +LA TI
Sbjct: 349 ELPKLGVKLKEEKDSLITITGGE-LKGAEVHGWDHRIVMSLALAGMVAGNTTIDTTESVA 407
Query: 430 KTFPDYFDVLSTF 442
++PD+F+ +S
Sbjct: 408 ISYPDFEDMSNL 420

>ref|ZP_06423357.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 317 str. F0108]
gb|EFC67605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 317 str. F0108]
Length = 415
Score = 193 bits (491), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 138/436 (31%), Positives = 220/436 (50%), Gaps = 60/436 (13%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V LP SKS+SNR L++ ALS + + NL N +D M+ AL + +++ RA
Sbjct: 15 VTLPASKSISNRALIMHALSGSSMLPQNLSNCDTRVMVRALSDMPKNIDV-----RA-- 67

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
AG AMR + A ++ G T L G RMR+RPI LV
Sbjct: 68 -----AGTAMRFMAAFLSCQKGEHT--LTGTQRMQRPIKPLV 103

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ +GAD++ PP+R+ G L GG+V++ G ISSQ++SA+LM AP ++
Sbjct: 104 DALRYVGADIEYEAKGYPPIRIYG-KPLEGGRVEMPGGISSQFISAILMIAPTLKKGLD 162

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+++ ++ S PY+++TL +M +G KA+ +D + +K GQ YK+ + +E D S+AS
Sbjct: 163 LKMTGQIASRPYIDLTLMMREYGAkadWTDI-NAISVKPGQ-YKA-RQYTIESDWSAAS 219

Query: 259 YFLAGAAITGG---TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTVTG 309
Y+ A++ V +EG S QGD + ++G K +++ T VT+
Sbjct: 220 YWYEMVALSNPDPTIVELEGLSENSKQGDSSVVRHIFSLGKTVFSKHPAGQLTKVTLKK 279

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
R L ++ + PD+A TL V P + ++S R+KET+R+ A++
Sbjct: 280 -----LRTRLPKLEYDFVNSPDLAQLTVVTCAMMGVPPHFHFKGLSSLRIKETDRIEALKK 333

Query: 370 ELTKLGASVEE-----GPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
E+ KLG + E D P ++ IDTY+DHRMA+AF+ A + I
Sbjct: 334 EMAKLGIVLREMAEGELAWDGMRCRPSDE----PIDTYEDHRMALAFAPVAFVNKEIKIN 389

Query: 424 DPGCTRKTFFPDYFDVL 439
PG K++P ++ L
Sbjct: 390 QPGVVSXSYPQFWSDL 405

>ref|YP_002565359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorubrum
lacusprofundi ATCC 49239]
sp|B9LUD2.1|AROAHALLT RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACM56289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorubrum
lacusprofundi ATCC 49239]
Length = 453

Score = 193 bits (491), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 155/447 (34%), Positives = 220/447 (49%), Gaps = 37/447 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-- 72
+ GT + P SKS ++R LL A S+G TV L+ S D A+ G +VE +
Sbjct: 10 VRGTTTRAPPSKSYTHRALLAAGYSDGATVRSPLV-SADTKATARAVTAFGGAVEPESGER 68

Query: 73 ---AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
A VV G G+ V D + N+G MR +TAA A G T VL G +
Sbjct: 69 FDDADALVVDGDFGRPAVPDDV----IDCANSGETTMRMLVTAALADG--TTVLTGDESL 122

Query: 130 RERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RP G L+ L LG + G P+ V+G L GG+V + G++SSQY++ALLMA
Sbjct: 123 RSRPQGPLLEALGDLGVRAESTRGNGQAPLVVSGP--LAGGEVAIPGNVSSQYVTALLMA 180

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-----EHSDSWDRFYIKGG 239
+ VEI++ L S PYV++TL L++ FG++A + + F + GG
Sbjct: 181 GAVTEEGVEIDLTTPLKSAPYVDITLELLDDFGIEATPVGDGGDALDGAAGAAGFVVDGG 240

Query: 240 QKYKSPKNAY-VEGDASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
Q Y +Y V GD SS SY +A A+ G V +EG S QGD E++E MG
Sbjct: 241 QSYAPAGGSYTVPGDFSSISYLVAAAGAVAAEPGEPVRIEGA-VPSAQGDSAIVEIVERMG 299

Query: 296 AKVTWTETSVTVTGPPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
A + W + +T R L ++V++ PD+ T+A + ADG T I +
Sbjct: 300 ADIEWDREAGVIT-----VRRSELGVEVDVGDTPDLLPTIAALGAVADGDTRIMNCEH 353

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK-LNVTADITYDDHRMAM-AFSLA 413
R KET+R+ A+ EL KLGA E PD + E L ++D DHR+ M A
Sbjct: 354 VRYKETDRVSAMAEELKLGAKTTEEPDTLTVHGSESDLRGASVDGRADHRIVMALAVAA 413

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLS 440

AE TIR +FP++FD ++
Sbjct: 414 LVAEGTTTIRGGEHVDVSFPNFFDAMA 440

>ref|ZP_03630896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [bacterium Ellin514]
gb|EEF58783.1| 3-phosphoshikimate 1-carboxyvinyltransferase [bacterium Ellin514]
Length = 426

Score = 193 bits (491), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 151/438 (34%), Positives = 217/438 (49%), Gaps = 66/438 (15%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA----D 70
+ + +PGSKS++NR L+LAAL++G T++ L SED M+ L+ LG VE +
Sbjct: 15 VRAEITVPGSKSITNRALILAAALADGRTILHGALWSEDTQAMVDCLQRLGFDVEVGIDPE 74

Query: 71 KAAKRAVVV-GCGGKFP-VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+++ R + V G G G K P A E + LF+GNAG A R L+A V G TY L GV R
Sbjct: 75 ESSDRITAVQGLGGKIPSGSANEPLDLFVGNAGTAARFLSAFVCL--GQGTYRLHGVKR 132

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M ERP L L++LG VD + PV ++G G G +S SSQ+ SALL+
Sbjct: 133 MHERPQAALFQALRELGYQVDS--PNNKLPVIIHGTGP-KKGTCSSVSIGESSQFASALLL 189

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A V+I + + PYV MT RL+E F +H +
Sbjct: 190 CAGKGRWSVKI-VGENTEESPYVMTSRLVESF---PQHGESEF----- 228

Query: 249 YVEGDASSASYFLAGAAI-----TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++E DASS SYF A I TV+V+ T+ Q D +F++ L++
Sbjct: 229 HIEPDASSGSYFWAAGKILSPDAKNPTVSVKEWPTSGWQIDAEFSKCLDL----- 278

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVA-LFADGPTAIRDVASWRVKETE 362
E R+ ++ D MT V+A L + P D+ RV+E E
Sbjct: 279 -----PETISRE-----GQLGDSIMTGIVMAPLSTHPVRFTDLGRLRVQECE 321

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEPVPTI 422
R+ A+RTEL + GA E D + P L+ I+TY+DHRMAM F++ + I
Sbjct: 322 RVHALRTELARCGAKAIETGDTLEVF-PGTLHGAEIETYNDRMAMCFAILGLKVSIGIKI 380

Query: 423 RDPGCTRKTFPDYFDVLS 440
++P C +KTFPD+F L+
Sbjct: 381 KNPACVKKTFPDFFQKLA 398

>ref|ZP_04999967.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces sp.
Mg1]
gb|EDX24478.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces sp.
Mg1]
Length = 450

Score = 193 bits (491), Expect = 4e-47, Method: Compositional matrix adjust.
Identities = 150/432 (34%), Positives = 217/432 (50%), Gaps = 29/432 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS++NR L+LAAL+ V L S D M ALR LG+ +E ++
Sbjct: 20 VHATVTVPGSKSVTNRALVLAALASEPGWVRRPLRSRDSQLMSDALRALGVGIEETVSSS 79

Query: 75 RAVVVGCGGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G + + A + +GNAG MR L T A G+ + DG PR ER
Sbjct: 80 SGGEGAGGEAWRIIPAALHGPATVDVGNAGTVMRFLPPVATLASGDIRF--DGDPRSYER 137

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G ++ L+ LGA +D G P+ V G G L GG V++ S SSQ++SALL++AP
Sbjct: 138 PLGQVITALRTLGARIDDD-GRGALPLTVQGGGALEGGTVEIDASNSSQFVSALLLSAPR 196

Query: 193 ALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK---YKSP--- 245
VE+ + D L S+P++ MT+ ++ G + + ++ GG+K SP
Sbjct: 197 FNQGEVVRHVGDNLPSMPHIRTVEMLRAAGAQVDTPEA-----GGEKDVWRVSPGAL 249

Query: 246 --KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++ VE D S+A FLA A ITGGTVTV + Q + MG T+

Sbjct: 250 LGRDMTVEPDLNAQPFLLAALITGGTVTVPDWPRRTTQPGDALRRIFTEMGGSCELTDA 309

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ TG G+ H IDV++ ++ ++ +A VA AD + +R VA R+ ET+R

Sbjct: 310 GLVFTG-----TGKIH--GIDVDLGEVVELTPGIAAVALADSESVLRGVAHLRLHETDR 362

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIR 423
+ A+ E+ LG V E D I P L TYDDHRMA A ++ A V I

Sbjct: 363 LAALTREINGLGGDVTEADGLRIR-PRPLRGFTFHTYDDHRMATAGAVIGLAVDGVLE 421

Query: 424 DPGCTRKTFFDY 435
+ T KT PD+

Sbjct: 422 NVATTAKTLPDF 433

>ref|ZP_07306373.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
viridochromogenes DSM 40736]
gb|EFL34742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
viridochromogenes DSM 40736]
Length = 438

Score = 193 bits (490), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 146/449 (32%), Positives = 220/449 (48%), Gaps = 36/449 (8%)

Query: 6 EIVLQPIKEISG----TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
+ L P SG TV +PGSKS++NR L+LA+LS + L S D M GALR

Sbjct: 7 DTALWPAPHASGAVDATVHVPGSKSVTNRALVLASLSSEPGLRRPLRSRDTLLMAGALR 66

Query: 62 TLGLSVE-----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
+G+ +E A R + G G V+ +GNAG MR L A

Sbjct: 67 AMGIEIEEGVGPDPGTGEAWRVLP TGLRG PATVD-----VGNAGTVMRFLPPVAALA 117

Query: 116 GGNATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
G + DG PR ERP+ ++ L+QLGA +D G P+ V+G G L GG+V +

Sbjct: 118 DGPVRF--DGDPRSRYERPLTGVIDALRQLGARIDDD-GRGALPLTVHGSAGLEGGQVAID 174

Query: 176 GSISQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSW--- 231
S SSQ++SALL++ P VE+ L S+P++ MT+ ++ G + + +S

Sbjct: 175 ASSSSQFVSALLSGPRFNQGVFVRHTGSTLPSMPHIRMTVDMLRAVGAQVDTPESGGEP 234

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVL 291
+ + + G ++ +E D S+A FLA A +TGG V + + Q + E+

Sbjct: 235 NVWRVTPGALLG--RDLVIEPDLNAQPFLLAALVTGGKVVIPDWPAHTTQPGDRLREIF 292

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR 351
MG TE + TG + IDV++ ++ ++ +A VA AD P+ +R

Sbjct: 293 TEMGGSCELTEYGLVFTG-----SGSVHGIDVDLGEVVELTPGIAAVALADSPSTLR 345

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
VA R+ ET+R+ A+ E+ +LG V E D I P +L+ TYDDHRMA A +

Sbjct: 346 GVAHLRLHETDRLAALTKELNGLGGDVTEADGLHIR-PRRLHGGVFHTYDDHRMATAGA 404

Query: 412 LAACAEVPTIRDPGCTRKTFFDYFDVLS 440
+ V I + T KT PD+ D+ +

Sbjct: 405 ILGLGVEGVQIENVATTAKTLPDFPDLT 433

>ref|YP_001192862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacterium
johnsoniae UW101]
gb|ABQ03543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacterium
johnsoniae UW101]
Length = 409

Score = 193 bits (490), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 138/423 (32%), Positives = 213/423 (50%), Gaps = 43/423 (10%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ + GSKS +NR+LLL AL T+ N NS+D M AL

Sbjct: 18 LNTGSKSETNRLLLKALFPNITLA-NTSNSDDSEVMQKALT----- 59

Query: 79 VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIGDLV 138

Sbjct: 60 G + D + +AG AMR LTA G V+ G RM+ERPI LV
----GNDEIVD-----IHHAGTAMRFLTAYFAVNEGREV-VMTGSSRMQERPIKILV 106

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+QLG ++ PP+R+ G + KV L+ ++SSQY+SALL+ A +E

Sbjct: 107 DTLRQLGVEISYEKEEGYPPIRIKG-KKVTASKVTLAANVSSQYISALLLVASKLENGLE 165

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + ++ SIPY++MTL L++ +K + + + K + K VE D SSAS

Sbjct: 166 LTLEGEITSIPYIKMTLALLKDLDIKTSFEGNVIKVFPKESVE---SKEMVVESDWSSAS 222

Query: 259 YFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
YF + A+ +T+ SLQGD + + E MG K T+ +T+ E

Sbjct: 223 YFFSLTALADAAKITLSSYKENS LQGDSELSLYEKMVGKTTFGNKM TL-----EKVAG 277

Query: 318 KHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + ++ +N PD+A T+ V L + + + ++KET+R+ A++TELTKLGA+

Sbjct: 278 FNYQDVNFELNNTPDIAQTIVVTCLGLGIGCHLTGLHTLKIKETDRLEALKTELTKLGAN 337

Query: 378 VEEGPDYCIITPPEKLVN-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTTPDYF 436
+ D + + +N I TY+DHRMAMAF+ A +VP+ I D G K++PD++

Sbjct: 338 ISVTNDSLTLVKSDTINHDVKIGTYNDHRMAMAFAPLAI-KVPIIIIEDAGVVS KSYPDFW 396

Query: 437 DVL 439
+ L

Sbjct: 397 NDL 399

>ref|ZP_06083401.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_22]
gb|EEZ04646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
2_1_22]
Length = 410

Score = 193 bits (490), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 221/435 (50%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 6 LIPPSVVTATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKALT----- 58

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R

Sbjct: 59 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 94

Query: 129 MRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+ + G L G ++ L G++SSQY+SALLM

Sbjct: 95 MQQRPIQILVNALRELGAIEIYVHNEGYPPLCIKG-AELKGNEITLKGNVSSQYISALLM 153

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S

Sbjct: 154 IGPALKDGLTLHLSGEIIISRPYINLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 211

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +

Sbjct: 212 -VESDWSAASYWYQIAALSPKAEIELLGLFPNSYQGDSRGAEVFSRLGITTEFTSQGVKL 270

Query: 308 TGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+

Sbjct: 271 KKTGKAP-----ERLEEDFIDIPDLAQTFVVTCALLNIPFRFTGLQSLKIKETDRIAL 324

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
R EL KLG ++E D ++ E+ I+TY+DHRMAMAF+ A + I +

Sbjct: 325 RAELKKLGYMIKEENDSILMWNGERCEPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAN 384

Query: 425 PGCTRKTTPDYFDVL 439
P K++P Y++ L

Sbjct: 385 PQVVTKSYPGWEDL 399

>ref|ZP_04545361.1| 3-phosphoshikimate 1-carboxy vinyl transferase [Bacteroides sp. D1]

ref|ZP_06724777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides ovatus SD
CC 2a]
ref|ZP_06767926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
xylanisolvens SD CC 1b]
gb|EEO50996.1| 3-phosphoshikimate 1-carboxy vinyl transferase [Bacteroides sp. D1]
gb|EFF55884.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides ovatus SD
CC 2a]
gb|EFG12355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
xylanisolvens SD CC 1b]
Length = 409

Score = 193 bits (490), Expect = 5e-47, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 221/435 (50%), Gaps = 45/435 (10%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P ++ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL
Sbjct: 5 LPPSVVTATQLPASKSISNRALIINALGKGIYPPENLSDCDDTQVMIKALT----- 57

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ KE + + AG AMR LTA ++ G T + G R
Sbjct: 58 -----EGKETIDIM--AAGTAMRFLTAYLSVTPGERT--ITGTAR 93

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA+++ PP+ + G L G ++ L G++SSQY+SALLM
Sbjct: 94 MQQRPIQLVNLRELGAIEYVHNEGYPPLCIKG-AELKGNEITLKGNVSSQYISALLM 152

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P + + + ++IS PY+ +TL+LM+ FG KA + S + + Q Y+S
Sbjct: 153 IGPALKDGLTLHLSGEIISRPYINLTQLMQDFGAKAAWT-SPNSISV-APQLYQSIPFK 210

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTSLQGDVKFAEVLEMMGAKVWTWTETSVTV 307
VE D S+ASY+ AA++ + + G S QGD + AEV +G +T V +
Sbjct: 211 -VESDWSAASYWYQIAALSPKAEIELGLFPNSYQGD SRGAEVFSRLGITTEFTSQGVKL 269

Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P + ++ + +PD+A T V + P + S ++KET+R+ A+
Sbjct: 270 KKTGKAP-----ERLEEDFIDIPDLAQTFVVTALNIPFRFTGLQSLKIKETDRIAAL 323

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFSLAACAEVPTVIRD 424
R EL KLG ++E D ++ E+ I+TY+DHRMAMAF+ A + I +
Sbjct: 324 RAELKKLGYMKEENDSILMWNGERCPEETPVIETYEDHRMAMAFAPAIIRHPNLLIAN 383

Query: 425 PGCTRKTFPDYFDVL 439
P K++P Y++ L
Sbjct: 384 PQVVTKSYPGYWEDL 398

>ref|ZP_07978939.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actG]
ref|ZP_07986138.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actF]
Length = 443

Score = 192 bits (489), Expect = 6e-47, Method: Compositional matrix adjust.
Identities = 148/437 (33%), Positives = 230/437 (52%), Gaps = 19/437 (4%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV++PGSKS++NR L+LAAL+ + L S D M ALRT+G+ +E +++
Sbjct: 20 VRATVRVPGSKSITNRALVLAALAAEPGWLRRPLRSRDTLLMASALRTMGVGIEETVSSE 79

Query: 75 RAVVVGCGGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VVG G + V A + + +GNAG MR L T A G + DG PR ER
Sbjct: 80 SCGVVGAGEAWRVIPAGLRGPATVDVGNAGTVMRFLPPVATLAEGAIRF--DGDPRSRYER 137

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L+ LGA +D P+ V G G L GGKV++ S SSQ++SALL++AP
Sbjct: 138 PLHGVIDALRALGARIDG-DRGALPLTVFGSGALDGGKVEVDASSSQFISALLLSAPR 196

Query: 193 ALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKSPKNA 248
VE+ L S+P++ M++ ++ G + + ++ + + + G ++
Sbjct: 197 FNQGVELRHTGATLPSLPHIRMSVDMLRAVGAQVDEPETGGEPNVWRVTPGALLG--RDL 254

Query: 249 YVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A FLA A +TGGTVT+ + Q + E+ MG TE +T+T
Sbjct: 255 TIEPDLNSAQPFLLAALVTGGTVTIPDWPAGTTQPGDRLREIFTEMGGACELTEAGLTLT 314

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G GR H IDV++ ++ ++ +A VA AD P+ +R VA R+ ET+R+ A+
Sbjct: 315 G-----TGRVH--GIDVDLGEVVELTGPGLAAVAALADSPSTLRGVAHLRLHETDRLAALT 367

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
E+ +LG V E D I P L+ TY+DHRMA A ++ A V I + T
Sbjct: 368 KEINELGGDVTETADGLHIR-PRPLHGGVFHTYEDHRMATAGAILGLAVPGVGIEINVATT 426

Query: 429 RKTFFPDYFDVLSFVKN 445
KT PD+ ++ + + N
Sbjct: 427 AKTLPDFPELWTGMLGN 443

>ref|ZP_06280883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACT-1]
gb|EFB80036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
ACT-1]
Length = 452

Score = 192 bits (489), Expect = 6e-47, Method: Compositional matrix adjust.
Identities = 150/453 (33%), Positives = 223/453 (49%), Gaps = 54/453 (11%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----- 68
+ TV +PGSKS++NR L+LA+L+ + L S D M ALR +G+ +E
Sbjct: 22 VDATVTVPGSKSVTNRALVLASLAAEPGWLRRPLRSRDTLLMADALRAMGVGIEETVSSS 81

Query: 69 -----ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
+ A R + G G V+ +GNAG MR L T A
Sbjct: 82 SASSPSAAASPSSGEAWRVIPAGLHGPAVD-----VGNAGTVMRFLPPVATLAD 132

Query: 117 GNATYVLVDGVPFRMRERPIGDLVVLGLQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G + DG PR ERP+ ++ GL+ LGA +D G P+ V+G G L GG V +
Sbjct: 133 GPVRF--DGDPRSRYERPLTGVIEGLRALGARIDDD-GRGALPLTVHGGGALEGGPVSIDA 189

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S SSQ++SALL++AP VE+ ++ S+P++ MT+ ++ G + + ++
Sbjct: 190 SSSSQVFSALLSAPRFNQGVFVRHTGAVLPSMPHIRMVTDMLRAVGAQVDEPET----- 244

Query: 236 IKGGQK---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKF 287
GG+ SP ++ +E D S+A FLA A +TGG VT+ + Q
Sbjct: 245 --GGEPNIWRVSPSALLGRDLTIEPDLNSAQPFLLAALVTGGRVTIPDWPERTTQPGDAL 302

Query: 288 AEVLEMMGAKVTWTETSVTVTGPPEPFGKRHLKAIDVNMNMPDVMATLAVVALFADGP 347
E+ MG TE +T TG GR H IDV++ ++ ++ +A VA AD P
Sbjct: 303 REIFTAMGGSCELTERGLTFTG-----TGRIH--GIDVDLGEVVELTGPGLAAVAALADSP 355

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMA 407
+ +R VA R+ ET+R+ A+ E+ +LG V E D I P L+ TYDDHRMA
Sbjct: 356 STLRGVAHLRLHETDRLAALTKEINELGGDVTETADGLHIR-PRPLHGGVFHTYDDHRMA 414

Query: 408 MAFSLAACAEVPTIRDPGCTRKTFPDYFDVLS 440
A ++ A V I + G T KT PD+ D+ +
Sbjct: 415 TAGAVIGLAVKVEIENVGTTAKTLPDFPDMWT 447

>ref|YP_677344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cytophaga
hutchinsonii ATCC 33406]
gb|ABG58004.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cytophaga
hutchinsonii ATCC 33406]
Length = 415

Score = 192 bits (489), Expect = 6e-47, Method: Compositional matrix adjust.
Identities = 141/432 (32%), Positives = 222/432 (51%), Gaps = 50/432 (11%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ T+ P SKS SNR+L++ AL+ + +DNL N+ D M+ L ++D

Sbjct: 20 VNHTITPPASKSESNRVLVIDALTGRKSQLDNLSNARDTQTMIRLL-----DSDSN-- 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
PV D + +AG MR LTA +A G + G PRM+ERPI

Sbjct: 71 -----PVWD-----VLDAGTTMRFLTA-FSAFNGKPRE-MTGTFRMKERPI 109

Query: 135 GDLVVGKQLGADVDCFLGTDCCPVRVNGIGG--LPGGKVKLSGSISSQYLSALLMAAPL 192
LV L++LGA ++ PP+ ++ +K+ G +SSQY++ALLM AP+

Sbjct: 110 KLLVDALRELGAVIEWEYKEKEGYPPILIHFPKPELAKTDYIKIKGDVSSQYITALLMIAPV 169

Query: 193 ALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ IE++ + S PY+EMTLRLME FGV +E W IK + P VE

Sbjct: 170 LPKGLTIELLGHVSGSKPYIEMTLRLMEHFGVTSE---WKDNIKISHQTYKPAQYKVES 225

Query: 253 DASSASYFLAGAAITG-GTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S +SY+ + AA+ + ++G SLQGD +++++ +G K +T + +T P

Sbjct: 226 DWSGSSYWFSAALAKEANIELKGYVKNLSLQGDHVIDIMDQLGVKTEFTADGLKLTQKP 285

Query: 312 REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ + + PD+A T+AV+ + + S R+KET+R+ AI+ EL

Sbjct: 286 VK-----GNLVWDFTDPCDLAQTAVAVILAAGVEGTLSGLQSLRIKETDRIAAIQNEL 338

Query: 372 TKLGA---SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEVPTIIRDPGC 427
K GA +E+ Y ++ K++ ++ TY+DHRMAMAF+ LA + VTI +P

Sbjct: 339 RKFGADMIEIEKDVITYKVVPGTFKVDGQSVHTYEDHRMAMAFAPLALLGK--VTIEEPSV 396

Query: 428 TRKTFPDYFDVL 439
K++P Y++ L

Sbjct: 397 VNKSYPYLEDL 408

>ref|ZP_08136605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
multiformis DSM 16608]
gb|EGC19693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
multiformis DSM 16608]
Length = 417

Score = 192 bits (489), Expect = 7e-47, Method: Compositional matrix adjust.
Identities = 142/452 (31%), Positives = 220/452 (48%), Gaps = 65/452 (14%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ + P + + ++LP SKS+SNR L++ AL+ G NL + +D ++ AL

Sbjct: 2 QYTITPPRHVDTRIQLPASKSISNRALIIHALTGGNITPANLSDCDDTEVIIRAL----- 56

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
A R V+ AG AMR +TA ++ G T + G

Sbjct: 57 -----AHRPEVIDIKA-----AGTAMRFMTAYLSVTEGEHT--ITG 90

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
RM+ RPIG LV L+ LGA+++ PP+R+ G L GG++++ G++SSQY+SA

Sbjct: 91 TERMKHRPIGLVDALRYLGAIEYAGEKGFPLRIRG-RQLEGGRLIIPGNVSSQYISA 149

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLM AP+ +E+++ ++S PY+++TL LM +FGV AE +D D +K + P

Sbjct: 150 LLMIAPILTGLEMKLTGGIVSRPYIDLTLHLMHQFGVSAEWTDI-DSITVKPQPYRQRP 208

Query: 246 KNAYVEGDASSASYFLAGAAIT---GGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+E D ++ASY+ A+T G V + G S QGD + ++G K + +

Sbjct: 209 YT--IENDWTAASYWYEVLAITDELGSKVVLPGMMDGSRQGDASVRYIFSLGLIKTAFAD 266

Query: 303 -----TSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
T T+T R L +D + PD+A TL P + S

Sbjct: 267 READRLTDLATLTHSRM-----LNRM DYDFTNQPDLAQTLIATCPVLGIPFHFTGLGSL 320

Query: 357 RVKETERMVAIRTELTKLGASVE-----EGPDYCIITPPEKLNVTADITYDDHRMA 407
R+KET+R+ A++TE+ KLG + EG D C E IDTY+DHRMA

Sbjct: 321 RIKETDRIEAMKTEMEKLGILHADSGTELSWEG-DRC-----EPAAQPVIDTYEDHRMA 374

Query: 408 MAFSLAACAEVPTIIRDPGCTRKTFPDYFDVL 439
M+F+ A + I P K++P Y++ L

Sbjct: 375 MSFAPLAIRLGRIGINHPEVVSXSYPHYWNL 406

>ref|ZP_05735072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella tanneriae
ATCC 51259]
gb|EEX72280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella tanneriae
ATCC 51259]
Length = 407

Score = 192 bits (489), Expect = 7e-47, Method: Compositional matrix adjust.
Identities = 142/440 (32%), Positives = 212/440 (48%), Gaps = 54/440 (12%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V L GSKSLSNR L++AAL++G + L +ED + AL+T
Sbjct: 12 LRGSVDLSGSKSLSNRALIIAALADGDYTLQGLSQAEDTRLAQALQT----- 59

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
Q+ + AG AMR LTA A+GG + L G RM++RPI
Sbjct: 60 -----SAAQVDIRGAGTAMRFLTAYYAASGG--AHCLTGSEMRKQRPI 100

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G LV L+ LGAD+D PP+R+ G L GG + LSGS+SSQY+SALL+ AP
Sbjct: 101 GPLVEALRSLGADIDYTEKEGFPPLRIRG-RQLRGGCLHLSGSVSSQYVSALLLIAPYLS 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKA--EHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ + + ++S PY+ MTL LM FG +A E D+ I Y+S VE
Sbjct: 160 SSLRLRLRLEGTIVSRPYINMTLALMRHFGAQAGWEAEDT---LIVAPAPYQSTARYRVEI 215

Query: 253 DASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA+ + A+ + + G + QGD + + +G K T+ +
Sbjct: 216 DWSSAACWYETVALATDPAARLLLRLGRLREETWQGDARVQDYFLPLGVKTTTFCAEGAVLEK 275

Query: 310 PPREFPGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ AI +++ PD+A +L V P + + R+KET+R+ A+
Sbjct: 276 TEMQS-----GAIVFDLSGQPDLAQSLVACAALQRPFRTGLQTLRIKETDRLAALAR 329

Query: 370 ELTKLGASVEEGPDYCI-----ITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
EL KLG +V D I + P L A TY+DHRMA+AF+ A + I +
Sbjct: 330 ELDKLGITVAVENDESIRSVTYASAPHLQPVA--TYEDHRMALAFAPCALRFPGLQIAE 387

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
P K++P +++ L + +K
Sbjct: 388 PAVVNKSYPGFWEALQSLLK 407

>ref|ZP_03678570.1| hypothetical protein BACCELL_02920 [Bacteroides cellulosilyticus
DSM 14838]
gb|EEF89483.1| hypothetical protein BACCELL_02920 [Bacteroides cellulosilyticus
DSM 14838]
Length = 417

Score = 192 bits (488), Expect = 9e-47, Method: Compositional matrix adjust.
Identities = 141/436 (32%), Positives = 216/436 (49%), Gaps = 57/436 (13%)

Query: 18 TVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T++LP SKS+SNR L+L AL++G NL + +D M+ AL
Sbjct: 14 TIQLPASKSISNRALILHALAQGHIAPSNLSDCDDTRVMIKALD----- 57

Query: 78 VVCGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
G G + AG AMR LTA ++ G T ++ G RM++RPI L
Sbjct: 58 --GNPGHIDIL-----AAGTAMRFLTAYLSVTPG--TRIITGTERMQQRPPIRIL 102

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L++LGA ++ PP+R+ G L G ++ L+G++SSQY+SALLM P+ +
Sbjct: 103 VDALRELGAQIEYAGKEGFPPLRITGTE-LTGEEISLAGNVSSQYISALLMIGPILKNGL 161

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ + ++IS PY+ +TL+LM+ FG A S S ++ G+ P VE D S A
Sbjct: 162 RLNLGTGEIISRPYINLTQLMKFEFGADAAWS-SESSITVRPGKYRDIPFT--VESDWSGA 218

Query: 258 SYFLAGAAI-----TG GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
SY+ A+ T + + G S QGD + AE+ +G T+T+ V +T

Sbjct: 219 SYWYQMVALLIQDNEKKESTKTEIKLPGLLPHSYQGDSEAEIFAKLGVHTTYTDQGVVLT 278

Query: 309 --GPPREFFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
G P + + ++ +PD+A T V + P + S ++KET+R+ A

Sbjct: 279 KMGTP-----VTCLKEDLVDIPDLAQTFVVTCLMNIPFRFTGLQSLKIKETDRIQA 330

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIR 423
+ TEL KLG V+ D +I E+ + I TY+DHRMAMAF+ A + I

Sbjct: 331 LITELNKLGYVVKSEQDSILIWNGERCEPASHPVIATYEDHRMAMAFAPAILRTPSIRIA 390

Query: 424 DPGCTRKTFFPDYFDVL 439

DP K++P Y++ L

Sbjct: 391 DPQVVSXSYPGYWEDL 406

>ref|ZP_02639510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens CPE str. F4969]
gb|EDT26807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens CPE str. F4969]
Length = 424

Score = 192 bits (487), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 132/438 (30%), Positives = 237/438 (54%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG

Sbjct: 2 KKVIITPSK-LKGSVKIPPSKSMARAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++

Sbjct: 61 ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRLVPIISLIKDNKVNFI 112

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+

Sbjct: 113 --GRGNLGRPLKTY---EIFEEQEIKYSYEEKLDLNLIEGSLKGGEFVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y

Sbjct: 167 ISGLLFTLPLLKEDSKIIITTELESKYIDLTLDLMDIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKAFAVLEMMGAKVTWTE 302
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA++ ++

Sbjct: 226 K-PMNYKVEGDYSQAAFYFSAGAL-GSEINCIDLDSLSSYQGDKECIEILERMGARLIESQ 283

Query: 303 -TSVTVTGPPREFFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+S+++ L ++ ++ PD+ L VVA + G T I + R+KE

Sbjct: 284 KSSLSII-----HGDLNGTIIDASQCPDIIPVLTVAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II ++L + ++ DHR+AM+ ++A+ C E

Sbjct: 336 DRLNAICTELNKLGADEKLDGLIIGVKELIGGEVYSHKHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFFPDYFD 437

V I++P C +K++P +++

Sbjct: 395 VIIKEPCVKKSYPGFWE 412

>ref|YP_003387743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirosoma linguale
DSM 74]
gb|ADB38944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirosoma linguale
DSM 74]
Length = 405

Score = 192 bits (487), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 143/435 (32%), Positives = 214/435 (49%), Gaps = 56/435 (12%)

Query: 15 ISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ T+ L SKS SNR L++ AL+ + NL + D M+ L++

Sbjct: 2 VRTTIPLASSKSESNRALIIDALTGFRCDLQNLSTARDTQTMIRLLKS----- 49

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

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          EDA +V      +AG MR LTA + G  T  + G PRM ERPI
Sbjct: 50  -----EDATADVL---DAGTTMRFLTAYFSVTGQQKT--MTGTPRMCERPI 90

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLMAAPL 192
          G LV  L+ LGAD+          PP+++NG          +LS  G +SSQY+SAL+M APL
Sbjct: 91  GILVDALRSLGADITYLRNEGYPPLQINGFSPSAESTNRLSIRGDVSSQYISALVMIAPL 150

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
          G + +E+  + S PY+EMTL M FG A+  W+  I          PK  +E
Sbjct: 151 LPGGLTLELTGAIGSRPYIEMTLEQMRYFG--ADVRADWETKTITVASSPYVPKPYAIES 208

Query: 253 DASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
          D S ASY+ + AA+          + + G  SLQGD  E++  +G + T+T++ V +T
Sbjct: 209 DWGASYWYSVAALAMDETAENLLGLKARSLQGD SAIVEIMRSLGVESTFTDSGVR LTK 268

Query: 310 PPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
          P +          +++ +  PD+A T+AV A          + + S ++KET+R+ A++
Sbjct: 269 IPTQ-----QSLTWDFTDPCDLAQTVAVCAAVKGVVLRMTGIESLKIKETDRVAALQA 321

Query: 370 ELTKLGA---SVEEGPDYCI----ITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTI 422
          EL K+GA  +E  Y +  I PP          IDTYDDHRMAMAF+  A + + I
Sbjct: 322 ELQKIGAELVELETNHLYEYVHQLAIAPP---GPATIDTYDDHRMAMAFAPVAMQK-EIII 377

Query: 423 RDPGCTRKTFFPDYFD 437
          +PG  K++P +++
Sbjct: 378 DEPGVVAKSYP SFWE 392

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>ref|ZP_07934447.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides eggerthii
1_2_48FAA]
gb|EFV30320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides eggerthii
1_2_48FAA]
Length = 424

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Score = 192 bits (487), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 142/452 (31%), Positives = 220/452 (48%), Gaps = 67/452 (14%)

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Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
          P +  ++LP SKS+SNR L+L AL+ G  + NL + +D  M+ AL
Sbjct: 8  PDAPLHAGIQLPASKSISNRALILHALAHGKQTLHNLSDCDDTRVMVRAL----- 57

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
          + + E + +  AG AMR LTA ++  G  V+ G RM+
Sbjct: 58  -----QGSPEHIDIM--AAGTAMRFLTAYLSVTPG--ARVITGTQRMQ 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
          +RPI LV L+QLGAD+          PP+ + G  L G ++ L+G+++SSQY+SALLM
Sbjct: 97  QRPILRLVDALRQLGADIKYTANEGFPPLHITG-SELQGENISLAGNVSSQYISALLMIG 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
          +  + + +  +IS PY+ +TL+L+ FG A+ S S +  + G  P  V
Sbjct: 156 AVLPGKLHLHLTGNIISRPIYNLTQLIHD FGGDAQWS-SENTITVHPGGYQDVPFT--V 212

Query: 251 EGDASSASYFLAGAAITGG-----TVTVEGCGTTSLQGDVKFAEVLEM 293
          E D S+ASY+  A+ G          T+ + G  S QGD + AE+
Sbjct: 213 ESDWSAASYWYQILALRGNEKRRMKNEESLSYKEETIELSGLFPHSYQGDSRGAEIFSR 272

Query: 294 MGAKVTWTETSV--TVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIR 351
          +G  +TE V  T+TG P          +  ++ +M  +PD+A T  V  + P
Sbjct: 273 LGVHTEYTERGVRLTLTGTP-----VTRLEEDMVDIPDLAQTFVVTCCLMNIPFRFT 324

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAM 408
          + S ++KET+R+ A+ TEL KLG +V  D ++  E+  +  I TY+DHRMAM
Sbjct: 325 GLQSLKIKETDRITALITELHKLGYAVRSEQDSILLWNGERCPAESTPLIATYEDHRMAM 384

Query: 409 AFSLAACAEVP-VTIRDPGCTRKTFFPDYFDVL 439
          AF+ AC  +P + I +P  K++P Y++ L
Sbjct: 385 AFA-PACITLPQLMIDEPQVVS KSYPGYWEDL 415

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>ref|ZP_02642799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium

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perfringens NCTC 8239]
gb|EDT78174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens NCTC 8239]
Length = 424

Score = 192 bits (487), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 132/438 (30%), Positives = 236/438 (53%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTL 64
++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LKGSVKIPPSKSMRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61 ANIKVEKDCLIINGENILKDSNYKVIDCNE-----SGSTLRFVLPISLIKDNKVNFI 112

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLGRPLKTY---EIFEEQEIKYSYEEKLDLNIEGSLKGGEFVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV +++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLKEDSKIITTELESKYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA++ ++
Sbjct: 226 K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCIDLSSYQGDKECIEILERMGARLIESQ 283

Query: 303 -TSVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284 KSSLII-----HGDNLGTIIDASQCPDIIPVLTVAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II + L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNLKGLADIKELKDGLIINGVKDLIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFPDYFD 437
V I++P C +K++P +++
Sbjct: 395 VIIKEPCVKKSYPGFWE 412

>ref|ZP_06005871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella bergensis
DSM 17361]
gb|EFA44799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella bergensis
DSM 17361]
Length = 418

Score = 191 bits (486), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 138/440 (31%), Positives = 224/440 (50%), Gaps = 48/440 (10%)

Query: 9 LQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVE 68
+ P ++ ++ LP SKS+SNR L++ AL+ + +NL + +D ++ AL
Sbjct: 8 IMPPSMLNASIALPSSKSIISNRALIINALAGARFMPENLSDCDDTEVVVKALT----- 60

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ PV D K AG AMR +TA + G +V+ G R
Sbjct: 61 -----NRPPVIDVKA-----AGTAMRFMTAYLAVTQGE--HVITGTRK 96

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M+ RPIG LV L++LGAD+D PP+R+ G LPGG++ + G +SSQY SAL+M
Sbjct: 97 MQHRPIGVLVDALRKLGLADIDYEGKQGFPLRIK-KALPGGRLVIPGDVSSQYTSALMM 155

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
P+ +E+ + ++S PY+++TL +M+++G A+ + D I+ Q Y S +
Sbjct: 156 IGPVLQNGLEHLHLAGNIVSRPYIDLTLYMMKQYGADADWTGG-DTITIR-PQNYTS-RPY 212

Query: 249 YVEGDASSASYFLAGAAITGG---TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW---T 301
+E D +SASY+ A+ T+ + G S QGD + ++G K + +
Sbjct: 213 VIENDWTSASYWYEMMALYDNHEDTLVLNGLADGSKQGD SAVKYIYSLGIKTAFENVES 272

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361

E VT R GR ++ +D + PD+A T+ D P ++S ++KET
Sbjct: 273 EHPTAVTLAHR--MGR--VQRLDFDFVNCPLAQTVVTSCCALDIPHFHTGLSSSLKIKET 328
Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVP 419
+R+ A++TEL KLG + D +I + + + IDTY+DHRMAMAF+ A
Sbjct: 329 DRIEALKTELRLKGLYLRSENDELWEHGRCDPSFEPIDTYEDHRMAMAFAPLAIRFP 388
Query: 420 VTIRDPGCTRKTFPDYFDVL 439
+ I +P K++P ++D L
Sbjct: 389 LQINNPQVVSYPKFWDDL 408

>ref|YP_003805618.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta smaragdinae DSM 11293]
gb|ADK83024.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta smaragdinae DSM 11293]
Length = 430

Score = 191 bits (486), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 153/435 (35%), Positives = 233/435 (53%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISG++K+PGSKS + R LL+A+ ++G +++ + L+S D L R+LG V ++
Sbjct: 17 ISGSLKIPGSKSHTIRALLIASAAQGRSIIQDPLDSSDTRAALSLCRSLGARVTEEQG-- 74
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R +V G GG A + + +GN+G ++ AA AA + DG ++R R
Sbjct: 75 RWIVEGTGG-----AMNQAHDVGNSGTSL--FLAAVAASDKAVSFDGDEQIRRRSA 126
Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L+ LGA++ C P V G L GGKV ++ +SQYLSALL+AAPL
Sbjct: 127 APLLDALRGLGAEIIESGEAGCAPFTVKGP--LQGGKVSIA-CPTSQYLSALLLAAPLTP 183
Query: 195 GDVEIEI-IDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKNAYVEG 252
EI + L PYVEMTL+ ++ G++ + W F + GGQ YK P +A V
Sbjct: 184 SGSSTEIEVSLLYERPYPVEMTLKWLDDQGIQYQRRGLEW--FLVPGGQHYK-PFSAAVPA 240
Query: 253 DASSASYFLAGAAITGGTVTVGCGTSTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D SSA++F AAITG + ++G T +QGD +LE MG +V+ + + + GP
Sbjct: 241 DFSSATFFFCAAAITGDKLFLKGLDPTDIQGDKMVLPILKMGCRVSPKDGGEIQGP-- 298
Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ L ++N +PD LA A FA G T + +V R+KET+R+ + ELT
Sbjct: 299 ----EEGLSGGTFDLNSIPDALPALAATACFAKGETQLTNVPQARIKETDRIAVMAQELT 354
Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTR 429
+GA + E D +I+ P+ L+ + + DHR+ MA ++AA A V I D G
Sbjct: 355 GIGAEIRELEDGLLISGRGPKGLSGGNVRGHDHRVIMAEIAALGAREEVIIDDDGAVA 414
Query: 430 KTFPDYFDVLSTFVK 444
TFP++F +L + K
Sbjct: 415 VTFPNFFSLDSIRK 429

>ref|YP_003399282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidaminococcus fermentans DSM 20731]
gb|ADB47967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidaminococcus fermentans DSM 20731]
Length = 430

Score = 191 bits (486), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 134/432 (31%), Positives = 222/432 (51%), Gaps = 21/432 (4%)

Query: 13 KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++GT+++P SKS+ +R L+ AAL++G++ V+ + S D+ LR LG + + +
Sbjct: 9 RSLTGTLRVPSKSMGHRALVCAALAQSSQVEGVSVSRDILATCDCLRQLGAVITSREE 68
Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G P + E + G +G +R L + A G+A + G ++ R
Sbjct: 69 TGGRTAFTVEGTRPHQVGTE---MDCGESGSTLRFLIP-LAALTGDA-FTFQSGSKLGS 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ V +Q G D P+ V G L G L G +SSQ++S LL A PL
Sbjct: 124 PLEPYEVIFRQQLVFRKGSARDNFPLTVQGP--LRPGHFTLPGDVSSQFISGLLFFALPL 181

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G+ +EI KL S Y+ +TL ++++G+ EH +++ R+ I G Q+Y+ P+ VEG
Sbjct: 182 LEGESTLEITGKLESQSYIALTSLALQKYGITIEH-ENYRRYRIPGNQQYQ-PREGAVEG 239

Query: 253 DASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S A+++L A + G T+++ G SLQGD +L+ MG +V + + P
Sbjct: 240 DYSQAAFVLT-AGMLGRTISLLGMDPDSLQGDKAIIPILQKMGQVVFEGDRLVSR--PG 296

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
P G ++ PD+ L V A + G T I R+KE +R+ A+ TEL
Sbjct: 297 TPIG-----TTIDAADCPDIIPVLTVAALSQGHTEIIHAERLRLKECDRLKAMATELN 350

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRK 430
KLGA + E PD I E+L+ +D ++DHR+AM+ ++A+ C E P+T+ C K
Sbjct: 351 KLGARITEKPDGLSIDGVEELSGGTVDWCNDHRIAMSLAVASILCRE-PLTLMGAECVSK 409

Query: 431 TFPDYFDVLSTF 442
++P+++ T
Sbjct: 410 SYPEFWQDFKTL 421

>ref|ZP_07310854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
griseoflavus Tu4000]
gb|EFL39223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
griseoflavus Tu4000]
Length = 438

Score = 191 bits (486), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 147/449 (32%), Positives = 223/449 (49%), Gaps = 36/449 (8%)

Query: 6 EIVLQPIKEISG----TVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALR 61
+ L P SG TV +PGSKS++NR L+LAAL+ + L S D M GALR
Sbjct: 7 DTALWPAPHASGAVDATVHVPGSKSVTNRALVLAALASEPGWLRRPLRSRDTLLMAGALR 66

Query: 62 TLGLSVE-----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
+G+ +E A R + G G V+ +GNAG MR L T A
Sbjct: 67 AMGVEIEEGVPGDGTGEAWRVLP TGLHGPATVD-----VGNAGTVMRFLPPVATLA 117

Query: 116 GGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
G + DG PR ERP+ ++ L++LGA +D P+ V+G G L GG V++
Sbjct: 118 DGPVRF--DGDPRSYPRLNGVIDALRRLGARIDDEE-RGALPMTVHGGGALDGGTVEVD 174

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW--- 231
S SSQ++SALL++AP VE+ L S+P++ MT+ ++ G + + S
Sbjct: 175 ASSSSQFVSALLSAPRFNQGEVVRHTGATLPSMPHIRMTVDMLRAVGAQVDTPESGGEP 234

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVL 291
+ + + G ++ VE D S+A FLA A +TGG V V + Q + E+
Sbjct: 235 NVWRVTPGALLG--RDLTVEPDLSNAQPFLAAALVTGGRVVVPDPAHTTQPGDRLREIF 292

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIR 351
MG TE+ + TG + +DV++ ++ ++ +A VA AD P+ +R
Sbjct: 293 TEMGGSCELTESGLVFTG-----SGSIHGVDVDLGEVGELTPGIAAVALADSPSTLR 345

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS 411
VA R+ ET+R+ A+ E+ +LG V E D I P +L+ TY+DHRMA A +
Sbjct: 346 GVAHLRLHETDRLAALKEINELGGDVETADGLHIR-PRRLHGGIFHTYEDHRMATAGA 404

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ A V I + T KT PD+ D+ +
Sbjct: 405 IIGLAVEGVQIENVATTAKTLPDFPDLWT 433

>ref|ZP_02951936.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens D str. JGS1721]
gb|EDT73125.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens D str. JGS1721]

Length = 424

Score = 191 bits (486), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 132/438 (30%), Positives = 236/438 (53%), Gaps = 32/438 (7%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2  KKVIITPSK-LRGSVKIPPSKSMAHRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65  --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61  ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRFLVPISLIKDNRVNFI 112

Query: 123  LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113  --GRGNLGRPLKTTY---EIFEEQEIKYSYEEELDLNIEGSLKGGEFKVKGNISSQF 166

Query: 183  LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167  ISGLLFTLPLLKDSKIIITTELESKGYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243  KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK-VTWT 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA+ +
Sbjct: 226  K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIENQ 283

Query: 302  ETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA+ + G T + + R+KE
Sbjct: 284  EESLSII-----HGDLNGTIIDASQCPDIIPVLTVVAVLSKGETRVINGERLRIKEC 335

Query: 362  ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II ++L + ++ DHR+AM+ ++A+ C E
Sbjct: 336  DRLNAICTELNKLADIKELKDGLIIGVKELIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420  VTIRDPGCTRKTFPDYFD 437
V I++P C +K++P +++
Sbjct: 395  VIIKEPDCVKKSYPGFWE 412
```

>ref|ZP_02630606.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens E str. JGS1987]
gb|EDT16474.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens E str. JGS1987]
Length = 424

Score = 191 bits (485), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 133/438 (30%), Positives = 235/438 (53%), Gaps = 32/438 (7%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2  KKVIITPSK-LKGSVKIPPSKSMAHRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65  --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61  ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRFLVPISLIKDNKVNFI 112

Query: 123  LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113  --GRGNLGRPLKTTY---EIFEEQEVKYSYEEENLDLNIIEGSLKGGEFKVKGNISSQF 166

Query: 183  LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167  ISGLLFTLPLLKDSKIIITTELESKGYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243  KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT- 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA++ +
Sbjct: 226  K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIESQ 283

Query: 302  ETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284  ERSLSII-----HGDLNGTIIDASQCPDIIPVLTVVAAVLSKGETRIINGERLRIKEC 335
```

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II + L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNKLKADIKELKDGLIINGVKDLIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFPDYFD 437
V I++P C +K++P +++
Sbjct: 395 VIIKEPDCVKKSYPGFWE 412

>ref|ZP_02865398.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens C str. JGS1495]
gb|EDS79458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens C str. JGS1495]
Length = 424

Score = 191 bits (485), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 133/438 (30%), Positives = 235/438 (53%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LKGSVKIPPSKSMHRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61 ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRFLVPISLIKDNKVNFI 112

Query: 123 LDGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLGRPLKTY--EIFDEQEIKYSYEEKLDLNLIEGSLKGGEFVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLLKDSKIIITTELESKYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT- 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA++ +
Sbjct: 226 K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIESQ 283

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284 ERSLSII-----HGDLNGTIIDASQCPDIIPVLTVAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II + L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNKLKADIKELKDGLIINGVKDLIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFPDYFD 437
V I++P C +K++P +++
Sbjct: 395 VIIKEPDCVKKSYPGFWE 412

>ref|YP_695141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens ATCC 13124]
sp|Q0TT99.1|ARO_A_CLOP1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG82786.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens ATCC 13124]
Length = 424

Score = 191 bits (485), Expect = 2e-46, Method: Compositional matrix adjust.
Identities = 133/438 (30%), Positives = 235/438 (53%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LKGSVKIPPSKSMHRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61 ANIKVEKDKLIINGENILKDSNYKVIDCNE-----SGSTLRFLVPISLIKDNRVNFI 112

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLKGKRPKTTY---EIFEEQEVKYSYEEENLDLNIEGSLKGGEFKVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLKEDSKIITTELESKGYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAK-VTWT 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA+ +
Sbjct: 226 K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIENQ 283

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284 EESLSII-----HGDNLGTIIDASQCPDIIPVLTVAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II ++L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNKLKADIKELKDGLIIGVKELIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFPDYFD 437
V I++P C +K++P +++
Sbjct: 395 VIKPEPCVKKSYPGFWE 412

>ref|ZP_06709873.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. e14]
gb|EFF92995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. e14]
Length = 442

Score = 191 bits (484), Expect = 3e-46, Method: Compositional matrix adjust.
Identities = 150/445 (33%), Positives = 221/445 (49%), Gaps = 40/445 (8%)

Query: 9 LQPIKEISG---TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M GALRT+G
Sbjct: 10 LWPAPHASGAVDATVHVPKSVTNRLVLAALASEPGWLRRLRSDTLMLAGALRTMG 69

Query: 65 LSVE-----ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTA 114
+ +E A A R + G G V+ +GNAG MR L
Sbjct: 70 VGIEETVSSASGAGASGEAWRVIPAGLHGPATVD-----VGNAGTVMRFLPPVAAL 120

Query: 115 AGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
A G + DG PR ERP+ ++ L+ LGA +D G P+ V+G G L GG V++
Sbjct: 121 ADGPVRF--DGDPKSYERPLHGVIALRALGARIDDD-GRGALPLTVHSGALDGGAVEI 177

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW-- 231
S SSQ++SALL++ P VE+ + L S+P++ MT+ ++ G + + +S
Sbjct: 178 DASSSSQFVSALLLSGPRFNQGEVVRHVGATLPSLPHIRMTVDMLRAVGAQVDTPESSGGE 237

Query: 232 -DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEV 290
+ + + G ++ VE D S+A FLA A +TGG V V + Q + E+
Sbjct: 238 PNVWRVTPGALLG--RDLTVEPDLNSAQPFLAAALVTGGKVVPDWPARTTQPGDRLREI 295

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAI 350
MG T+ + TG G H IDV+++++ ++ +A VA AD P+ +
Sbjct: 296 FTEMGGSCELTDYGLVFTG-----SGAVH--GIDVDLSEVGELTPGIAAVALADSPSTL 348

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
R VA R+ ET+R+ A+ E+ +LG V E D I P +L+ TYDDHRMA A
Sbjct: 349 RGV AHLRLHETDRLAALTKEINELGGDVTETADGLHIR-PRRLHGGIFHTYDDHRMATAG 407

Query: 411 SLAACAEVPTIRDPGCTRKTFPDY 435
++ A V I + T KT PD+
Sbjct: 408 AIIGLAVEGVQIENVATTAKTLPDF 432

>ref|ZP_03458009.1| hypothetical protein BACEGG_00780 [Bacteroides eggerthii DSM 20697]
gb|EEC54903.1| hypothetical protein BACEGG_00780 [Bacteroides eggerthii DSM 20697]
Length = 424

Score = 190 bits (483), Expect = 3e-46, Method: Compositional matrix adjust.
Identities = 141/452 (31%), Positives = 219/452 (48%), Gaps = 67/452 (14%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEAD 70
P + ++LP SKS+SNR L+L AL+ G + NL + +D M+ AL
Sbjct: 8 PDAPLHAGIQLPASKSISNRALILHALAHGKQTLHNLSDCDDTRVMVRAL----- 57

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + E + + AG AMR LTA ++ G V+ G RM+
Sbjct: 58 -----QGSPEHIDIM--AAGTAMRFLTAYLSVTPG--ARVITGTQRMQ 96

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RPI LV L+QLGAD+ PP+ + G L G ++ L+G++SSQY+SALLM
Sbjct: 97 QRPILRLVDALRQLGADIKYTANEGFPPLHITG-SELQGNEISLAGNVSSQYISALLMIG 155

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+ + + + +IS PY+ +TL+L+ FG A+ S + + G P V
Sbjct: 156 AVLPGKGLHLHLTGNIISRPIYNLTQLIHDFGGDAQWSAE-NTITVHPGGYQDVFT--V 212

Query: 251 EGDASSASYFLAGAAITGG-----TVTVEGCGTTSLQGDVKFAEVLEM 293
E D S+ASY+ A+ G T+ + G S QGD + AE+
Sbjct: 213 ESDWSAASYWYQILALRGNEKRRMKNEESLKSYYEETIELSGLFPHSYQGDSRGAEIFSR 272

Query: 294 MGAKVTWTETSV--TVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR 351
+G +TE V T+TG P + ++ +M +PD+A T V + P
Sbjct: 273 LGVHTEYTERGVRLLTLTGTP-----VTRLEEDMVDIPDLAQTFVVTCLMNIPFRFT 324

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAM 408
+ S ++KET+R+ A+ TEL KLG +V D ++ E+ + I TY+DHRMAM
Sbjct: 325 GLQSLKIKETDRITALITELHKLGYAVRSEQDSILLWNGERCAPASAPLIATYEDHRMAM 384

Query: 409 AFSLAACAEVP-VTIRDPGCTRKTFPDYFDVL 439
AF+ AC +P + I +P K++P Y++ L
Sbjct: 385 AFA-PACITLPQLMIDEPQVVSXSPYGYWEDL 415

>ref|YP_001295176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacterium
psychrophilum JIP02/86]
emb|CAC82655.1| 5-enolpyruvylshikimate 3-phosphate synthase [Flavobacterium
psychrophilum]
emb|CAL42356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacterium
psychrophilum JIP02/86]
Length = 409

Score = 190 bits (483), Expect = 3e-46, Method: Compositional matrix adjust.
Identities = 132/433 (30%), Positives = 216/433 (49%), Gaps = 53/433 (12%)

Query: 17 GTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
T+K+ GSKS +NR+LLL AL T+ DN+ +S+D M+ AL
Sbjct: 14 STIKISGSKSETNRLLLLQALYPNITL-DNISSSDDSQVMIKAL----- 56

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
A + ++ + +AG AMR LTA G +L G RM+ERPI
Sbjct: 57 -----ASKTQEIDIHAGTAMRFLTAYFAQKEGKEV-ILTGSSRMKERPIKI 102

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
LV L+QLGA+++ P+++ G + K+ L ++SSQY+SALL+ AP
Sbjct: 103 LVEALQQLGAIEYVENEGFAPIKIAG-KKIVQHKISLLANVSSQYISALLLIAPKLENG 161

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS----WDRFYIKGGQKYKSPKNAYVEG 252
+E+ ++ ++ S PY++MTL L+ G++ D+ +F I Q +E
Sbjct: 162 LELTLVGEIASTPYIKMTLALLNDLGIETSFIDNKISVLPQFIIHNSQ-----FTIES 214

Query: 253 DASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ETSVTVTG 309
D SSASYF + A++ G +T+ SLQGD AE+ + G + + +++++T
Sbjct: 215 DWSSASYFYISIIALSEIGTRITLSSYQNSLQGDCVLAIEYKDFGVETVFNLNKTISIT- 273

Query: 310 PPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
L I+ +N PD+A T+AV + + + ++KET+R+ A++
Sbjct: 274 ----KINNCQLSTINYQLNNAPDIAQTIAVTCFGLRVGCHLTGLHTLKIKETDRLEALKV 329

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
ELTKLGA++ + + ++ I TY DHRMAMAF+ A + I D G

Sbjct: 330 ELTKLGATISVTNNSLTLEGSSNIHSDIKIKTYQDHRMAMAFAPLAL-RTSIIIEDAGVV 388

Query: 429 RKTFPDYFDVLST 441

K++P++++ L +

Sbjct: 389 SKSYPNFWNDLQS 401

>ref|YP_003383038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kribbella flavida DSM 17836]

gb|ADB34239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kribbella flavida DSM 17836]

Length = 423

Score = 190 bits (483), Expect = 3e-46, Method: Compositional matrix adjust.

Identities = 149/436 (34%), Positives = 229/436 (52%), Gaps = 26/436 (5%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-E 68

+P + G V +PGSKS+SNR L+LAAL++G + + LL + D M AL LG+ + E

Sbjct: 11 RPTGAVDGRVTVPKSGKSLSNRALVLAALADGPSTLSGLLAARDTALMRAALAALGVGITE 70

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

D +V G K + G AG MR + A G + DG P

Sbjct: 71 HD-----GLVTVTPGSL-----KGPADVDCLAGTVMRFVPPVAALADGVVAF--DGDY 118

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

RERP+ ++ L+ LG +D GT P VNG G + GGKV L S SSQ++SALL+

Sbjct: 119 ARERPMMHVILGALRTLGVTTIDH-GTGRMPYAVNGSGAVRGKVTLTASGSSQFVSALLL 177

Query: 189 AAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247

A V+I K + S P+++M++ ++ GV+ + S+ +R+ + G +

Sbjct: 178 AGARYDEGVDIRHDGKPVPSQPHLDMSVAMLRERGVQVDDSEP-NRWIVAPGPIQA--LD 234

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307

A +E D S+A+ FLA A +TGG+VTV G + Q + E+ GA+V+ +TV

Sbjct: 235 AAIEPDLSNAAPFLAAAVVTGGSVTVTGWPAVTTQPGGQLPEIFSRFGAEVSLDGGDLTV 294

Query: 308 TGPPREPFGKHLKADIVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367

G R + +D+++++ ++ LA VA+ ADGP+ +R +A R ET+R+ A+

Sbjct: 295 RGTGR-----IAGVDLDLSEVGELTPVLAAVAVLADGPSYLRGIAHLRNHETDRLAAL 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGC 427

TELT LG V + D I P+ L+ TY DHRMA A ++ A + I +

Sbjct: 348 ETELTAALGGDVNQATADGLEIR-PKPLHGGGLFGTYHDHRMAHAAAVVGLAVDGIENIAT 406

Query: 428 TRKTFPDYFDVLSTFV 443

T KT P++ ++ ST V

Sbjct: 407 TAKTLPEFPELWSTLV 422

>ref|YP_001823822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces griseus subsp. griseus NBRC 13350]

dbj|BAG19139.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptomyces griseus subsp. griseus NBRC 13350]

Length = 450

Score = 190 bits (482), Expect = 4e-46, Method: Compositional matrix adjust.

Identities = 149/453 (32%), Positives = 222/453 (49%), Gaps = 54/453 (11%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----- 68

+ TV +PGSKS++NR L+LA+L+ + L S D M ALR +G+ +E

Sbjct: 20 VDATVTVPGKSVTNRALVLAASLAEPGWLRRPLRSRDTLLMADALRAMGVGIEETVSS 79

Query: 69 -----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116

+ A R + G G V+ +GNAG MR L T A

Sbjct: 80 SASSPSAAASPDSSEAWRVIPAGLHGPAVD-----VGNAGTVMRFLPPVATLAD 130

Query: 117 GNATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG 176

G + DG PR ERP+ ++ GL+ LGA +D G P+ V+G G L GG V +

Sbjct: 131 GPVRF--DGDPRSYPRLTGVIIEGLRALGARIDDD-GRGALPLTVHGGGALEGGPVSIDA 187

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFY 235

S SSQ++SALL++AP VE+ ++ S+P++ MT+ ++ G + + ++
Sbjct: 188 SSSSQFVSALLSAPRFNQGVFVRHTGAVLPSPHIRMVTVMLRAVGAQVDEPET----- 242
Query: 236 IKGGQK---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKF 287
GG+ SP ++ +E D S+A FLA A +TGG VT+ + Q
Sbjct: 243 --GGEPNVVRVSPSALLGRDLTIEPDLSNAQPFLAALVTGGRVTIPDWPERTTQPGDAL 300
Query: 288 AEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGP 347
E+ MG TE +T TG GR H IDV++ ++ ++ +A VA AD P
Sbjct: 301 REIFTAMGGSCELTEHGLTFTG-----TGRIH--GIDVDLGEVGEITPGIAAVAALADSP 353
Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMA 407
+ + VA R+ ET+R+ A+ E+ +LG V E D I P L+ TYDDHRMA
Sbjct: 354 STLSGVAHLRLHETDRLAALTKEINELGGDVTETADGLHIR-PRPLHGGVFHTYDDHRMA 412
Query: 408 MAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
A ++ A V I + G T KT PD+ D+ +
Sbjct: 413 TAGAVIGLAVKGEIENVGTTAKTLPDFPDMWT 445

>ref|YP_134905.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloarcula
marismortui ATCC 43049]
gb|AAV45199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloarcula
marismortui ATCC 43049]
Length = 429

Score = 190 bits (482), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 146/431 (33%), Positives = 217/431 (50%), Gaps = 20/431 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEVDVHYMLGALRTLGLSVEADKAAK 74
+ GT + P SKS ++R +L A ++G V D L+ S D + A+ G SV +
Sbjct: 10 VEGTAQAPPSKSYTHRAVLAAGYADGAVVHDPLV-SADTKATMRAVEAYGGSVSLAEDES 68
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPI 134
V G G+ D + N+G MR +TA TAA + VL G +R RP
Sbjct: 69 TVEVTGFGDGRPETPDDV----IDCANSGETTMRVLTA--TAALQDDLAVLTGDESLRSRPQ 122
Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ + QL D + P+ V G G+ GG V++ G +SSQY++ALLMA ++
Sbjct: 123 GPLLDAIGQLNGDAESTRHNGQAPLVVGG--GIDGGAVEIPGDVSSQYITALLMAGAVSP 180
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
++I++ +L S PYV++TL +++ FGV AE +D+ F + GGQ Y Y V GD
Sbjct: 181 DGIDIDLTTTELKSSPYVDITLEVLDAFGVDAEKTADAG--FTVDGGQTYVPDGGDYNVPGD 238
Query: 254 ASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SS SY LA A+ S QGD ++L+ MGA + W E +T
Sbjct: 239 FSSMSYLLAAGALAAEDGLQVTSAPFSAQGDAAIVDILDRMGADLDWDEEHGEIT----- 293
Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ L I+V + PD+ T+A + ADG T I D R KET+R+ A+ ELTK
Sbjct: 294 -VSQSELTGIEVGVEDTPDLLPTIATLGAAADGVTRITDAEHVRYKETDRVSAMAEELTK 352
Query: 374 LGASVEEGPDYCIITPPEK-LNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 431
+GA VEE D + + L T ++ DHR+ M+ ++A A+ T+ +
Sbjct: 353 MGAEEVEHQDELFFVYGADSDLVGTTVEGRADHRIIMSLAVAGLVADGETTVTGAHVVDVS 412
Query: 432 FPDYFDVLSTF 442
FPD+FDVL +
Sbjct: 413 FPDFFDVLDSL 423

>ref|YP_003091787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter heparinus
DSM 2366]
gb|ACU03725.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter heparinus
DSM 2366]
Length = 419

Score = 190 bits (482), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 148/433 (34%), Positives = 223/433 (51%), Gaps = 46/433 (10%)

Query: 12 IKEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
IK+I+ + L GSKS SNR L+++ALSEG VDNL ++ D + L+ +G + D
Sbjct: 12 IKDINAEIALTGSKSESNRALIISALSEGVLKVDNLSDAVIDTVTLNNILKAIGKENPDPT 71

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
F V+ +G+AG AMR LTA ++ G + L G RM+E
Sbjct: 72 F-----FSD-----VGHAGTAMRFLTAYLSITRG--MFYLTGSGRMKE 108

Query: 132 RPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L++LGA + + G D PP+ +N VK+ G+ISSQYLSALLM A
Sbjct: 109 RPIKLLVEALQKLGAGIK-YSGQDGFPPLEINKDFRQASRIVKIQGNISSQYLSALLMIA 167

Query: 191 P-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P L LG + +EI +L S PY+EMTL +++ G+ EH WD I Q+
Sbjct: 168 PSLPLG-LSLEIEGELTSRPYLEMTLSMLQDAGI--EH--RWDNNTIHIDQQPFKAAELI 222

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VE D S+ASY+ + AA+ +T+ SLQGD K +++ G + + + +
Sbjct: 223 VEPDWSAASYWYSIAALADHAEITLPLNKQKSLQGDSKIRDIMVAFGVRTSSIPNGIALK 282

Query: 309 GPPREPFGGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G +N+ PD+A T+ V A + + + ++KET R++A++
Sbjct: 283 S-----GTSVAITEVLNLKDCPDLAQTIIIVCAAAGLNLSTGLTLKIKETNRILALQ 336

Query: 369 TELTKLGASV-EEGPDYCI---ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
EL K+G + EE Y + ++ PEK+ TYDDHRMAMAF+ + + +
Sbjct: 337 QELIKIGVVLKEENEVYTLNCDQLSFPEKVTFA--TYDDHRMAMAFAPLSFFIKEIEME 393

Query: 424 DPGCTRKTFPDYF 436
D K++PDY+
Sbjct: 394 DYQVVEKSYPDYV 406

>ref|NP_629359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
coelicolor A3(2)]
ref|ZP_05523740.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces lividans
TK24]
ref|ZP_06528581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces lividans
TK24]
sp|Q9K4A7.1|ARO2_STRCO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 2;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase 2; Short=EPSP synthase 2; Short=EPSPS 2
emb|CAB94597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
coelicolor A3(2)]
gb|EFD66831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces lividans
TK24]
Length = 438

Score = 190 bits (482), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 147/446 (32%), Positives = 222/446 (49%), Gaps = 36/446 (8%)

Query: 9 LQPIKEISG----TVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M ALRTLGL
Sbjct: 10 LWPAPHASGAVDATVHVPGSKSVTNRALVLAALASEPGWLRRLRSRDTLLMAEALRTLGL 69

Query: 65 LSVEADKAAK-----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +E + R + G G V+ +GNAG MR L T A G
Sbjct: 70 VEIEEGVGPEGTGEFWRVIPAGLRGPATVD-----VGNAGTVMRFLPPVATLADGA 120

Query: 119 ATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSI 178
+ DG PR ERP+ ++ L+ LGA +D G P+ V+G G L GG V++ S
Sbjct: 121 VRF--DGDPRSRYERPLHGVIDALRVLGARIDDD-GRGALPLTVHGGGALEGGPVEIDASS 177

Query: 179 SSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSW---DRF 234
SSQ++SALL++ P VE+ L S+P++ MT+ ++ G + + +S + +
Sbjct: 178 SSQFVSALLLSGPRFNQGVVVRHTGSALPSMPHIRMVTDMLRAVGAQVDTPESSGGEPNVW 237

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G ++ VE D S+A FLA A +TGG V + + + Q + E+ M
Sbjct: 238 RVTGPALLG--RDLTVEPDLSNAQPFLLAAALVTGGKVVIPDWPSRTTQPGDRLREIFTDM 295

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
G T+ + TG + IDV++++ ++ +A VA AD P+ +R VA
Sbjct: 296 GGSCELTDFGLVFTG-----SGAIHGIDVDLSEVGELTPGIAAVALADSPSTLRGVA 348

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
R+ ET+R+ A+ E+ +LG V E D I P +L+ TYDDHRMA A ++
Sbjct: 349 HLR LHETDRLAALTKELNELGGDVTETADGLHIR-PRRLHGGVFHTYDDHRMATAGAVLG 407

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLS 440
A V I + T KT PD+ D+ +
Sbjct: 408 LAVEGVQIENVATTAKTLPDFPDLWT 433

>ref|YP_003575186.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella ruminicola
23]
gb|ADE82596.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella ruminicola
23]
Length = 416

Score = 190 bits (482), Expect = 4e-46, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 226/436 (51%), Gaps = 47/436 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ T++LP SKS+SNR L++ ALS G + NL + +D ++ ALR +
Sbjct: 10 ERLAQITQLPASKSISNRALIIYALSGGRNLPQNLSDCDDTEVIIIEALRYM----- 60

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
P E + + AG AMR +TA ++ G T+V+ G RM+ R
Sbjct: 61 -----PDE-----INIKAAGTAMRFMTAYLSVMRG--THVITGTERMQRH 98

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L++LGA ++ PP+++ G L GG++ + G++SSQY+SALLM P+
Sbjct: 99 PIAILVDALRKLGAQIEYVQGEFPPLKITGYK-LQGGELSIPGNVSSQYISALLMIGPM 157

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ +++ +IS PY+++TL +M FG +A+ S + D + + YK ++ ++E
Sbjct: 158 LEDGLTLQLTGDIISRPYIDLTLWMMGEFGAEAKWSSA-DTITV-AHKPYKG-RDYFIES 214

Query: 253 DASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S ASY+ A++ V + G S+QGD + ++G K T+ G
Sbjct: 215 DWSGASYWYEMVALSKDRDAEVKLTGLMDGSMQGDSTSRYSLLGVKTTF---ETQKKG 271

Query: 310 PPREPFGGRKHLKAI---DVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P+ +K+ + + + PD+A T V D P + +++ ++KET+R+ A
Sbjct: 272 VPQMVTLLKKNRGRGVGKLEYDFVNAPDLAQTFVVTCAALDIPHFGLSTLKIKETDRIAA 331

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAEVPVIR 423
++ E+ KLG + + D + E+ IDTY+DHRMA+AF+ A + + I
Sbjct: 332 LKKEMLKLGVIHDANDSELYWDGERCEPDLQAGIDTYEDHRMALAFAPYALRQDGLIIN 391

Query: 424 DPGCTRKTFPDYFDVL 439
+P K++P ++D L
Sbjct: 392 NPQVVTKSYPKFWDDL 407

>ref|ZP_08085077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oralis
ATCC 33269]
gb|EFZ36700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella oralis
ATCC 33269]
Length = 414

Score = 189 bits (481), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 136/428 (31%), Positives = 214/428 (50%), Gaps = 41/428 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I +KLP SKS+SNR L++ AL+ G+ + +N+ + +D ++ ALR + ++
Sbjct: 11 IDTIKLPASKSISNRALIIYALTGGSLLPENISDCDDTSVIVHALRYMPEVID----- 64

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ AG AMR LTA + A G+ +++ G RM++RPI
Sbjct: 65 -----IKAAGTAMRFLTAYLAATDGH--HIITGTDRMQQRPI 99

Query: 135 GDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
LV L+ LGAD+ +LG + PP+ + G L GG ++++G +SSQY+SALLM P
Sbjct: 100 KILVEALRYLGADI-TYLGKEGYPPLEIKG-RQLDGGHLEIAGDVSSQYISALLMIGPAL 157

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+E+++ ++ S PY+E+TL +M+ FG AE SD D I P +E D
Sbjct: 158 KNGLELKLNGEIASRPYIELTLWMMKEFGADAEWSDI-DTITIMPKSYQSRPYT--IESD 214

Query: 254 ASSASYFLAGAAI--TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
S ASY+ A+ + + G S QGD + ++G K T+
Sbjct: 215 WSGASYWYEIMALGNKDAKIRLRGLTDGSKQGDVSVVKYLFSLGVTTFENRKENRASDV 274

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ +D + PD+A T V + P +AS R+KET+R+ A+R EL
Sbjct: 275 ILTRHEGAVPRLDYDFINSPDLAQTFVCCALMEIPHFHTGLASLRKETDRIEALRKEL 334

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAEVPVITRDPGCTR 429
KLK V+E +I E T +IDTY+DHRMA++F+ AA +TI P
Sbjct: 335 KKLGYLVKESNGSELIWAGEHCTPTPESIDTYEDHRMALSFAPAAYRFPGITINHPQVVT 394

Query: 430 KTFPDYFD 437
K++P +++
Sbjct: 395 KSYPAFWN 402

>ref|ZP_02180832.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Flavobacteriales bacterium ALC-1]
gb|EDP72300.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Flavobacteriales bacterium ALC-1]
Length = 407

Score = 189 bits (481), Expect = 6e-46, Method: Compositional matrix adjust.
Identities = 142/441 (32%), Positives = 223/441 (50%), Gaps = 44/441 (9%)

Query: 6 EIVLQPIKEIS-GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+I +Q K I+ VK+ GSKS SNR+LLL AL +++NL NS+D M AL+
Sbjct: 2 DISIQSKSLINFENVKITGSKSESNRLLLLQALYP-EILIEENLSNDDSVLMQKALK--- 57

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+K ++V + +AG AMR LTA ++ + V+
Sbjct: 58 -----SKESIVD-----IHHAGTAMRFLTAYLSIQE-DEEVVIT 90

Query: 125 GVPRMRERPIGLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RM+ERPI LV L+ LGAD+ PP+++ G L KV L ++SSQY+S
Sbjct: 91 GSSRMKERPIKILVEALRVLGADISYLENEGFPPLKIVG-KKLSKNKVTLEANVSSQYIS 149

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+ A +E+ + K+ S+PY++MTL L+ GV+ D ++ +K
Sbjct: 150 ALLLIASKLEDGLELTLNGKITSVPYIKMTLSLLNEIGVETSFVD--NKIEVKPNILELK 207

Query: 245 PKNAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
P+ VE D SSASYF + A++ G +T+ SLQGD A++ + G +
Sbjct: 208 PQTLVVESDWSSASYFFSIIALSEVGTETITISSYKKESLQGDSVLAKIYQNFQVDTHFNS 267

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
S+ + G + + +++ PD+A T+AV A + + + ++KET+
Sbjct: 268 LSIRLVKT-----GDVKVSGLVFHLSDAPDIAQTIAVTAFLGVECYMTGLHTLKIKETD 322

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVT 421
R+VA++TEL KLGA V D + + +IDTY DHRMAMAF+ + +T
Sbjct: 323 RLVALKTELEKLGAEVIITEDSLRVKASNTIKTNISIDTYKDHRRMAMAFAPLGL-KTDLT 381

Query: 422 IRDPGCTRKTTFPDYFDVLSTF 442
I+ K++P ++ L+T
Sbjct: 382 IKKADVVSXSYQFWGDLTTI 402

>ref|YP_003129415.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorhabdus utahensis
DSM 12940]
gb|ACV10682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorhabdus utahensis

DSM 12940]
Length = 428

Score = 189 bits (480), Expect = 7e-46, Method: Compositional matrix adjust.
Identities = 148/432 (34%), Positives = 218/432 (50%), Gaps = 24/432 (5%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V+ P SKS ++R +L A +EG TV D L S D +GA+ G SVE +
Sbjct: 10 VTGQVQAPPKSYTHRAILAAAGYAEGATVRDPL-ESADTEATMGAVEAYGGSVE--RGVD 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G G+ V + N+G MR +TA TAA + VL G +R RP
Sbjct: 67 ALEVTGFDGRPAVPSDIVNCE---NSGTTMRLVTA--TAALADGITVLTGDDSLRSRPQ 120

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ + QL + P+ V G + GG V + G +SSQY++ALLMA +
Sbjct: 121 GPLLDIAIGQLDGRAESTRANGQAPLVVKGP--VDGGTVSIPGDVSSQYITALLMAGAITE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
+EI + +L S PYV++T+ +++ FGV E + + F + GGQ Y Y V GD
Sbjct: 179 EGIEIALETELKSAPYVDITIEVLDAFGVDVESTAAG--FDVAGGQTYDPAGGEYAVPGD 236

Query: 254 ASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SS SY LA GA +TV G S QGD ++LE MGA ++W + +T
Sbjct: 237 FSSISYLLATGALAAPDGLTVTGA-RPSAQGDSAIVDILERMGADISWDRDAGEIT---- 291

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
R L ++V++ PD+ T++V+ ADG T I D R KET+R+ A+ ELT
Sbjct: 292 --VSRSSLGVEVSVADTPDLLPTISVLGAADGDTRIVDCEHVRYKETDRVAAMAEELT 349

Query: 373 KLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPG-CTRK 430
+GASV E + I + L+ +D DHR+ M+ ++A TI G
Sbjct: 350 AMGASVTEEQEVLTIHGDDTDLGSAVVDGRADHRIVMSLAVAGLVADGETIVQGGEHVDV 409

Query: 431 TFPDYFDVLSTF 442
+FP++FDV+ +
Sbjct: 410 SFPNFFDVIESI 421

>ref|ZP_04704720.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces albus
J1074]
ref|ZP_06593432.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces albus
J1074]
gb|EFE83893.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces albus
J1074]
Length = 450

Score = 189 bits (480), Expect = 8e-46, Method: Compositional matrix adjust.
Identities = 149/436 (34%), Positives = 226/436 (51%), Gaps = 23/436 (5%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----AD 70
+ TV++PGSKS++NR L+LAAL+ + L S D M ALRTLG+ +E +D
Sbjct: 20 VEATVQVPGSKSVTNRALVLAALAAEPGWLRRPLRSRDTVLMAEALRTLGVGIEETVSSD 79

Query: 71 KAAKRAVVVGCGGKFPV--EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AA + + G + + + +GNAG MR L T A G+ + DG PR
Sbjct: 80 SAAPGSTLAKGGEAWRIIPSGLRGPATVDVGNAGTVMRFLPLATLADGDIRF--DGDPR 137

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
ERP+ ++ L+ LGA +D P+ V+G G L GG V++ S SSQ++SALL+
Sbjct: 138 SYERPLHGVIDALRALGARIDDD-DRGSLPMTVHGTGSLDGGTVEIDASSSSQFVSALLL 196

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKS 244
+AP VE+ I +L S+P++ MT+ ++ R G + + +S + + + G
Sbjct: 197 SAPRFNQGEVVRHIGPRLPSMPHIRMVTDMLRRVGAQVDEPESGGEPNVWRVTPGALLG- 255

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETTS 304
++ VE D S+A FLA A +TGG V V + Q + E+ MG TE
Sbjct: 256 -RDLTVEPDLNAQPFLAAALVTGGRVVPDPAHTTQPGDRLREIFTTMMGGSCLETEAG 314

Query: 305 VTVTGPMPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

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      + TG      GR H   IDV++ ++ ++   +A VA  ADG + +R VA  R+ ET+R+
Sbjct: 315 LVFTG-----SGRVH--GIDVDLGEVGE LTPGIAAVALADGESVLRGV AHLRLHETDRL 367

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRD 424
      A+  E+ +LG V E D   I P L+      TYDDHRMA A ++      V I +
Sbjct: 368 AALTKEINELGGDVTETADGLRIR-PRPLHGGVFHTYDDHRMATAGAILGLVVKGV E IEN 426

Query: 425 PGCTRKTFPDYFDVLS 440
      T KT PD+ D+ +
Sbjct: 427 VATTAKTLPDFPDLWT 442

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>gb|EGC87543.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella
denticola CRIS 18C-A]
Length = 417

Score = 189 bits (480), Expect = 8e-46, Method: Compositional matrix adjust.
Identities = 141/455 (30%), Positives = 224/455 (49%), Gaps = 71/455 (15%)

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Query: 6   EIVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      + ++ P + +   + LP SKS+SNR L++ AL+ G + +NL + +D ++ AL
Sbjct: 2   QYMITPPRHVDTRILLPASKSISNRALIIHALTGGNVMPENLSDCDDTKVIIRAL----- 56

Query: 66  SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      + R V+      + AG AMR +TA ++   G T + G
Sbjct: 57  -----SHRPEVID-----IKAAGTAMRFMTAYLSVTEGEHT--ITG 90

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSA 185
      RM+ RPIG LV L+ LGA+++   PP+R+ G L GG++++ G++SSQY+SA
Sbjct: 91  TERMKHRPIGVLVDALRYLGA EIEYAGEKGFPPLRIRG-RQLEGGRL EIPGNVSSQYISA 149

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      LLM AP+   +E+++   ++S PY+++TL LM +FGV AE +D D +K + P
Sbjct: 150 LLMIAPVLSKGLEMKLTGGIVSRPYIDLTLHLMHQFGVSAEWTDI-DSITVKPQPYRQRP 208

Query: 246 KNAYVEGDASSASYFLAGAAIT---GGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTE 302
      +E D ++ASY+   A+T G V + G S QGD + ++G K + +
Sbjct: 209 YT--IENDWTAASYWYEV LALTD ELGAKVVLP GMLDGS RQGD S AVRYIFSLLG IKTAFAD 266

Query: 303 -----TSVTVTGPPREPFGGRKH---LKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDV 353
      T T+T      +H L +D + PD+A TL P +
Sbjct: 267 READRLTDTALT-----RHSCMLNRMDYDFTNQPDLAQTLIATCPVLGIPFHFTGL 317

Query: 354 ASWRVKETERMVAIRTELTKLGASVE-----EGPDYCIITPPEKLNVT AIDTYDDH 404
      S R+KET+R+ A++TE+ KLG + EG D C E IDTY+DH
Sbjct: 318 GSLRIKETDRIEAMKTEMEKLYILHADSGTELSWEG-DRC-----EPAAQPVIDTYEDH 371

Query: 405 RMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVL 439
      RMAM+F+ A + I P K++P Y++ L
Sbjct: 372 RMAMSFAPLAIRLGRIGINHPEVVSKSYPHYWNDL 406

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>ref|YP_003357655.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocella
paludicola SANA E]
dbj|BAI62672.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocella
paludicola SANA E]
Length = 430

Score = 189 bits (479), Expect = 9e-46, Method: Compositional matrix adjust.
Identities = 152/430 (35%), Positives = 214/430 (49%), Gaps = 36/430 (8%)

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Query: 14  EISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      E+ G V+ P SKS ++R +++ +L + + LL S D +GA R +G E D
Sbjct: 18  EVYGEVEAPP SKSYTHRSIVIGSLGHYSKIEKPLL-SADTLATVGACRAMG--AEIDVKG 74

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      + G G+ V D + N+G +R T+ A G V G +R RP
Sbjct: 75  DYLEIAGVIGRPKVPDD---VVNAANS GTTLRLCTSM AALADG--ATVFTGDSSLRSRP 128

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLSGSISSQYLSALL 187
      G L+ L LGA C R NG+ G + GG++ + G ISSQ++S+LL

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Sbjct: 129 NGPLIKALNDLGAI-----CFSTRHNLAPIVQGPMKGGEIFIEGGISSQFISLL 180

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
++ P A D I I +L S PYVE+TL +ME+ G K S + F+I+ Q Y+ K+

Sbjct: 181 ISCPFARRDTTININGELKSKPYVEVTLEMMKAGGKV--STDFKEFHIESDQDYEL-KS 237

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSASY LA A+ G VTV S QGD E L MGA V W TV

Sbjct: 238 YRVPGDFSSASYMLAAGALAG-KVTVANL-FESKQGDAAIMEYLLDMGANVWDTEKGTV 295

Query: 308 TGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
T + L+ ID++ PD+ TLAV+A A G T I + A R KET+R+ A+

Sbjct: 296 T-----VEQAGLRGIDIDAGATPDLVPTLAVLAACAKGTTRITNAAHVRYKETDRLHAM 349

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
TEL K+GA + E PD +I +L +D YDDHR+ MA ++A A +I

Sbjct: 350 ATELKKMGADITEEPDGLVINGG-RLKGAKVDGYDDHRIVMALAVAGLMASGTTSIDTAE 408

Query: 427 CTRKTFPDYF 436

++P +F

Sbjct: 409 SVDISYPGFF 418

>ref|YP_685260.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
methanogenic archaeon RC-I]
sp|Q0W6Q9.1|AROA_UNCMA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAJ35934.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
methanogenic archaeon RC-I]
Length = 422

Score = 189 bits (479), Expect = 9e-46, Method: Compositional matrix adjust.
Identities = 154/429 (35%), Positives = 227/429 (52%), Gaps = 33/429 (7%)

Query: 14 EISGTVKLPGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKA 72
++ G+V P SKS ++R + + ++ + LL S D + A R G + +

Sbjct: 9 DVWGSVDAPPSKSYTHRAIAIGSMGHYAKITGPLL-SADTLATVSACRAFGADIRISGDT 67

Query: 73 AKRAVVVGCGGKFP--VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ A V+G + P V DAK N+G +R L +++ A AT V G +R

Sbjct: 68 VEIAGVIG-KPRVPEDVIDAK-----NSGTTLR-LCSSIAALAEAT-VFTGDSSLR 116

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP G L+ L LGA GT P+ ++G+ + GG++ ++GSISSQ++S+LL++

Sbjct: 117 KRPNGPLIKALNDLGAVCYSTRGTGTAPLIHGV--MKGGRISINGSISSQFISLLISC 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P A D I I +L S PYVE+TL ++E+ G + E +++ F I+ Q Y + V

Sbjct: 175 PFAKNDTTILIEGELKSKPYVEVTLEMLEKAGCRIE--TNFEFRQCCQDYNLGEY-RV 231

Query: 251 EGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET--SVTVT 308
GD SSASY LA AA+TG VTV G S QGD E L MGA V W E +VTV

Sbjct: 232 PGDFSSASYPLAAAATGSRVTV-GNLFPSKQGDAAILEHLLDMGANVFWDEEMGTVTVE 290

Query: 309 GPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G GR H ID++ + PD+ TLAV+A A+G T I + R KET+R+ A+

Sbjct: 291 G-----GRLH--GIDIDAGQTPDLVPTLAVLAACAEGTTHINNAEHVRYKETDRLRAMA 342

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA-CAEVPVTIRDPGC 427
TEL K+G +EE D I +L +D +DDHR+ MA ++A A+ TI

Sbjct: 343 TELRKMGVQIEERQDGLDIEGG-RLTGATVDGHHDDHRIVMALAVAGLAADGQTTISTAES 401

Query: 428 TRKTFPDYF 436

++P +F

Sbjct: 402 VDISYPAFF 410

>ref|ZP_06587010.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces
roseosporus NRRL 15998]

gb|EFE77471.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces roseosporus NRRL 15998]
Length = 450

Score = 189 bits (479), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 152/463 (32%), Positives = 224/463 (48%), Gaps = 58/463 (12%)

Query: 9 LQPIKEISG----TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LA+L+ + L S D M ALR +G
Sbjct: 10 LWPAPHASGAVDATVTVPGSKSVTNRALVLASLAAEPGWLRRPLRSRDTLLMAEALRAMG 69

Query: 65 LSVE-----ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMR 106
+ +E + A R + G G V+ +GNAG MR
Sbjct: 70 VGIEETVSSSSASSPSAAASPDSSGEAWRVIPAGLHGPATVD-----VGNAGTVMR 120

Query: 107 SLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGG 166
L T A G + DG PR ERP+ ++ GL+ LGA +D G P+ V+G G
Sbjct: 121 FLPPVATLADGPIRF--DGDPRSRYERPLTGVI EGLRTL GARIDDD-GRGALPLTVHGGGA 177

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA 225
L GG V + S SSQ++SALL++ P VE+ ++ S+P++ MT+ ++ G +
Sbjct: 178 LEGGPVSIDASSSSQFVSALLSGPRFNQGV EVRHTGAVLP SMPHIRMTVDMLRAVGAQV 237

Query: 226 EHSDSWDRFYIKGGQK---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCG 277
+ ++ GG+ SP ++ +E D S+A FLA A +TGG VT+
Sbjct: 238 DEPET-----GGEPNVWRVSPSALLGRDLTIEPDL SNAQPFLAALVTGGRVTIPDWP 290

Query: 278 TTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTL 337
+ Q E+ MG TE +T TG GR H IDV++ ++ ++ +
Sbjct: 291 ERTTQPGDALREIFTAMGGSCELTERGLTFTG-----TGRH--GIDVDLGEVGELTPGI 343

Query: 338 AVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 397
A VA AD P+ + VA R+ ET+R+ A+ E+ +LG V E D I P L+
Sbjct: 344 AAVAALADSPSTLSGVAHLRLHETDRLAALTK EINELGGDVAETADGLHIR-PRPLHGGV 402

Query: 398 IDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTFPDYFDVLS 440
TYDDHRMA A ++ A V I + G T KT PD+ D+ +
Sbjct: 403 FHTYDDHRMATAGAIIGLAVKGVEIENVGTTAKTLPDFPDMWT 445

>ref|YP_002478927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774]
gb|ACL48249.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774]
Length = 484

Score = 189 bits (479), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 157/471 (33%), Positives = 223/471 (47%), Gaps = 65/471 (13%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV---EADKAA 73
TV P SKS+S+R L+ AAL+ GT++V + L S D+ L G ++ E+ A+
Sbjct: 24 TVTAPASKSVSHRYLMGAALAGGTSIVRHTLESRDLETRAILCAAGATMAELPESTPAS 83

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G A + + +G R LTA + A G + + G RM ERP
Sbjct: 84 GAWQVTGMNGAPRGGTAAAPLSCDVEESGTTTCRLLTAVLAA--GQGVFRIHGAARMHERP 141

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPVRVNGIGGLP---GGKVKLSGSISSQYLSALLMAA 190
I +L L LG DCP + G P GG V+L ISSQY S LL+AA
Sbjct: 142 IAE L D A L A A L G T Q T S F E E K P D C P P C V L T A H G L D P A R C G G I V E L G M D I S S Q Y F S G L L L A A 201

Query: 191 PLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKA E-----HSDSWDRF- 234
P+ + + + K +S PYV +TL+ + +G++ E +W R
Sbjct: 202 PMGPAPLTLALGGRKAVSWPYVGLTLQCLTDY G I R F E V Q T R R D I G A P W Q P M G D G A W R R L D 261

Query: 235 -YIKGGQK---YKSPKNA---YVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKF 287
+ G + Y P A VEGD S ASY LA AI V VEG SLQGD
Sbjct: 262 EALPGCLRITVYPGPYRAGEYTV EGDWSGASYLLAAGAIGRRPVRVEGLRADSLQGD RAM 321

Query: 288 AEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGP 347
+L+ MGA+V +VTV P R L +D++M PD+ T+A VA FA G

Sbjct: 322 LNILQRMGARVDVQPLAVTVY-PSR-----LHGVDLDMGHCPDLVPTVATVAAFAQGS 373

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEE-----GPDYCIITPPE 391
T IR+VA R KE++R+ A TEL K G V+E PD+ I+ P+

Sbjct: 374 TRIRNV AHLRHKESDRIKAPATELGKAGVVVDELSDGMLVNLGGRNNGKPDHPIL--PD 431

Query: 392 KLNVT AIDTYDDHRMAMAFSLAACAEVPVTIR---DPGCTRKTFPDYFDV 438
++A ++DHR+AM+ +L +R DP K+FP ++++

Sbjct: 432 GQTLISA---HNDHRIAMSLALLDLCRSEAVVRSRLDDPSVVGKSFQFWNI 479

>ref|ZP_04711269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces roseosporus NRRL 11379]
Length = 452

Score = 188 bits (478), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 152/463 (32%), Positives = 224/463 (48%), Gaps = 58/463 (12%)

Query: 9 LQPIKEISG----TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LA+L+ + L S D M ALR +G

Sbjct: 12 LWPAPHASGVVDATVTVPGSKSVTNRALVLASLAAEPGWLRRPLRSRDTLLMAEALRAMG 71

Query: 65 LSVE-----ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMR 106
+ +E + A R + G G V+ +GNAG MR

Sbjct: 72 VGIEETVSSSSASSPSAAASPDSSGEAWRVIPAGLHGPATVD-----VGNAGTVMR 122

Query: 107 SLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG 166
L T A G + DG PR ERP+ ++ GL+ LGA +D G P+ V+G G

Sbjct: 123 FLPPVATLADGPIRF--DGDPRS YERPLTGVI EGLRTL GARIDDD-GRGALPLTVHGGGA 179

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA 225
L GG V + S SSQ++SALL++ P VE+ ++ S+P++ MT+ ++ G +

Sbjct: 180 LEGGPVSIDASSSSQFVSALLSGPRFNQGV EVRHTGAVLPSMPHIRMVTVDM LRAVGAQV 239

Query: 226 EHSDSWDRFYIKGGQK---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCG 277
+ ++ GG+ SP ++ +E D S+A FLA A +TGG VT+

Sbjct: 240 DEPET-----GGEPNVWRVSPSALLGRDLTIEPDLSNAQPFLLAALVTGGRVTIPDWP 292

Query: 278 TTSLQGDVVKFAEVLMMGAKVWTETSVTVTGPPREPFGRKHLKAIDVNMNKM P DVAMTL 337
+ Q E+ MG TE +T TG GR H IDV++ ++ ++ +

Sbjct: 293 ERTTQPGDALREIFTAMGGSCELTERGLTFTG-----TGRIH--GIDVDLGEV GELTPGI 345

Query: 338 AVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A 397
A VA AD P+ + VA R+ ET+R+ A+ E+ +LG V E D I P L+

Sbjct: 346 AAVAALADSPSTLSGVAHLRLHETDRLAALKEINELGGDVAETADGLHIR-PRPLHGGV 404

Query: 398 IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
TYDDHRMA A ++ A V I + G T KT PD+ D+ +

Sbjct: 405 FHTYDDHRMATAGAIIGLAVKGVEIENVGTTAKTLPDFPDMWT 447

>ref|ZP_04696087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces roseosporus NRRL 15998]
Length = 452

Score = 188 bits (478), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 152/463 (32%), Positives = 224/463 (48%), Gaps = 58/463 (12%)

Query: 9 LQPIKEISG----TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LA+L+ + L S D M ALR +G

Sbjct: 12 LWPAPHASGAVDATVTVPGSKSVTNRALVLASLAAEPGWLRRPLRSRDTLLMAEALRAMG 71

Query: 65 LSVE-----ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMR 106
+ +E + A R + G G V+ +GNAG MR

Sbjct: 72 VGIEETVSSSSASSPSAAASPDSSGEAWRVIPAGLHGPATVD-----VGNAGTVMR 122

Query: 107 SLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG 166
L T A G + DG PR ERP+ ++ GL+ LGA +D G P+ V+G G

Sbjct: 123 FLPPVATLADGPIRF--DGDPRS YERPLTGVI EGLRTL GARIDDD-GRGALPLTVHGGGA 179

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA 225

L GG V + S SSQ++SALL++ P VE+ ++ S+P++ MT+ ++ G +
Sbjct: 180 LEGGPVSIDASSSSQVFSALLSGPRFNQGVVRHTGAVLPSPHIRMVTVMLRAVGAQV 239
Query: 226 EHSDSWDRFYIKGGQK---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCG 277
+ ++ GG+ SP ++ +E D S+A FLA A +TGG VT+
Sbjct: 240 DEPET-----GGEPNVVRVSPSALLGRDLTIEPDLNAQPFLLAALVTGGRVTIPDWP 292
Query: 278 TTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTL 337
+ Q E+ MG TE +T TG GR H IDV++ ++ ++ +
Sbjct: 293 ERTTQPGDALREIFTAMGGSCELTERTGLTFTG-----TGRIH--GIDVDLGEVGEITPGI 345
Query: 338 AVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 397
A VA AD P+ + VA R+ ET+R+ A+ E+ +LG V E D I P L+
Sbjct: 346 AAVAALADSPSTLSGVAHLRLHETDRLAALTKEINELGGDVAETADGLHIR-PRPLHGGV 404
Query: 398 IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
TYDDHRMA A ++ A V I + G T KT PD+ D+ +
Sbjct: 405 FHTYDDHRMATAGAIIGLAVKGVEIENVGTTAKTLPDFPDMWT 447

>ref|XP_001449723.1| hypothetical protein [Paramecium tetraurelia strain d4-2]
emb|CAK82326.1| unnamed protein product [Paramecium tetraurelia]
Length = 1118

Score = 188 bits (477), Expect = 1e-45, Method: Compositional matrix adjust.
Identities = 138/439 (31%), Positives = 227/439 (51%), Gaps = 42/439 (9%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ GSKS++NR+LLL++LSEG + ++N +S+D ML +L+ L L + ++ G
Sbjct: 25 IHGSKSITNRVLLLSLSEGISSLNPFYSDDTKAMLSLQELRLCEVQTHSKHNLILEG 84
Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
C G+F K+E + + +G R L + A GN T + G R+ ERPI ++V
Sbjct: 85 CQGQF---YKKEYTINVKESGTCARFL-LPIAALIGNVTII--GAQRIYERPIQEMV-- 135
Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD-VEI 199
+ L +V P +V I G +K+ +SSQ++S +LM+AP D I
Sbjct: 136 -EALDLNVIYQLKEGQLPFKV--IDGKFAKHIIKISQLSSQFVSGILMSAPYFPNDETLLI 192
Query: 200 EIID-----KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
EIID ++S Y+EMT++LM +GV+ E S +F +K G YK+ + +E DA
Sbjct: 193 EIIDCNENETIVSESYIEMTIQLMNIYGVRVERL-SKTKFLVKKG-VYKA-QTYDIEPDA 249
Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
++ SY L + GG ++E + LQGD +F +V+E MG +V + +
Sbjct: 250 TALSVDLLHIGLNGG--SIETKKISKLQGDQFLDVIEQMGQVVRREQGFYKII----- 301
Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ LK DVN D ++LA++ +G I+ + + RVKE +R+ A+ L K+
Sbjct: 302 -KNQDLKPDVNCINFSDTFISLALLMSSIEGQCIKGIENQVRKECDRIKAVTENLIKV 360
Query: 375 GASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSL-----AACAEVPVTI 422
G + + +I +K N I+TY+DHR+AMAFS+ + + I
Sbjct: 361 GVVCLQQNNEILIRGKRYQKYNRYRKDITINTYNDHRIAMAFSILGGHFEKVQYQYRIII 420
Query: 423 RDPGCTRKTFPDYFDVLST 441
+ C RKTFPD+++ + +
Sbjct: 421 DNKDCVRKTFPDYFNHIQS 439

>gb|ADW03510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
flavogriseus ATCC 33331]
Length = 462

Score = 188 bits (477), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 149/436 (34%), Positives = 214/436 (49%), Gaps = 42/436 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----- 68
+ TV +PGSKS++NR L+LA+LS + L S D M ALR LG+ +E
Sbjct: 23 VDATVTVPGSKSVTNRALVLSLSSEPGWLRRLRSRDTLLMAQALRALGVGIEEGVGP 82

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A R + G G V+ +GNAG MR L A G + DG PR
Sbjct: 83 GSGEAWRVIPAGLHGPARVD-----VGNAGTVMRFLPPVACLADGPVHF--DGDPR 131

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
ERP+ ++ LK LGA +D G P+ V+G G L GG V + S SSQ++SALL+
Sbjct: 132 SYERPLHGVIDALKSLGARIDDD-GRGTLPLTVHGAGALDGGPVSVDASSSSQFVSALLL 190

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK---YKS 244
+ P VE+ L S+P++ MT+ ++ G + + ++ GG+ S
Sbjct: 191 SGPRFNQGVVEVRHTGATLPSMPHIRMVTDMLRSVGAQVDEPET-----GGEPNVWRVS 243

Query: 245 P-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
P ++ VE D S+A FLA A +TGG VT+ + Q E+ MG
Sbjct: 244 PSALLGRDLTVEPDLSNAQPFLAAALVTGGRVTIPDWPLRTTQPGDALREIFTAMGGVCE 303

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
TE +T TG G H IDV++++ ++ +A +A AD P+ +R VA R+
Sbjct: 304 LTERGLTFTG-----TGSVH--GIDVDLSEVGELTPGIAAALADSPSTLRLGVHLRLH 356

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
ET+R+ A+ E+ LG V E D I P L+ TYDDHRMA A ++ A
Sbjct: 357 ETDRLAALTKEINLGGDVTETADGLRIV-PVPLHGGTFHTYDDHRMATAGAIIGLAVAG 415

Query: 420 VTIRDPGCTRKTFPDY 435
V I + G T KT PD+
Sbjct: 416 VEIENVGTTAKTLPDF 431

>ref|ZP_04685981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
ghanaensis ATCC 14672]
Length = 438

Score = 188 bits (477), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 146/441 (33%), Positives = 216/441 (48%), Gaps = 36/441 (8%)

Query: 9 LQPIKEISG----TVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M G LR LG
Sbjct: 10 LWPAPHASGAVDATVHVPKSVTNRLVLAALASEPGWLRRLRSDTLTLLMAGGLRALG 69

Query: 65 LSVE-----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +E A R + G G V+ +GNAG MR L T A G
Sbjct: 70 VEIEEGVGPDTGEAWRVLP TGLHGPA TVD-----VGNAGTVMRFLPPVATLADGP 120

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ DG PR ERP+ ++ L++LGA +D P+ V+G G L GG V + S
Sbjct: 121 VRF--DGDPRS YERPLNGVIDALRRLGARIDDD-DRGALPMTVHGGGALDGGTVSVDA 177

Query: 179 SSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSW---DRF 234
SSQ++SALL++AP VE+ L S+P++ MT+ ++ G + + +S + +
Sbjct: 178 SSQFVSALLLSAPRFNQGVEVRHTGSTLPSLPHIRMVTDMLRAVGAQVDTPESGGEPNVW 237

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G ++ +E D S+A FLA A +TGG V V + Q + E+ M
Sbjct: 238 RVTPGALLG--RDLTIEPDLSNAQPFLAAALVTGGKVVPDPWPARTTQPGDRLREIFTEM 295

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
G TE + TG + IDV++ ++ ++ +A VA AD P+ +R VA
Sbjct: 296 GGSCLETFYGLVFTG-----SGSIHGIDVDLGEVGELTPGIAAVALADSPSTLRLGVA 348

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R+ ET+R+ A+ E+ +LG V E D I P +L+ TY+DHRMA A ++
Sbjct: 349 HIRLHETDRLAALTKEINELGGDVTETADGLHIR-PRRLHGGVFHTYEDHRMATAGAVIG 407

Query: 415 CAEVPVTIRDPGCTRKTFPDY 435
A V I + T KT PD+
Sbjct: 408 LAVEGVQIENVATTAKTLPDF 428

>ref|YP_860405.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gramella forsetii
KT0803]

emb|CAL65337.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gramella forsetii
KT0803]
Length = 405

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 144/427 (33%), Positives = 218/427 (51%), Gaps = 45/427 (10%)

Query: 13 KEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKA 72
K + +++ GSKS SNR+L+L AL + +NL NS+D + AL
Sbjct: 10 KNLISELQITGSKSESNRLLILQALYPDIIQI-ENLSNSDDTTVLKNALEK----- 58

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G G V D + +AG AMR LTA + G + G RM ER
Sbjct: 59 -----GSG-----VID-----IHHAGTAMRFLTAYFASKEG-CDVEITGSKRMTER 98

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL-LMAAP 191
PI LV L+++GA+++ PP+ + G L VKL ++SSQY+SAL L+ A
Sbjct: 99 PIRLLVDALQRMGANIEYKNEVGYPPLLIK-G-KKLHVDSVKLHANVSSQYVSALMLIGAS 157

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L G +EI + ++ S PY+ MTL +M+ G+K D DR YI+ K +P VE
Sbjct: 158 LPKG-LEIILEQQITSTPYILMTLEIMQHAGIKGTFKD--DRIYIEPA-KSIAPATIAVE 213

Query: 252 GDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSASYF + AAIT + + TS QGD AE+ + G + + E S+ +
Sbjct: 214 SDWSSASYFYISAAITDTAEIKLSNRYKTSRQGDSCLAIEYKHFGVETEFQENSIVLKKQ 273

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R I ++ PD+A T+AV L + + + ++KET+R+ A++ E
Sbjct: 274 EGTRSSR-----ICEDLRNSPDIAQTIAVTCALGLECKLEGLHTLKIKETDRLQALKNE 328

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT-ITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
+ K A VE D+ + P + LN ++TY+DHRMAMAF+ A +VP++I+D
Sbjct: 329 MEKFSAKVEITNDHLHLLPCKSLNENVEVETYNDRMAMAFAPLA-QKVPLSIKDADVVS 387

Query: 430 KTFPDYF 436
K++PD++
Sbjct: 388 KSYPDFW 394

>gb|ADY13184.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Spirochaeta sp.
Buddy]
Length = 430

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 144/433 (33%), Positives = 222/433 (51%), Gaps = 30/433 (6%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ G +++PGSKS + R +LLA L++G T ++N L S D L A R G V D++ +
Sbjct: 10 LKGKIQVPGSKSHTIRSVLLATLAQQQTCIENPLASGDGLSALRAARAFGAIV--DQSQQ 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV G GG V + + N+G T+ G V+ G ++R RPI
Sbjct: 68 RWVVQGRGGLNLLVPQDVVDTK---NSGTTTCLFTSVAALVDGYT--VITGDEQIRRRPI 121

Query: 135 GDLVVGLKQLGADVDCFL---GTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
LV L LGA FL CPPV V G+ L GG+V + G +SQY+S+LL++AP
Sbjct: 122 LGLVEALNTLGAT--AFLTRPKQGCCPPVVVKGL--LQGGEVSIEGK-NSQYVSSLLSAP 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA I + + L PYV++TL M+R GV+ E+ + + RF I+GGQ+Y N +
Sbjct: 177 LAKRTTVIHVHNAL-EKPYVQLTLDWMKRLGVEVENPEQYTRFTIEGGQRYHG-GNFLIP 234

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ETSVTVTGP 310
D S+ ++ L AAIT + + G + QGD + E+L A + E + + G
Sbjct: 235 ADWSAVAFPLVAAAITSNDLVLTGLDFSDSQGDKRIVEILTSFRANIQRQGEGLRIMGN 294

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G + ++++ +PD LAV+A A+G T ++ R KET+R+ + +
Sbjct: 295 APLQGG-----LTIDLSIDIPDALPALAVLATQAEGQTVFINLEHVRQKETDRVEEMTLK 348

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF---SLAACAEVPVTIRDPGC 427
L LG ++ D ++ P ++ + + DDHR+AMA LAA E+ VT D C
Sbjct: 349 LNALGCNLRMENDCLVVEGPTRIQSGIVSSDDHRIAMALVVAGLAAQGEIVVT--DAQC 406

Query: 428 TRKTFPDYFDVLS 440
+FP +F L+
Sbjct: 407 ADVSFPGFFSKLA 419

>ref|NP_561612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens str. 13]
sp|Q8XMJ2.1|AROA_CLOPE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB80402.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens str. 13]
Length = 424

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 130/437 (29%), Positives = 232/437 (53%), Gaps = 30/437 (6%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LRGSVKIPPSKMAHRAIICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + D E +G +R L ++
Sbjct: 61 ANIKVEKDKLIINGENILKDSNYKFIDCNE-----SGSTLRFLVPISLIKDNRVNFI 112

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLGRPLKTTY---EIFEEQEIKYSYEEENLDLNIIEGSLKGGEFVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y+++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLKDDSKIIITTELESKYIDLTLDMEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGTVTVEGCGTTSLQGDVKFAEVLEMMGAK-VTWT 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE MGA+ +
Sbjct: 226 K-PMNYKVEGDYSQAIFYFSAGAL-GSEINCLDLSSYQGDKECIEILEGMGARLIESQ 283

Query: 302 ETSVTVTGPPREPFPGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284 ERSLSII-----HGDNLGTIIDASQCPDIIPVLTVVAAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ AI TEL KLGA ++E D II + L + ++ DHR+AM+ ++A+ + V
Sbjct: 336 DRLNAICTELNKLGDADIKELKDGLIINGVKDLIGGEVYSHKDHRIAMSLAIASTRCKKEV 395

Query: 421 TIRDPGCTRKTFPDYFD 437
I++P C +K++P +++
Sbjct: 396 IIEKPCVKKSYPGFWE 412

>ref|ZP_06576756.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces
ghanaensis ATCC 14672]
gb|EFE67217.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2 [Streptomyces
ghanaensis ATCC 14672]
Length = 441

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 146/446 (32%), Positives = 219/446 (49%), Gaps = 36/446 (8%)

Query: 9 LQPIKEISG---TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M G LR LG
Sbjct: 13 LWPAPHASGAVDATVHVPGSKSVTNRALVLAALASEPGWLRRLRSRDTLLMAGGLRALG 72

Query: 65 LSVE-----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +E A R + G G V+ +GNAG MR L T A G
Sbjct: 73 VEIEEGVPGDGTGEAWRVLPGLHGPATVD-----VGNAGTVMRFLPPVATLADGP 123

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ DG PR ERP+ ++ L++LGA +D P+ V+G G L GG V + S
Sbjct: 124 VRF--DGDPRSRYERPLNGVIDALRRRLGARIDDD--DRGALPMTVHGGGALDGGTVSVSDASS 180

Query: 179 SSQYLSALLMAAPLALGDVEIEII--DKLISIPYVEMTLRLMERFGVKAHSDSW---DRF 234
SSQ++SALL++AP VE+ L S+P++ MT+ ++ G + + +S + +
Sbjct: 181 SSQFVSALLSAPRFNQGVFVRHTGSTLPSLPHIRMTVDMLRAVGAQVDTPESSGGEPNVW 240

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G ++ +E D S+A FLA A +TGG V V + Q + E+ M
Sbjct: 241 RVTPGALLG--RDLTIEPDLNAQPFLAAALVTGGKVVPDWPARTTQPGDRLREIFTEM 298

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVA 354
G TE + TG + IDV++ ++ ++ +A VA AD P+ +R VA
Sbjct: 299 GGSCELTEYGLVFTG-----SGSIHGIDVDLGEVGELTPGIAAVALADSPSTLRGVA 351

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R+ ET+R+ A+ E+ +LG V E D I P +L+ TY+DHRMA A ++
Sbjct: 352 HLRHETDRLAALTKEINELGGDVTETADGLHIR--PRRLHGGVFHTYEDHRMATAGAVIG 410

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFDVLS 440
A V I + T KT PD+ ++ +
Sbjct: 411 LAVEGVQIENVATTAKTLPDFPELWT 436

>ref|ZP_02635555.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens B str. ATCC 3626]
gb|EDT24150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
perfringens B str. ATCC 3626]
Length = 424

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 132/438 (30%), Positives = 232/438 (52%), Gaps = 32/438 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEVDHYMLGALRTL 64
+++++ P K + G+VK+P SKS+++R ++ A+LS+G +V+ N+ SED+ + +++LG
Sbjct: 2 KKVIITPSK-LKGSVKIPPSKMAHRAICASLSKGESVISNIDFSEDIIATMEGMKSLG 60

Query: 65 --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE DK + + V D E +G +R L ++
Sbjct: 61 ANIKVEKDCLIINGENILKDSNYKVIDCNE-----SGSTLRFLVPISLIKDNRVNFI 112

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ ++ + + + +N G L GG+ K+ G+ISSQ+
Sbjct: 113 --GRGNLGRPLKTTY---EIFEEQEVKYSYEEENLDLNIEGSLKGGEFKVKGNISSQF 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL PL D +I I +L S Y++TL ++E+FGV ++++ + F IKG Q Y
Sbjct: 167 ISGLLFTLPLLKEDSKIIITTELESKYIDLTLDMIEKFGVTIKNNN-YREFLIKGNQSY 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK-VTWT 301
K P N VEGD S A+++ + A+ G + +S QGD + E+LE M A +
Sbjct: 226 K-PMNYKVEGDYSQAAFYFSAGAL-GSEINCIDLDLSSYQGDKECIEILERSASLIKNQ 283

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E S+++ L ++ ++ PD+ L VVA + G T I + R+KE
Sbjct: 284 EESLSII-----HGDNLGTIIDASQCPDIIPVLTVAALSKGETRIINGERLRIKEC 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
+R+ AI TEL KLGA ++E D II ++L + ++ DHR+AM+ ++A+ C E
Sbjct: 336 DRLNAICTELNKLKADIKELKDGLIINGVKELIGGEVYSHKDHRIAMSLAIASTRCKE-E 394

Query: 420 VTIRDPGCTRKTFFPDYFD 437
V I +P C +K++P +++
Sbjct: 395 VIISEPDCVKKSYPGFWE 412

>ref|YP_003488703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces scabiei
87.22]
emb|CBG70146.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces scabiei
87.22]

Length = 443

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 148/451 (32%), Positives = 220/451 (48%), Gaps = 41/451 (9%)

Query: 9 LQPIKEISG----TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M GALR +G
Sbjct: 9 LWPAPHASGAVDATVHVPKSVTNRALVLAALASEPGWLRRLRSRDTLLMAGALRAMG 68

Query: 65 LSVE-----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT 113
+ +E A R + G G V+ +GNAG MR L
Sbjct: 69 VGIEETVSSSSSGAGSGEAWRVLP TGLHGPATVD-----VGNAGTVMRFLPPVAA 119

Query: 114 AAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK 173
A G + DG PR ERP+ ++ L+ LGA +D G P+ V+G G L GG V
Sbjct: 120 LADGPIRF--DGDPRSYPRLHGVLDALRALGARIDDD-GRGALPLTVHSGALDGGPVAA 176

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSW- 231
+ S SSQ++SALL++AP VE+ L S+P++ MT+ ++ G + + +S
Sbjct: 177 IDASSSSQFVSALLSAPRFNQGVVRHTGSTLPSLPHIRMTVDMLRSVGAQVDTPESSG 236

Query: 232 --DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAE 289
+ + + G ++ +E D S+A FLA A +TGG + + + Q + E
Sbjct: 237 EPNVWRVTPGALLG--RDLTIEPDLNAQPFLAAALVTGGKIVIPDWPARTTQPGDQLRE 294

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTA 349
+ MG TE + TG G H IDV++++ ++ +A VA AD P+
Sbjct: 295 IFTEMGGICELTEYGLVFTG----SGAVH--GIDVDLSEVGELTPGIAAVALADSPST 347

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
+R VA R+ ET+R+ A+ E+ +LG V E D I P L+ TYDDHRMA A
Sbjct: 348 LRGVAHLRLRHETDRLAALTKEINELGGDVTEADGLHIR-PRPLHGGVFHTYDDHRMATA 406

Query: 410 FSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
++ A V I + T KT PD+ D+ +
Sbjct: 407 GAIIGLAVEGVRIENVATTAKTLPDFPDLWT 437

>ref|YP_001512899.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkaliphilus
oremlandii OhILAs]
sp|A8MH16.1|AROAL_KOO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABW18903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkaliphilus
oremlandii OhILAs]
Length = 427

Score = 187 bits (476), Expect = 2e-45, Method: Compositional matrix adjust.
Identities = 147/447 (32%), Positives = 238/447 (53%), Gaps = 29/447 (6%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
+ V+ I+ ISG+VK+PG KS+S+R ++L ++S+GTT V ++L SEDV +G + LG+
Sbjct: 2 DFFVVKIEAISGSVKVPGDKSISHRSIILGSISKGTTYVRDILLSEDVQRTIGFFKKLGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
S+E ++ V+ G +ED + Q L +GN+G + R L ++ G YVL+
Sbjct: 62 SIE-----QKNKVIALKG-MAIEDFRPYTQELDMGNSGTSARLLGLIS--GSPHAYVLN 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G P +++RP+ + L+Q+GA ++ D P+++ G G L G KL + S+Q S
Sbjct: 114 GDPFLKRPMPKRVTKPLEQMGHIEYLEREDLLPIKIG-GNLRGIHYKLPVA-SAQIKS 171

Query: 185 ALLMAAPLALGDVEIEIIDLKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
AL++A G IE + + + + E+ +++ FG E ++ + IKG Q+ +
Sbjct: 172 ALILAGLHCSGKTVE--EPVATRDHTEI---MIQHFGGTVEKNNHF--IQIKGNQRLLA 224

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V GD SSA++ L +AI + +E G + + VLE MGA++ E
Sbjct: 225 -NEVLVPGDISAFLVLSAIVPKAELMIEDVGLNPTRSGI--LHVLESMEGARMEELEE 281

Query: 304 SVTVTGPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358

V V G +H LKA+ + + +P D LAV A A+G T IRD +V
Sbjct: 282 RV-VNGERVGNILIRHSCSLKAVTIEGDIPTLIDEIPILAVAATQAEGITVIRDAQELKV 340

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KE+ R+ + ++L K+GA++E D II P KL ID+ DHR+AMAF++A AE

Sbjct: 341 KESNRIDTVVSQQLKMGANIEASHDGMIIQGPTKLGATIDSEFDHRIAMAFVAGMVAE 400

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVK 444

I C +FP++ ++L K
Sbjct: 401 GETKILKSECIASVFPFETELKKISK 427

>ref|NP_347531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
acetobutylicum ATCC 824]
sp|Q97KM2.1|ARO_A_CLOAB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK78871.1|AE007605_4 5-enolpyruvylshikimate-3-phosphate synthase [Clostridium
acetobutylicum ATCC 824]
gb|ADZ19946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
acetobutylicum EA 2018]
Length = 428

Score = 187 bits (475), Expect = 3e-45, Method: Compositional matrix adjust.
Identities = 136/438 (31%), Positives = 223/438 (50%), Gaps = 41/438 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD--- 70
+ G +K+P SKSL +R ++ AALSE + ++N+ S+D+ + LG + D

Sbjct: 11 LKGDIKIPPSKSLGHRAIICAALSEESTIENISYSKDIKATCIGMSKLGALIIEDAKDN 70

Query: 71 ---KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
K K+ +V +KE+V + +G +R L N V DG

Sbjct: 71 STLKIKKQKLV-----SKEKVYIDCSESGSTVRFLIPISLIEERNV--VFDGQG 117

Query: 128 RMRERPIGDL--VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ RP+ + K++ P+++ G L G L G+ISSQ++S

Sbjct: 118 KLSYRPLDSYFNIFDEKEIAYS---HPEGKVLPLQIKG--RLKAGMFNLPGNISSQFISG 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ + P GD I I L S+ YV+MT+ ++++FG++ E+ ++ F+IKG QK K

Sbjct: 173 LMFSLPLFLEGDSIINITTNLESVGYVDMTIDMLKKFGIEIENK-AYKSFFIKGNQKCKGT 231

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
K VEGD S A+++L+ A I G + + +SLQGD ++L+ MG + E S

Sbjct: 232 KYK-VEGDFSQAAFWLS-AGILNGNINCKDLNLISSLQGDVKVILDILKKMGGAID--EKSF 287

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ H I ++ ++ PD+ L+VVA ++G T I + A R+KE++R+

Sbjct: 288 SSK-----KSTHTGIVIDASQCPDLVPILSVVAALSEGTTKIVNAARLRIKESDRLK 339

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRD 424
A+ TEL KLGA V E D +I EKL +++++DHR+AMA +AA E VTI

Sbjct: 340 AMATELNKLGAEEVVELEDGLLIEGKEKLKGGEVESWNDHRIAMALGIAALRCEESVTING 399

Query: 425 PGCTRKTFPDYFDVLSTF 442

C K++P ++ L
Sbjct: 400 SECVSKSYPQFWSDLKQL 417

>ref|ZP_08160034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus albus 8]
gb|EGC02053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus albus 8]
Length = 409

Score = 187 bits (474), Expect = 3e-45, Method: Compositional matrix adjust.
Identities = 146/428 (34%), Positives = 223/428 (52%), Gaps = 39/428 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72

K++SG V P SKS ++R+L+ AAL+EG +V+D L S D+ + A+R LG + +

Sbjct: 8 KKLSGEVTPPPSKSAHRMLIAAALAEGNSVIDRLYPSVDILTTVDAMRQLGAEITVE-- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132


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      +RAVV G      + A E+ +      +G +R L      A G AT++ G ++ ER
Sbjct: 66  GERAVVKG-----IVKAPEKAVIDCCESGSTLRFLIPVAAALGVEATFL--GRGKLPER 117

Query: 133  PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      PI +      + G + D + GT P + G L GG ++ G ISSQ+++ LL+A PL
Sbjct: 118  PITPYLQEFKPHGVEFD-YSGT--MPFTIKG--RLTGGVFEIDGGISSQFITGLLLAMPL 172

Query: 193  ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
      I++ KL S PYV+MT +ME GV+AE SDS F + GQKY+ P + VEG
Sbjct: 173  TKEGGAIKLTSKLESRPYVDMTRGVMEELGVRAEVSDSG--FEVAAGQKYQ-PFSGAVEG 229

Query: 253  DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      D S ++F A+ G V + G S QGD K E+ M + +
Sbjct: 230  DHSQGAFFEVADAL-GSKVEISGLNVNSFQGDKKIIEICREM----VYNKDGA----- 277

Query: 313  EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
      L+ +V+++ +PD+ LAV+A F DG + I A R+KE++R+ A+ L
Sbjct: 278  -----LRPFVVDSDIPDLVPILAVLASFCDGESRITGAARLRIKESDRLAAMEETLN 330

Query: 373  KLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
      LG V D II + L + ++DHR+AMA ++AA E P+ I C RK
Sbjct: 331  ALGGDVTATEDSLIIRGRDTLAGGVTVSAHNDHRIAMAMAIATRCEKPIIIEGAECVRK 390

Query: 431  TFPDYFDV 438
      ++PD+++V
Sbjct: 391  SYPDFWEV 398

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>ref|YP_003196823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Robiginitalea
      biformata HTCC2501]
gb|EAR14361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Robiginitalea
      biformata HTCC2501]
      Length = 409

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Score = 187 bits (474), Expect = 4e-45, Method: Compositional matrix adjust.
Identities = 141/436 (32%), Positives = 210/436 (48%), Gaps = 50/436 (11%)

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Query: 13  KEISGTVKLPKSKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      + + + + GSKS SNR+LLL AL G + NL NS+D M GL+ AD
Sbjct: 11  QRLQQDITITGSKSESNRLLLRALYPGIEI-RNLSNSDDARVMQN-----GLASGADTV 64

Query: 73  AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGVPVRMRER 132
      + +AG AMR LTA + G L G RM+ER
Sbjct: 65  D-----IHHAGTAMRFLTAYFASREGREV-TLTGSQRMKER 99

Query: 133  PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      PI LV L+ LGA++D CPP+R+ G L +V L +SSQY+SALL+ AP
Sbjct: 100  PIEILVEALRDLGAEIDYLENPGCPPLRIRG-KRLEKSEVTLPADVSSQYISALLLIAPS 158

Query: 193  ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-AYVE 251
      + + + + S+PY+ MTL L++R GVK E D I+ P++ VE
Sbjct: 159  LPNGLTLHLEGTITVSPYIRMTLGLLDRLGVKTEFRDQ----TIRVEHAASLPESICTVE 214

Query: 252  GDASSASYFLAGAAI--TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT- 308
      D SSASYF + A+ TG + + SLQGD E+ +G + + + + +T
Sbjct: 215  SDWSSASYFYSLVALSPTGSGIQLRSFRGDSLQGDVLPFIFGQLGVESHFEDDRLEITR 274

Query: 309  -GPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
      G P F R ++ + PD+A TLA + + + ++KET+R+VA+
Sbjct: 275  SGDPDSDFFR-----CDLIRSPDLAQTLAACCFLGIGGICELTGLHTLTKIKETDRLVAL 327

Query: 368  RTELTKLKASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
      EL KLGA + + P ++ + I TY+DHRMAMAF+ + + I D G
Sbjct: 328  ENELKKLGAEIRVTDKSLHLEPSRRIVAMQRIPTYNDHRMAMAFAPLGL-KTDLVIEDAG 386

Query: 427  CTRKTFPDYFDVLSTF 442
      K++PD+++ L
Sbjct: 387  VVSKSYPDFWEDLEAL 402

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>ref|ZP_01119134.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polaribacter irgensii

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23-P]
gb|EAR11801.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Polaribacter irgensii
23-P]
Length = 409

Score = 187 bits (474), Expect = 4e-45, Method: Compositional matrix adjust.
Identities = 133/429 (31%), Positives = 224/429 (52%), Gaps = 46/429 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ + + GSKS SNR+L+L L T+ DNL +S+D +M AL + +++
Sbjct: 11 QKINEEITISGSKSESNRLLILQNLFSSEITI-DNLSDDDAVHMQHALSSNTETID---- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+G+AG AMR LT+ G VL G RM+ R
Sbjct: 66 -----IGHAGTAMRFLTSTYFAVKSGREV-VLTGSERMQNR 99

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV LK LGA++ PP+R+ G + V+++G++SSQY+S+LL+ A
Sbjct: 100 PIEILVNALKDLGAEISYEEKVGYPPIRIKG-KKVTKETVQINGNVSSQYISSLLLIAAK 158

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+EIE++ ++ SIPY++MTL L+ + G++A + + K K + VE
Sbjct: 159 LEKGLEIELLGEITSIPYIQMTLSLLNQLGIEASFVGNKIKVLSK--KIIKKQTVIVES 215

Query: 253 DASSASYF--LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSASYF + ++ G ++ + SLQGD AE+ G + + + +
Sbjct: 216 DWSSASYFYFISVASSEIGTSIQLSAYKKESLQGDSCLAIEIYTHFGVTTVFGQNFIL-- 272

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTA-IRDVASWRVKETERMVAIRT 369
+E R L+ +++++ PD+A T+AV FA+G + + + + ++KET+R+ A++
Sbjct: 273 KKEQKSR--LETLEIDLKNAPDIAQTIAVTC-FAEGISCNLSGLHTLKIKETDRLEALKD 329

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
ELTKLGA +E + ++ AI TY+DHRMAMAF+ A +VP+ I +
Sbjct: 330 ELTKLGAVIEVTNKSLLHGRSFDMHANIAIKTYNDHRMAMAFAPLAL-KVPIKILNAEVV 388

Query: 429 RKTFFPDYFD 437
K++ +++
Sbjct: 389 TKSYQKFWE 397

>ref|ZP_07289137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. C]
gb|EFL17506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. C]
Length = 448

Score = 187 bits (474), Expect = 4e-45, Method: Compositional matrix adjust.
Identities = 153/442 (34%), Positives = 221/442 (50%), Gaps = 46/442 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---- 68
+ + TV +PGSKS++NR L+LAAL+ V L S D M ALR LG+ +E
Sbjct: 18 QAVHATVTVPGSKSVTNRALVLAALAAEPGWRRPLRSRDSQLMSDALRALGVGIEETVS 77

Query: 69 -----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
A R + G V+ +GNAG MR L T A G+ +
Sbjct: 78 SSSADGDSGEAWRIIPAALHGPATVD-----VGNAGTVMRFLPPVATLADGDIRF- 127

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
DG PR ERP+G ++ L+ LGA +D G P+ V G G L GG V++ S SSQ+
Sbjct: 128 -DGDPRSRYERPLGQVITALRALGARIDDD-GRGALPMTVQGGGALEGGTVEIDASNSQF 185

Query: 183 LSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+SALL++AP VE+ + KL S+P++ MT+ ++ G + + ++ GG+K
Sbjct: 186 VSALLLSAPRFNQGVVHRVGGKLPSPHIRTVDMLRAAGAQVDTPEA-----GGEK 238

Query: 242 ---YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+P ++ VE D S+A F+A A ITGGTVTV + Q E+
Sbjct: 239 DVWRVAPGALLGRDMVVEPDLSNAQPFMAAALITGGTVTVDPWPLRTQPGDALREIFTA 298

Query: 294 MGAKVTWTETSVTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
MG TE + TG G+ H IDV++++ ++ +A VA AD + +R V
Sbjct: 299 MGGSCELTEAGLVFTG-----TGKIH--GIDVDLSEVGELTPGIAAVALADSESVLRGV 351

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLA 413
A R+ ET+R+ A+ E+ LG V E D I P KL+ TYDDHRMA A ++
Sbjct: 352 AHLRLHETDRLAALTAETINGLGGDVTEDEDGLRIR-PRKLHGGVFHTYDDHRMATAGAVI 410

Query: 414 ACAEVPVTIRDPGCTRKTFPDY 435
A V I + T KT PD+
Sbjct: 411 GLAVPGVEIENVATTAKTLPDF 432

>ref|ZP_05004205.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
clavuligerus ATCC 27064]
ref|ZP_06773553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
clavuligerus ATCC 27064]
gb|EDY48504.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
clavuligerus ATCC 27064]
gb|EFG09152.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
clavuligerus ATCC 27064]
Length = 440

Score = 186 bits (473), Expect = 4e-45, Method: Compositional matrix adjust.
Identities = 148/444 (33%), Positives = 224/444 (50%), Gaps = 42/444 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----- 68
+ TV +PGSKS++NR L+LAAL+ + L S D M ALR LG+ +E
Sbjct: 20 VDATVTVPGSKSVTNRALVLAALAAEPGWLRRLPLRSRDTLLMAQALRALGVGIEEGVGP 79

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + R + G G V+ +GNAG MR L T A G + DG PR
Sbjct: 80 GEGESWRVIPAGLHGPAITVD-----VGNAGTVMRFLPPVATLADGPVRF--DGDPR 128

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
ERP+ ++ L+ LGA +D G P+ V+G G L GG+V++ S SSQ++SALL+
Sbjct: 129 SHERPLHGVIDALRALGARIDDE-GRGALPLTVHSGALDGRVEIDASSSSQFVSALLL 187

Query: 189 AAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK---YKS 244
+ P VE+ I +L S+P++ MT+ ++ G + + ++ GG+ S
Sbjct: 188 SGPRFNQGVQEVHRHIGARLPSMPHIRMVTDMLRAVGAQVDEPET-----GGEPNVWRVS 240

Query: 245 P-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
P ++ +E D S+A FLA A +TGG VTV T+ Q + MG
Sbjct: 241 PSAVLGRDITIEPDLNAQPFLAAALVTGGRVTVDPWFPTTTQPGDALRTIFTGMGGSCE 300

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
T+ +T TG R ++ IDV++++ ++ +A VA AD P+ +R VA R+
Sbjct: 301 LTDRGLTFTGSGR-----VRGIDVDLSEVGELTPGIAAVALADSPSTLRGVHLRLH 353

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP 419
ET+R+ A+ E+ LG V E D I P L+ TYDDHRMA A ++ A
Sbjct: 354 ETDRLAALTKIENNLGGDVTEDEDGLHIR-PRPLHGGVFHTYDDHRMATAGAIIGLAVEG 412

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
V I + T KT PD+ + +T +
Sbjct: 413 VEIENVATTAKTLPDFPRMWTML 436

>ref|ZP_06823528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SPB74]
gb|EDY44204.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SPB74]
Length = 446

Score = 186 bits (473), Expect = 4e-45, Method: Compositional matrix adjust.
Identities = 142/437 (32%), Positives = 228/437 (52%), Gaps = 19/437 (4%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV++PGSKS++NR L+LAAL+ + L S D M ALRT+G+ +E +++
Sbjct: 23 VRATVRVPGSKSITNRALVLAALAAEPGWLRRLPLRSRDTLLMASALRTMGVGIEETVSSE 82

Query: 75 RAVVVCGCGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ G G + V A + + +GNAG MR L T A G + DG PR ER

Sbjct: 83 SCGLAGAGEAWRVIPAGLRGPATVDVGNAGTVMRFLPPVATLAEGAIRF--DGDPRSYER 140

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L+ LGA +D P+ V G G L GGKV++ S SSQ++SALL++AP

Sbjct: 141 PLHGVIDSLRALGARIDG-DRGALPLTVFGSGALDGGKVEVDASSSSQFISALLSAPS 199

Query: 193 ALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKSPKNA 248
VE+ L S+P++ MT+ ++ G + + ++ + + + G ++

Sbjct: 200 FNQGVELRHTGATLPSLPHIRMTVDMLRAVGAQVDEPETGGEPNVWRVTPGALLG--RDL 257

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A FLA A +TGGTVT+ + Q + E+ MG TE + ++

Sbjct: 258 TIEPDLNAQPFLLAALVTGGTVTIPDWPARTQPGDRLREIFTEMGGACELTEAGLALS 317

Query: 309 GPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G R ++ +DV++ ++ ++ +A VA AD P+ +R VA R+ ET+R+ A+

Sbjct: 318 GTGR-----VRGVDVLDGEVGLTPGIAAVALADSPSTLRGVAHLRLHETDRLAALT 370

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
E+ +LG V E D I P L+ TY+DHRMA A ++ A V I + T

Sbjct: 371 KEINELGGDVTEADGLHIR-PRPLHGGVFHTYEDHRMATAGAILGLAVPGVEIENVATT 429

Query: 429 RKTFFPDYFDVLSTFVK 445
KT PD+ ++ + + N

Sbjct: 430 AKTLPDFELWTGMLGN 446

>ref|ZP_07280355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. AA4]
gb|EFL08724.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. AA4]
Length = 431

Score = 186 bits (473), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 154/432 (35%), Positives = 227/432 (52%), Gaps = 23/432 (5%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ V++PGSKS++NR +LAAL+ T V + L+S D ML AL +LG E

Sbjct: 21 LDAAVRVPKSKSITNRAYVLAALAGAPTRVRHPLDSRDTRLMLAALASLGALSEETIDGF 80

Query: 75 RAVVVGK-GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+G GG+ +E + LGNAG R A T G A+ + DG +R RP

Sbjct: 81 LVHPLGTIGGR-----GDETTVALGNAGTVARFTPALATL--GEASVLFDGDEAIRRRP 132

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG L+ L++LGA +D G D PP V+G GGL GG+V L S SSQ+LSALL+A P

Sbjct: 133 IGPLLAALRKLGARIDG-GRDAPPFTVHSGGLRGGRVDLDSSASSQFLSALLLAGPAF 191

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V + ++ S P++ MTL ++ RFG E S F+++ K P+ VE

Sbjct: 192 ERGVTVRLVGGAPPSEPHIAMTLDMLRRFGATVERS GP--EFHVEP-AKLSCEPY-VVEP 247

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A+ F+A A + GGTV V G + Q ++ +GAK T + + VTG

Sbjct: 248 DLSTAAPFVAAAVVGGGTVRVHGWPKQTTQPGDWLRLGLVAELGAKATLDDDGLVVTGGGA 307

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
P ID+++++ ++ +A + FA+GP++I VA R ET+R+ A+ TEL+

Sbjct: 308 FP-----GIDLDLHEVGELTPVIAAMLCFAEGPSSITGVAHLRGHETDRLTALATELS 360

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432
LGA V E D IT P ++ TY+DHR+ MA ++ V + +P KTF

Sbjct: 361 GLGARVTELEDGLEIT-PAPMHGGVFRTYEDHRLVMAAAVLGLRVPGVLVENPETVGKTF 419

Query: 433 PDYFDVLSTFVK 444
P + + S V

Sbjct: 420 PKFVETWSDAVS 431

>ref|YP_003781065.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
ljungdahlii DSM 13528]
gb|ADK15963.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
ljungdahlii DSM 13528]

Length = 426

Score = 186 bits (473), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 131/431 (30%), Positives = 221/431 (51%), Gaps = 26/431 (6%)

```
Query: 7   IVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
          + ++P K + G +++P SKS+ +R L+ +AL++G + + N+ SED+ AL LG+
Sbjct: 4   VSIKPTK-LKGQIQVPPSKSVCHRALICSALAQGESNIKNVDFSEDIEATCSALEALGVD 62

Query: 67  VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
          ++ DK + G + + F +G +R L G T+ G
Sbjct: 63  IKRDKHT-----LNVGTGNSVIRMKNSNIHCF--KSGSTIRFLIPIAATLGEKVTF--GE 113

Query: 127  PRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
          ++ ERP+ + F G P+ +NG L G+ ++ G+ISSQ++S L
Sbjct: 114  DKLIERPLDVYIDFKQKIFYRNFQGK--LPLTING--KLKPGEYRVKGNISSQFISGL 169

Query: 187  LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
          L A PL GD +I + +L S YV++TL ++ERFGV + D + F I G Q YK
Sbjct: 170  LFALPLLDGDSKIVVTTELESKSYVDITLDMLERFGVYVDKKD-YREFLINGKQTYKK-N 227

Query: 247  NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVT 306
          N +EGD S A++++ A+ G + SLQGD +L+ MG ++ E T
Sbjct: 228  NCSIEGDFSQAFAFWMTAGALGDGII-CSSLNMNSLQGDKAVIRILKDMGVEIE--EKGDT 284

Query: 307  VTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
          + P E G ++ ++ PD+ LA +A + G T I + A R+KE++R+ A
Sbjct: 285  LKVNPSETHGTY-----IDASQCPDLVPVLAALASVSSGTEITNAARLRIKESDRLKA 338

Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV-PVTIRDP 425
          I TEL K+GA V+E D II E+L + ++ DHR+AMA ++ + V P+ +++
Sbjct: 339  ISTEELNKIGADVKEREDGLIINGKERKGGKVTSWRDHRIAMALAVVSSKCVNPMIMKEA 398

Query: 426  GCTRKTFPDYF 436
          +K++P ++
Sbjct: 399  EYVKKSYPGFW 409
```

```
>ref|YP_003480512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natrialba magadii
ATCC 43099]
gb|ADD05950.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natrialba magadii
ATCC 43099]
Length = 432
```

Score = 186 bits (473), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 154/450 (34%), Positives = 224/450 (49%), Gaps = 49/450 (10%)

```
Query: 7   IVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
          + + P + ++GT + P SKS ++R +L A +E TTV D L +++
Sbjct: 6   VTITPSR-VAGTARAPPSKSYTHRAILAAGYAEQTTVRDALWSADT----- 50

Query: 67  VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLG-----NAGIAMRSLTAAVTA 114
          +A RAV + GG +D+ E++ F G N+G MR +TAA
Sbjct: 51  ----QATARAVDL-FGGNVERQDSTLEIEGFSGRPGVPADVIDCDNSGTTMRLVTAAAAAL 105

Query: 115  AGGNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
          A G T VL G +R RP G L+ + LG + G P+ V G L GG V +
Sbjct: 106  ADG--TSVLTGDESLRSRPQGPLLEAVADLGGEALSTRNGQAPLVVTGP--LSGGTVSI 161

Query: 175  SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
          G +SSQY++ALLMA + + IE+ L S PYV++TL ++E FGV+A +D+ F
Sbjct: 162  PGDVSSQYITALLMAGAVTDEGLVIELETALKSAPYVDITLEVLEAFGVEARKTDTG--F 219

Query: 235  YIKGGQKYKSPKNAY-VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLE 292
          ++GGQ Y Y V GD SS SY L AGA G V +EG S QGD ++++
Sbjct: 220  SVEGGQTYDPADGEYAVPGDFSSISYPLAAGAIAGDGGVRIEGA-HPSAQGDTAIVDIVD 278

Query: 293  MMGAKVWTETSVTGTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRD 352
          MGA V W + T+ K L+ I+V++ PD+ T+A + ADG T I +
Sbjct: 279  RMGATVDWDRSGGTI-----DVQAKTLEGIEVSVEDTPDLLPTIATLGAVADGDTHITN 332
```

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK-LNVTAIDTYDDHRMAMAFS 411
R KET+R+ A+ EL KLG E D + E L ++ DHR+ MA +
Sbjct: 333 AEHVRYKETDRVSAMAEELGKLGVEETEEQDSLTVHGDESVELEGATVEGRGDHRIIMALA 392

Query: 412 LAA-CAEVPVTIRDPGCTRKTFPDYFDVLS 440
LA AE TIR +FP +F++L+
Sbjct: 393 LAGLVAEGETTIRGAEHVDVSFPGFEMLA 422

>ref|ZP_01733382.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium BAL38]
gb|EAZ96451.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium BAL38]
Length = 422

Score = 186 bits (473), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 136/432 (31%), Positives = 215/432 (49%), Gaps = 40/432 (9%)

Query: 17 GTVKLPGSKSLNRILLALAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
++K+ GSKS +NR+LLL AL V++N NS+D ML AL
Sbjct: 14 ASIKITGSKSETNRLLLQALYPNL-VLENTSNSDDSETMLKAL----- 56

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGN-----ATYVLDGVPRMRE 131
+P K + + +AG AMR LTA A VL G RM++
Sbjct: 57 ----TNTHYSPITK---TIDVHHAGTAMRFLTAFFAIQERKDLSDLAEVVLTGSERMKQ 109

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI LV L QLGA++ PP+R+ G L KV L ++SSQY+SALL+ AP
Sbjct: 110 RPIKILVDALNQLGAIEISYEENEGFPPLRIK-GKLTESKVS LPA NVSSQYISALLLIAP 168

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+E+ + ++ SIPY++MTL L+ GV+ + + +K + + K VE
Sbjct: 169 KLENGLELTLEGEITSIPYIKMTLALLNEIGVETSFEN--NLITVKSSEVEINSKLITVE 226

Query: 252 GDASSASYFLAGAAIT--GGT VTVEGCGTTS LQGDVKFAEVLEMMGAKVTW-TETSVTVT 308
D SSASY+ A++ G +++ SLQGD E+ + G + + ++ S+T++
Sbjct: 227 SDWSSASYWFSIVALSEIGTQISLSSYKQNSLQGDSALIEIYKDFGVETVFNSDNSITIS 286

Query: 309 GPPREPFRGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
++ L + +N PD+A T+ V + + + ++KET+R+ A++
Sbjct: 287 ---KKQVHNSQLATCNSQLNNCPDIAQTIVVTCFGLGIGCDLFLGLHTLKIKETDRLEALK 343

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
EL KLG A + + + P +N I TY DHRMAMAF+ A +VP+ I D
Sbjct: 344 VELIKLGADISVTNLSLHNP SAIINKDIVIKTYQDHRMAMAFAPLAL-KVPIIIDAEV 402

Query: 428 TRKTFPDYFDVL 439
K++P +++ L
Sbjct: 403 VSKSYPTFWEDL 414

>gb|AAS77246.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
bacterium]
Length = 272

Score = 186 bits (473), Expect = 5e-45, Method: Compositional matrix adjust.
Identities = 118/272 (43%), Positives = 166/272 (61%), Gaps = 12/272 (4%)

Query: 169 GGVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD 228
GG+ L S+SSQ++SALLM APL +++ ++ + P+++MTL LM+R+G ++
Sbjct: 10 GGETTLDASLSSQFVSALLMPAPLWPRGLKLN VVG D-TARPFIDMTLTLMDRWGATSDVK 68

Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFA 288
+ + GGQ+Y++ + VE DAS ASYF A AA+ GGTVT+ S+QGD+
Sbjct: 69 G--NVIVVPPGGQRYRA-IDFMVEPDASGASYFAAAAALIGT VTTLARLNAGSVQGD LGLL 125

Query: 289 EVLEMMGAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNMPDVMATLAVVALFADGPT 348
VLE MGA+ W S+ V G R L +DV+MN MPD+ TLA +A FA PT
Sbjct: 126 RVLERMGARTQWNRDSIEVIGTGR-----LAGVDVDMNAMPDMVPTLAAIAPFASSPT 178

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM 408

IR+VA R E++R+ A+ TEL +LGA+V E D I P L I+TYDDHR+AM
Sbjct: 179 RIRNVAFIRHHESDRLRALATELRLRGATVNEFEDGLGIE-PSVLKPATIETYDDHRIAM 237

Query: 409 AFSLAACAEVPTIRDPGCTRKTFPDYFDVLS 440
AFS+ V I++PGC KT+P +FD L+

Sbjct: 238 AFSVVGLKLAGVRIKNPGCVSKTYPGFFDDLA 269

>ref|YP_003327067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylanimonas
cellulosilytica DSM 15894]
gb|ACZ31509.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylanimonas
cellulosilytica DSM 15894]
Length = 444

Score = 186 bits (472), Expect = 6e-45, Method: Compositional matrix adjust.
Identities = 152/434 (35%), Positives = 226/434 (52%), Gaps = 34/434 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ +V++PGSKSL+NR+L+LAAL++G V+ L S D M+GALR+LG+ + E D +

Sbjct: 24 LDASVEIPGSKSLTNRLVLAAALADGPGVLRGALRSRDADLMIGALRSLGVRIEEGDAPS 83

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G P+ +V + G AG MR L A G + DG P R RP

Sbjct: 84 TLHVTPG-----PL---TGDVDIDCGLAGTVMRFLPPVAALAAGPVRF--DGDPHARVRP 133

Query: 134 IGDLVVGLKQLGADVDCF-----LGTDCPPVR----VNGIGGLPGGKVKLSGSISSQY 182
+ ++ L LG ++ G PP V G GGL GG+V + S SSQ+

Sbjct: 134 MRPVLAALAAALGVEITRTDDAGPDDAGRAGPPSHLPFTVGGRGGLRGQVVDASASSQF 193

Query: 183 LSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+S LL+AA + + I L S+P++EMT+ + GV + DS D ++

Sbjct: 194 VSGLLLAAARFDEGLSLRHIGTTLPSVPHIEMTVATLREVGVVVD--DSRDGIWVVEPGP 251

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ ++ VE D S+A+ FLA A + GG+V+V G TT+ Q +LE MG + +

Sbjct: 252 IAA-RDVRVEPDLNSNAAPFLAAALVAGGSVSVPGWPTTTTQPGALVPGLLERMGGTASLS 310

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ +TVT G + IDV+++ ++A T A +A AD P+ +R +A R ET

Sbjct: 311 DGVLTVT-----GDGTIHGIDVDLHAAGELAPTFAALAAALADSPSRLRGIAHLRGHET 363

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
+R+ A+ TE+T+LG EE D +IT P L+ TY DHRMA + +L A A V

Sbjct: 364 DRLAALATEITRLGGQAEETRDGLVIT-PRPLHGGLWHTYADHRMATSGALLALATPDVL 422

Query: 422 IRDPGCTRKTFPDY 435
+ D T KT PD+

Sbjct: 423 VEDVETAKTLPDF 436

>ref|YP_001394188.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium kluyveri
DSM 555]
ref|YP_002471169.1| hypothetical protein CKR_0704 [Clostridium kluyveri NBRC 12016]
sp|A5N6A9.1|ARO_A_CLOK5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B9DZT0.1|ARO_A_CLOK1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EDK32840.1| AroA [Clostridium kluyveri DSM 555]
dbj|BAH05755.1| hypothetical protein [Clostridium kluyveri NBRC 12016]
Length = 426

Score = 186 bits (472), Expect = 7e-45, Method: Compositional matrix adjust.
Identities = 137/433 (31%), Positives = 223/433 (51%), Gaps = 28/433 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+ + P K + G VK+P SKS+ +R L+ A+LS G + + N+ SED+ AL++LG+

Sbjct: 4 VSINPTK-LEGQVKIPPSKSVCHRALICASLSSGVSNTITNVDFSEIEATCEALKSLGVI 62

Query: 67 VEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126

Sbjct: 63 +E + + G + K V F +G +R L G T+ +G
IEKGNS-----LSIKGNSLVKKNVHCF--QSGSTLRFLLIPLAATLGEEITFTGEG- 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
++ ERP+ K G P+ +NG L G ++ G +SSQ+++ L

Sbjct: 115 -KLVERPLNVYIDIFKSQKIYKTESGK--LPLTING--KLKSGDYRVRGDVSSQFVTGL 169

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L A PL GD +IEI +L S YV++T+ ++ +FGV + S S+ F IKG Q YK

Sbjct: 170 LFALPLLSGDSKIEITTELESKSYVDITIDMLGKFGVCVDGS-SYREFIIKGNQTYKEV- 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +EGD S +++L A+ G +T G T SLQGD +L+ MG ++ E +

Sbjct: 228 DCNIEGDFSQVAFWLVMGALGKG-ITCMGLDTSLQGDRIIVHILKDMGVEIEEKENECIE 286

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V P + G + +++++ PD+ LA +A + G T I + A R+KE++R+ A

Sbjct: 287 VN--PSKTTG-----VVIDVSQCPLVPVLAALASVSHGTTEIINAARLRKESDRLKA 338

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
I +EL K+GA V E D II E L + ++ DHR+AMA + + C E P+ I

Sbjct: 339 ITSELNKGAEVIEKEDSLIIHGKLNKGGNVTSWKDHRIAMALAAVSSKCTE-PLVIEG 397

Query: 425 PGCTRKTFFPDYFD 437
C +K++P +++

Sbjct: 398 AECVKKSYPGFWE 410

>ref|ZP_07385752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus
curdolanolyticus YK9]
gb|EFM12900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus
curdolanolyticus YK9]
Length = 430

Score = 186 bits (471), Expect = 8e-45, Method: Compositional matrix adjust.
Identities = 148/440 (33%), Positives = 231/440 (52%), Gaps = 22/440 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++ P + G ++ SK+ + R LL+AAL+EGT+ + +SED M +R LG

Sbjct: 2 DVIVTPTPRLQDIALSSKNYTTRYLLVAALAEGTSTIYYPAHSESDAMRRRCIRDLAGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE D+ ++ + G G + D KE L +GNAG +R L A + + T+V

Sbjct: 62 VVEEDE--EKITITGFGR--PSDVKE---LNVGNAGAVLRFLMA-IASLSPEVTFVNTY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+V L+QLGA ++ G P+ + G G L GGK+ +SG+ISSQ+LSA

Sbjct: 114 PDSLGRPHDDLIVSLEQLGASIEHNEGK--LPITIRG-GQLKGGKITVSGNISSQFLSA 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL P+ D EIE++ L S + TL ++E+ G+ S+ + I G QKY++

Sbjct: 171 LLFLTPMLEEDSEIEVLHDLKSKIVIGQTLVIEQAGIVIHASEDLMHYRIPGRQKYEA- 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
K V+GD ++ LA AA+T VT+ G S QG+ +VL MM +T V

Sbjct: 230 KTYRVQGDYPGSAAVLAAAATVSDVTLRGLEEKSKQGERAIVDVLMMNVPLTHDNAV 289

Query: 306 TVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G + LKA++ + + D + + A+FA+G + +V + R KE +R+

Sbjct: 290 RVQGNGK-----LKALEFDGDVATDAVLAMVAAVFAEGTSRFYNVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
EL K GA+VEE I+ PE + ID + DHR+ MA ++ ++ P+ I

Sbjct: 343 DYLNELRKAGANVEERQSEIIVHGRPEGVEGGVEIDAHYDHRVIMALTVVGLRSKQPIRI 402

Query: 423 RDPGCTRKTFFPDYFDVLSTF 442
RD K++P YFD L

Sbjct: 403 RDAHHVAKSYPIYFDHLKAL 422

>ref|YP_004160822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides

helcogenes P 36-108]
gb|ADV43236.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides
helcogenes P 36-108]
Length = 422

Score = 186 bits (471), Expect = 8e-45, Method: Compositional matrix adjust.
Identities = 146/441 (33%), Positives = 214/441 (48%), Gaps = 63/441 (14%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
++LP SKS+SNR L+L AL+ G NL + +D M+ AL
Sbjct: 15 IQLPASKSISNRALILHALAHGNITPCNLSDCDDTRVMIRAL----- 56

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
E + + AG AMR LTA + G T V+ G RMR+RPI LV
Sbjct: 57 -----NGNPEHIDILA--AGTAMRFLTAYFSVIPG--TRVITGTERMQRPIHILV 103

Query: 139 VGLKQLGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L++LGA ++ PP+R+ G L G ++ L+G++SSQY+SALLM + +
Sbjct: 104 DALRKLGAQIEYEGNEGFPLRITGTE-LRGEISLAGNVSSQYISALLMTGAILPKGLH 162

Query: 199 IEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + +IS PY+ +TL+LM FG KA+ +S + + G P VE D S+AS
Sbjct: 163 LHLTGNIIISRPYINLTQLMRDFGAKAD-WNSSENSITVSPGGYQDVPFT--VESDWSAAS 219

Query: 259 YFLAGAAITGG-----TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
Y+ A++G TV + G S QGD + AE+ +G + V
Sbjct: 220 YWYQTVALSNGRHMNAGSAEISSPTVDLLGLFPHSHQGDSTRGAEIFSRLGVHTEYIGHGV 279

Query: 306 --TVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
T TG P E HL +M +PD+A T AV + P + S ++KET+R
Sbjct: 280 RLQTGTGPVE----HLTE---DMVDIPDLAQTFAVTCCLMNIPFRFTGLQSLKIKETDR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVP- 419
+ A+ TEL KLG V D + ++ A I TY+DHRMAMAF+ AC +P
Sbjct: 332 INALITELHKLGYIVRSEQDSILSWNGDRCPAEAAPTISTYEDHRMAMAF+PACFMLPR 390

Query: 420 VTIRDPGCTRKTFPDYFDVLS 440
+ I +P K++P Y++ L
Sbjct: 391 LKIDEPQVVSXSYPAYWEDLQ 411

>ref|ZP_01252676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychroflexus torquis
ATCC 700755]
gb|EAS72545.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychroflexus torquis
ATCC 700755]
Length = 409

Score = 186 bits (471), Expect = 8e-45, Method: Compositional matrix adjust.
Identities = 137/423 (32%), Positives = 223/423 (52%), Gaps = 43/423 (10%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ + GSKS+SNR L+L A + L + +D + AL TL
Sbjct: 15 LHITGSKSISNRYLILKAQFPNIEL-SGLSDCDDTRVLHKALTTL----- 58

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
++ +E+ + +AG AMR LTA +++ N VL G RM ERPIG LV
Sbjct: 59 -----KEKGDEIDIH--HAGTAMRFLTAYLSSLP-NLEVVLKSGKRMHERPIGILV 106

Query: 139 VGLKQLGADVDCFLGTD-CPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
+++LG + +LG++ PP++++G L K+ + S+SSQY++AL++ AP +
Sbjct: 107 EAMRELGGHIK-YLGSEGFPLKIHG-KSLQKDKISIPASVSSQYITALLIAPSFKNGL 164

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYK-SPKNAYVEGDASS 256
I + K+ S PY+ MT ++ GV+ + +S +I+ K K PK VE D SS
Sbjct: 165 TIYLSQSVTSKPYLMMTAASLKSIGVEVDLQES----HIQVHPKTKIEPKTIAVESDWSS 220

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFP 315
ASYF + A+ G + SLQGD K AE ++ G + + S+ ++
Sbjct: 221 ASYFYSCLALMDQGEFELSTFQKNSLQGDVKFAEFYKLFGIETRFKGDSSILISKAGVLL 280

Query: 316 GRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375

K I++++N PD+A T+AV L + + + +VKET+R+VA++TE+ K G
Sbjct: 281 PEK----IELDLNDTPDLAQTIAVTCLGLNIACNLTLGLHTLKVKETDRLVALKTEIEKFG 336

Query: 376 ASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
A VE + ++P L + ++ TY DHRMAMAF+ A +V +TI +P K+FPD

Sbjct: 337 AVEEISNESLQLSPKANLKESVSVQTYQDHRMAMAFAPLAI-KVDLTILNPEVVSFSFPD 395

Query: 435 YFD 437

+++

Sbjct: 396 FWE 398

>ref|YP_009687.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
vulgaris str. Hildenborough]
gb|AAS94946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
vulgaris str. Hildenborough]
gb|ADP85595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
vulgaris RCH1]
Length = 439

Score = 186 bits (471), Expect = 9e-45, Method: Compositional matrix adjust.
Identities = 157/448 (35%), Positives = 226/448 (50%), Gaps = 48/448 (10%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V P SKSLS+R L+ AAL+ G + V+++L S D+ LR G +E +A +V

Sbjct: 6 VTAPPSKSLSHRALIGAALAAGESTVEHVLESRLDTCADILRAAGAHIE-RRAPGSYLV 64

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G G P + V + +G R LTA + A G + + G PRM ERPIG+L

Sbjct: 65 RGVAGT-PAGGFAPVSCDVHESGTTCRLLTAVLAA--GMGRFRIHGAPRMHERPIGELT 121

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG + PP+ ++ G+ GG+V + SSQYLS LL+AAPL G +

Sbjct: 122 DALASLGVQIAFEARAGFPPLVIDA-AGMRGGEVSGIMDESSQYLSGLLLAAPLTQG-MT 179

Query: 199 IEIIDK-LISIPYVEMTLRLMERFGVK--AEHSDSWD-----RFYI 236
+ + K ++S PYV +TL+ +E FG+ E D+ D RF +

Sbjct: 180 VNVAGKSVVSWPYVGLTLQTLDFGIDFTVETRDVAPWGAVDWRSLHEAVPGLVRFVRV 239

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+ G Y++ + VEGD S ASYFLA A+ V VEG SLQGD ++L MGA

Sbjct: 240 RPGM-YRA-GSYRVEGDWSGASYFLAAGAVGPRPVRVEGLRVDLSLQGDRLDILTAMGA 297

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPATAIRDVASW 356
+ E V V P L ++V+M PD+ T+A VA FA G T +R+VA

Sbjct: 298 DIRPGEHGVVHPAP-----LHGVEVDMGHCPDLVPTVAAVAFAATGRTVVRNVAHL 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTIDTYDDHRMAMAF 410
R+KE++R+ A EL + G + EE D ++ T P L + DHRMAM+

Sbjct: 350 RIKESDRIAAPVGLRAGVNAEERADGLVQGGALATEPGTL----FSAHGDHRMAMSL 405

Query: 411 SLAACAEVPTIRDPGCTRKTFPDYFDV 438
+L V V + DP C K+FP ++++

Sbjct: 406 ALLGLGGVDVRLDDPSCVSKSFPFWEL 433

>ref|NP_824218.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
avermitilis MA-4680]
sp|Q82IU1.1|AROA_STRAW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC70753.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
avermitilis MA-4680]
Length = 446

Score = 186 bits (471), Expect = 9e-45, Method: Compositional matrix adjust.
Identities = 149/459 (32%), Positives = 221/459 (48%), Gaps = 44/459 (9%)

Query: 9 LQPIKEISG---TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
L P SG TV +PGSKS++NR L+LAAL+ + L S D M ALR +G

Sbjct: 10 LWPAPHASGAVDATVHVPGSKSVTNRALVLAALASEPGWLRRLRSRDTLLMAALREMG 69

Query: 65 LSVEADKA-----AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA 110
+ +E + A R + G V+ +GNAG MR L
Sbjct: 70 VGIEETVSSSSVGGGSDGSGEAWRVIPAALHGPATVD-----VGNAGTVMRFLPP 120

Query: 111 AVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG 170
A G + DG PR ERP+ ++ L+ LGA +D G P+ V+G G L GG
Sbjct: 121 VAALADGPPIRF--DGDPRSYERPLNGVIDALRALGARIDDD-GRGALPLTVHGGGALDGG 177

Query: 171 KVKLSGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSD 229
V + S SSQ++SALL++ P VE+ L S+P++ MT+ ++ G + + +
Sbjct: 178 PVAIDASSSSQFVSALLSGPRFNQGVFVRHTGSTLPSMPHIRMTVDMLRAVGAQVDTPE 237

Query: 230 SW---DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
S + + + G ++ VE D S+A FLA A +TGG V + + Q K
Sbjct: 238 SGGEANVWRVTPGALLG--RDLTVEPDLNAQPFLLAALVTGGKVVIPDWPERTTQPGDK 295

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADG 346
E+ MG TE + TG G H IDV++++ ++ +A VA AD
Sbjct: 296 LREIFTMGGSCELTEQGLEFTG-----SGAVH--GIDVDLSEVGELTPGIAAVALADS 348

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRM 406
P+ +R VA R+ ET+R+ A+ E+ +LG V E D I P +L+ TYDDHRM
Sbjct: 349 PSTLRGVHLRLHETDRLAALTKEINELGGDVTETADGLSIR-PRRLHGGIFHTYDDHRM 407

Query: 407 AMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
A A ++ A V I + T KT PD+ D+ + + N
Sbjct: 408 ATAGAIIGLAVDGVQIENVATTAKTLPDFDLWTGMLGN 446

>ref|YP_004003933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermus
fervidus DSM 2088]
gb|ADP77171.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanothermus
fervidus DSM 2088]
Length = 423

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 135/436 (30%), Positives = 225/436 (51%), Gaps = 27/436 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++ + I G VK P SKS ++R +++A+L++ + + N L ++D + A G
Sbjct: 2 DLIVKKTGEGIEGNVKAAPPKSYTHRAVLIASLADNISHLKNPLVAKDTCSSVEACEAFGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY--VL 123
++ + A +V G GK E + +GN+G +R +TA G A Y +L
Sbjct: 62 KIDIKRNA--WIVKGVNGKV----ITPENVIDVGNSGTTLRIMTAV----AGLAKYYTIL 111

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G +R RP+ L+ L+ LG P+ V G G GG ++ G+ISSQ++
Sbjct: 112 TGDKSIRSRPMQPLNLSRLDLGVVAFSSRNNGRAPIIIVKG--GYEGGYTEIPGNISSQFI 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL+ P ++++II +LIS PYV+MT+ +M++F K E + +Y++ YK
Sbjct: 170 SALLIIGPYGSKPLKLIIGELISKPYVDMTVEVMKKFDKIEREK--NTYYVE-PNGYK 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
S K + +EGD SSASY + AI GG V+++ S Q D +++ MG + +
Sbjct: 227 SCKYS-IEGDFSSASYIVGATAIAGGKVSIKNLFKDSKQADKLILDIISEMGVDIKIKKN 285

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V L IDVN+ PD+ T+AV+ A G T I + R KET+R
Sbjct: 286 EIIVCSHG-----ELHGIDVNLKNSPDLLPTVAVLGAAAKGRTKIYGIRHARFKETDR 338

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ EL+KLG V+E D II + +D+++DHR+ MA +L + + I+
Sbjct: 339 IAMCAKELSKLGIKVKELDDGLIINGGN-IKGGIVDSHNDHRLVMALTLGLKK-GIKIK 396

Query: 424 DPGCTRKTFPDYFDVL 439
+ + +FPD+ V+
Sbjct: 397 NAEAYKISFPDFVKVM 412

>ref|YP_003402990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloterrigena
turkmenica DSM 5511]
gb|ADB60317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloterrigena
turkmenica DSM 5511]
Length = 434

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 150/445 (33%), Positives = 213/445 (47%), Gaps = 53/445 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G+ + P SKS ++R +L A ++ TV D L +++ +A
Sbjct: 10 VAGSARAPPSKSYTHRAILAAGYADEATVRDALWSADT-----QATA 51

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLG-----NAGIAMRSLTAAVTAAGGNATYV 122
RAV + G DA E+ F G N+G R +TAA A G T V
Sbjct: 52 RAVDLFGGDVTRAGDATLEIDGFDGRPEVPADVIDCANS GTTTRLVTA AAAALADG--TTV 109

Query: 123 LDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G +R RP G L+ L LGA+ G P+ V G L GG V + G +SSQY
Sbjct: 110 LTGDESLRSRQGPLLEALTDLGAEAYSTRGNGLAPLVVTGP--LSGGTVSIPGDVSSQY 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ALLMA + +EI++ +L S PYV++TL ++ FGV A +D + F + GGQ Y
Sbjct: 168 ITALLMAGAVTDEGIEIDLETELKSAPYVDITLEVLADFGVDARETD--EGFAVDGGQSY 225

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ Y V GD SS SY LA AI G V +EG S QGD E++E MGA
Sbjct: 226 RPAGGEYAVPGDFSSISYPLAAGAIAGNEGDGVRIEGA-NPSAQGDTAIVEIVERMGADA 284

Query: 299 TWTETS--VTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
W S + V+ P L I+V++ PD+ T+A + ADG T I +
Sbjct: 285 DWDRESGVIDVSSAP-----LTGIEVDVEDTPDLLPTIATLGAVADGDTRITNAEHV 336

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAA- 414
R KET+R+ A+ EL KLG E D + + +L + DHR+ MA +LA
Sbjct: 337 RYKETDRVSAMAEELGKLGVTETTERDSLTVHGSDSRLEGATVQGRADHRIIMALALAGL 396

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVL 439
AE TI +FP +F++L
Sbjct: 397 VAEGETTIEGADHVDVSFPGFFELL 421

>ref|ZP_06253467.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella copri DSM
18205]
gb|EFB34131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella copri DSM
18205]
Length = 414

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 131/432 (30%), Positives = 214/432 (49%), Gaps = 41/432 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++++ ++ LP SKS+SNR L++ A++ NL + +D ++ ALR + +
Sbjct: 9 RQLNASINLPASKSISNRALVINAMAGCKLQPRNLSDCDDTEVIIAALRDMPDVIN---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ AG AMR +TA ++A G T + G RM+ R
Sbjct: 65 -----IKAAGTAMRFMTAYLSATPGEHT--ITGTERMQNR 97

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV L+ LGAD+ PP+ + G L GG +++ G+ISSQY+SALLM P+
Sbjct: 98 PIAILVDALRYLGADIQYEKKEGYPLHIVG-KPLEGGHLEVVGNISSQYISALLMIGPI 156

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+E+++ ++ S PY+++TL M+ FG AE +D D +K Q Y + +E
Sbjct: 157 LKNGLELKLGTGEIASRPYIDLTLWTMQNFGASAEWTDV-DTITVK-PQPYSCVADYTIEN 214

Query: 253 DASSASYFLAGAAITGG---TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S++SY+ A+ G V +EG +S QGD + ++G K + V
Sbjct: 215 DWSASSYWYEMMALNGNPDSEVRLEGLFDSSKQGDVVKYIFSLLGVKSEFENRD--VLS 272

Query: 310 PPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P + R L D + + PD+A T+ V +AS ++KET+R+ A++
Sbjct: 273 PVKLVQVRCLLPRFDYDFSGSPDLAQITIVVACCALGVKFKFTGLASLKIKETDRIEALKK 332

Query: 370 ELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEVPTIRDPGC 427
EL K+G + + D +I E + IDTY+DHRMA+AF+ A + I +P
Sbjct: 333 ELKKVGYVIYDENDNTLIWDGETCEPSFEPIIDTYEDHRMALAFAPLAFKFPQIEINNPEV 392

Query: 428 TRKTFPDYFDVL 439
K++P Y++ L
Sbjct: 393 VSKSYPHYWEDL 404

>ref|YP_003200775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nakamurella
multipartita DSM 44233]
gb|ACV77786.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nakamurella
multipartita DSM 44233]
Length = 428

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 141/428 (32%), Positives = 222/428 (51%), Gaps = 26/428 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSL+NR L+LAA + +++ L S D M ALR LG +E+
Sbjct: 17 VTATVPVPGSKSLTNRALVLAQAQAVAPSLIPAPLRSRDTLMAAALRALGTGIESAGPGG 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA-AVTAAGGNATYVLDGVPRMRERP 133
R +V P A + G AG MR L A TA G + DG R RP
Sbjct: 77 RDWLV-----TPAPLAGP-AHVDCGLAGTVMRFLPPLAATATG---PIIFDGDEAARRRP 127

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ LG VD D P V+ G +PGG V++ S SSQ++S LL++AP
Sbjct: 128 MATVLDALRALGVRVDG----DRLPFTVHADGRVPGGTVRIDASASSQFVSGLLLSAPSF 183

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G +E+ + S+P++EMT++ + GV+ + + DR+ ++ G P + +E
Sbjct: 184 AGGIEVRHEGAAPVPSLPHIEMTVQALRGVGVVRVDDATP-DRWRVEPGPV--QPWTSTIEP 240

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A+ FLA AA+TGGTDTV + Q +L MGA+V+ +TV+GP R
Sbjct: 241 DLSNATPFLAAAAVTGGTVTVPHPWAATTQAGDAIRGLLTAMGARVSIGPDGLTVSGPDR 300

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
L+ + +++ + ++ T+A +ALFADGP+ + + R ET+R+ A+ ++
Sbjct: 301 -----LRGLTADLHDVGELTPTVAAIALFADGPSRLTGIGHLRGHETDRLAALAQDIQ 353

Query: 373 KLGASVEEGPDYCIITPPEKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTF 432
+G V+E PD I P+ L+ + DHRMA A ++ V + D T KT
Sbjct: 354 AVGGRVDEAPDGFTIH-PQPLHGGPWAAFADHRMATAGAIVGLRVPGVLVDDVATTAKTL 412

Query: 433 PDYFDVLS 440
P + D+ +
Sbjct: 413 PGFADMWT 420

>ref|YP_003103946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinosynnema mirum
DSM 43827]
gb|ACU40100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinosynnema mirum
DSM 43827]
Length = 420

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 141/422 (33%), Positives = 211/422 (50%), Gaps = 27/422 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKS++NR L+LAA+++ +V+ L S D M ALR LG +E
Sbjct: 14 VNATVPVPGSKSITNRALVLAADIADAPSVLRAPLRSRDTLLMAEALRALGARIEDGPDGS 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G + + ++ G AG MR L A G V DG + R RP+

Sbjct: 74 WLVRPG-----ELRGSARVDCGLAGTVMRFLPPVAALAAGE--VVFDGDEQARVRPM 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLA 193
G ++ L+ LGADV D P + G GGLPGG+V + S SSQ++S LL++ A

Sbjct: 124 GTVLGALRALGADVGD---DALPFTLRGAGGLPGGEVVIDASASSQFVSGLLLSGARYD 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G V + + S+P++EMT+ ++ GV + S D + ++ G + VE D

Sbjct: 180 KGVVVAHEGEPVPSLPHIEMTVAMLREAGVVVDDSGR-DTWRVEPGPVAG--REWDVEPD 236

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+ FLA AA+TGG V V G + Q +L MG V + V G

Sbjct: 237 LSNATPFLAAAAVTGGEVLVPGWPAATTQAGDAIRGILAEAGCSVELGADGLRVRG---- 292

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L+ +D+++ + ++ T+ +A+FA GPT +R +A R ET+R+ A+ E+

Sbjct: 293 ----GELRGVLDLHDVGELTPTVVALAVFASGPTVLRGIAHLRGHETDRLAALVAEVNG 348

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFT 433
LG EE D +I P L Y DHRMA A ++ V + D G T KT P

Sbjct: 349 LGGDAEETEDGLLIR-PRALRGGTWRAYADHRMATAGAIVGLRVPGVEVDDIGTTSKTIP 407

Query: 434 DY 435
D+

Sbjct: 408 DF 409

>ref|YP_004103569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus albus 7]
gb|ADU20935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus albus 7]
Length = 409

Score = 185 bits (470), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 152/439 (34%), Positives = 222/439 (50%), Gaps = 40/439 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I + P K + GTV P SKS ++R+L+ AAL+EGT+V+D L S D+ + A+R LG

Sbjct: 2 DIKITPTK-LHGTVTTPPSKSAHRMLIAAALAEAGTSVIDRLYPSVDIMTTVEAMRQLG- 59

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
E D RAVV G GG A E L +G +R L A G ++ G

Sbjct: 60 -AEIDVNGDRAVVRGIGG-----APESAVLDCCESGSTLRFLIPVAAALGVRTFL--G 110

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ ERPI + G + D + P +NG L GG+ ++ G ISSQ+++

Sbjct: 111 RGKLPERPITPYLEEFPCGHVEFDY---NNTMPFTING--KLTGGRYEIDGGISSQFITG 165

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A PL EI + L S PYV+MT+ +M ++GV E ++ + F I GQK+ +

Sbjct: 166 LLLALPLTGERSEIVLTSHLESRPYVDMTIDVMRKYGVNVEVTE--NSFIIPEGQKFVAC 223

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
A VEGD S ++F ++ G V + G S QGD K E+ E

Sbjct: 224 DGA-VEGDHSGGAFFEVANS-LSGSEVDIRGLNVNSFQGDKKIIEICE-----EMVY 272

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G P+ PF V+ +PD+ LAV+ F G + I D A R+KE++R+

Sbjct: 273 NKKGMKP-PF-----TVSAADIPDLVPI LAVLGSFCGGESRITDAARLRLKESDRLA 323

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT-ITYDDHRMAMAFSLAAC-AEVPVTIR 423
A+ L LG V D II E L A + ++DHR+AMA ++AA E PV IR

Sbjct: 324 AMEETLNALGGDVTTATADSLIIGKESLAGGAEVSAHNDHRIAMAMAIAATRCEDPVIIR 383

Query: 424 DPGCTRKTFTPDYFDVLSF 442
C RK++PD+++V +

Sbjct: 384 GAECVRKSYPDFWEVYRSL 402

>ref|ZP_04853058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
oral taxon 786 str. D14]
gb|EES72779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
oral taxon 786 str. D14]

Length = 430

Score = 185 bits (469), Expect = 1e-44, Method: Compositional matrix adjust.
Identities = 147/441 (33%), Positives = 232/441 (52%), Gaps = 24/441 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++P E+ G + SK+ + R LL+AAL+EGT+ V +SED M + LG
Sbjct: 2 DVIVRPTPELKGEIGALSSKNYTTRYLLVAALAEGTSTVYYPAHSESDAMRRCIADLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D+ ++ V+ G G + +D KE L +GNAG +R L A + + T+V
Sbjct: 62 VLEEDE--EKIVITGFGR--PKDVKE---LNVGNAGAVLRFLLMA-IASLCPEVTFVNTY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+ L QLG +V G P+ + G G GKG+++SGS+SSQYLSA
Sbjct: 114 PDSLGRPHDDLIDALGQLGVEVSHNEGK--LPITIRG-GAPKGGKIRVSGSVSSQYLSA 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL PL D EIE+++ L S TL ++E+ G+ SD + F + G Q Y++
Sbjct: 171 LLFLTPLLDEDESEIEVLNLDLKSQVVGQTLVLEQAGIVIHASDDYMHFRVPGRQSYQA- 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
K V+GD ++ LA AA+T V V S QG+ +VL+MM +T + +V
Sbjct: 230 KTYTVQGDYPGSAAILAAAVTKSDVKVHRLAEHSKQGERAVVDVLQMMDVPLTHQDGTV 289

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G R L+ ++ + + D + + A+FADG + +V + R KE +R+
Sbjct: 290 HVQGNR-----LRPVEFDGDAATDAVLAMVAAVAFADGTSRFYNVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
TEL K GA+VEE I+ P I+ + DHR+ MA ++ C E P+
Sbjct: 343 DFLTELKAGANVEERQSEIIVHGRPSGLEGGVTINAHYDHRVIMALTVVGLRCRE-PLV 401

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I+D K++P +FD +++
Sbjct: 402 IKDAHVAKSYQPFFDHITSL 422

>ref|YP_922900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nocardioide sp.
JS614]
gb|ABL81213.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nocardioide sp.
JS614]
Length = 430

Score = 185 bits (469), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 142/438 (32%), Positives = 223/438 (50%), Gaps = 31/438 (7%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + V LPGSKSL+NR L+LAA+++G +VV L S D M AL LG V+ A
Sbjct: 19 RPVDVAVTLPGSKSLTNRALVLAAMADGPSVRRALRSRDSMLMAAALTALGSQVDTTGA 78

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G F + + G AG MR + + G ++ DG P MR+R
Sbjct: 79 DWLVTP----GAF-----DRDAAVDCGLAGTVMRFVPPVAGLSTGAVSF--DGDPHMRKR 127

Query: 133 PIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG+++ L+ LG V+ D P V+G G + GG V + S SSQ++SALL+A
Sbjct: 128 PIGEILGALRTLGVSVGE----DTLPFTVHGSGTVRGTVVVDASASSQFISALLLAGAR 183

Query: 193 ALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
V++ K + S+P+++MT+ ++ GV+ + +D+ +R+ + G + +E
Sbjct: 184 YDHGVDVRHDGKPVPSLPHIDMTVAMLRHGVGEVDGADA-NRWRVAPGPVRA--VDHLIE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE----TSVTV 307
D S+A+ FLA AA++GGTV V ++ Q ++L MG +V + + T + V
Sbjct: 241 PDSLNAAPFLALAAVSGGTVVVRDWPSTTQAGDALRDILTAMGCEVGFVDGPDSTGLRV 300

Query: 308 TGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
T G L IDV+++ + ++ +A + A+ P+ +R +A R ET+R+ A+
Sbjct: 301 T-----GSGTLLGIDVDLHNVGELTPAVALCALAEAPSHLRGIAHIRGHETDRLAAL 353

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
TEL+ LGA V E D I P L+ TY DHRMA A + A V + +
Sbjct: 354 ATELSGLGADVTEHADGLSIR-PAPLHGGVFHTYADHRMAHAGVIIGAAVEDVLVENVAT 412

Query: 428 TRKTFPDYFDVLSTFVKV 445
T KTFPD+ S ++
Sbjct: 413 TGKTFPDFAGFWSGLIEE 430

>ref|YP_003012523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
JDR-2]
gb|ACT02437.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
JDR-2]
Length = 430

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 146/443 (32%), Positives = 231/443 (52%), Gaps = 22/443 (4%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++ P + G ++ SK+ + R LL+AAL++GT+ + +SED M +R LG
Sbjct: 2 DVIVTPTPTLQGEIQALSSKNYTTRYLLVAALADGTSTIYPAHSESDAMRRCIRDLAG 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE D ++ V+ G G ++ K+ QL +GNAG +R L A + + + T++
Sbjct: 62 IVEEDD--EKIVITGFG-----KNPKDVDQLDVGNGAVLRFLMA-IASLCPDVTFINRY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+ L Q+G ++ G P+R+ G G GGK+++SG++SSQ+LSA
Sbjct: 114 PDSLGRPHNDLIDALQMGVKIEHNEGK--LPIRIQG-GAPKGGKIQVSGNVSSQFLSA 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL PL D EIE++ L S V TL ++E+ G+ S+ + I G QKY++
Sbjct: 171 LLFLTPLLEEDSEIEVLHDLKSKVVVGQTLEVLEQAGIVIHASEDLMHYRIPGNQKYEAK 230

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSV 305
K V+GD ++ LA AA+T V V S QG+ +VL MM +T V
Sbjct: 231 KYV-VQGDYPGSAAIAAAAVTNSDVIVHRLAENSKQGERAVVDVLRMMEVPLTHENGIV 289

Query: 306 TVTGPPPREPFRKHLKAIDVNMNKMPPVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G + LKA++ + +K D + + A+FA+G + DV + R KE +R+
Sbjct: 290 HVKGNGK-----LKAVEFDGDKATDAVLAMVAAVFAEGTSRFYDVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPTI 422
EL K GA+VEE I+ PE + I+ + DHR+ MA ++ A+ P+ I
Sbjct: 343 DYLNELRKAGANVEERQAEIIVHGRPEGVEGGVEINAHYDHRVIMALTVVGLRAKNPIRI 402

Query: 423 RDPGCTRKTFPDYFDVLSTFVKV 445
RD K++P YFD L N
Sbjct: 403 RDAHVAKSYPIYFDHLKALGAN 425

>ref|ZP_05858117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella veroralis
F0319]
gb|EEX18046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella veroralis
F0319]
Length = 417

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 132/443 (29%), Positives = 222/443 (50%), Gaps = 53/443 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ ++ P + I + LP SKS+SNR L++ AL++ + +NL + +D +L A
Sbjct: 2 QYIITPPQHIDTRITLPASKSVSNRALIVQALTKEGILPENLSDCDDTKVILQAF----- 56

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
S +D +A +G AMR LTA + + G +++ G
Sbjct: 57 SQPSDVIDIKA-----SGTAMRFLTAYLCLSQGE--HIITG 90

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
RM+ RPI LV L+ LGAD+D PP+R+ G L GG++ + G++SSQY+SA
Sbjct: 91 TERMKHRPIKILVDALRYLGADIDYIGNEGYPLRIRGCE-LEGGQLVIPGNVSSQYVSA 149

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLM AP+ +++++ ++S PY+++TL +M FGV AE ++ +D +K Q +
Sbjct: 150 LLMIAPILTKGLDLKLTGEIVSRPYIDLTLHIMHEFGVAAEWTN-FDTISVKPQQYTR-- 206

Query: 246 KNAYVEGDASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ +E D ++ASY+ A+ G V + G S QGD + ++G K +
Sbjct: 207 RTYTIENDWTAASYWYEILALQEDLDGEVVLSSGLKDGSRQGDAAVRYIFSLGIKTNFAR 266

Query: 303 -----TSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
T T+T R L +D + PD+A TL P + S
Sbjct: 267 KDAEGLTDTATLTHRTR-----MLNRMDDYDFINHPDLAQTLLAACPVLGIPFHTGLNSL 320

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK---LNVTAIDTYDDHRMAMAFSLA 413
R+KET+R+ A++TE+ KLG ++ D + E+ +++ I+TY+DHRMAM+F+
Sbjct: 321 RIKETDRIEAMKTEMAKLGIVLQSRNDELGSWEGERCEPVSLPVINTYEDHRMAMSFAPL 380

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYF 436
A + I P K++P ++
Sbjct: 381 AIKLGEIRIDHPEVVTKSYPHFW 403

>ref|YP_003118554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Catenulispora
acidiphila DSM 44928]
gb|ACU76713.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Catenulispora
acidiphila DSM 44928]
Length = 454

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 140/430 (32%), Positives = 213/430 (49%), Gaps = 26/430 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ V++PGSKS +NR LLLAAL + + + L + D M+GALR LG+ V+A +
Sbjct: 16 RPVTADVRVPGSKSATNRALLAALGDSPSTITGGLRARDSVLMIGALRALGVEVDAGED 75

Query: 73 AKRAVV-VGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
V + + DA ++ +G AG MR L A G + DG P R
Sbjct: 76 FDAPVWRITPPAQLRGGDAGAPAKVDVGLAGTVMRFLPPVAALAAGQVYF--DGDYARA 133

Query: 132 RPIGDLVVLGLQLGADVD-----CFLGTDCCPPVRVNGIGGLPGKVKLSGSISSQYLSAL 186
RP+G L+ L+ LG +D F P V G G + GG V+L + SSQ++SAL
Sbjct: 134 RPMGTLLQSLRDLGVRIDDDGDRGTF-----PFLVEGAGQVAGGLVELDATASSQFISAL 187

Query: 187 LMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+A L VE+ + I S P+++MT+ + G + S+ R+ +
Sbjct: 188 LLAGSRYLKGVEVRHVGGPIPSQPHIDMTVEFVRAAGGTVDASEP-GRWVVT--PSVLRG 244

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ +E D S+A+ FLA A +TGGTVT+ + Q +L MGA+V T +
Sbjct: 245 REWSIEPDLNSAAPFLAAALVTGGTVTIPDWAATTQAGDASRHLLREMGARVELTPAGL 304

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV+ G + ++ ++ + ++ TLA VA AD P+ + R ET+R+
Sbjct: 305 TVS-----GGAGVHGMEADLRDVGELTPTLAAVAALADSPSRFTGIGHLRGHETDRLA 357

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ E+ LG V E PD +I P K++ TYDDHRMA A ++ A V + D
Sbjct: 358 ALAREINGLGGDVVEPDGILLIR-PAKMHSGVFATYDDHRMATAGAVLGLAVPGVEVEDI 416

Query: 426 GCTRKTFFDY 435
T KT PD+
Sbjct: 417 AATGKTLPDF 426

>ref|YP_182676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermococcus
kodakarensis KOD1]
sp|Q5JFT3.1|ARO_A_PYRKO RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
dbj|BAD84452.1| 5-enolpyruvylshikimate-3-phosphate synthase [Thermococcus

kodakarensis KOD1]
Length = 399

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 147/440 (33%), Positives = 220/440 (50%), Gaps = 43/440 (9%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
++++P+ E+ G + P SKS ++R LA L+EG + ++N L +D + A+R+ G
Sbjct: 1 MIIRPVDEVGRGELNAPPSKSYTHRAYFLALLAEGESTIENPLVCDDTLATIEAIRSFGAG 60

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V+ + VV P E+ ++ +G R TA GG ++DG
Sbjct: 61 VDG-----KTVV-----PPEPSPGF-VYARESGTTARFSTALAGGIGGKT--LIDGA 105

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
R+RERP+ LV LK LGA+VD F P+ V G + G+V + S SSQ++S L
Sbjct: 106 RRLRERPMDGLVKALKGLGAEDVGF----SLPLTVKGP--VKSGRVSDASKSSQFVSGL 159

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSP 245
L+ VE +S PY+EMTLR ME FGV+ E S++ + G +YK P
Sbjct: 160 LLLGAEVGLKVEAR---NPVSKPYIEMTLRTEAFGVEFEREGFSFEVYPGVKGTRYKVP 216

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
GD S+AS+FLA A+ G V V +Q D+ F + LE GA+V V
Sbjct: 217 -----GDYSTASFFLAAGALY-GKVRVNNLLREDVQADMAFLDALEEFGARVKRGRDYV 269

Query: 306 TVTGPPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G LKA+ ++ + PD LAVVA +A+G + IR R KE++R+
Sbjct: 270 KVEG-----GELKAVALDCSDFPDSFPILAVVAAYAEGRSVIR-ARQLRFKESDRVR 320

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRD 424
A+ L+++G V E D I ++T++DHR+AMA S+AA A P I D
Sbjct: 321 AMAVNLSRMGVKVRLEDGLEIEGGRPRGAK-VETFNDHRIAMAMSIAALGATGPSIID 379

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
K+ P +FD L ++
Sbjct: 380 TESVSKSHPGFFDDLRLLE 399

>ref|YP_304445.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina
barkeri str. Fusaro]
gb|AAZ69865.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina
barkeri str. Fusaro]
Length = 443

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 162/424 (38%), Positives = 223/424 (52%), Gaps = 21/424 (4%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G V P SKS ++R + LAALS+ +TV L+ S D + A G VE ++
Sbjct: 23 IKGEVFAPPSKSYTHRAVTLAALSKESTVRHPLI-SADTLATVRASEMFGALVEREE--D 79

Query: 75 RAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R ++ G GK V D + N+G +R +TA AA + VL G +R RP
Sbjct: 80 RLIIHINGKPNVPDD---VIDAANSGTTLRFMATV--AALTDGITVLTGDASLRTRPN 133

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ L +LG G + P+ V G GL G V + GSISSQ++SALL+ PLA
Sbjct: 134 GPLLEVLNRLGVKACSTRGNERAPLVVKG--GLKGQDVSIDGSISSQFISALLITCPLAE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYVEGD 253
+ I K+ S PYV++TL ++E GVK DS RF I G QKY K+ V GD
Sbjct: 192 NSTILSITGKIKSRPYVDITLEMLELAGVKVHIDDSNGTRFIIPGKQKYDF-KDYTVPGD 250

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSASY LA AA+T G+ VTV+ S QGD E L+ MGA +TW + + VT
Sbjct: 251 FSSASYLLAAAAMTDGSEVTVKNL-FPSKQGDKVIETLQMGADITWDKEAGNVTVK-- 307

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + LKAI + PD+ T+AV+A A G + I + R KET+R+ A+ TEL
Sbjct: 308 ---GGRQLKAITFDAGANPDVPTVAVLA AVAKGTSRIENAEHVRVKETDRLRALATELP 364

Query: 373 KLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTF 432
KLG ++E D IT KL+ ++ +DDHR+ MA S+A I ++
Sbjct: 365 KLGVDLKEERDSLITITGG-KLHGASVHGWDHRIVMALSVAGIVAGNTKIDTTESASISY 423

Query: 433 PDYF 436
P++F
Sbjct: 424 PEFF 427

>ref|YP_003646068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tsukamurella
paurometabola DSM 20162]
gb|ADG77729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tsukamurella
paurometabola DSM 20162]
Length = 430

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 140/422 (33%), Positives = 208/422 (49%), Gaps = 27/422 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV LPGSKS++NR +LAA + + + N L S D M L LG+ V
Sbjct: 19 VTGTVALPGSKSITNRAYILAAQASSASTLTNTLRSDTDLMARGLTALGVDVNFLTDTT 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
AV G A + G AG MR L AAG + DG P+ R RP+
Sbjct: 79 VAVTGG-----ALHGAAVDCGLAGTVMRFLPP--LAAGARGSSRFDDGPQARIRPL 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G ++ L+ LGA +D D P ++G G + GG V + S SSQ++S LL++ P
Sbjct: 128 GTVLDALRGLGARIDG---DGLPFTMHGEGPIRGTTVIDASASSQFVSGLLLSGSPSFA 183

Query: 195 GDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
V + K + S+P++EMT+ ++ G + ++ GG + VE D
Sbjct: 184 EGVTVHHGDKPVPSPHIEMTVDMLRAAGADVDTAEPTNTRVAPGGLHAH---DWTVEPD 240

Query: 254 ASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+ FLA AAITGG VTV S Q V+FA++L MGA+VT + ++T
Sbjct: 241 LSNATVFLAAAAITGGAVTVPHWNPQSTQPGVQFADILAEMGAEVTHADGALTGR----- 295

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G L +D ++ + ++ T+A +A AD P+ +R +A R ET+R+ A+ E++
Sbjct: 296 --GTGGLHGVDWDLRDIGELTPTVAALALADTPSHLRGIAHLRGHETDRLAALTAEISA 353

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
LG E D I P L+ +Y DHRMA A ++ V + D T KT P
Sbjct: 354 LGGHCTETEDGLRIE-PATLHGGLWHSYADHRMATAGAILGLVTTGVQVEDIATTAKTMP 412

Query: 434 DY 435
D+
Sbjct: 413 DF 414

>ref|YP_002309425.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Azobacteroides pseudotrichonymphae genomovar. CFP2]
dbj|BAG84014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Azobacteroides pseudotrichonymphae genomovar. CFP2]
Length = 426

Score = 184 bits (468), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 135/444 (30%), Positives = 217/444 (48%), Gaps = 66/444 (14%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEG-TTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
I+ +V+LP SKS+SNR+L+L ALS+ ++NL +S+D + AL++
Sbjct: 13 INTSVQLPASKSISNRVLILNALSKNDIYFIENLSDDTQALQYALQS----- 61

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++V +G AG +MR LTA ++ GN + + G RM+ RP
Sbjct: 62 -----DDVDFDIGAAGTSMRFLTAYLSQRKGN--WSITGTERMKNRP 101

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I L L QLGA++ PP+ + G L GG + L G ISSQY+SAL+M AP+

Sbjct: 102 IWILTDALCQLGAEISFLEKKGFPLYIVG-KKLRGGSISLDGGISSQYISALMMIAPVL 160

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS--WDRFYIKGGQKYKSPKNAYVE 251
+ +++ +IS PY+ MT+RLME FG++ E ++ W R Q Y+ + VE

Sbjct: 161 EQGLTMQLEGIIISRPYIGMTIRLMEVFGIRVEWEENIIWIR-----PQLYRMHSSFKVE 215

Query: 252 GDASSASYFLAGAAITGGTVTVE--GCGTTSLQGDVKFAEVLEMMGAKVTW-----TE 302
D S+ASY+ A+ +E G S+QGD + + E +G + +

Sbjct: 216 SDWSAASYWYEIIALASKDSLIELLGLENSIQGDAQGRFLFEKLGVTMTFVFTTLGER 275

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
++ T P P R + + N PD+ T V + P + + S R+KET+

Sbjct: 276 KEISTTSLPILP--RFTGEMLSYNFVNEPDLVQTFVVSCLLNIPFCFKGLQSLRIKETD 333

Query: 363 RMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
R+ A++ E+ KLG ++E + C ++ + I TY+DHRMAMAF+

Sbjct: 334 RITALQKEMRKLYLIRIKDCTGDTMEWKGERC-----KQEDNPVILTYEDHRMAMAFAP 388

Query: 413 AACAEVPVTIRDPGCTRKTTFPDYF 436
++I P K++P+Y+

Sbjct: 389 VCLKLKKISIDTPEVVSXSYPNYW 412

>ref|ZP_05130027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp.
7_2_43FAA]
gb|EEH96921.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp.
7_2_43FAA]
Length = 431

Score = 184 bits (467), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 128/426 (30%), Positives = 226/426 (53%), Gaps = 22/426 (5%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++GTVK+P SKS+S+R ++ AAL GT+ ++N+ S+D++ + A+ LG + +K

Sbjct: 10 KLNQTVKVPSPKSMRAIICAALGRGTSTIENIDYSDDINATIDAMVALGAVI--NKER 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 133
+ ++ G + V++A + +G +R + G ++ G + +RP

Sbjct: 68 DKVVISGIYREDAVKNAVRYIDC--NESGSTLRFIIPISLLFDGMTKFI--GKGNLGRK 123

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ K+ G + V+ G L G+ L G+ISSQ+++ LL + PL

Sbjct: 124 LDITYFDIFKEQGIKYNVENELNMIVK---GMLKPGEFSLPGNISSQFITGLLFSPLPL 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD +I I + S Y+++TL M+ FG++ E+ D + F I+G QKY S +N VEGD

Sbjct: 180 DGDSKINISTNIESKGYIDLTLDCMKDFGIEIENRD-YKEFIIRGNQKYIS-RNYRVEGD 237

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S A+++LA A+ G V + SLQGD + ++LE MGAK + ++ +

Sbjct: 238 YSQAAFYLAADAL-GSDVAITDLKKNLSLQGDKEVIDILERMGAKFIVDKNNIKCNVEDK- 295

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L + ++ ++ PD+ ++VA A G T I + R+KE +R+ A+ TEL K

Sbjct: 296 -----LVSTVIDASQCPDIIPVISLVAALAKGRTEIINAGRLRIKCDRLKAVATELNK 349

Query: 374 LGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAACAEV-PVTIRDPGCTRKT 431
LGA + E D II ++L + ++ DHR+AM ++A+ + P+ + D C K+

Sbjct: 350 LGAKIVEKEDGLIIDGVDELQGGVEVSWKDHRIAMTLAIASTRCINPIELTDYDCIAKS 409

Query: 432 FPDYFD 437
+P +F+

Sbjct: 410 YPGFFE 415

>ref|ZP_01059205.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leeuwenhoekiella
blandensis MED217]
gb|EAQ51037.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leeuwenhoekiella
blandensis MED217]
Length = 407

Score = 184 bits (467), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 139/435 (31%), Positives = 216/435 (49%), Gaps = 57/435 (13%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++G +K+ GSKS SNR+LLL AL G + +NL NS D M AL
Sbjct: 11 QLAGEIKITGSKSESNRLLLLQALFGGFKI-ENLSNSHDSQVMQKAL----- 56

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
A +E + + +AG AMR LTA A G T +L G RM+ERP
Sbjct: 57 -----ASKEKTVDIHHAGTAMRFLTAYFAAFEGRET-ILTGSSRMQERP 99

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
IG LV L+ LGAD+ P+ + G L V + ++SSQY+SAL+M
Sbjct: 100 IGLLDALRDLGADISYMNNEGYAPLLIKG-KKLTSTVSFAANVSSQYISALMMVGASL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---- 249
+EI+++ ++ S+PY+EMT L+ + G+++ +G Q P A
Sbjct: 159 PNGIEIDLVGQITSVPYIEMTRSLTLQLGIESS-----FEGQQINIKPAGAINVSE 209

Query: 250 --VEGDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VE D SSASY+ + A+ + + SLQGD AE+ + +G + T+ +VT
Sbjct: 210 MVVESDWSSASYYYYSLVALCDKAKLKISSYKENSLSQDQSVLAELYQLGVETTFEANA 269

Query: 307 VTGPPREFFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ E + + + + PD+A T+AV + + + +KET+R+ A
Sbjct: 270 L-----EKVEKPKPRRVEFDLANSPIAQTIAVTCYGLGVCGLYGLHTLTKIKETDRLEA 324

Query: 367 IRTELTKLGA--SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
++ ELTKLGA SV + + + +VT I TY DHRMAMAF+ A P+ D
Sbjct: 325 LKAELTKLGAHISVTDKSLHLEGETNFSQDVT-IKTYQDHRMAMAFAPFAL-RAPILFED 382

Query: 425 PGCTRKTFPDYFDVL 439
K++PD+++ L
Sbjct: 383 AEVVNKSYPDFWEDL 397

>ref|YP_001620220.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acholeplasma
laidlawii PG-8A]
gb|ABX80844.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acholeplasma
laidlawii PG-8A]
Length = 418

Score = 184 bits (467), Expect = 2e-44, Method: Compositional matrix adjust.
Identities = 136/427 (31%), Positives = 225/427 (52%), Gaps = 34/427 (7%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SG VK+ SKSLS+R +L AAL+ G + +DN+L+S+D+ AL++LG ++
Sbjct: 13 NLSGEVKIVSSKSLSHRYVLAALAHGQSKIDNILDSDDLIATQSALKSLGATIN----- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-LDGVPRMRER 132
+ ++ GGK V+ E + F +G +R L T+ + +P +
Sbjct: 68 -QGLI--TGGK--VQRVHETIDCF--ESGSTLRFLIPVAMLQDKPVTFTGKNQLPFRTQE 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+L Q D +L P+ V+G L GG L G +SSQ+++ LL A PL
Sbjct: 121 MYENLFKETYQFEHPKDKWL-----PLTVSG--PLKGGTYHLRGDVSSQFITGLLYALPL 173

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D EI + L S+ YV+MTL ++++FG+K + + + I G Q Y +P N VEG
Sbjct: 174 APNDSEIILTSLESVGVDMTLDVLDKFGIKI--IKTVNGYKIPGNQHY-NPGNYSVEG 230

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S A++F+A A + G + + SLQGD + ++ MG +T T V P +
Sbjct: 231 DFSGAAFFVA-AGLLAGPIHLTNLNHSLQDKEIIDLAVKMGGDITPTSEGYLVK-PSK 288

Query: 313 EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
LK I +++ ++PD+ L V+ A+G T I + + R+KE++R+ A+ T L
Sbjct: 289 -----LKGISIDVGQIPDLGPILMVLGALAEGTTIIHNASRLRIKESDRLNAMVTNLK 341

Query: 373 KLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
LGA+++E D I KL + +Y DHR+AM+ ++A+ E P+T+ D K

Sbjct: 342 ALGANIKEIGDTVEIKGVSKLKGGLVSSYKDHRIAMSMASIMCEQPITLDDETVVSK 401

Query: 431 TFPDYFD 437

++P++F+

Sbjct: 402 SYPNFFE 408

>ref|ZP_08043247.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haladaptatus
paucihalophilus DX253]
gb|EFW93058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haladaptatus
paucihalophilus DX253]
Length = 429

Score = 184 bits (467), Expect = 3e-44, Method: Compositional matrix adjust.
Identities = 149/433 (34%), Positives = 213/433 (49%), Gaps = 26/433 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
E+SGT + P SKS ++R +L A S G V D L+ S D + A+ G V

Sbjct: 8 SELSGTARAPPSKSYTHRAILAAGYSGGALVFDPLI-SADTKATMRAVDAFGGDVT--DT 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G GG+ + L N+G R ++ TAA + V G +R R

Sbjct: 65 GEAIEIDGFGGEPTIPGDV---LDCANS GTTTRLVSG--TAALVDGITVFTGDASLRSR 118

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P G ++ + QLG + G P+ + G + GG V + G +SSQY+SALLMA L

Sbjct: 119 PQGPMLSAIDQLGGRGESTRGNGKAPLVLKGP--ISGGTVSIPGDVSSQYVSALLMAGAL 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VE 251
V I++ +L S PYV++TL L++ FGV AE D + + GGQ Y+ Y V

Sbjct: 177 TDEGVTIDLETELKSAPYVDITLELLDDFGVTAEKRDGG--YRVDGGQFYEPSDGEYHVP 234

Query: 252 GDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SS SY LA A+ V +EG S QGD +VL+ MGA + W +T

Sbjct: 235 GDFSSISYLLAAGAVAADDDERVRIEGA-YPSAQGDTFIVDVLDRMGADIEWNRNDGVLT 293

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+ L + V++ PD+ T+A + ADG T I + R KET+R+ +

Sbjct: 294 -----VRQSSLSGVTVDVGDTPDLLPTIAALGAIADGETRIENCEHVRYKETDRVAVMA 347

Query: 369 TELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAACAEVPVT-IRDPG 426
EL+ LGASVEE D I E L + +D + DHR+ MA ++A A T + D

Sbjct: 348 KELS NLGASVEEEDDALTIYGDENLVGSVVDGHGDHRIVMALAVAGLAADGTTMVADAE 407

Query: 427 CTRKTFPDYFDVL 439

+FPD+FDVL

Sbjct: 408 HVDVSFPDFFDVL 420

>ref|ZP_02076942.1| hypothetical protein EUBDOL_00735 [Eubacterium dolichum DSM 3991]
gb|EDP11557.1| hypothetical protein EUBDOL_00735 [Eubacterium dolichum DSM 3991]
Length = 421

Score = 183 bits (465), Expect = 4e-44, Method: Compositional matrix adjust.
Identities = 124/426 (29%), Positives = 216/426 (50%), Gaps = 31/426 (7%)

Query: 16 SGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+G++ +P SKS+S+R ++ AAL+ G +++ N+ S+D+ + ++ LG S+ D +

Sbjct: 11 TGSIHIPPSKSM SHRAIICAALAHGESIIQNVAYS KDILATIEGMKQLGASIRKDGST-- 68

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ + F AKE +F +G +R + + T+ G R+ +RP

Sbjct: 69 -LYIRGVQS FQQLAAKE---IFCNESGSTLRFFIPIFSLCNQDITFTGQG--RLLD RP-- 120

Query: 136 DLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+++ AD+ G D P ++ L G L G +SSQ++S LL A PL

Sbjct: 121 -----QKVYADIFHKQGLDFTHTPSGIHIHQLQAGGYTLKGDVSSQFISGLLFALPLL 174

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D I I S Y+++TL +MERFGVKA + D + YI G Q+Y++ N +EGD

Sbjct: 175 TEDSTIHIEPPFESRSYIDL TLEMMERFGVKAYRDEF-TLYIPGNQQYQAC-NYTI EGD 232

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S ++F AI+ G +T+ G +S QGD + ++L+ GA + + + P +
Sbjct: 233 YSQLAFFAVLGAISNG-ITLHGVTSPSSKQGDQIIDLKQFALIDTLKDGRIH--PAK 289

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G+ +N+ PD+ + V+ ++ +G T I + + R+KE++R+ A+ EL K
Sbjct: 290 LIGQA-----INLENCPLDGPVCLGMYGEGTTHIYNASRLRIKESDRIAAMEEELRK 343

Query: 374 LGASVEEGPDYCIITP-PEKLNVTADTYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKT 431
G ++ PD I P + T++ ++DHR+ MA S+AA A I D K+
Sbjct: 344 FGTNITSTPDITIQHNPNPICQTSLYGHNDHRIVMALSAAMASRQEAIEDAQAIKES 403

Query: 432 FPDYFD 437
+P +F+
Sbjct: 404 YPTFFE 409

>ref|ZP_02437127.1| hypothetical protein BACSTE_03400 [Bacteroides stercoris ATCC 43183]
gb|EDS14254.1| hypothetical protein BACSTE_03400 [Bacteroides stercoris ATCC 43183]
Length = 424

Score = 183 bits (464), Expect = 5e-44, Method: Compositional matrix adjust.
Identities = 137/447 (30%), Positives = 215/447 (48%), Gaps = 65/447 (14%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ ++LP SKS+SNR L+L AL+ G + NL + +D M+ AL
Sbjct: 12 MHAAIRLPASKSISNRALILHALAHGRQTLNLSDCDDTRVMVRAL----- 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ E + + AG AMR LTA ++ G ++ G RM++RPI
Sbjct: 58 -----QGNPEHIDIM--AAGTAMRFLTAYLSVTPG--VRIITGTQRMQQRPI 100

Query: 135 GDLVVLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L L+QLGA+++ PP+R+ G L G ++ L+G++SSQY+SALLM +
Sbjct: 101 RILTDALRQLGANIEYAGNEGFPPLRITG-SELQGCEISLAGNVSSQYISALLMIGAVLP 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ + + +IS PY+++TL+L+ FG AE S GG + P VE D
Sbjct: 160 QGLHLHLTGCIISRPYIDLTLKLIRDFGGHAEWSSSENSITVYPGGYR-DVPFT--VESDW 216

Query: 255 SSASYFLAGAAITGG-----TVTVEGCGTTSIQGDVKFAEVLEMMGAK 297
S+ASY+ A+ G TV + G S QGD + AE+ +G
Sbjct: 217 SAASYWYQILALRGNEERKTGSGELPKGNEEETVELLGLFPHSYQGDSRGAEIFSRGLGVH 276

Query: 298 VTWTETSV--VTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
+T+ V T+ G P + ++ +M +PD+A T V + P + S
Sbjct: 277 TEYTDKGVRLLTAGTP-----VDRLEEDMVDIPDLAQTFVVTCLMNIPFRFTGLQS 328

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTADTYDDHRMAMAFSL 412
++KET+R+ A+ EL KLG +V D ++ E+ + I TY+DHRMAMAF+
Sbjct: 329 LKIKETDRITALIAELRKLGYAVRSEQDSILLWEGERCAPESAPVIATYEDHRMAMAFAP 388

Query: 413 AACAEVPTIRDPGCTRKTFPDYFDVL 439
A A + I +P K++P Y++ L
Sbjct: 389 ACIALPQIRIDEPQVVSXSYPGYWEDL 415

>ref|ZP_04820906.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
El str. 'BoNT E Beluga']
gb|EES48191.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
El str. 'BoNT E Beluga']
Length = 433

Score = 183 bits (464), Expect = 5e-44, Method: Compositional matrix adjust.
Identities = 130/431 (30%), Positives = 226/431 (52%), Gaps = 30/431 (6%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK+P SKS+++R ++ AAL +G + + N+ S+D+ + A+R+LG + +

Sbjct: 10 KLKGEVKIPPSKSMHRGVICAALGDGISKIRNINYSDDIRATINAMRSLGAIITKEDGY 69

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF----LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + E K+ ++L +G +R L G++ ++ G +

Sbjct: 70 LHIIGI-----KSECKKNIELNRTIDCNESGSTLRFLVPISCIFEGSSRFI--GKGNL 121

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ G G +R+ GI L G+ KL G ISSQ++S +L

Sbjct: 122 GKRPLDITYEIFDNQGIKYSYKKGK--LDLRIQGI--LKYGEFKLRGDISSQFISGMLFT 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
PL GD +I I +L S Y+++TL M FG++ ++++ F IKG Q YKS ++

Sbjct: 178 LPLLEGDSKIIITTELESKGYIDLTLSSAMDFGIEV-INNNYREFIIKGNQTYKS-RDYR 235

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+EGD S A++FL A+ V + SLQGD + E+LE M K+ + S + G

Sbjct: 236 IEGDYSQAFFLVADALK-SEVFINDLKLESLQGDKEVIEILERMNMKIKNIDNS--LLG 292

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
PRE +L+A ++ ++ PD+ +++ + +G T I +V R+KE +R+ A+ +

Sbjct: 293 IPRE----NLEATIIDGSQCPDIIPVISLASSLCNGRTEIINVGRLEKICDRLSAVAS 347

Query: 370 ELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
EL KLGA++ E D II + L + ++ DHR+AM ++A+ C E P+ + D

Sbjct: 348 ELNKLGANIEKEDSLIIDGVKTLKGGVKVWSHKDHRIAMMLAIASTVCME-PIILEDYE 406

Query: 427 CTRKTFPDYFD 437
C K++P++FD

Sbjct: 407 CISKSYPEFFD 417

>ref|YP_967917.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
vulgaris DP4]
gb|ABM29490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio
vulgaris DP4]
Length = 439

Score = 182 bits (463), Expect = 6e-44, Method: Compositional matrix adjust.
Identities = 156/447 (34%), Positives = 221/447 (49%), Gaps = 46/447 (10%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V P SKSL+R L+ AAL+ G + V+++L S D+ LR G +E A +V

Sbjct: 6 VTAPPSKSLSHRALIGAALAAGESTVEHVLESRDLTCTADILRAAGAHIE-RCAPGSYLV 64

Query: 79 VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G G P + V + +G R LTA + A G + + G PRM ERPIG+L

Sbjct: 65 RGVAGT-PAGGFEAPVSCDVHESGTTTCRLLTAVLAA--GMGRFRIHGAPRMHERPIGELT 121

Query: 139 VGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LG + PP+ ++ G+ GG+V + SSQYLS LL+AAPL G

Sbjct: 122 DALASLVQIAFEARAGFPPLVIDA-AGMRGGEVSGIMDESSQYLSGLLLAAPLTQGMTV 180

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWD-----RFYIK 237
++S PYV +TL+ +E FG+ E D+ D RF ++

Sbjct: 181 NVAGTSVVSWPYVGLTLQTLEDFGIDFTVETRDVAPWGAVDWRSLEAVPGLVRFVR 240

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Y++ + VEGD S ASYFLA A+ V VEG SLQGD ++L MGA

Sbjct: 241 PGM-YRA-GSYRVEGDWSGASYFLAAGAVGPRPVRVEGLRVDLSLQGDRAALLDILTAMGAD 298

Query: 298 VTWTETSVTVTGPPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
+ E V V P L ++V+M PD+ T+A VA FA G T +R+VA R

Sbjct: 299 IRPGEHVVVHPAP-----LHGVEVDMGHCPDLVPTVAAVAFAFATGRTVVRNVHLR 350

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADTYDDHRMAMAFS 411
+KE++R+ A EL + G + EE D ++ T P L + DHRMAM+ +

Sbjct: 351 IKESDRIAAPVGELRRAGVNAERADGLVVQGGALATEPGTL----FSAHGDHRMAMSLA 406

Query: 412 LAACAEPVVTIRDPGCTRKTFPDYFDV 438
L V V + DP C K+FP ++++

Sbjct: 407 LLGLGGVDVRLDDPSCVSKSFPFWEL 433

>ref|YP_001922269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
E3 str. Alaska E43]
sp|B2UYK7.1|ARO_CLOBA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD52475.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
E3 str. Alaska E43]
Length = 433

Score = 182 bits (463), Expect = 6e-44, Method: Compositional matrix adjust.
Identities = 133/431 (30%), Positives = 227/431 (52%), Gaps = 30/431 (6%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK+P SKS++R ++ AAL +G + + N+ S+D+ + A+R+LG + K
Sbjct: 10 KLGKEVKIPPSKSMHRGVICAALGDGISKIRNINYSDDIRATINAMRSLGAIIT--KED 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF---LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ ++G E K+ ++L +G +R L G++ ++ G +
Sbjct: 68 EYLHIIG---IKSECKKNIELNRTIDCNESGSTLRFLVPISCIFEGSSRFI--GKGNL 121

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ G G +R+ GI L G+ KL G ISSQ++S +L
Sbjct: 122 GKRPLDTYYEIFDNQGIKYSYKKGK--LDLRIQGI--LKYGEFKLRGDISSQFISGMLFT 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
PL GD +I I +L S Y+++TL M FG++ ++++ F IKG Q YKS +
Sbjct: 178 LPLLEGDSKIIITTELESKGYIDLTLSSAMDFGIEI-INNNYREFIIKGNQTYKSI-DYR 235

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+EGD S A++FL A+ V + SLQGD + E+LE M K+ + S+ G
Sbjct: 236 IEGDYSQAFFLVADALKS-EVFINDLKLESLQGDKEVIEILERMNMKIKNIDNSLL--G 292

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
PRE +L+A ++ ++ PD+ +++ A +G T I +V R+KE +R+ A+ +
Sbjct: 293 IPRE-----NLEATIIDGSQCPIIPVISLAASLCNGRTEIINVGRRLRIKCDRLSAVAS 347

Query: 370 ELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
EL KLGA++ E D II + L + ++ DHR+AM ++A+ C E P+ + D
Sbjct: 348 ELNKLGANIEEKEDSLIIDGVKTLKGGVKVWSHKDHRIAMMLAIASTVCME-PIILEDYE 406

Query: 427 CTRKTFPDYFD 437
C K++P++FD
Sbjct: 407 CISKSYPEFFD 417

>ref|ZP_07085696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chryseobacterium
gleum ATCC 35910]
gb|EFK36524.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chryseobacterium
gleum ATCC 35910]
Length = 408

Score = 182 bits (463), Expect = 7e-44, Method: Compositional matrix adjust.
Identities = 138/436 (31%), Positives = 222/436 (50%), Gaps = 49/436 (11%)

Query: 18 TVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV++ GSKS+SNR+L+L +L + NL NS+D + AL ++
Sbjct: 14 TVQISGSKSISNRLILLESLSFNSIKI-GNLSNSQDTQLKKAL-----SENTD 60

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
VV + +AG AMR LT+ + G T +L G RM+ERPI +L
Sbjct: 61 VVD-----IHHAGTAMRFLTSYYSIQEGKTT-ILTGSGRMKERPIKNL 102

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ LG +++ PP+++ G + V + +ISSQ++++LL+ A +
Sbjct: 103 VSALRDLGVEIEYMENEGFPPLKIRG-RKITQTSVNVNANISSQFITSLLLIAGKLENGL 161

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV-----EG 252
+I ++ ++ S Y+EMTL ++ +FG+++ S++ IK + + KNA V E
Sbjct: 162 QINLVGEVTSRSYIEMTLDTLTKFGIQS----SFEGNSIKV-EPFTPDKNAEVVHYEVES 216

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLE-MMGAKVTWTETSVTVTGPP 311
D SSASYF + A+ T+ ++ S QGD A + E G K T++E +T P
Sbjct: 217 DWSSASYFYFICALGRKTIHLKSFYKESTQGDSALAGIYEKFFGIKTTFSEDEHQLTLEP 276

Query: 312 REPFGKHLKAIIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ F + I ++MN PD+A TL V A P I + + RVKET+R++A+ EL
Sbjct: 277 QPDFSFP--EKIVLDMNCPDIAQTLCTVTAALKIPFEISGLGTLRVKETDRLLALYNEL 334

Query: 372 TKLGASVEEGPDYCI--ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
KLG E D I I+ E ++ TY DHRMAM+F+ C +TI D
Sbjct: 335 QKLGTTET-EITDLTIQSI SFKEPQEHSVKTYQDHRMAMSF-A PFCLIQELTIEDEDVVE 392

Query: 430 KTFPDYFDVLSTFVKN 445
K++P +++ L + + +
Sbjct: 393 KSYPMFWEDLESILTH 408

>gb|EFP93820.1| pentafunctional AROM polypeptide [Puccinia graminis f. sp. tritici
CRL 75-36-700-3]
Length = 1560

Score = 182 bits (462), Expect = 1e-43, Method: Compositional matrix adjust.
Identities = 139/387 (35%), Positives = 211/387 (54%), Gaps = 41/387 (10%)

Query: 86 PVEDAKEEVQLFLGNAGIAMRSLTAAVT----AAGGNATYVLDGVPRMRERPIGDLVVGL 141
P D K ++LGNAG A R LT + ++ V+ G RM+ERPIG LV L
Sbjct: 400 PAPDGK---HVYLGNAGTAARFLT TVCSLVKSQVSNQSSTVITGNARMQERPIGPLVDTL 456

Query: 142 KQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEI 201
+ G +D C P+R++ G PGG ++L+ S+SSQY+S++L++AP A V + +
Sbjct: 457 RTNGVQIDYLRNEGCLPLRISPEDGFP GGMIELAASVSSQYVSSVLSAPFAQAPVTLSL 516

Query: 202 I-DKLISIPYVEMTLRLMERFGVKAHSDS-----WDRFYIKGGQKYKSPKNAYVEGDA 254
+ +IS PY+++T+ +M FG++ E + + I G YK+P +E DA
Sbjct: 517 VGGAVISQPYIDITISMSTFGIQVERVKDPATGLPSNTYRIPNG-TYKNPPVYEIESDA 575

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPRE 313
SSA+Y LA AA+ G ++T+E G+ SLQGD +FA +VLE MG +V TE V GP
Sbjct: 576 SSATYPLAMAALNGLSITLETIGSGSLQGD AQFAKKVLEPMGCQVIQTERETKVIGPS-- 633

Query: 314 PFGRKHLKAI-DVNMNMPDVAMT----LAVVALFADG----PTAIRDVASWRVKETERM 364
L+ + +++M +M D +T L V A ++ T I +A+ RVKE R+
Sbjct: 634 --AVSELRLQLGEIDMEEMTDAFLTACVVLGVAAQHSEKEQRMSTRIIGIANQRVKECNRI 691

Query: 365 VAIRTELTKLGASVEEGPDYCI--TPPEKL----NVTADITYDDHRMAMAFSLAACAEV 418
A+ EL K+G +E D + TP + L + I+ YDDHR+AMAFS+ V
Sbjct: 692 AAMVAELGKMGIIHAQELEDGIEVFGTPVDALAKRGDQVRINCYDDHRIAMAFSV--LGTV 749

Query: 419 P----VTIRDPGCTRKTFPDYFDVLST 441
P + + + C KT+P ++D LST
Sbjct: 750 PGGKGLILNEKRCVEKTWPSWDDLST 776

>ref|ZP_01890962.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [unidentified
eubacterium SCB49]
gb|EDM43733.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [unidentified
eubacterium SCB49]
Length = 409

Score = 182 bits (462), Expect = 1e-43, Method: Compositional matrix adjust.
Identities = 134/426 (31%), Positives = 209/426 (49%), Gaps = 48/426 (11%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+KL GSKS +NR+L+L AL G + N S+D M+ AL + G ++
Sbjct: 17 IKLGGSKSEANRLVLQALFSGIEIT-NCSTSDSQTMMNALSSDGNLID----- 65

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
+ +AG AMR LTA G L G RM +RPIG LV
Sbjct: 66 -----VSHAGTAMRFLTAYFATQDGREV-TLTGSKRMLQRPIGLLV 105

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
LK LGAD+ PP+ + G L +V ++ ++SSQY+SAL++ AP ++
Sbjct: 106 DALKALGADISYVKNIYGPPLLIRG-KQLKANEVTIAANVSSQYISALMLIAPSLPEGLK 164

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKSPKNAYVEGDAS 255
I + + S+PY+ MTL+L+++ G + D+ R I G +K + VE D S
Sbjct: 165 IRLDGNVTSVPYINMTLQLLQGLGFEFGFEDNVVRVLPGAITGVKKIR-----VESDWS 218

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S SY A+T G +T SLQGD +++ + +G + + E +VT
Sbjct: 219 SVSYLYGLIALTQSGKLTSTTFKKESLQGDAAALSDIYQELGVETIFNEDD-SVTLQKISE 277

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ HL + N+ PD+A T+AV + + + ++KET+R+ A++ EL KL
Sbjct: 278 VTKAHL---EFNLINTPDIAQTIAVTCFGLGVSCTLTGLHTLKIKETDRFLALKVELEKL 334

Query: 375 GASVEEGPDYCIITPPEKLVN-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFF 433
GA V + ++ + AIDTY DHRMAMAF+ + +TI + K+FP
Sbjct: 335 GAQVHITENSLMLEKSTAIKAGVAIDTYQDHRMAMAF-PLVLKTSLTINEADVVSFSFP 393

Query: 434 DYFDVL 439
++++VL
Sbjct: 394 EFWEVL 399

>gb|AAT74841.1| AROM polypeptide [Tetrahymena thermophila]
Length = 1577

Score = 182 bits (462), Expect = 1e-43, Method: Composition-based stats.
Identities = 133/444 (29%), Positives = 223/444 (50%), Gaps = 33/444 (7%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
++L GSKS++NR+L+L+AL + + N+L +ED M+ +L+TLG A V
Sbjct: 382 IQLAGSKSITNRVLILSALLDKEIQLQNVLFADTEVMMKSLQTLGACSIQQLDANTVKV 441

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G GG F +D KE +++ N+G + R + + + N + V+ RM+ERPI DL+
Sbjct: 442 KNGGAFNFQDEKE---IYVNNSGTSARFICSMMLLLKPNQSVVIRCCERMKERPIKDLI 498

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L + + P RV GG + ++ ISSQY++ +LMAAP AL V
Sbjct: 499 EALSDF-LNFYELEKEFYLPFRVTKKYEFKGGDIHINSKISSQYVTGILMAAPYALEPVR 557

Query: 199 IEI--IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA-YVEGDAS 255
+ + +++ S P+++MT +M++FG + + + F I KY PK + Y+E DA+
Sbjct: 558 VILSQTEQITSEFFIQMTFDMMKQFGSNI-YREKQNIIFNIS-NTKYLYPKESYYIEPDAA 615

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
+ASY +A A + + ++G SLQGD+KF E L +G V + + V + G
Sbjct: 616 TASYDMAWAVLNQKKIIKGFQIHSQGLKFTKLVGLGYCVEYNDVGVIIRG----DL 671

Query: 316 GRKHLKAIDVNMNMKMPDVAMTLAVV--ALFADGPTA--IRDVASWRVKETERMVAIRTEL 371
+K + N D +T ++ AL + + I ++A+ RVKE +R+ A+ L
Sbjct: 672 PQKECTQTTFDFNDCTDTFITFGIILAALENNNNQSYKIVNIANQRVKECDRIHALSLNL 731

Query: 372 TKLGASVEEGPDYCIITPPEKLVN-TAIDT-----YDDHRMAMAFSLAAC----- 415
K G E D I P +K + D+ ++DHR+ MAFS
Sbjct: 732 KKFGIKTIEYDDGIEIFPNKKQLLEQCDKQSIIECFNDHRLGMAFSQLGNFIKKNKGQ 791

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVL 439
+ + + + C +KTFP +++ L
Sbjct: 792 NSLDIILDEGDCVKKTFPSFYNHL 815

>ref|YP_003871327.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Paenibacillus polymyxa E681]
gb|ADM70789.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Paenibacillus polymyxa E681]
Length = 430

Score = 182 bits (461), Expect = 1e-43, Method: Compositional matrix adjust.
Identities = 145/440 (32%), Positives = 226/440 (51%), Gaps = 22/440 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++P + G + SK+ + R LL AAL+EG + + +SED M + LG
Sbjct: 2 DVIVRPTPSLQGEIGALSSKNYTRYLLTAALAEGQSTIYYPAHSESDAMRRCIADLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D ++ V+ G G + KE L +GNAG +R L + + + T+V
Sbjct: 62 VLEEDD--EKIVITGFGSH--PQAVKE---LNVGNAGAVLRFLMG-IASLCADVTFFVNTY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+ L QLG VD G P+R+ G G GGK+++SGS+SSQYLSA
Sbjct: 114 PDSLGRPHDDLIDALGQLGVKVDHREGK--LPRIQG-GQAKGGKIQVSGSVSSQYLSA 170

Query: 186 LLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL PL D EIE++ L S + TL +++ G+ SD + F + G Q Y+ P
Sbjct: 171 LLFLTPLLEEDSEIEVLHDLKSKVIGQTLEVLQEAGIIHASDDYMSFRVPGRQSYQ-P 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V+GD ++ LA AA+T VT+ S QG+ +VL MM +T +V
Sbjct: 230 RTYTVQGDYPGSAAVLAATAVNSDVTIHLKEQSKQGERAIVDVLRMMEVPLTHENDTV 289

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G R LKA++ + + D + + A+FA+G + +V + R KE +R+
Sbjct: 290 VVKGNR-----LKAVEFDGDAATDAVLAMVAAVFAEGTSRFYNVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
ELTK GA VEE I+ PE + I+ + DHR+ MA ++ ++ P+ I
Sbjct: 343 DYLNELTKAGARVEERQAEIIVHGRPEGVEGGVEINAHFDRHVIMALTIVGLRSQKPLVI 402

Query: 423 RDPGCTRKTFFPDYFDVLSTF 442
+D K++P YFD L+T
Sbjct: 403 KDAHVAKSYPQYFDHLTTL 422

>ref|ZP_06475046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia symbiont of
Datisca glomerata]
gb|EFD28258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia symbiont of
Datisca glomerata]
Length = 440

Score = 182 bits (461), Expect = 1e-43, Method: Compositional matrix adjust.
Identities = 151/430 (35%), Positives = 221/430 (51%), Gaps = 29/430 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV +PGSKS +NR L+LAA+S GT+ + L S D M AL LG++V D
Sbjct: 19 RPVDATVTMPGSKSATNRALILAAISAGTSRLTRPLRSRDSLLMAALGELGVAVVDDHD 78

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G++P++ A ++ GNAG R A T A G+ V DG PRMRER
Sbjct: 79 DWL-----VHGRYPLQ-AAPARVDCGNAGTVARFTPALATLAHGD--VVFDGDPRMRER 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ L+ L+ LGA +D D P+ V+G G LPGG V + S SSQ +S LL+AAP
Sbjct: 131 PLTPLLDALRTLGAADG----DRMPLTVHGRGHLPGGAVTVDASTSSQLVSGLLLAAPR 186

Query: 193 ALGDVEIEIIL-DKLISIPYVEMTLRLMERFGVKA-----HSDSWDRFYIKGGQKYKSPK 246
V + + +L S PY+EMT+ + G E R+ + G +
Sbjct: 187 YDQGVTVRHVGTRLPSPWPLEMTVADLRVAGAAVEVDVDRRPGGEARWSVAAGPLHA--H 244

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +E D +SAS FLA AA TGG V + ++Q ++L MG T T +
Sbjct: 245 DRVIEPDINSASAFLLAAAAATGGRVVLADWPSGTVPGRMLPDLLTAMGCVCVCTLT+TAGLE 304

Query: 307 VTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V GP R L+ IDV+++ + A TL +A+ AD P+ +R +A R++ET+R+ A
Sbjct: 305 VRGPGR-----LRGIDVDLSDYGEAAPTTLALAVLADSPSRRLRGIAHLRLQETDRLGA 357

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426

+ EL +LGA + D ++ P L +D DHR+AMA+++ V + D
Sbjct: 358 LAAELGRLGADITVTDDGLAVS-PAPLTGARLDPRADHRLAMAYAVVGLVVPGLVDDIA 416

Query: 427 CTRKTFPDYF 436
T KT P YF

Sbjct: 417 TTGKTVP-YF 425

>ref|YP_003257006.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blattabacterium sp.
(Periplaneta americana) str. BPLAN]
gb|ACX83863.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blattabacterium sp.
(Periplaneta americana) str. BPLAN]
Length = 416

Score = 182 bits (461), Expect = 1e-43, Method: Compositional matrix adjust.
Identities = 128/433 (29%), Positives = 217/433 (50%), Gaps = 60/433 (13%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G+V + GSKS+SNR+L+L A+ ++NL N ED + +L + ++
Sbjct: 16 GSVSITGSKSVSNRLLILKAVYPDDIQIENLSNCEDTQVLKKSLSNSTSNILD----- 67

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ +AG AMR LT+ ++ G +L G RM+ERPI
Sbjct: 68 -----IHAGTAMRFLTSYLSVQEGKEV-ILTGSNRMKERPISV 105

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
LV LK+LG+++ PP+++ G + GG++ ++ ISSQY+S+L++ A
Sbjct: 106 LVEALKKLGSEIYYLEKVGYPPIKIFG-KKIFGGEIDINAKISSQYISSLMLIASTFQMG 164

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPNAYVEGDASS 256
++I + + + SIPY++MT L+ G+KA D +I G++ K K+ +E D SS
Sbjct: 165 LKIYLNENITSIPIKMTFDLLILAGIKAFWKDKI--IHIHPGKE-KGQKHFSIESDWSS 221

Query: 257 ASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLE-MMGAKVTWTETSVTVTG----- 309
ASY+ + I + +T+ SLQGD + + + E G + ++ +T+
Sbjct: 222 ASYYYYSMVTIAKSKHMTLSSYKNESLQGDREVSSIYEKYFGISTIFDKSIITLNKRLNFI 281

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
PPR I++++NK PD+A T+ V ++ + + ++KET+R+ A++
Sbjct: 282 PPR-----IINLDLNKTPDLAQITIVVTCSAIGIRCHLKGLETIKIKETDRLRLAKN 332

Query: 370 ELTKLGASVE-----EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
EL K G ++ E D+ K+N I TY DHRMAM+FS P+ I
Sbjct: 333 ELFKFGIKIKITNSCLEITDFFQKEINSKIN---IKTYQDHRMAMSFSPFGLL-YPIQIE 388

Query: 424 DPGCTRKTFPDYF 436
DP K++PD++
Sbjct: 389 DPNVVEKSYPDFW 401

>ref|YP_003096551.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Flavobacteriaceae
bacterium 3519-10]
gb|ACU08489.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Flavobacteriaceae
bacterium 3519-10]
Length = 410

Score = 181 bits (460), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 138/432 (31%), Positives = 211/432 (48%), Gaps = 50/432 (11%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+++ GSKS+SNR+L+L L + ++ NL +S+D + AL +DK
Sbjct: 13 TIEISGSKSISNRLLILQHLVKNIKII-NLSDSQDTQLLQEALN-----SDKDL---- 60

Query: 78 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+ + +AG AMR LT+ G T L G RM++RPI +L
Sbjct: 61 -----IDVHHAGTAMRFLTSYFAIQDGK-TVTLTGSAARMKQRPKLN 101

Query: 138 VVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ LGAD+ PP+++ G L V +S ISSQ++++L++ +
Sbjct: 102 VDALRDLGADIQYLENEGFPPLKIVG-KNLEKNTVTISADISSQFITSMLLVGAKLENGL 160

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYKSPKNAYVEG 252
+I + K+ S PY+EMTL+++ E + W I QK P VE
Sbjct: 161 QINLSGKITSKPYLEMTLKILRTL----EIPNQWTGNTISISPAIRSQKSSQPVFPVVES 216

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D SSASYF + AAI+ TV + SLQGD E+ T +E + +
Sbjct: 217 DWSSASYFYSLAAISRETVNLRCFKPYSLQGDSVLKEIYWKFFGVNTISEGAESRISLMP 276

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
EPF ++I ++MN PD+A TL V A P I +A+ +VKET+R++A++ EL
Sbjct: 277 EPFFSLP-ESISLDMNDPCDIAQTLCTATALQIPFGITGLATLKVKETDRLLALKNELF 335

Query: 373 KLGASVEEGPDYC----IITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
K+G VE D P E + I TY+DHRMAM+F+ C +TI +
Sbjct: 336 KIGCIVEITDDSISSVKFFDPNENI---CIATYNDHRMAMSFA-PYCLVKSLTIENAEVV 391

Query: 429 RKTFFPDYFDVLS 440
K++P ++D L+
Sbjct: 392 EKSYPKFWDDLN 403

>ref|ZP_03293534.1| hypothetical protein CLOHIR_01484 [Clostridium hiranonis DSM 13275]
gb|EEA84856.1| hypothetical protein CLOHIR_01484 [Clostridium hiranonis DSM 13275]
Length = 443

Score = 181 bits (460), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 135/448 (30%), Positives = 225/448 (50%), Gaps = 40/448 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I ++P K +SG V +P SKS ++R L+ AALSEG +++N+ S+D+ L A+++ G
Sbjct: 2 DIRIKPSK-LSGDVTIPPSKSFARALICAALSEGKSIINNIELSDDIKATLEAVKSFGA 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGN---AGIAMRSLTAAVTAAGGNATYV 122
K ++ + K E+ + + L + N +G +R + G +
Sbjct: 61 ---VSKVGDTISIEIGIRKNAGEEIEITDNDLHIINCNESGSTLRFMIPIAAVLGYKCRFE 117

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVD---CFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+ G + +RP+ + G + +L D G L G+ + G+IS
Sbjct: 118 MSG--NLGKRPLDVYYDIFDKNGVKYKGENYLEID-----GKLGAGEYDIPGNIS 166

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+++ +L A + D I I+D + S Y+++TL ++ FG++ EH D + +F IKG
Sbjct: 167 SQFITGMLFALSMLLEDDSVINILDNIESKSYIDITLASLKDFGIEIEH-DEYRKFRICKGN 225

Query: 240 QKYKSPK-----NAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
QKY + N Y VEGD S ++FL AI G V V+G S+QGD ++LE
Sbjct: 226 QKYNCKRENLDCEYTVEGDFSQGAFFLCADAI-GNDVNVKGLRRNSIQGDKATVDILER 284

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDV 353
MG + + E L + ++ PD+ L+V A FA+G T I +
Sbjct: 285 MGCERYVDECDDI-----KMKVNSLNSTVIDATDCPDIIPLVSVCAAFANGTTEIVNA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCII--TPPEKLN-VTAIDTYDDHRMAMAF 410
R+KE +R+ AI EL+KLGA++EE D II +KL + ++ DHR+ M
Sbjct: 338 KRLRIKCDRLSAINELSKLGANIEREDSLIYNGNKKLKGCEVWSHKDHRICMML 397

Query: 411 SLAAC-AEVPVTIRDPGCTRKTFFPDYFD 437
S+A+ E + I+D C K++P +F+
Sbjct: 398 SIASTICEEEIIVIKDAECISKSYPRFFE 425

>ref|YP_003301285.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermomonospora
curvata DSM 43183]
gb|ACY99247.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermomonospora
curvata DSM 43183]
Length = 425

Score = 181 bits (459), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 138/438 (31%), Positives = 213/438 (48%), Gaps = 34/438 (7%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA---DK 71

++ TV LPGSKS++NR L+LAAL+E T + L+S D M LR LG+ V+A D
Sbjct: 15 LAATVVLPGSKSMTNRALILAAALAEETRIVRPLHSRDTELMAQGLRELGVVDAEGDDW 74

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
G G V + +G AG MR L G T +DG PR R+

Sbjct: 75 LVTPGDHAGPAGP-----VHVDVGLAGTVMRFLPPVAALTRGQVT--IDGDPRARQ 123

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+ LGA++D G C P V+G G L GG V + S SSQ +S LL+AAP

Sbjct: 124 RMPRIIDALRALGAEIDDG-GRGCLPFTVHGRGSLAGGSVTIDASASSQLVSGLLLAAP 182

Query: 192 LALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKSPKN 247
VE+ + S P++ MT+R+++ G E + R ++GG++

Sbjct: 183 RFTKGVEVRHEGPPVPSAPHLAMTVRMLQDAGAVVETGRNLWRVAPGPLRGGEQ----- 236

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E D S+A+ FL A + GG VTV G + Q +L MG +V+ +TV

Sbjct: 237 -VIEPDLSNAAQFLGAALVAGGRVTVPGWPAETTQPGDALRHLLAEMGGRVSLGPQGLTV 295

Query: 308 TGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G L+ + ++ + ++ +A +A AD P+ + +A R ET+R+ A+

Sbjct: 296 -----HGDGTLRGLRADLRDVGELTPVIAAALADSPSRLTGTIAHLRGHETDRLAAL 348

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
E+ LG V PD I P L+ + TYDDHRM MA ++ A + + +

Sbjct: 349 ADEINALGGDVRRLLPDGLEIR-PRPLHGGLVRTYDDHRMVMAAAVLGLAVEGIVVENVAT 407

Query: 428 TRKTFPDYFDVLSTFVKN 445
KT P + ++ + ++

Sbjct: 408 VGKTLPGFTELWTGMLEG 425

>ref|YP_003178454.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halomicrobium mukohataei DSM 12286]
gb|ACV48747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halomicrobium mukohataei DSM 12286]
Length = 430

Score = 181 bits (459), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 148/434 (34%), Positives = 214/434 (49%), Gaps = 31/434 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT + P SKS ++R +L A ++G V D L+ S D + A+ G V

Sbjct: 10 VGGTARAPPSKSYTHRAILAAGYADGAVVHDPLV-SADTRATMRVATFAGGGVALRDEET 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G G+ D + N+G R +TA TAA G+ VL G +R RP

Sbjct: 69 VLDVTGFDGRPETPDDV---IDCANSGETTTLVTA--TAALGDGLTVLTGDESLRSRPQ 122

Query: 135 GDLVVGLK-QLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
G L+ + L + G P+ V G + GG+V + G +SSQY++ALLMA +

Sbjct: 123 GPLLDAITTDLGDAESTRGNGQAPLVVGG--AVDGGEVSIIPGDVSSQYITALLMAGAVT 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEG 252
G +++ + +L S PYV++TL ++ FG++AE + D F + GGQ Y Y V G

Sbjct: 181 DGGIDVHLETTELKSAPYVDITLEVLADFGIEAEA--TPDGFAVPGGQSYAPTDGEYHVP 238

Query: 253 DASSASYFLAGAAIT---GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSS--VTV 307
D SS SY LA A+ G T+T S QGD +++ MGA V W + + V

Sbjct: 239 DFSSISYLLAAGALASEDGLTIT---SAYPSAQGDTAIVDIVREMAGVDWDREAGEIEV 295

Query: 308 TGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
T P L ++V++ PD+ T+A + ADG T I D R KET+R+ A+

Sbjct: 296 TSAP-----LSGVEVSVADTPDLLPTIATLGAAADGTTTRIVDCEHVRYKETDRVSAM 347

Query: 368 RTELTKLASVEEGPDYCIITPPEK-LNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDP 425
LTK+GASVEE + I E L +D DHR+ MA S+A A+ T+

Sbjct: 348 AEALTKMGASVEERQETLTIHGGESDLQGATVDGRADHRIIMALSIAGLVADGTTTVDGI 407

Query: 426 GCTRKTFPDYFDVL 439
+FPD+FDVL

Sbjct: 408 EHVDVSFPDFFDVL 421

>ref|YP_003636308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulomonas
flavigena DSM 20109]
gb|ADG74109.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cellulomonas
flavigena DSM 20109]
Length = 443

Score = 181 bits (458), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 143/427 (33%), Positives = 214/427 (50%), Gaps = 23/427 (5%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKSLSNR L+LAAL++G + + +LL S D M GAL TLG+ V+
Sbjct: 18 LDATVAVPGSKSLSNRYLVLAALAQQGPSTLRSLLVSRDTRLMAGALETLGVQVD---LGG 74

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
AV V G + V + G AG MR L A A G + G RP+
Sbjct: 75 DAVGVTPGAL-----RGHVTVDCLAGTVMRFLPAVAALADGPVHF--KGDVEALVRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
G L+ L+ L VD P V+G G + GG+V + S SSQ++S LL+AA
Sbjct: 127 GPILLRALQALDVRVDEEGEPGHLPTTVHGTGAVRGGQVDVDASGSSQFVSGLLLAASRFD 186

Query: 194 LGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G L S+P++ MT+ +M GV + S + +++ G ++ +VE D
Sbjct: 187 QGLTVRHTGPTPLPSLPHIRMTVEVMRAAGVVDDSRP-EIWHVEPGPVAG--RDVHVEPD 243

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+ FL A + GG+V V G T+ Q ++L MGA V +TVT
Sbjct: 244 LSNAAPFLCAAMVAGGSVRVPWPATTTQPGGLLPDILTRMGATVALDGDVLTVT----- 298

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G ++ +D+++ ++A T+A +A+ D PT +R + R ET+R+ A+ E+T+
Sbjct: 299 --GTGEVRGVDLDRAGEIAPTIAALAVHGDSPTRLRGIGHLRGHETDRLAALAAEITR 356

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTTFP 433
LG E+ D +IT P L+ TY DHRMA A +L V + D T KT P
Sbjct: 357 LGGQCEQTS DGLVIT-PRTLHGGVWGTYADHRMATAGALVGLRVPGVEVEDVATTAKTLP 415

Query: 434 DYFDVLS 440
+ D+ +
Sbjct: 416 GFADLWA 422

>ref|ZP_06300243.1| hypothetical protein pah_c197o073 [Parachlamydia acanthamoebae str.
Hall's coccus]
gb|EFB40684.1| hypothetical protein pah_c197o073 [Parachlamydia acanthamoebae str.
Hall's coccus]
Length = 449

Score = 181 bits (458), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 143/423 (33%), Positives = 215/423 (50%), Gaps = 22/423 (5%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +P SKS + R +L A L++G +VV + L S D + M+ A R LG +E
Sbjct: 32 LTGEIGIPPSKSHTLRAILFATLAKGKSVVHHYLASPDYAMIEACRHLGAKIEVFPTCI 91

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR-ERP 133
+ G G GK A E + GN+GI +R TA A G+ V+ G +R +RP
Sbjct: 92 E--IRGTGGKI----AYAENVIDAGNSGIVLRFCTA--IGALGSLPIVITGDHSIRHQR 143

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+ GL QL G G PV + G + GK ++G SQ +SALL+AA A
Sbjct: 144 MQPLLEGLSQLGVSQSSMRGDGFAPVIIQG--PIKSGKTVINGE-DSQPVSAALLIAAFA 200

Query: 194 LGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G +EI ++ P++ +TL ++R G+ E+ + + + G Y+ + V GD
Sbjct: 201 EGSIEI-VVKNPGETPWINLTNLNWLDRLGIPYENHN-FTHYRLFNGACYEG-FDYTVPGD 257

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313

SSA++ +A A +T + V +QGD + V + MGAK+ + ET +
Sbjct: 258 FSSAAFPiAAALVTDSELVVRNIDMHDVQGDKELLSVFQRMGAKLHFDQTNILL---V 313

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G K L I V++N D L+V+A FADG T IR+ A R KE R+ +I TEL K
Sbjct: 314 KRGGK-LSGISVDINNFIIDSITILSVLACFADGETHIRNAAIARRKECNRITSIATELRK 372

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTF 432
+GA V E D I+ LN + +Y DHRM M+ ++AA A + C KTF
Sbjct: 373 MGADVSELEDGLIVR-KSILNGAQLHSYQDHRMVMSLTVAALGARGETLLTSTECVSKTF 431

Query: 433 PDY 435
P +
Sbjct: 432 PTF 434

>ref|YP_003935682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sticklandii DSM 519]
emb|CBH20777.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS) [Clostridium sticklandii]
Length = 428

Score = 181 bits (458), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 120/433 (27%), Positives = 228/433 (52%), Gaps = 21/433 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ ++P KE+SG + +P SKS+S+R ++ A+LS G + + N++ S+D+ A++ LG
Sbjct: 2 KVKVIEP-KELSGEISIPPSKISHRVIAAASLSSGVSEISNIVMSKDIKATCEAMKQLG 60

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ KA V + G + K + +G +R + + +++
Sbjct: 61 AEISEVKAENERVKLIKIEVFKAPKASIDC--NESGSTLRFMIPIAMMSNSEISFI-- 116

Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G ++ ERP+ + G + + P+++NG L G + G +SSQ+++
Sbjct: 117 GKGLVERPLDVYKIFDEQGIHYET--KDNKLPLKING--SLTPGTFDIRGDVSSQFIT 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L+ PL D +I I +L S Y+++T+ ++ ++G+ E+ D + FYIKG Q YK+
Sbjct: 173 GLMFVLPPLASDSKISITGELESKGYIDLTISVLSKYGIVIENDD-YKAFYIKGRQVYKA 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ VEGD S A+++L A G +T +SLQ D + ++++ M K++ + S
Sbjct: 232 C-DYRVEGDFSQAQFWLV-AGCLGEKITSRDLNESSLQADKEVIDIIKSMAGKISCEDNS 289

Query: 305 VTVTGPPEPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ K ++ +++PD+ L+V+A + G T +++ A R+KE++R+
Sbjct: 290 FIAQ-----KSQTKRTVIDASQIPDIIPVLSVLASVSKGTTIVKNGARLRIKESDRL 341

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIR 423
A +TEL KLGA ++E D II KL +D+++DHR+AMA ++A+ E V I
Sbjct: 342 TATKTELNLKGADIKEEGDTLIIKGVSKLRGANVDSWNDHRIAMAMAVASIRCEGSVID 401

Query: 424 DPGCTRKTFPDYF 436
K++P+++
Sbjct: 402 GASSVDKSYPNFW 414

>ref|ZP_06919663.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus ATCC 29083]
gb|EDY54251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sviveus ATCC 29083]
Length = 441

Score = 181 bits (458), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 138/434 (31%), Positives = 215/434 (49%), Gaps = 28/434 (6%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE----AD 70
+ TV +PGSKS++NR L+LAAL+ + L S D M ALR +G+ +E D
Sbjct: 20 VDATVHVPGSKSVTNRALVLAALASEPGWLRRLRSRDTLLMAAALREMGVGIEEGVGP 79

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V+ G + P + +GNAG MR L A G + DG PR
Sbjct: 80 GTGETWRVLPAGLRGPA-----TVDVGNAGTVMRFLPPVAALADGPIHF--DGDPRSY 130

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
ERP+ ++ L+ LGA +D G P+ V+G G L GG V++ S SSQ++SALL++
Sbjct: 131 ERPLTGVIALRALGARIDDD-GRGALPLTVHGGGALDGGPVEIDASSSSQFVSALLLSG 189

Query: 191 PLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKSPK 246
P VE+ L S+P++ MT+ ++ G + + +S + + + G +
Sbjct: 190 PRFNQGVVHRHTGSALPSMPHIRMTVDMLRAVGAQVDTPESGGEPNVWRVTPGALLG--R 247

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VE D S+A FLA A +TGG V + + Q + ++ MG TE +
Sbjct: 248 DLTVEPDLNALPFLAALVTGGKVVIPDWPARTTQPGDRLRKIFTMGGSCELTEYGLV 307

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
TG + ID ++ ++ ++ +A VA AD P+ +R V+ R+ ET+R+ A
Sbjct: 308 FTG-----SGAIHGIDADLGEVGLTPGIAAVALADSPSTLRGVSHLRLHETDRLAA 360

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPG 426
+ E+ +LG V E D I P +L+ TY+DHRMA A ++ A V I +
Sbjct: 361 LTKEINELGGDVTETADGLHIR-PRRLHGGIFHTYEDHRMATAGAVIGLAVEGVQIENVA 419

Query: 427 CTRKTFPDYFDVLS 440
T KT PD+ D+ S
Sbjct: 420 TTAKTLPDFPDMWS 433

>ref|YP_003968514.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ilyobacter polytropus
DSM 2926]
gb|ADO84166.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ilyobacter polytropus
DSM 2926]
Length = 422

Score = 181 bits (458), Expect = 3e-43, Method: Compositional matrix adjust.
Identities = 128/426 (30%), Positives = 225/426 (52%), Gaps = 26/426 (6%)

Query: 14 EISGTVKLPKSGKSLSNRILLALASEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
+++G V +P SKSLS+R ++ A+++G + V NL+ S+D+ + A+ LG+S+ K
Sbjct: 9 KLNGEVIIPPSKSLSHRAIIAGAMAKGKSNVTNLIMSDDIEATIEAMEALGVSI--SKGE 66

Query: 74 KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G G ++E + +G +R L A G ++ +G R+ +RP
Sbjct: 67 HEVDIEGTGTL-----VRKESTINCRESGSTVRFLVPISLLADGEVKFIGEG--RLAKRP 119

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ G + G D P+ + G L GG+ K+ G++SSQ+++ L+ P
Sbjct: 120 LTTFFNIFNDFGVKYE--RGKDYLPLTIKG--KLTGGRYKMKGNVSSQFITGLMYTLPKL 175

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D IEI L SI YV++TL ++++ G++ E+ D + F+IKG Q++K P N VEGD
Sbjct: 176 KEDSVIEITTPLESIGYVDLTLDMLKKSGIEIENKD-YKEFHIKGNQEFK-PVNYRVEGD 233

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S ++++ A + G + G SLQGD + +++ MG V T +T
Sbjct: 234 YSQGAFWMVAATLGAGLDCI-GLEKDSLQGDKEILDITKMGGIVKDTTKGLT-----S 286

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
F + ID +++ PD+ + V+A ++G T I + R+KE++R+ A+ TEL K
Sbjct: 287 EFTKTKGAVID--LSQCPDLGPVITVMASVSEGETRIVNAQRLRIKESDRITAMVTELNK 344

Query: 374 LGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
+GA + E D II +KL A + +++DHR+AMA ++A+ E + I +K+
Sbjct: 345 VGADITETEDGMIIRGVKKLKGAKVSSWNDHRIAMAMAVASTQCEEAIIIEGAESVKKS 404

Query: 432 FPDYFD 437
+P ++D
Sbjct: 405 YPHFWD 410

>ref|ZP_07356893.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
3_1_syn3]
gb|EFL87297.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfovibrio sp.
3_1_syn3]
Length = 481

Score = 180 bits (457), Expect = 3e-43, Method: Compositional matrix adjust.
Identities = 154/481 (32%), Positives = 220/481 (45%), Gaps = 68/481 (14%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-----D 70
TV P SKSLS+R L+ AAL+ G + V + L S D+ L G +EA
Sbjct: 12 TVTAPASKSLSHRYLIGAAAGGESTVRHTLESVDLECTRAILCGAGARMEALDASGNGA 71

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G P + + +G R LTA + A G + + G RM
Sbjct: 72 GNNSGWRVQLGGLGAPRGGRPLDCDVRESGTTCLRLTAVL--AAGEGLFRVHGSKRMH 129

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIG---GLPGGKVKLSGSISSQYLSALL 187
ERPIGDL L +LGA V CPP+ + G L G + L +SSQY S LL
Sbjct: 130 ERPIGDLTDALTRLGAGVAFEGKPGCPPLLLQAHGLNPALADGIIHLGMDMSSQYFSGLL 189

Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGV-----KAEHSDSWD----- 232
+AAP + +E+ K +S PYV +TL+ + FG+ + + W
Sbjct: 190 LAAPFCATPLSVELAGRKAVSWPYVGLTLQCLTDFGISFSVETRKNEAAPWQTLPEGDWR 249

Query: 233 -----RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLO 282
R ++ G Y+ P + VEGD S ASYFLA A+ V V G SLQ
Sbjct: 250 DLAEARPGCLRVTRPG-AYR-PGDTVEGDWSGASYFLAAGALGRRAVRVRGLRADSLQ 307

Query: 283 GDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVAL 342
GD +L+ MGA++ +VTV P E L + ++M PD+ T+AV+A
Sbjct: 308 GDRAMLGILQKMGARLEVEPDVTVY--PSE-----LHGVALDMGSCPDVPTVAVLAA 359

Query: 343 FADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT----- 388
FA G T I +VA R+KE++R+ A TEL K G +V+E D +++
Sbjct: 360 FAKGSTRISNVAHLRIKESDRINAPATELAKTGVTVDELSDGMLVSGTGGTGMGGRLRN 419

Query: 389 ---PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIR----DPGCTRKTFPDYFDVLST 441
P + ++DHRMAM+ +L + + +R DP RK+FP ++DV S
Sbjct: 420 RPAAPRLPEGATLSAHNDHRMAMSLALLGLRDPGLRVRRERLDDPTVVRKSFQFQWDVWSR 479

Query: 442 F 442
Sbjct: 480 L 480

>ref|ZP_07578367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotogales
bacterium mesG1.Ag.4.2]
gb|EFN46113.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotogales
bacterium mesG1.Ag.4.2]
Length = 429

Score = 180 bits (457), Expect = 3e-43, Method: Compositional matrix adjust.
Identities = 133/440 (30%), Positives = 227/440 (51%), Gaps = 23/440 (5%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I +SG + +PGSKS + R +L+AA+++G + + N L SED A R G
Sbjct: 2 IAFASKHNLSGKLSVPGSKSHIRAVLIAAMAKGVSTIRNPLPSEDCLAATRAARAFGSD 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-LDG 125
V+ +K G K P +D + GN+G TA +G + YV L G
Sbjct: 62 VKIEKGVTIKSSPEGLKIP-DDVID-----CGNSGTTFYFATAI---SGTSLDYVVLTG 112

Query: 126 VPRMRERPIGDLVVGLKQLGA-DVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
++R RP+ L+ +++LGA V +D PV V G + G + G +S QY+S
Sbjct: 113 DYQIRRRPVVKLLLEAMRKLGAFVTTTRSDSDAAPVIVKG--PMRAGTIVFDGKMS-QYIS 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYK 243
+L+A+ G IE+ K I PY++MT+ M G++ ++ + ++ F ++G Q YK
Sbjct: 170 GMLLASARLEGKTRIEV-QKAIERPYLQMTVDWMSEHGIEVKYDEKNYSFFEVEGPNQYK 228

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + + D S ++ L A +T + +E + QGD ++L+ MG VT +
Sbjct: 229 -PVDTAIPSDWESVAFPLVAALVTDSELVIEDLDLSGSQGDVAVIVDILKEMGGNVTLNRS 287

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
S ++ + G L+ I ++ + +PD L V A +A+G T + + S RVKET+R
Sbjct: 288 SNSL-----KAVGGTKLRGITIDCSDIPDALPILTVAAACYAEGDVTLTGIESIRVKETDR 342

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT-I 422
+ ++ EL+K+GAS+E+ II +KL + ++DHR+AM+ S+A VT +
Sbjct: 343 VEVMKRELSKMGASIEDTDHQMIIHGKKLTGAKVQSHDDHRVAMSLSVAGLFSEGVTEV 402

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
+ C +FP +F+++++
Sbjct: 403 SNAECVSVSFPGFELMNSI 422

>ref|YP_003947542.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus
polymyxa SC2]
gb|ADO57301.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus
polymyxa SC2]
Length = 430

Score = 180 bits (457), Expect = 3e-43, Method: Compositional matrix adjust.
Identities = 145/440 (32%), Positives = 226/440 (51%), Gaps = 22/440 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++P + G + SK+ + R LL AAL++G + + +SED M + LG
Sbjct: 2 DVIVRTPSLQGEIGALSSKNYTTRYLLTAALADGQSTIYYPAHSESDAMRRRCITDLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D ++ V+ G G + KE L +GNAG +R L + + + T+V
Sbjct: 62 VLEEDD--EKIVITGFGSH--PQAVKE---LNVGNAGAVLRFLMG--IASLCPDVTFFVNTY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+ L QLG VD G P+R+ G G GGK+++SGS+SSQYLSA
Sbjct: 114 PDSLGLKRPDLDLIDALGQLGVKVDHREGK--LPRIQGGQAKGGKIEVSGSVSSQYLSA 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL PL D EIE++ L S + TL +++ G+ SD + F + G Q Y+ P
Sbjct: 171 LLFLTPLLEEDSEIEVLHDLKSKVVIGQTLEVLQEAGITIHASDDYMSFRVPGRQSYQ-P 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V+GD ++ LA AA+T VT+ S QG+ +VL MM +T +V
Sbjct: 230 RTYTVQGDYPGSAAVLAAAAVTNSDVTIHLRLKEQSKQGERAIVDVLRMMEVPLTHENDTV 289

Query: 306 TVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G R LKAI+ + + D + + A+FA+G + +V + R KE +R+
Sbjct: 290 VVGKNGR-----LKAIEFDGDAATDAVLAMVAAVFAEGTSRFYNVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
EL+K GA VEE I+ PE + I+ + DHR+ MA ++ A+ P+ I
Sbjct: 343 DYLNELSKAGARVEERQAEIIVHGRPEGVEGGVEINAHYDHRVIMALTVVGLRAQKPLVI 402

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
+D K++P YFD L+T
Sbjct: 403 KDAHVVAKSYPQYFDHLTTL 422

>ref|YP_004099765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Intrasporangium
calvum DSM 43043]
gb|ADU49038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Intrasporangium
calvum DSM 43043]
Length = 475

Score = 180 bits (457), Expect = 4e-43, Method: Compositional matrix adjust.
Identities = 152/437 (34%), Positives = 216/437 (49%), Gaps = 37/437 (8%)

Query: 11 PIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-A 69
P + + TV LPSKSL+NR L+LAAL+ + + L S D M ALR LG+ ++

Sbjct: 39 PDRPVHATVLLPGSKSLTNRYLVLAALAGDRSRLRAPLRSRDTLLMADALRALGVRIDDV 98

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
D A V P E + +V++ G AG MR L A A G LDG P+

Sbjct: 99 DPDGDVAGSVDPDWLVSPPEHLRGDVRIDCGLAGTVMRFLPAVAALARGPVH--LDGDPQA 156

Query: 130 RERPIGDLVVGKQLGA--DVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
R RP+G ++ L+ LG D D +L P+ V+G G + GG V + S SSQ++SAL

Sbjct: 157 RVRPMGPVLESLRALGVELESDGYL-----PLTVHGRGSRVGGSVTMDASSSSQFVSAL 211

Query: 187 LMAAPLAGDVEIEIIDK---LISIPYVEMTLRLMERFGVKAHS--DSWDRFYIKGGQK 241
L+A A D I I + + S P++ MT+ + G + S D+W +

Sbjct: 212 LLAG--ARYDEGITIHHRGRPVPSQPHILMTVETLRDAGALVDDSEPDTW-----RV 261

Query: 242 YKSPKNAY---VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
S NA +E D S+A F+A A +TGGTV + G + Q E+L+ MGA V

Sbjct: 262 EPSEINALDVSIEPDLNAGPFVAAALVTGGTVRIPGWPQYTTQAGDLMREILD TMGADV 321

Query: 299 TWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
+TV G L ID++++ ++ T+A +A A P++IR VA R

Sbjct: 322 RLDRHGLTV-----IGSGELVGIDIDLHDAAE LPTVAALAA LASTPSSIRGVAHIRG 374

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEV 418
ET+R+ A+ EL LG +V E D I P L+ TY DHRMA A ++

Sbjct: 375 HETDRLAALTAELGSLGGAVTETEDGLRIA-PAPLHGGRFRTYHDHRMATAGAI VGLRVH 433

Query: 419 PVTIRDPGCTRKTFFPDY 435
VT+ D T KT PD+

Sbjct: 434 GVTVEDIETTSKTLPDF 450

>ref|ZP_03700952.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium MS024-3C]
gb|EEG43261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium MS024-3C]
Length = 417

Score = 180 bits (456), Expect = 4e-43, Method: Compositional matrix adjust.
Identities = 139/442 (31%), Positives = 219/442 (49%), Gaps = 61/442 (13%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ + + GSKS +NR+LLL AL ++ DNL NSED +A +

Sbjct: 16 LKAQIAITGSKSETNRLLLLQALFPVLSI-DNLSNSEDA-----QAMQ 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V +K V ++ +AG AMR LTA G + +L G RM+ERPI

Sbjct: 58 RGVA-----SSKGTVDIY--HAGTAMRFLTAYATQPG-VSIILTGSERMQERPI 104

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G LV L+ LGA++ PP+ + G + V+L+ +SSQY+SALL+

Sbjct: 105 GILVDALRNLGAEISYVKNEGYPPLAIKG-SEITQDSVQLNAGVSSQYISALLLVGARLK 163

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS-----PKN 247
+ + + K+ S+PY++MTL+L+E+ GVK + GQ+ K ++

Sbjct: 164 NGLTLALEGKITSVPYIKMTLKLLEKIGVKTKFE-----GQEIKVFPASDVFSQS 213

Query: 248 AYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VE D SSASY+ + A++ G V++ SLQGD ++ +G + T+ + +

Sbjct: 214 MVVESDWSSASYYSIALSDVGSEVSLSSYTPDSLQGDVAVLRDIYSHLGVTTFKKDQL 273

Query: 306 TV--TGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P + K L +++ PD+A T+AV + + + +KET+R

Sbjct: 274 VLAKVAAPSDAILEKGLAW---DLSNAPDIAQTIAVSCFGLGVACDLTGLHTLKIKETDR 330

Query: 364 MVAIRTELTKLGASV---EEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
+VA+ EL+KLGA + E+ K +VT I TY DHRMAMAF+ A VP+

Sbjct: 331 LVALENELSKLGAGLHITEKSLHLAAFNGSIKAHVT-IGTYHDHRMAMAFAPLAL-RVPI 388

Query: 421 TIRDPGCTRKTFFPDYFDVLSTF 442
I D G K++PD++ + T

Sbjct: 389 AIEDAGVVNKSYPDFWTDKMTL 410

>ref|YP_004273047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter saltans
DSM 12145]
gb|ADY51225.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter saltans
DSM 12145]
Length = 412

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 138/434 (31%), Positives = 216/434 (49%), Gaps = 52/434 (11%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K I+ T++L GSKS SNR L++ ALS+G ++NL ++ D +V D
Sbjct: 12 KNINQTIETLTSKSESNRALIIQALSKGKVQIENLSSAAD-----TVTLDN 58

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K A + +G AG AMR L + +T G N VL G RM++R
Sbjct: 59 LKNA-----AGNIAEANVGPAAGTAMRFLASYLTVKGINT--VLGTGTERMQR 104

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG LV L+ +G ++ PP+++ VK+ G ISSQY+++LL+ A
Sbjct: 105 PIGILVDALRHIGGEIVYIENEGFPPLQIPSQFIQKSEAVKIKGDISSQYITSLLLIASF 164

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ +EI +L S PYVEMTL +E+ G+K +W+ I + + VE
Sbjct: 165 LPKGLTLEIEGELTSRYPVEMTLGFLEQCGIKY---TWNDNKIAIPHQEFNESKLIVEP 220

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV---TVT 308
D S+ASY+ A AA+ T+T+ SLQGD E++ G K T+ ET + V+
Sbjct: 221 DWSAASYWYAFALADSATITLPYLRQNSLQGD SAIVEIMSHFGVKTTFNETGLILEKVS 280

Query: 309 GPPREPFGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P F ++ PD+A T+ VV+ + + ++KET+R+ A++
Sbjct: 281 TPLDSKF-----FDLKNCPDLAQTVIVVSAALGHEATFTGLETLKIKETDRIKALQ 331

Query: 369 TELTKLGAS-VEEGPDYCI---ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+L K+G +E+ +Y + + PEK+ I+TY+DHRMAMAF+ A V I
Sbjct: 332 EQLAKIGVKLIEKDLNYTLDCSGLHFPEKI---FINTYEDHRMAMAFAPLALFVKEVEIE 388

Query: 424 DPGCTRKTFPDYFD 437
+ K++P Y++
Sbjct: 389 EERVVDKSYPHYWE 402

>ref|ZP_06200730.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D20]
ref|ZP_07940229.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
4_1_36]
gb|EFA21855.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp. D20]
gb|EFV24529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
4_1_36]
Length = 438

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 146/459 (31%), Positives = 217/459 (47%), Gaps = 77/459 (16%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ ++LP SKS+SNR L+L +L+ G + NL + +D M AL
Sbjct: 11 LHAAIQLPASKSISNRALILHSLAHGNILPRNLSDCDDTIVMTRALD----- 57

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G G + AG AMR LTA ++ G T ++ G RM++RPI
Sbjct: 58 -----GNPGHIDIL-----AAGTAMRFLTAYLSVTPG--TRIITGTQRMQQRPI 99

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
LV L++LGA ++ PP+R+ G L G ++ L+G++SSQY+SALLM +
Sbjct: 100 RILVDALRELGARIEYVGNEGFPPLRITGTE-LTGSEISLAGNVSSQYISALLMIGTVLP 158

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ + + +IS PY+ +TL+LM FG +A+ S D + G +P VE D
Sbjct: 159 KGLRLHLTGDIISRPYINLTQLMRDFGAQADWV-SEDCITVSPGGYTDPFT--VESDW 215

Query: 255 SSASYFLAGAAITG-----GTVTVE--GCGTTSLQGDVKF 287
S+ASY+ AI G T +E G S QGD +
Sbjct: 216 SAASYWYQMAIEGKNEKIKGGDRSSAKESDSTKEEAHTAEIELLGLFAHSYQGDSRG 275

Query: 288 AEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKA--IDVNMNMPDVAMTLAVVALFAD 345
AEV +G +T+ V +T RK A +D +M +PD+A T V D
Sbjct: 276 AEVFTRLGVHTEYTDGRGVKLT-----RKGT PATRLDEDMVDIPDLAQTFVVTCLMD 327

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A--IDTYD 402
P + S ++KET+R+ A+ TEL KLG V D ++ E+ A I TY+
Sbjct: 328 IPFRFTGLQSLKIKETDRITALITELRKLGYVVRSEQDSILLWDGERCPADADPVIATYE 387

Query: 403 DHRMAMAFSLAACAEVP-VTIRDPGCTRKTFPDYFDVLS 440
DHRMAMAF+ AC +P + I +P K++P Y++ L
Sbjct: 388 DHRMAMAF+ PACLVLPQIRINEPQVVTKSYPAYWEDLQ 425

>ref|ZP_02861638.1| hypothetical protein ANASTE_00845 [Anaerofustis stercorihominis DSM 17244]
gb|EDS73128.1| hypothetical protein ANASTE_00845 [Anaerofustis stercorihominis DSM 17244]
Length = 412

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 132/437 (30%), Positives = 220/437 (50%), Gaps = 46/437 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I + P K + G V +P SKS+++R ++ AALS+G +V+DN+ S+D+ + A+++G
Sbjct: 2 DNIKITPNK-LKGKVNIPPSKSMRAHRAICAALSKGKSVIDNIELSDDIIATISAVKSMG 60

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D R V + P E + + +G +R G T++
Sbjct: 61 AKVTTDN--RKVTIEGILNSPKE---SDFTVDCNESGSTLRFFVPITMLLKGEKTFI-- 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + G ++ + D + V+G L ++ G ISSQ+++
Sbjct: 113 GKGNLGKRPLDVFNIFDKQG--IEYYYEKDILNLTVDG--RLKADTFEVRGDISSQFIT 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LL PL GD +I I L S Y+++TL ++E+FG+K ++D + F IKG Q+YK+
Sbjct: 169 GLLFTLPLLEGDSKIVITTDLESKSYLDLTLSMLEKFGIKIINND-YKEFIKGNQEYKA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD---VKFAEVLEMMGAKVTWT 301
+ VEGD S A++FL+ A G + V G TSLQGD +K+ +VL KV
Sbjct: 228 -MDYTVVEGDYSQAFFLS-ANYLGSDIDVLGLDDTSLQGDKEIKWIDVLNSSEKVV-- 282

Query: 302 ETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
++ PD+ L V A G T I + R+KE
Sbjct: 283 -----IDAANCPDIIPVLTVCAALTKGETRIINAGRLRIKEC 319

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPV 420
+R+ AI EL+KLGA + E D +I E L +D++ DHR++M+ ++A+ A+ +
Sbjct: 320 DRLNAISKELSKLGAKEIENEDNLVIEGVESLKGKIVDSHKDHRISMSMAIASTAAKDDI 379

Query: 421 TIRDPGCTRKTFPDYFD 437
I+D C RK++P +F+
Sbjct: 380 IIKDYMCVRKSYPTFFE 396

>ref|ZP_00959872.1| hypothetical protein ISM_08555 [Roseovarius nubinhibens ISM]
gb|EAP78334.1| hypothetical protein ISM_08555 [Roseovarius nubinhibens ISM]
Length = 385

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 137/415 (33%), Positives = 210/415 (50%), Gaps = 43/415 (10%)

Query: 34 LAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEE 93
+AAL++GT+ + LL S+D +M+ ALR +G+ +E + + + G GG + +
Sbjct: 1 MAALAQGTSTLTGLLRSDDRHMMTALRQMGVEIE-ELSETSLRITGQGGL-----RQPD 54

Query: 94 VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG 153

LFLGNAG A+R LTAAV G T + G M+ RPI L+ L LG V
Sbjct: 55 APLFLGNAGTAVRFLTAVALVDGPVT--ITGDEHMQNRPIAPLIDTLVSLG--VAAKAP 110

Query: 154 TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVE 212
 T CPPV + G G G V +SG++SSQY+SA+++ A +A + I I K+ ++ Y++
Sbjct: 111 TGCPPVEIMGTGAFTGTDVTVSGALSSQYISAIMILAAMAKDETRIHIEGGKIGAVGYLQ 170

Query: 213 MTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVT 272
 +T +M FG + + +R I+ G Y++ A +E DAS+A+Y A +TGG +
Sbjct: 171 ITAAMVRAFGAEVSFP-AENRIVIQPG-GYRAADYA-IEPDASAATYLVAAEVLTTGGEID 227

Query: 273 VEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFRKHLKAIDVNMNKMMPD 332
 + Q D ++ P P ++ ++M D
Sbjct: 228 TGAEPASMNQPDAAAHALIAAF-----PDMP-----AEIEGSMQMD 263

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE--EGPDYCIITPP 390
 TLAV+A F P +A+ RVKE +R+ A+R LT++ A + EG D + P
Sbjct: 264 AIPTLAVLAAFNTRPVRFTGIANLRVKECDRVEALRDGLTRIRADLATVEGDDLIVHADP 323

Query: 391 E---KLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
 + ID+Y DHR+AM F+LA +TI DP C KTFP+Y+ VL +
Sbjct: 324 ALSGQTQPARIDSYADHRIAMCFALAGLRIHGITIEDPCVSKTFPNYWAVLES 378

>ref|ZP_07717729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromicrobium marinum
DSM 15272]
gb|EFQ82964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeromicrobium marinum
DSM 15272]
Length = 425

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 148/440 (33%), Positives = 222/440 (50%), Gaps = 29/440 (6%)

Query: 9 LQPIKE--ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
 L P ++ + G V +PGSKSL+NR L+LAA+++G + + L S D M+GAL LG
Sbjct: 8 LAPHRDSPVVGVRVIVPGSKSLTNRALVLAADVADGPSTLRRALGSRDTSMLMIGALTALGAE 67

Query: 67 VEAD--KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 V D + R + G G V+ G AG MR + A AA G A D
Sbjct: 68 VTRDGLEWTVRPLDTGRTGAVAVD-----CGLAGTVMRFPVA--LAALGRARVTFD 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
 G R RERP+ + L++LG +VD G P V+G GG+ GG++++ S SSQ++S
Sbjct: 117 GDERARERPMAATTIGSLRRLGVEVDD-RGAGSLPFTVHGQGGVRRGRLEIDASASSQFVS 175

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
 ALL+AAP + +++ D L S P++ MT+ + GV D R+ ++ G
Sbjct: 176 ALLLAAPRFVEGLDLHHTGDTLPSAPHIAMTVAQLRDRGVVH--DDVTRWRVEPGPVAA 233

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTET 303
 + + +E D S+A F+A A +T G VTV + Q + + E G
Sbjct: 234 T--DLEIEPDLNAGVFVAAALVTAGEVTVRHWPAATDQAGDAWRTITEAFGGTAHREGD 291

Query: 304 SVTVTGPPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
 V TGP R L +D+++ + ++A +A VA FAD P+ +R +A R ET+R
Sbjct: 292 DVVFTGPDR-----LAGVDLDRDVGELAPVVAVAFAADRSTLRGIAHLRGHETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIR 423
 + A+ TE+ +LG V E PD I P L+ + TY DHRMA A + A V +
Sbjct: 345 LAALATEINRLGGDVSETPDGLEIR-PRPLHGDVVRTYHDHRMAHAHVLLALRVDPVFVE 403

Query: 424 DPGCTRKTFPDYFDVLSTFV 443
 + T KT+P++ V V
Sbjct: 404 NVVTTVKTYPNFAPVWERLV 423

>ref|ZP_07607719.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
violaceusniger Tu 4113]
gb|EFN16825.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
violaceusniger Tu 4113]
Length = 458

Score = 180 bits (456), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 138/437 (31%), Positives = 219/437 (50%), Gaps = 36/437 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---ADK 71
++ TV +PGSKS++NR L+LAAL+ + L S D M ALR +G+ +E +D
Sbjct: 24 VAATVTVPGSKSVTNRGLILAAALAEPGWLRRLRSRDTLLMAAALRAMGVGIEETVSDG 83

Query: 72 A-----AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
A A R + G G ++ +GNAG MR L A G
Sbjct: 84 ALGSGGPSGGGEAWRVIPAGLHGPATID-----VGNAGTVMRFLPPVAALADGPVH 134

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ DG PR ERP+ ++ L+ LGA +D G P+ V+G G L GG V++ S SS
Sbjct: 135 F--DGDPRSHERPLHGVIDALRALGARIDDD--GRGALPMTVHGGGALDGGPVRIDASSSS 191

Query: 181 QYLSALLMAAPLALGDVEIEIIDK-LISIPYVEMTLRLMERFGVKAHSDSW-DRFYIKG 238
Q++SALL++AP VE+ I L S+P++ MT+ ++ G + + +++ +R +
Sbjct: 192 QFVSALLLSAPRFNQGEVVRHIGAALPSLPHIRMTVDMLRAAGARVDTAEAGGERGVWRV 251

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ VE D S+A+ FLA A +TGG VT+ + Q + + MG
Sbjct: 252 APSALLGRDLVVEPDLSNAAPFLAAALVTGGRVTIPDWPDRTTQPGDELRRIFTEMGGSY 311

Query: 299 TWTETSVTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
T+ +T TG R + ID +++++ ++ +A VA AD + +R +A R+
Sbjct: 312 DLTDAGLTFTGTGR-----ITGIDADLHEVGELTPVIAAVALADSESVLRGIAHLRL 364

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
ET+R+ A+ E+ +LG V E D I P L+ TY+DHR+A A ++ A
Sbjct: 365 HETDRLAALAKEINELGGDVAETEDGLRIR-PRPLHGGIFHTYEDHRLATAAAVLGLAVD 423

Query: 419 PVTIRDPGCTRKTFPDY 435
V + + T KT PD+
Sbjct: 424 GVLVENVSTTAKTLPDF 440

>ref|YP_003958696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium limosum
KIST612]
gb|ADO35733.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium limosum
KIST612]
Length = 402

Score = 179 bits (455), Expect = 5e-43, Method: Compositional matrix adjust.
Identities = 134/408 (32%), Positives = 209/408 (51%), Gaps = 39/408 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK- 71
K++ GT+ +P SKS+S+R ++ AALS+GT+V+ N+L S+D+ A+ LG ++ ++
Sbjct: 9 KKLGGTICIPPSKSVSHRAVMCAALSQGTSVITNILLSDDITATCKAMEILGAEIKYEEN 68

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
KR + G P + K + +G +R + + N+ + G R+ E
Sbjct: 69 EEKRFTLTITGVSHPDTEGK---TIDCIESGSTLRFIPLLALKARNSRVI--GRGRLVE 123

Query: 132 RPIG-----DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQ 181
RP+ D+ + G ++ CF GT P G +L+GSISSQ
Sbjct: 124 RMPQPPYDIFEEQDITYQKETEGQELPLCFTGTLKP-----GAYRLNGSISSQ 171

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+++ LL A PL GD IEI L S PY+++TL +ME+FG+ + D + F I G Q+
Sbjct: 172 FITGLLFALPLLDGDSVIEITPLESRPYIDITLDVMEKFGIAVVNED-YHLFRIAGNQ 230

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y + ++ VEGD S +++L G I G E + S QGD E+++ MG V T
Sbjct: 231 YMA-RDYRVEGDFSQGAFWLVGG-ILGKKTDCEDLQASSQGDKAIEIIQAMGGNVAQT 288

Query: 302 ETSVTVTGPPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E VT P G H VN+++ PD+ L V+A + G T I A R KE+
Sbjct: 289 EKGY-VTKP-----GSTH--GAVNVNSQCPDLVPVLTVLAALSQGTTEIVGAARLRFKES 340

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409

+R+ A+ LT LGA + E P+ I E +D+++DHR+AMA
Sbjct: 341 DRLAAMNEVLTTLGAKLTEHPEGMTIEGVEHFTGGVVD SHNDHRIAMA 388

>ref|ZP_02428786.1| hypothetical protein CLORAM_02197 [Clostridium ramosum DSM 1402]
gb|EDS17413.1| hypothetical protein CLORAM_02197 [Clostridium ramosum DSM 1402]
Length = 426

Score = 179 bits (455), Expect = 6e-43, Method: Compositional matrix adjust.
Identities = 124/425 (29%), Positives = 223/425 (52%), Gaps = 25/425 (5%)

Query: 14 EISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V++P SKSL++R ++ A+L++G + +DN+ S+D+ + A+++LG +E K
Sbjct: 10 KLSGVVQVPPSKSLAHRRAIICASLAKGISRIDNIEYSKDIQATIKAMQSLGKIE--KYD 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G K+ ++ +G +R + A +V G + +RP
Sbjct: 68 DYLIIDGTTY-----TKQNSEIDCEESGSTLRFMVPIAIVEENKAHFV--GRGNLGKRP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ ++ D + V IG L K+ G+ISSQ+++ LL A PL
Sbjct: 121 LNTFYEIFER--QNIGYLYKEDILDLYV--IGKLKPDHYKVPGNISSQFITGLLFALPLL 176

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD IEI L S Y+++TL+++ ++G+K ++D + F + G Q+Y++ + VE D
Sbjct: 177 DGDSIIIEITSPLESKYIDLTLQMLNQYGIKIVNND-YKSFIVMGKQEYQA-HDYRVEAD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S A+++L AI G V + SLQGD E LE MGAK++ + VTG
Sbjct: 235 FSQAAYFLVAGAI-GNDVVLTDNLDSLQGDKATLEFLEAMGAKISVVSDGIKVTG---- 289

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++L A V+ ++ PDV ++V A G + + + R+KE +R++A R++L +
Sbjct: 290 ----ENLAATIVDASQCPDVIPVVSVALALAQGKSDVINAKRLRIKCDRIIATRSQLNE 345

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTF 432
LG +V E PD I + ++ DHR+AM ++AA + PV I + C K++
Sbjct: 346 LGGTVTELPDGMTIRGVNEFTGGNCSSFADHRIAMMLAIAATRSSQPVIDNMECVEKSY 405

Query: 433 PDYFD 437
P++++
Sbjct: 406 PNFWE 410

>ref|YP_565758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcoides
burtonii DSM 6242]
sp|Q12X18.1|AROAMETBU RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABE52008.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanococcoides
burtonii DSM 6242]
Length = 427

Score = 179 bits (455), Expect = 6e-43, Method: Compositional matrix adjust.
Identities = 149/429 (34%), Positives = 218/429 (50%), Gaps = 21/429 (4%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + P SKS ++R + +AALS+ +++ L S D + A LG +E D
Sbjct: 10 VHGEIFAPASKSYTHRAITVAALSK-ESIIHRPLISADTQSTIKACEMLGAYIEKD--GD 66

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ ++ G G+ D +V GN+G +R +TA AA G T VL G +R RP
Sbjct: 67 KLLISGVDGEPQTPDNVIDV----GNSGTTLRFMFTA--IAALGQGTTLTGDNSIRSRPN 120

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ L LG G C P+ V G GL G K+ GSISSQ++SALL+A PL
Sbjct: 121 GPLLQVLNDLVGQSISTRGDGCAPIVVTG--GLKGAIKIDGSISSQFISALLLACPLTK 178

Query: 195 GDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEGD 253
+ I +L S PYV++TL ++E+ G + D+ + +F I G QKY+ K V GD

Sbjct: 179 NSTTSLIKGELKSRPYVDVTLTDILEKAGAEIYLEDNQNLKFIIPGNQKYR-LKEYTVPGD 237

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313

SSASY LA AA+T + V S+QGD ++L+ MGA + W + TV E

Sbjct: 238 FSSASYLLAAAAMTDTKIKVNNL-YPSMQGDAAIIDILKEMGANIYWNKEEGTV-----E 291

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373

G K L I ++ PD+ T+AV+ A+G T I + R KET+R+ A+ EL K

Sbjct: 292 VNGGK-LHGITMDAGATPDLVPTVAVLGAVAEGETVITNAEHVRYKETDRLHAMAVELDK 350

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFF 433

+G S E D I E L + + DHR+ M+ +LA TI ++P

Sbjct: 351 MGISTSEKDKLTIKGGE-LKGADVHGWHDRIVMSLTLAGMIAGDTTIDTAEAFISYP 409

Query: 434 DYFDVLSTF 442

++FD + +

Sbjct: 410 NFFDSMRSI 418

>ref|YP_002959959.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermococcus
gammatolerans EJ3]
gb|ACS34095.1| 3-phosphoshikimate 1-carboxyvinyltransferase (aroA) [Thermococcus
gammatolerans EJ3]
Length = 398

Score = 179 bits (454), Expect = 7e-43, Method: Compositional matrix adjust.
Identities = 138/431 (32%), Positives = 210/431 (48%), Gaps = 42/431 (9%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66

++++P+ + G V+ P SKS ++R LA L++G + ++ L S+D L A+R G

Sbjct: 1 MIVEPVDWLEGKVRAPPSKSYTHRAFFLALLADGESTIEEPLVSDDTEATLNIRAFAE 60

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126

+ ++ P E K E+ +G R A + A G + V+DG

Sbjct: 61 ADWNRVVP-----PEELRKAIEIN--ARESGTTARISVAVASLARGRS--VIDGQ 105

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

R+RERP LV L+ LG V G P + GG+PGG+V + S+SSQ+++AL

Sbjct: 106 GRLRERPFAPLVRALRSLGVTVR---GEKLP---IEVFGGMPGGRVSVSDASLSSQFVTAL 159

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

L+ A VE E K +S PY+EMTLR ME FGV E + F G K+ P

Sbjct: 160 LILASKVGMRVEFE---KAVSKPYIEMTLRTMEAFGVTFERNGGVRVFPGVKGTKFHP- 215

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306

GD SSAS+FL A+ G V VE +Q D+ E+L +GA V V

Sbjct: 216 -----GDYSSASFFLVAGALY-GRVVRVENLDPGDVQADMAIVEILGEIGANVKVGGDYVE 269

Query: 307 VTGPPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366

V+ R L+ ++N + PD+ L+V+A +A+G + IR R KE++R+ A

Sbjct: 270 VS-----RGELRGFEINCSDFPDLFPILSVLAAYAEGRSVIRG-RQLRYKESDRVRA 320

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEVPVTIRD 425

+ L + G V E D I V ++ ++DHR+AMA + L A I++

Sbjct: 321 MAVNLRAGIKVRELEDGLEIHGGRPRGVV-VEFDNDRVAMAMAVLGLGARGKTVIKNE 379

Query: 426 GCTRKTFFPDYF 436

K++P +F

Sbjct: 380 RVVAKSYPGFF 390

>ref|YP_003241998.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
Y412MC10]
gb|ACX64191.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus sp.
Y412MC10]
Length = 430

Score = 179 bits (453), Expect = 9e-43, Method: Compositional matrix adjust.
Identities = 149/441 (33%), Positives = 227/441 (51%), Gaps = 24/441 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

+++++P + G + SK+ + R LL+AAL+EGT+ + +SED M +R LG
Sbjct: 2 DVIVRPTPIKGEIGALSSKNYTTRYLLVAALAEGTSTIYYPAHSESDAMRRRCIRDIGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D+ ++AV+ G G K P D KE L +GNAG +R L VTA T+V

Sbjct: 62 VIEEDE--EKAIVITFGG-KSP-RDVKE---LNVGNAGAVLRFLMG-VTALSKEVTFVNAY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLP-GGKVKLSGSISSQYLS 184
+ +RP DL+ L QLG +V+ G +R GG P GGK+ +SG +SSQYLS

Sbjct: 114 PESLGKRPHDDLITLGLGVEVEHNDGRLPITIR----GGQPKGGKLTVSGEVSSQYLS 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL PL D EI + L S + TL ++E+ G+ + +D + F + GGQ Y++

Sbjct: 170 ALLFLTPLLAEDSEITVTGDLKSKVIGQTLLEVLEQAGITITQAADDYTFFRVPGGQSYEA 229

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K V+GD ++ LA AA+T VT+ S QG+ +VL MM +T +

Sbjct: 230 -KTYTVQGDYPGSAAVLAAAATQSDVTIRNLSEDSKQGERAIIIDVLRMMEVPLTHENG 288

Query: 305 VVTGTPPREPFGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V G + LKA+ + + D + + A+FA+G + +V + R KE +R+

Sbjct: 289 VHVQ-----GNRTLKALQFDGAATDAVLAMVAAAVFAEGTSRFFYNVENLRYKECDRI 341

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVT 421
TEL K GA+VEE I+ P I+ + DHR+ MA ++ A P+

Sbjct: 342 TDYLTELRLKAGANVEERQAEIIVHGRPGGVEGGVEINAHYDHRVIMALTVVGLRAGQPIR 401

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I+D K++P YFD +

Sbjct: 402 IKDAHVAKSYPQYFDHMKAL 422

>ref|ZP_04564427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mollicutes bacterium
D7]
gb|EEO33118.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coprobacillus sp. D7]
Length = 426

Score = 179 bits (453), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 124/425 (29%), Positives = 222/425 (52%), Gaps = 25/425 (5%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V++P SKSL++R ++ A+L++G + +DN+ S+D+ + A+++LG +E K

Sbjct: 10 KLSGVVQVPSPKSLAHRRAIICASLAKGISRIDNIEYSKDIQATIKAMQSLGTKIE--KYD 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
++ G K+ ++ +G +R + A +V G + +RP

Sbjct: 68 DYLIIDGTTY-----TKQNSEIDCEESGSLRFMVPIAIVEENKAHFV--GRGNLGRK 120

Query: 134 IGDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ ++ D + V IG L K+ G+ISSQ+++ LL A PL

Sbjct: 121 LNTFYEIFER--QNIGYLYKEDILDLYV--IGKLPDHYKVPGNISSQFITGLLFALPLL 176

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD IEI L S Y+++TL+++ ++G+K ++D + F + G Q+Y++ + VE D

Sbjct: 177 DGDSIIIEITSPLESKYIDLTLQMLNQYGIKIVNND-YKSFIVMGKQEYQA-HDYRVEAD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S A+++L AI G V + SLQGD E LE MGA++ + VTG

Sbjct: 235 FSQAAYFLVAGAI-GNDVVLTDNLDSLQGDKATLEFLEAMGAKISVVSDGIKVTG---- 289

Query: 314 PFGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++L A V+ ++ PDV ++V A G + + + R+KE +R++A R++L +

Sbjct: 290 ----ENLAATIVDASQCPDVPVVSVALALAQGKSDVINAKRLRIKECDRIIATRSQ 345

Query: 374 LGASVEEGPDYCIITPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTF 432
LG +V E PD I + ++ DHR+AM ++AA + PV I + C K++

Sbjct: 346 LGGTVTELPDGMTIRGVNEFTGGNCSSFADHRIAMMLAIAATRSSQPVVIDNMECVEKSY 405

Query: 433 PDYFD 437
P +++

Sbjct: 406 PSFWE 410

>ref|YP_003860848.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Maribacter
sp. HTCC2170]
gb|EAR00814.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Maribacter
sp. HTCC2170]
Length = 409

Score = 179 bits (453), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 136/437 (31%), Positives = 214/437 (48%), Gaps = 56/437 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ +V++ GSKS SNR LLL AL ++ +NL NS+D M +
Sbjct: 13 LNSSVQITGSKSESNSRLLQLALYPNISI-ENLSNSDDAEVM-----Q 54

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ + + G ++ + +AG AMR LT A+ + VL G RM ERP+
Sbjct: 55 KGLAISNG-----EVDIHAGTAMRFLTGYF-ASQPDKEVVLTSQRMTERPV 101

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
LV LK LGAD++ PP+++ + +V L +ISSQY+S+LL+ AP
Sbjct: 102 KVLVDALKNLGADIEYVNEGYPPIKI-KGKKIQKHQVSLPANISSQYISSLLLIAPSLE 160

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA----- 248
+E+ ++ ++ S+PY++MTL L+ + GV+ SD+ + PKN
Sbjct: 161 NGLELNLVGEITSVPYIKMTLGLLNQIGVETSFSDNIKVL-----PKNNVGRTEL 211

Query: 249 YVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VE D SSASYF + A++ G + + SLQGD A + E G T+ +
Sbjct: 212 VVESDWSASASYFYSIVALSKVGSEIKLGSYKRDSLQGDSVLANIYESFGVDITTFVNNEIV 271

Query: 307 VTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+T L I+ ++ PD+A T+AV L +R + + ++KET+R+VA
Sbjct: 272 LTKTQ----DCSLDLIECDLANAPDIAQTIQIAVTCLGLGIGCELRLGLHTLTKIKETDRLVA 326

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLN-VAIDTYDDHRMAMAFSLAACAEVPVITRDP 425
+ ELTK GA V + + + ++DTY+DHRMAMAF A + I D
Sbjct: 327 MHDELTKFGADVVTNETLTLKKSNSIKSGVSVDTYNDHRMAMAFGLPAL-KTSFNINDA 385

Query: 426 GCTRKTFPDYFDVLSTF 442
K++PD++ L T
Sbjct: 386 EVVSKSYPDFWKDLET 402

>gb|EFS56521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL046PA2]
gb|EFS58295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL036PA1]
gb|EFS60329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL036PA2]
gb|EFS88775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL036PA3]
gb|EFT04632.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL002PA2]
gb|EFT57376.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL002PA3]
Length = 429

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 219/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTPGSKSQTNRALVLAALSDGPSVLEGLASRDSYLSAGLQLLGADIQPIGPS 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+

Sbjct: 126 IAPVLNGLRQLGVEVD---SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E

Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+

Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMAMVSRVDGSMITIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ A VA A G + IR VA R ET+R+ A+ EL

Sbjct: 297 ---GWQELRPLDVLHEASELTPVFAAVASLARGSRIRGVAHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K

Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+

Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|ZP_03702032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium MS024-2A]
gb|EEG42069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium MS024-2A]
Length = 405

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 134/432 (31%), Positives = 218/432 (50%), Gaps = 45/432 (10%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+ P G++ + GSKS +NR+LLL AL G + N NS+D M AL+T +

Sbjct: 5 IAHPNGHCEGSINITGSKSETNRLLLLQALFNGFEL-KNTSNSDDSKVMQKALQTSSDRI 63

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + +AG AMR LTA + G + VL G

Sbjct: 64 D-----IHHAGTAMRFLTAYFSHIQGRSV-VLTGSS 93

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM+ERPI LV L+ +GA + PP+++G L GGKV+L +SSQY+SALL

Sbjct: 94 RMQERPIQILVDALRDIGASISYEKEEGFPPLKIHG-KKLAGGKVELPADVSSQYISALL 152

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ P+ +E+ ++ K+ SIPY++MTL L+ GV S S++ I + K+

Sbjct: 153 LLGPVLEQGELHLVKGITSIPYIDMTLSLLNSLGV---STSFEGLICVSPMKEIKKD 208

Query: 248 -AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VE D SSASYF + AA++ + + SLQGD + + + + E

Sbjct: 209 IQIVESDWSSASYFFSIAALSETAEIHLTSFRKESLQGDVLSRIYDNLNVSSH-EGDT 267

Query: 306 TVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ +P ++ ++++K PD+A T+AV + + + ++KET+R+

Sbjct: 268 LILKKENKPLP---TSLKLDLSKAPDIAQTIAVSCYGLGIGCDLVGLHTLKIKETDRLE 323

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TEL+KLGA+++ + ++P +I TY+DHRMAMAF+ A ++P+ I

Sbjct: 324 ALNTELSKLGATIKVTENSLHSPGINFKENCISIPTYNDHRMAMAFAPLAL-KIPLQIEA 382

Query: 425 PGCTRKTFPDYF 436
K++PD++

Sbjct: 383 SDVVSksYPDFW 394

>ref|YP_327187.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natronomonas
pharaonis DSM 2160]
sp|Q3IQG6.1|AROANATPD RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS

emb|CAI49630.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natronomonas pharaonis DSM 2160]
Length = 438

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 144/449 (32%), Positives = 209/449 (46%), Gaps = 53/449 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV+ P SKS ++R +L A +G TV + L + AD A
Sbjct: 10 VNGTVRAPPSKSYTHRAILAAGYGDGATVKNPLFS-----ADTRAT 50

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLG-----NAGIAMRSLTAAVTAAGGNATYV 122
V GG D EV F G N+G MR TA T A + V
Sbjct: 51 ARAVEAYGGTTEQADDDLEVTGFDGTPGTPKDVINCANS GTTMRLLTA--TGALVDGLAV 108

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G +R RP G L+ L QLGA + P+ V G + GG++ + G +SSQY
Sbjct: 109 LTGDESLRSRPQG PLLDALDQLGARAESTRENGQAPLVVGG--DIDGGELAIRGDVSSQY 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-----HSDSWDR 233
++ LLMA + ++IE+ L S PYV++TL ++ FGV AE S D
Sbjct: 167 ITGLLMAGAVTESGIDIELTTALKSAPYVDITLEVLA DFGVDAEVIGGDDSEVRSAGADG 226

Query: 234 FYIKGGQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLE 292
F + GGQ Y Y V GD SS SY LA A+ V S QGD +LE
Sbjct: 227 FRVDGGQSYAPT DGTYHVP GDFSSMSYLLAAGALAADEEVVAGAHPSAQGDAAIVSILE 286

Query: 293 MMGAKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRD 352
MGA + W +T + L ++V + PD+ T+AV+ ADG T I D
Sbjct: 287 SMGADIEWNRRDGRIT-----VRQSSLSGVEVG VADTPDLLPTIAVLGAAADGETRITD 340

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSL 412
R+KET+R+ A+ TEL +LG +E D ++ ++ + +DDHR+ M+ ++
Sbjct: 341 CEHVR LKETDRVAAMATELERLGVETDEYEDELVVYGG-GIDGGTVAGHDDHRIVMSLAV 399

Query: 413 AA-CAEVPVTIRDPGCTRKTFPDYFDVLS 440
A A+ VTI++ +FP +F+ L+
Sbjct: 400 AGLVADGEVTIKNADHVDVSFSPFFETLA 428

>gb|EFS39990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium acnes HL110PA1]
Length = 429

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 220/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSDGPSVLEGLASRDSYLSAGLQLLGADIQPIGPGS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERP 133
V+ G P+E G AG MR L G +V D + RP
Sbjct: 77 VQVMPGLAHPTGPPIE-----CGMAGTVMRFLPVVAALVPGQTRFVGD--EQASRRP 125

Query: 134 IGD LVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD---SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVPVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTaidTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTdNGLDITGRGADKLHGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+
Sbjct: 414 TMPQFPQMwanLVee 428

>gb|EFT73592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL046PA1]
Length = 429

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 220/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPgSKSLsnrilllaalsegTtVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSdGpSVLEGLASRDSYLSAGLQLLGADIQPIGPGS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD---SDRLPFSLNAPDRMCGQKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIdKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLrHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTvtVEGCGTtSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLdHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTaidTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTdNGLDITGRGADKLHGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+
Sbjct: 414 TMPQFPQMwanLVee 428

>ref|ZP_06426967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes SK187]
ref|ZP_06430273.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes J165]
gb|EFD02856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes SK187]
gb|EFD06502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes J165]
gb|EFS35562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL013PA1]
gb|EFS42868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL110PA2]
gb|EFS46258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL087PA2]
gb|EFS50406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL025PA1]
gb|EFS54005.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL059PA1]
gb|EFS63165.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL063PA1]
gb|EFS65130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL063PA2]

gb|EFS76055.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL086PA1]
gb|EFS79507.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL005PA4]
gb|EFS81787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL050PA1]
gb|EFS84168.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL050PA3]
gb|EFS87295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL001PA1]
gb|EFS95389.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL067PA1]
gb|EFS99838.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL027PA1]
gb|EFT02046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL002PA1]
gb|EFT06645.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL082PA1]
gb|EFT11690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL037PA1]
gb|EFT22795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL072PA2]
gb|EFT25526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL110PA3]
gb|EFT49811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL053PA2]
gb|EFT56692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL027PA2]
gb|EFT60517.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL072PA1]
gb|EFT64073.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL110PA4]
gb|EFT70764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL059PA2]
gb|EFT75702.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL050PA2]
gb|EFT80709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL030PA2]
Length = 429

Score = 178 bits (452), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 220/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTPVPGSKSQTNRALVLAALSDGSPVLEGLASRDSYLSAGLQLLGADIQPIGPGS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHTPGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD----SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPTVIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+
Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|NP_070326.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Archaeoglobus fulgidus DSM 4304]
sp|O28775.1|ARO_AARCFU RecName: Full=Probable 3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAB89746.1| 5-enolpyruvylshikimate 3-phosphate synthase (aroA) [Archaeoglobus fulgidus DSM 4304]
Length = 416

Score = 178 bits (451), Expect = 1e-42, Method: Compositional matrix adjust.
Identities = 141/431 (32%), Positives = 217/431 (50%), Gaps = 32/431 (7%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
EI G K P SKS ++R + A+LS VV+ L+ SED L A + +G +V K
Sbjct: 9 EIRGKAKPPASKSYTHRAFIAASLSPSARVVNPLI-SEDTISTLNACKRIGAAVL--KKG 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G G + E N+G +R T ++ + + V+DG +R+RP
Sbjct: 66 NEWLFSGVGD-----VEAEGYFNFANS GTTLRIFTGLLSLSPFRS--VVDGDESLRKR 117

Query: 134 IGD LVVLGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
G+LV+ L +LGA F G + PP V G+ + GG+V++ SSQ++S+LL A
Sbjct: 118 NGELVLALSGLGAR---FKGREPYTPPFSVQGV--IKGGEVEIEAP-SSQFVSSLLFALS 171

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA GD + + +K+ S PY+++TL ++ GVK E ++ ++I G Q +K + V
Sbjct: 172 LAEGDSSLRV-EKVKSQPYIDVTLDLVRESGVKVEREGNF--YHIPGSQSFKL-RRYDVP 227

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSASY +A A + G V +EG S QGD K ++ MG V W + +
Sbjct: 228 ADFSSASYLIA-AGLIAGEVVLGEM-FESAQGDRIKIDICREMGGSVEWDKRGVIRAE- 284

Query: 312 REPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R L+ ++V+ + +PD+ T+AV+A A G T I + R+KE +R+ I L
Sbjct: 285 -----RSELEGVEVDASDIPDLVPTIAVLA AVAKGKTRIYNAEHLRIKEIDRIEGIHQNL 339

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 431
LG + D II + +D++ DHRMA+AFSL V R+ +
Sbjct: 340 KALGVESKPLKDGLI IKGGKGEFRGVVDSFGDHRMALAFSLGLLG-EVKCRNAEVVSVS 398

Query: 432 FPDYFDVLSTF 442
FP YF VL +
Sbjct: 399 FPGYFRVLESL 409

>ref|XP_001434983.1| hypothetical protein [Paramecium tetraurelia strain d4-2]
emb|CAK67586.1| unnamed protein product [Paramecium tetraurelia]
Length = 1468

Score = 178 bits (451), Expect = 2e-42, Method: Composition-based stats.
Identities = 141/450 (31%), Positives = 231/450 (51%), Gaps = 42/450 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I + + GSKS++NR+LLL++LSEG + ++N +S+D ML +L+ L L +
Sbjct: 368 DIRPSKPIHGSKSITNRVLLSSLSEGISLNNFYDSDDTKAMLNLSQELRLCEIQTHSK 427

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ GC G+G ++E + + +G R L + A GN T + G R+ ERP
Sbjct: 428 HNLILEGCGGQF----YQKEYTINVKESGTCARFLL-PIAALIGNVTII--GAQRIYERP 480

Query: 134 IGD LVVLGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++V + L +V P +V I G G +K+ +SSQ++S +LMAAP
Sbjct: 481 IQEMV---EALNLNVKYLEKEGQLPFPK--IDGKLGKHIKIKSQLSSQFVSGILMAAPYF 535

Query: 194 LGD-VEIEIID-----KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247

D IEIID ++S Y+EMT++LM +GVK E S +F +K G YK+ +
 Sbjct: 536 PNDETLIEIIDCKENETIVSESYIEMIQLMNIYGVKVERI-SKTKFLVKKG-IYKA-QT 592
 Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
 +E DA++ SY L + GG ++E + LQGD +F +V+E MG +V + +
 Sbjct: 593 YDIEPDATALSYDLLHIGLNGG--SIETKKISKQLQGAQFLDVIEQMGMQVREQGFYKI 650
 Query: 308 TGPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
 + LK DV+ D ++LA++ +G I+ + + RVKE +R+ A+
 Sbjct: 651 -----IKNQDLKPQDVDCINFSDTFISLALLMSSIEGQCIKGIENQVRKECDRIKAV 703
 Query: 368 RTELTKLGASVEEGPDYCIITPP--EKLN----VTAIDTYDDHRMAMAFSLAACA----- 416
 L K+G + +I +K N I+TY+DHR+AMAFS+
 Sbjct: 704 TENLVKVGVCVLSQNNELIRGKRYQKYNQYRKDVIINTYNDHRIAMAFSILGGHFEKVQ 763
 Query: 417 -EVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
 + + I + C RKTFFD+++ + + N
 Sbjct: 764 YQYRIIIDNKDCVRKTFPDPFYNIQSLGLN 793

>ref|YP_004092883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ethanoligenens
 harbinense YUAN-3]
 gb|ADU28152.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ethanoligenens
 harbinense YUAN-3]
 Length = 425

Score = 178 bits (451), Expect = 2e-42, Method: Compositional matrix adjust.
 Identities = 144/437 (32%), Positives = 221/437 (50%), Gaps = 33/437 (7%)

Query: 14 EISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
 ++ G V P SKS ++R ++ AAL++G + S+D+ +GA+R LG S+ A+ A
 Sbjct: 10 KLVGGVTPPPSKSAAHREGIICAALAKGAGRITPFAESDDMRATIGAMRALGASIRAEDGA 69
 Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 133
 + G + + +G +R L G A + +G R+ +RP
 Sbjct: 70 -----LLVNGTDTFRNVSGTIDCL--ESGSTLRFLPIAAVCG--ADFTFEGHGRLPKRP 120
 Query: 134 IGDVLVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
 IG + L + G V C P +R G L G L G+ISSQ+++ LL+A PL
 Sbjct: 121 IGPYLDCLPKAG--VTCLTEGGLPLSIR----GALRPGTFTLPGNISSQFITGLLLALPL 174
 Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
 GD I + L S+ Y+++TL ++ FG+ E + D + + G Q+Y +P++ VEG
 Sbjct: 175 LDGDSRIRLTTPLSVGYIDLTLVDLHAFGI--EIRQTADGYDVPKGQRY-TPRDFTVEG 231
 Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
 D S A+++LA A+ GG+VTV G T S QGD ++LE GA++T VT P
 Sbjct: 232 DWSQAAPFLAAGAL-GGSVTVRGMRTDSKQGDKAIVDLLEQFGARITRGPDGVTAAVAP- 289
 Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
 L I ++ ++PD+ LA A FA G T I++ A R+KE++R+ I LT
 Sbjct: 290 -----LHGIAIDAAQIPDLVPILAATACFASGTTTIQNAARLRIKESDRLHTIAVGLT 342
 Query: 373 KLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACA EV-PVTIRDPGCT 428
 LGA +EE PD +I P ++T +D DHR+ MA S+AA V I
 Sbjct: 343 ALGARIEELPDGLVIRGPLS-SITEPPVLDGAGDHRIVMALSVAAAHTVCGAKISGAEAI 401
 Query: 429 RKTFFPDYFDVLSTFVK 445
 RK++P +F T N
 Sbjct: 402 RKSYPAFFADFHTLGGN 418

>gb|EFT10607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
 acnes HL082PA2]
 Length = 429

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
 Identities = 140/435 (32%), Positives = 220/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 ++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++

Sbjct: 17 LAGRVTPVPGSKSQTNRALVLAALSDGPSVLEGLASRDSYLSAGLQLLGADIQPIGPGS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P+E G AG MR L G +V D + RP

Sbjct: 77 VRVMPGLAHTPGPIE-----CGMAGTVMRFLPVVAALVPGQTRFVGD--EQASRRP 125

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+

Sbjct: 126 IAPVLNGLRQLGVEVD----SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E

Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGT VTVVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+

Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL

Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K

Sbjct: 354 KLGVEVQQT DNGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVKN 445
T P + + + V+

Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|YP_075248.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Symbiobacterium thermophilum IAM 14863]
dbj|BAD40404.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Symbiobacterium thermophilum IAM 14863]
Length = 449

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 149/451 (33%), Positives = 215/451 (47%), Gaps = 36/451 (7%)

Query: 6 EIVLQPIKEISGTVKLP GSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ + P + GTV P SK+ + R LL AAL+EG +++ SED + L LG

Sbjct: 2 DVRVYPATRLGTVNPPSSKNYTTRYLLAAALAEGESLIRYPAESEDAAALKRCLADLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ D R G + P L GNAG +R L A A T+V D

Sbjct: 62 ELIPDGPHLRVRGFGANPRNPG-----TLNPGNAGAVLRFLMAVCAATLDEITFVTDY 114

Query: 126 VPRMRERP IGD LVVGLKQLGADVDCFLGT-----DCPPVRVNG-----IGGLP 168
+ RP GDL+ L QLGA V+ G PP +G L

Sbjct: 115 AESLGRRPHGDLLDALAQLGAQVESREGRLPITIRTGPPAGAGSRSGWERPPSGRVGRRLR 174

Query: 169 GGVKVLKSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHES 228
GG V++SGS+SSQY SALL AAPL DV IE+ + S P + TL++++ G++ E

Sbjct: 175 GGTVRVSGSVSSQYTSALLFAAPLIGEDVTIEVTGDMKSRPPIRQTLQVLQEAGIRVEAG 234

Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVVEGCGTTS LQGDVKFA 288
D RF+I GGQ+Y+ P+ V GD A+ +A AA+ VT+ QG+ +

Sbjct: 235 DDLRRFHIPGGQRYR-PREYTVPGDYPGAAALMAAAVVPDVTIPRLFPDE-QGERQAI 292

Query: 289 EVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPT 348
+VL MGA + V + G GR L+ + + + D + L A+ A+G T

Sbjct: 293 DVL RAMGADIAHDGQQVWIRG-----GRP-LRGVRFDGDPFTDAVLALTA AAVLAEGET 345

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRM 406
+V + R KE +R+ R EL KLGA V E D I+ PE + +++ DHR+

Sbjct: 346 VFYNVENLRYKECDRISDYRAELNKL GARVAEERDKLIVRGRPEGVEGGVTVESRIDHRV 405

Query: 407 AMAFSLAAC-AEVPVTIRDPGCTRKTFPDYF 436
M ++ A A PV IRD K++P +F

Sbjct: 406 IMGLTIVALRAREPVVIRDAHVAKSYPAFF 436

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>ref|ZP_02950383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium butyricum
5521]
ref|ZP_04529172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium butyricum
E4 str. BoNT E BL5262]
gb|EDT74654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium butyricum
5521]
gb|EEP52635.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium butyricum
E4 str. BoNT E BL5262]
Length = 435
```

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 127/427 (29%), Positives = 216/427 (50%), Gaps = 18/427 (4%)

```
Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ G VK+P SKS+++R ++ AALS+GT V N+ S+D+ + A+++LG +E
Sbjct: 9 KKLKGGVKIPPSKSMRAHRAVICAALSDGTCKVSNIDFSDIIATVEAMKSLGAIIEKKDD 68

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + +E + +G +R L G +V G + +R
Sbjct: 69 CLEVIGIKSPENKLNNSSTDERIIDCNESGSTLRFLVPIAALFEGVKNKFV--GRGNLGR 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ G G + + G L G+ K+ G+ISSQ+++ LL PL
Sbjct: 127 PLDTYYEIFDNQGIKYSYKEGI----LDLKTGKGLKCGEFKVKGNISSQFITGLLFTLPL 182

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
GD +I I +L S Y+++TL M FG++ +++ ++ F IKG Q YKS + VEG
Sbjct: 183 LDGDSKIVITTELESKGYIDLTLASMRDFGIEIINNYYE-FIIKGNQNYKSI-DYRVEG 240

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVGFVLEMMGAKVTWTETSVTVTGPPR 312
D S A++FL A + V V SLQGD + ++LE MG + + + T
Sbjct: 241 DYSQAFFLCADAASN-EVVVNDLNLNSLQGDKEVIDILERMGVNIKENDKGIIGTVD-- 297

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
K LK+ ++ ++ PD+ +++ A DG T + + R+KE +R+ A+ +EL
Sbjct: 298 -----KKLKSTIIDGSQCPDIIPVVSALAASLDCGTTEVINAGRLRIKECDRLAAVTSELN 352

Query: 373 KLGASVEEGPDYCIITPPEKLN-VTAIDTYDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
KLGA + E D II KL + ++ DHR+AM ++A+ E P+ I+D C K
Sbjct: 353 KLGAKITEKEDGLIIEGVSKLKGCTVWSHKDHRIAMTLAIASTICEEPIIIEKDYECVTK 412

Query: 431 TFPDYFD 437
++P++++
Sbjct: 413 SYPEFWN 419
```

```
>ref|YP_706273.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus jostii
RHA1]
sp|Q0S2X1.1|AROARHOSR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG98115.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus jostii
RHA1]
Length = 438
```

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 144/434 (33%), Positives = 222/434 (51%), Gaps = 34/434 (7%)

```
Query: 18 TVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS++NR L+LAAL++G + + L S D M+ ALRTLGS+S+E A +
Sbjct: 21 TVALPGSKSITNRALILAALADGPSTLTGALRSRDTLMIETALRTLGISLET-VGADTTL 79

Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
V G P++ + L AG MR L A G + DG + R RP+ +
Sbjct: 80 RVTPG---PLQGGAVDCGL----AGTVMRFLPPVAALASGTVHF--DGDEQARTPLDTI 130

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
+ L+ LGAD+D P V G G L GG+V + S SSQ++S LL++A V
Sbjct: 131 LDALRGLGADIDGA----SLPFTVRGAGSLRGGRVTIDASGSSQFVSGLLLSAAAFDEGV 186
```

Query: 198 EIEIIDKLI-SIPYVEMTLRLMERFGVKAE-----HSDSWDRFYIKGGQKYKSPKNAYV 250
+ K + S+P+++MT+ ++ GV+ +D+W + + +
Sbjct: 187 TVHHDGKTVPSMPHIDMTVEMLRESGVEVTTPATGGEADTW-----RVSPGVVRAVDRAI 241

Query: 251 EGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
E D S+A+ FLA AA+TGG VTV + + Q E+L MGA V ++TV GP
Sbjct: 242 EPDLNATAFLAAAAVTGGEVTVPLWPSRTTQPGDAIREILLAMGADVRLDGANLTVRGP 301

Query: 311 PREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ L ID++++ + ++ T+A +A ADGP+ +R +A R ET+R+ A+ E
Sbjct: 302 -----QQLTGIDIDLHDVGELTPTVAALALADGPSHLRGIAHLRGHETDRLAALAHE 354

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
+ LG +V E D I P L+ +Y DHRMA A ++ + I D G T K
Sbjct: 355 INSLGNGVTETEDGLTIV-PAGLHGGTWRSYADHRMATAGAIVGLRVDGIRIEDVGTAK 413

Query: 431 TFPDYFDVLSTFVK 444
T P + ++ +T +
Sbjct: 414 TLPGFENLWATMLS 427

>ref|ZP_06406159.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 299 str. F0039]
gb|EFC70644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prevotella sp. oral
taxon 299 str. F0039]
Length = 432

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 128/440 (29%), Positives = 220/440 (50%), Gaps = 40/440 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
I +QP +SG V++P SKS++NR +++ ALS T+ N +DV ML ++ G
Sbjct: 16 NISIQPPTSLSGNVEIPTSKSIANRSIVIDALSNNSTTFQGAANCDVAVMLNGIK--GE 73

Query: 66 SVEADKAAKRAVVVGC GGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ E D A +G AMR LTA + N+T++L G
Sbjct: 74 TCELDIMA-----SGTAMRFLTA-YWSIQPNSTHILTG 105

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
RM++RPI LV L+ LGAD++ PP+++NG L GG + + +SSQY+SA
Sbjct: 106 TERMKQRPIKVLVDSLRTLGLADIEYMEKEGYPLKING-KSLEGGMITMPADVSSQYVSA 164

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLM APL + + + + S Y+++T+ +M ++G K +D D ++ ++Y++
Sbjct: 165 LLMIAPLFTKGLTLTLKGTIASRSYIDLITIDIMTKYGAHVHTDV-DTIKVE-PKRYEAT 222

Query: 246 KNAYVEGDASSASYFLAGAAITG---GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-T 301
+ +E D +SASY+ A++ +T++G +S QGD + ++G K +
Sbjct: 223 QRM-IENDWTSASYWYLHLALSDCQEAITMQGLSESSKQGDSVVRYLFSLLGIKTAFIK 281

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
ET+ T + + + + PD+A T+ V + +++ ++KET
Sbjct: 282 ETTNNNTTKMVLKSKDKMKVSMMLHYDFINAPDLAQTMMVACVAMGISFRFTGLSTLKIKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVP 419
R+ A+++EL KLG V + E+ VT+ I+T++DHRMA+AFS
Sbjct: 342 NRIAALQSELLKLG FVVNNDKSDLSWNGERCAVTSTDINTFEDHRMALAFSALTYLFPN 401

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
+TI K++P ++ L
Sbjct: 402 ITINAANVVSKSYPHFWSEL 421

>ref|YP_004255775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
proteolyticus MRP]
gb|ADY26158.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
proteolyticus MRP]
Length = 438

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.

Identities = 150/438 (34%), Positives = 207/438 (47%), Gaps = 19/438 (4%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ V+ P +SGTV+ SK+ + R LL AAL+EG +VV + +SED +L LR G
Sbjct: 9 DAVVHPTARLSGTVQAQPSKNYTTRFLAALAEGESVVRGVASSEDAAEALLSCLRAWGA 68

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + A V G G + P D + EV GNAG R L A V A V D
Sbjct: 69 RIEL--SGGDAYVTGFGAR-PSPDTRLEV---GNAGAVARFLA-VAALTSGTEVVTDS 120

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+GDL+ L LG V G P V V+G G GG V +S SSQ+LS
Sbjct: 121 PHSLGQRPMGDLLAALTALGLTVQSAAGGRLP-VTVSG-GPALGGPVSVSAEQSSQFLSG 178

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL AAPL ++I + L S P + TL + RFGV+ E + R + G Q+Y++
Sbjct: 179 LLFAAPLLERGLDITVTGHLRSEPPIRQTLDTLRRFGVQVEAATDLRIRVPGAQRYQA- 237

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V GD ++ L AI G VTV G LQG+ +VL MG + +V
Sbjct: 238 GDYRVPGDYPGSAALLVAGAILPGEVTVAGLDPHDLQGERLALDVLREMGTDLRREGDAV 297

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G L + + + D L A A+G T +VA+ R+KE +R+
Sbjct: 298 TVRGG-----SPLHGVTRDGDPTDAVQVLCAAAAAAEGCTTWHNVATLRLKECDRIS 350

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRD 424
R EL +LG E D + +D + DHRM M SL A PVTI
Sbjct: 351 DTRAELLRLGLVQARETADSLTVCAGAVRGNVTVDGHGDHRMIMLLSLLGLRASGPVTITG 410

Query: 425 PGCTRKTFPDYFDVLSTF 442
RK++P++F L
Sbjct: 411 AHHIRKSYPEFFAHLQAL 428

>ref|ZP_04383385.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus
erythropolis SK121]
gb|EEN89377.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus
erythropolis SK121]
Length = 437

Score = 177 bits (450), Expect = 2e-42, Method: Compositional matrix adjust.
Identities = 144/432 (33%), Positives = 219/432 (50%), Gaps = 42/432 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ V LPKSGS++NR L+LAAL++G + + L S D M+ ALR LG+ V EA A
Sbjct: 18 VDAVVTLPGKSIITNRLILAAALADGPSTITGALRSRDADLMIAALRDLGIGVEEAGDAT 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G P+ + + L AG MR L A G + DG + R RP
Sbjct: 78 TLRITPG-----PLRGGEVDCGL----AGTVMRFLPPLAAMADGIVHF--DGDEQARTRP 126

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G ++ L+ LGA ++ D P V G G L GG V + S SSQ++S LL++A
Sbjct: 127 LGTILEALRGLGARIEG----DALPFTVTGTGSLRGGTVTIDASGSSQFVSGLLLSAAAF 182

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA-----HSDSWDRFYIKGGQKYKSPK 246
V + K + S+P+++MT+ ++ GV +D+W + P
Sbjct: 183 EEGVTVHHDGKPVSPMPHIDMTVEMLREAGVSVTTPATGGDADTW-----RVAPGPV 234

Query: 247 NAY---VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
A +E D S+A+ FLA AA+TGGTV+V +++ Q +L MGA VT +
Sbjct: 235 RAVDWAIEPDLSNATPFLAAAATGGTVSVPMWPSSTTQPGDAIRVILASMGADVTIADG 294

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+TV GP + L+ ID++++ + ++ T+A +A A+G + +R +A R ET+R
Sbjct: 295 VLTVRGP-----EKLRGIDIDLHDVGLTPTVAALAALAEGTSHLRGIAHLRGHETDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ E+ KLG SV E D I P E L+ +Y DHRMA A ++ V +
Sbjct: 348 LAALADEINKLGGSVTETDDGLTIVPAE-LHGGQWLSYADHRMATAGAIIGLVVDGVEVD 406

Query: 424 DPGCTRKTFFDY 435
D G T K T P +
Sbjct: 407 DVGTTAKTLPGF 418

>ref|ZP_06263110.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes J139]
gb|EFB88606.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes J139]
Length = 429

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 219/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSDGPSVLEGALASRDSYLSAGLQLLGADIQPIGPS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD---SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGMAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRLPLDVLHEASELTPVVAASLASLRGSRIRGVAHIRGHETDRLAALHEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVKN 445
T P + + + V+
Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|YP_001031078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocorpusculum
labreanum Z]
sp|A2SU05.1|AROAMETLZ RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABN07811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanocorpusculum
labreanum Z]
Length = 422

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 139/425 (32%), Positives = 217/425 (51%), Gaps = 26/425 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADK 71
+ISG V P SKS ++R LLA+L++G +VV + L ED L A++ LG +V E D
Sbjct: 8 SQISGCVHAPPSKSHTHRAFLASLAKGESVVLSPLLGEDTLATLSAVKALGANVCEGDD 67

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R + G P+ + + N+G ++R L + G + D +
Sbjct: 68 ---RITIQGGLNHLAPL---PKGTVINCKNSGTSIRMLAGIASRLDGTTEFTGDA--SLCS 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ L+ L +LGA V G C P + G + GG V + G +SSQ++S LL++AP

Sbjct: 120 RPMKPLLDALSELGAGVTSNNG--CAPFTITGP--VSGGDVHIRGDVSSQFISGLLISAP 175

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L D I + L S PYV+MT+ M++ GV E + D + ++ GQ Y S ++ V

Sbjct: 176 LGKADTRIHLTTPLTSTKPYVDMTISAMKKHGVSVETIE--DGYLVRSGQVYSS-EDVQVG 232

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD SSA++ A AA+ G + V G QGD +LE GA V +VT+

Sbjct: 233 GDYSSAAFLFAAALAG-EIAVSGLDPADPQGDQVVISILETFGAGVVRDGENVTIR--- 288

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ LKA D+++ PD+ +AV+A A G + + A R KE++R+++ L

Sbjct: 289 -----KAALKAADIDLANAPDLFPIIAVLASQAKGTSRLYGAAHLRFKESDRIMSTVLFL 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
+GA + E D CI+T P L+ + T+ DHR+ MA ++A A+ T+ D GC

Sbjct: 344 RSMGADISETEDGCIVTGPANLSGANVTTFGDHRIMMASAVAGLIADSTTTTVDDAGCCAV 403

Query: 431 TFPDY 435

++P +

Sbjct: 404 SYPGF 408

>ref|ZP_02620468.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
C str. Eklund]

gb|EDS78226.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
C str. Eklund]

Length = 435

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 129/444 (29%), Positives = 233/444 (52%), Gaps = 37/444 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E I + P E++G + +P SKSL++R ++ A LS+G + ++N++ SED+ + +++LG

Sbjct: 2 ENIKITP-SELNGEINIPPSKSLAHRAIISAGLSGVSNIENIIFSEDIKSTIRGMKSLG 60

Query: 65 LSV-----EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
+ + E K+ R + G + + E + +G +R L A

Sbjct: 61 IKIDDITNENKSLGRKTLKVIGKEKLI---LENDTIDCSESGSTLRFILPIALRAEKAV 117

Query: 120 TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
T+ G ++ RP+ + G + + P+ V+G + G+ + G+IS

Sbjct: 118 TFT--GRGKLVSRPLDVYINIFEDQG--IKYKTTNNQLPLTVDG--KINSGEFHVKGNIS 171

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
SQ+++ L+ P GD +I II +L S YV++T+ ++++FGV+ E+++ + F IKG

Sbjct: 172 SQFITGLMYTLPFLDGDGSKIIITELESRGYVDLTIDMLKKFGVEIENNN-YKEFIKGN 230

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
QK S ++ V+GD S ++F+ A I G V SLQGD ++++ MGA +

Sbjct: 231 QKSTS-RDYRVQGDGFSQGAFFIV-AGILGSKVKTLDLDDISLQGDKAIIDIVKKMGANIK 288

Query: 300 ----WTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVAS 355
+ ET + T I ++ ++ PD+ LAV+ + G T I +

Sbjct: 289 VGRDYIETKSKT-----HGITIDASECPDLVPI LAVLGAVSHGTTKIINAER 336

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
R+KE +R+ A+ TEL+K+GA ++E D II KL +D+++DHR+AMA ++A+

Sbjct: 337 LRIKECDRLKAMATELSKIGADIKELEDGLIIGKYKLKGGVVDSDWHDRIAMAMAIASI 396

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFD 437

C E PV I++ K++PD+++

Sbjct: 397 KCTE-PVIIQNSMAVNKSYPDFWE 419

>gb|EFT64948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL060PA1]

Length = 429

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 140/437 (32%), Positives = 220/437 (50%), Gaps = 27/437 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 15 RLLAGRVTVPGSKSQTNRALVLAALS DGPSVLEGLVLSRDSYLSAGLQLLGADIQPIGP 74

Query: 73 AKRAVVVCGGKGF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V+ G P+E G AG MR L G +V G +
Sbjct: 75 GSVRVMPGLAHTGPTE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASR 123

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI ++ GL+QLG +VD +D P +N + G KV + + SSQ++SALL+A+
Sbjct: 124 RPIAPVNLNGLRQLGVEVD----SDRLPFSLNAPDRMCGPKVTIDSATSSQFISALLASA 179

Query: 192 LALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+++ + SIP++ MT ++ GV SD + ++ G + + +
Sbjct: 180 RFPQIGIDL RHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHVVRPGPIHA--LDDVI 236

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
E D ++A+ FLA A I GG VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 237 EPDLTNAAVFLAAALIVGGAVTVPGWPTDSTQPGAQFMGIAEKMGMVSRVDGSMTIAAQ 296

Query: 311 PREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ E
Sbjct: 297 -----GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALHE 351

Query: 371 LTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
L KLG V++ + IT +KL+ Y DHRMA A +L V + D CT
Sbjct: 352 LAKLGVEVQQTNDGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCT 411

Query: 429 RKTFFPDYFDVLSTFVKN 445
KT P + + + V+
Sbjct: 412 SKTMPQFPQMWANLVEE 428

>ref|YP_002783591.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus opacus
B4]
sp|C1B1F1.1|AROA_RHOOB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAH54646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus opacus
B4]
Length = 438

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 144/440 (32%), Positives = 221/440 (50%), Gaps = 46/440 (10%)

Query: 18 TVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV LPGSKS++NR L+LAAL++G + + L S D M+ ALRTLGL+ +E
Sbjct: 21 TVALPGSKSITNRALILAALADGPSTLTGALRSRDTLMDALRTLGLIGIET----- 72

Query: 78 VVCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMREPI 134
GG + A ++ + G AG MR L AGG + DG + R RP+
Sbjct: 73 ---AGGDTTLRVAPGPLRGGA VDCGLAGTVMRFLPPVAALAGGTVDV--DGDEQARTRPL 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L+ LGAD+D D P V G G L GG+V + S SSQ++S LL++A
Sbjct: 128 DTILNALRGLGADIDG----DSLPTTVRGAGSLRGGRVTIDASGSSQFVSGLLLSAAAFD 183

Query: 195 GDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA-----HSDSWDRFYIKGGQKYKSPKN 247
V + + S+P+++MT+ ++ GV+ +D+W + P
Sbjct: 184 EGVTVVHHDGTTVPSPHIDMTVEMLRSGVEVSTPATGGEADTW-----RVSPGPVR 235

Query: 248 A---YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 304
A +E D S+A+ FLA AA+T G VTV + Q E+L MGA V +
Sbjct: 236 AVDRVIEPDLNATAFLAAAVTCGEVTVPLWPAETTQPGDAIREILLAMGADVRRDGAN 295

Query: 305 VTVTGPVREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TV GP + L ID++++ + ++ T+A +A ADGP+ +R +A R ET+R+
Sbjct: 296 LTVRGP-----QQLTGIDIDLHDVGE LPTVAALAAALADGPSHLRGIAHLRGHETDRL 348

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424

A+ E+ LG +V E D I P + L+ +Y DHRMA A ++ + I D
Sbjct: 349 AALAHEINSLGGNVTEDEDGLTIVPAD-LHGGTWRSYADHRMATAGAIVGLRVDGIEIED 407
Query: 425 PGCTRKTFFPDYFDVLSTFVK 444
G T K T P + ++ +T +
Sbjct: 408 IGTTAKTLPGFENLWATMLS 427

>ref|ZP_02422012.1| hypothetical protein EUBSIR_00853 [Eubacterium siraeum DSM 15702]
gb|EDS01327.1| hypothetical protein EUBSIR_00853 [Eubacterium siraeum DSM 15702]
Length = 405

Score = 177 bits (449), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 136/433 (31%), Positives = 209/433 (48%), Gaps = 44/433 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I + P K +SG + +P SKS+S+R+L+ AA +GTT +DNLL D+H + AL LG+
Sbjct: 2 DKITPSK-LSGKLIVPPSKSISHRMLICAAFCDDGTTHIDNLLCEMDLHATINALTALGV 60
Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + G P E K V F +G +R + +A G A + G
Sbjct: 61 KINGKDGSDYDIT----GITQSE--KAAVDCF--ESGSTLRFMIPIFSAFGCEAEFT--G 110
Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ ERPI L+ + + GA T P R+ G L GGK + GS+SSQ+++
Sbjct: 111 RGKLPERPITPLIEPMTENGA----VFETLSMPYRIK--GKLSGGKYYIDGSVSSQFITG 164
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL A + D EI + L S PYV +T+ M++FGV S++ + ++IKGGQKY+ P
Sbjct: 165 LLFALSVLKSKDSEIILTTSLKSKPYVNITIDCMKQFGVGV--SETENGYFIKGGQKYQ-P 221
Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
N VE D S +++FLA A G + + S+QGD ++ E
Sbjct: 222 HNCTVEADMSQSAFFLA-ANCAGSDIELTNLNLNSVQGDKAIVDIAEKFR----- 270
Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
L ID + +PD+ +AV+ F + P I + R+KE +R+
Sbjct: 271 -----NGGDLVIDA--SDIPDLVPAIAVMMSFREKPCRIINCERLRIKECDRLA 318
Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV-PVTIRD 424
A + LG + I P E + Y+DHR+AMA ++AA V I+
Sbjct: 319 ATTELINDLGKAISTENSIEIFPVEAFKGGTVRNYNDHRIAMAGAVAATRSTGEVLIIG 378
Query: 425 PGCTRKTFFPDYFD 437
CT K++P +FD
Sbjct: 379 AECTNKSYPGFFD 391

>ref|YP_003937400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
sticklandii DSM 519]
emb|CBH22495.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Clostridium sticklandii]
Length = 468

Score = 177 bits (448), Expect = 3e-42, Method: Compositional matrix adjust.
Identities = 128/440 (29%), Positives = 232/440 (52%), Gaps = 26/440 (5%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ + P K++SG + +P SKS+S+R ++ A+LS+G + + N++ S+D+ + A++ G+
Sbjct: 40 VTINP-KKLSGEISIPPSKSMHRAIIAASLSDGMSKITNVVLSDDIIATINAMKNFGVE 98
Query: 67 VEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D A R + G K V + + +G +R L + G
Sbjct: 99 IEVQDNADLRKTAIIKGNKNLVYTGN---IDCNESGSTLRFILPFAGLMDEEVKFT--G 153
Query: 126 VPRMRERPIGDLVVGL--KQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
++ ERP+ D+ + KQ ++ + P+ VNG L G+ +L G ISSQ++
Sbjct: 154 KGKLVERPL-DVYEIFDKQ---NISYRNEENKLPVNVNG--KLKAGEFQLRGDISSQFI 207
Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

+ L+ PL D +I I L S YV+MT+ ++ FG+ E+ + + FYIKG Q YK
Sbjct: 208 TGLMFVLPLLDSDSKIIITDLESKGYVDMTIDTLKVFGILLENKE-YKEFYIKGNQAYK 266

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + VEGD S A++++ AI G + + SLQ D K ++ + MGA + E
Sbjct: 267 A-REYKVEGDFSQAAFWIVAGAI-GDKIICKDVNLESLQADKKIIDIAMGADIKKLED 324

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G G HLK+++++ +++PD+ + V+A ++G T I + + R+KE++R
Sbjct: 325 -----GHIEVNSG--HLKSMEIDASQIPDIIPVICVMASMSGETRIINASRLRIKESDR 377

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ + +EL+KLGA + E D II +L + +++DHR+AMA ++A+ ++ V I
Sbjct: 378 IKSTVSELSKLGADITEHEDSIIINGKTQLTGKGLSSWNDRHRIAMAMAIASIRCQLEVEI 437

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
K++P +++ T
Sbjct: 438 SGAEAVSKSYPHFWEDFKTL 457

>gb|EFT77790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL030PA1]
Length = 429

Score = 177 bits (448), Expect = 4e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 219/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALS DGPSVLEGLVLSRDSYLSAGLQLLGADIQPIGPS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N L G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD----SDRLPFSLNAPDRLCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + S P++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHDGASVPSTPHIAMTCAMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLASLARGSRIRGVHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVKN 445
T P + + + V+
Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|ZP_03290752.1| hypothetical protein CLONEX_02970 [Clostridium nexile DSM 1787]
gb|EEA81116.1| hypothetical protein CLONEX_02970 [Clostridium nexile DSM 1787]
Length = 422

Score = 176 bits (447), Expect = 4e-42, Method: Compositional matrix adjust.
Identities = 135/441 (30%), Positives = 218/441 (49%), Gaps = 40/441 (9%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P K SG + +P SKSL++R ++ A L+ G +V+ N+ S D+ + +R LG S++
Sbjct: 5 ITPAKIDSGNITIPPSKSLAHRAIICACAPGRSVISNIDYSVDIRATIEGMRHLGASIK 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVL 123
DK D E Q + +G +R + G AT+
Sbjct: 65 EDKDTLFI-----DGIETFQYDGDVVNCHESGSTLRFFLPLFSLTGKRATF-- 110

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G R+ ERP + ++ G D F+ T P + ++G L G++ L G++SSQ++
Sbjct: 111 SGSKRLIERPQNVYEMLFQEQGID---FVRT-YPNIIIDG--RLKPGELTLKGNVSSQFI 164

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ LL A PL D +I I S YV++T++++RF + E+ D++ IKG Q+Y+
Sbjct: 165 TGLLFALPLLEADSKIHIEPPFESRSYVDLTIQMLKRFQIIVEYEDAY-TLAIKGNQQYQ 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + VEGD S F A + +V G SLQGD K ++ + M A + +
Sbjct: 224 -PTDVLVEGDYSQL-VFWASLGVLNHSEVETHGLDLHSLQGDKKTIDIFQSMNAGIKVLDD 281

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
F L +++N PD+ L +A A+G T ++ R+KE++R
Sbjct: 282 GYQ-----FCPGTLNGTVIDLNDPCDLPMLFALATQANGKTTFQNAGRLRIKESDR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAMAFS-LAACAEVPV 420
+ A+ TEL KLG S+ IT P KL NVT + ++DHR+ MA S LA A+ P+
Sbjct: 334 IEAMETELKKLGCSISSTFGTVTITGPVKLQGNVT-LHGNDHRIVMALSI LATIAD EPI 392

Query: 421 TIRDPGCTRKTFPDYFDVLST 441
TI D K++P +F L++
Sbjct: 393 TIDDAQAISKSYPGFFKDLAS 413

>ref|ZP_04057460.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
gingivalis ATCC 33624]
gb|EEK14869.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
gingivalis ATCC 33624]
Length = 405

Score = 176 bits (447), Expect = 5e-42, Method: Compositional matrix adjust.
Identities = 137/427 (32%), Positives = 208/427 (48%), Gaps = 54/427 (12%)

Query: 18 TVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+ + GSKS SNR+LLL L + +N+ S+D M L LG
Sbjct: 17 TLNIGGSKSESNRLLLLKQLFPSLEI-ENISPSKDTMEMSRGLHLLG----- 62

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
EE+ + G+AG AMR LTA A + VL G RM++RPIG L
Sbjct: 63 -----EEINV--GDAGTAMRFLTAYY-ACCTDRKVVLTSERMQQRPILG 105

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+QLGA +D PP+ + G + GG++ + ++SSQYLSALL+ +
Sbjct: 106 VEALRQLGASIDYLSTEGFPPLSITG-KHIEGGELTIKANVSSQYLSALLLVGSTFPKGL 164

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP---KNAYVEGD 253
+ + ++ S+PY+ MTL L+ + G++A D+ Y +P + VE D
Sbjct: 165 TLHLEGEITSLPYLRMTLALLNQLGIEAVLEDNIIITV-----YHTPEVEAQTIVVEPD 217

Query: 254 ASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
SSASYF + A++ G ++ + SLQGD A++ + G K + + +
Sbjct: 218 WSSASYFYSMIALSEVGSSFLNHYKESLQGDRIADIYQSFGVKTIFWRDKIQLI-KE 276

Query: 312 REPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R+ F N+ PD+A T+AV + + + +KET R+ A+R E+
Sbjct: 277 RDDFS----TIFSYNLMDCPDIAQTIAVTCFGLGVECFSLGLHTLNKETNRLEALRDEI 332

Query: 372 TKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
TKLG V I P K+ NV +I TY DHRMAMAF+ C +VP+TI
Sbjct: 333 TKLGGEVHISQGEIWIWGPVKIARNV-SIATYGDHRMAMAF-PLCLKVPLTIEKGVEV 390

Query: 430 KTFPDYF 436
K++P+++
Sbjct: 391 KSYPNFW 397

>ref|YP_004045439.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Riemerella
anatipestifer DSM 15868]
gb|ADQ81933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Riemerella
anatipestifer DSM 15868]
gb|EFT36070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Riemerella
anatipestifer RA-YM]
Length = 410

Score = 176 bits (447), Expect = 5e-42, Method: Compositional matrix adjust.
Identities = 133/430 (30%), Positives = 208/430 (48%), Gaps = 42/430 (9%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ + GSKS SNR+L+L L G ++NL N++D + AL +
Sbjct: 17 ISISGSKSESNRLLILQRL-LGDLQINNLSNAQDTQLLQKALYS----- 59

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
+EV + + +AG AMR LT+ G T +L G RM++RPI LV
Sbjct: 60 -----NDEV-IDIHAGTAMRFLTSYFVIQEGRTT-ILTGSDRMKQRPIAPLV 105

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
LK LGA++ CPP+++ G L +V +S +SSQ++S+LL+ A ++
Sbjct: 106 EALKSLGAEITYLEKEGCPPLKIVG-KKLYKNEVSISAESVSSQFISLLLVAGFLENGLK 164

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I ++ + S PY+EMTL+++ G++ E + K VE D SSAS
Sbjct: 165 IALVGHITSRPYLEMTLKM LSDLGIETFEKGTIEVKPLKELATDNKEYTVESDWSAS 224

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL-EMMGAKVTWTETSVTVTGPPPREPFGR 317
YF + AI V +E TS+QGD ++ + G + + V P ++ +
Sbjct: 225 YFYSLVAIGKKQVALESFKETSMQGDALVKIYRDFGVETQFQNGERLVLTPIKD--FK 282

Query: 318 KHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ LK I+++MN PD+A T+ V A I +A+ +VKET+R+VA++ EL K+G
Sbjct: 283 QPLK-INLDMNDCPDIAQTVCVTAAALGVHFQIEGLATLKVKETDRLVALKNELLKIGLE 341

Query: 378 VEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
E D I V I TY DHRMAM+F+ A + I D K++P
Sbjct: 342 TEITEDS--IKSARFFQVEEIPCIKTYHHRMAMSFAPYALVG-DIKIEDASVVEKSYPY 398

Query: 435 YFDVLSTFVK 444
+++ T K
Sbjct: 399 FWEDFKTLK 408

>ref|YP_879090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium novyi NT]
sp|A0Q388.1|AROALCLONN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK62560.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium novyi NT]
Length = 435

Score = 176 bits (447), Expect = 5e-42, Method: Compositional matrix adjust.
Identities = 129/444 (29%), Positives = 233/444 (52%), Gaps = 39/444 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E I + P E++G + +P SKSL++R ++ A LSEG + ++N++ SED+ + +++LG
Sbjct: 2 ENIKIIP-SELNGEINIPPSKSLAHRAIISAGLSEGVSNINIIFSEDIKATIRGMKSLG 60

Query: 65 LSVE-----ADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +E K ++R+ + G K +E+ + +G +R L A
Sbjct: 61 IEIEDITNEYKKGSRSTLKVIGKEKLTLEND----TIDCESGSLRFLIPIALRAEKE 116

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
T+ G ++ RP+ + G + + P+ V+G + G+ + G++
Sbjct: 117 VTFT--GRGKLVSRPLDVYYNIFENQG--IKYKTSNNELPLTVDG--KINPGEFHVKGNV 170

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQ+++ L+ P GD +I I +L S YV++T+ +++FGV+ E+++ + F IKG
Sbjct: 171 SSQFITGLMYTLFPLDGDGSKIIITTELESKGVDLTIDTLKKFGVEIENNN-YKEFIK 229

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298

QK S ++ V+GD S ++F+ A I G V SLQGD +++++ MGA +
Sbjct: 230 NQKSTS-RDYRVQGDFFSQGAFFIV-AGILGSNVKTLDLDDSLQGDKAIIDIVKMGANI 287
Query: 299 T----WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
+ ET + T I ++ ++ PD+ LAV+ + G T I +
Sbjct: 288 KVGRDYIETKKSKT-----HGITIDASECPDLVPILAVLGAVSHGTTKIINAE 335
Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
R+KE +R+ A+ TEL+K+GA ++E D II KL +D+++DHR+AMA ++A+
Sbjct: 336 RLRIKEDRLKAMATELSKIGADIKELEDGLIIGKYKLKGGVVDWNDHRIAMAMAIAS 395
Query: 415 --CAEVPVTIRDPGCTRKTFPDYF 436
C E PV I++ K++PD++
Sbjct: 396 IKCTE-PVIIQNSMAVNKSYPDFW 418

>ref|YP_055974.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes KPA171202]
gb|AAT83016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes KPA171202]
Length = 429

Score = 176 bits (447), Expect = 5e-42, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 219/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSDGPSVLEGVLASRDSYLSAGLQLLGADIQPIGPGS 76
Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125
Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N L G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD----SDRLPFSLNAPDRLCGPKVTIDSATSSQFISALLLASARF 181
Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + S P++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHDGASVPSTPHIAMTCAMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238
Query: 253 DASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGAIVSRVDGSMITIAAQ-- 296
Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALHEHELA 353
Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGKFGCYADHRMAHAGALLGLVIDGVLEDDITCTSK 413
Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+
Sbjct: 414 TMPQFPQMWANLVEE 428

>ref|ZP_01882742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter sp. BAL39]
gb|EDM37644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pedobacter sp. BAL39]
Length = 417

Score = 176 bits (447), Expect = 6e-42, Method: Compositional matrix adjust.
Identities = 139/438 (31%), Positives = 219/438 (50%), Gaps = 50/438 (11%)

Query: 13 KEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K I + L GSKS NR L+++ALS+G V N+ S+ AD
Sbjct: 13 KHIHTEITLTGSKSECNRALIISALSKGAVAVANM-----SIAADTV 54
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
++ P + + +G AG AMR LTA ++A G+ + L G RM++R

Sbjct: 55 TLARILKQVSTHNPQQTVD-----VGPAGTAMRFLTAFLSALPGD--FRLTGTERMQR 107

Query: 133 PIGDLVVLGKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
 PIG L LK +GA++ +LG + PP+ +NG VK+ G ISSQY+SALLM AP

Sbjct: 108 PIGILSEALKTIGANI-SYLGEEGYPPLHINGPLNQSADTVKIKGDISSQYISALLMVAP 166

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
 + +EI +L S+PYV+MTL ++ G+ H S + IK Q +K+ VE

Sbjct: 167 RLPEGLTLEIEGELTSVPYVKMTLDMLTEAGIS--HEWSAQQISIK-PQSFKA-TTLTVE 222

Query: 252 GDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
 D S+ASY+ + AA+ + + SLQGD + E++ G + T + ++

Sbjct: 223 PDWSAASYWYSIAALASESAIELPYLKEKSLQGDSRIREIMTAFGLHTSNTANGIALSKI 282

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
 P F + L ++ PD+A T+ V A A + + ++KET+R+ A++ E

Sbjct: 283 P-AAFTDEVL-----DLKDCPDLAQTVIVCAAAMKKNLAFTGLETLIKETDRIKALQNE 336

Query: 371 LTKLGASVEEGPDYCIITP-----PEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
 L K+G ++ E D+ + T PE++ TY+DHRMAMAF+ + V +

Sbjct: 337 LAKIGVTLTE--DHLVYTLNCDGLHFPERVTFA---TYEDHRMAMAFAPLSLLINEVVLE 391

Query: 424 DPGCTRKTFPDYFDVLST 441
 + K++PD++ L T

Sbjct: 392 EMDVVEKSYPDFWKDLQT 409

>ref|YP_003513920.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stackebrandtia
 nassauensis DSM 44728]
 gb|ADD44827.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stackebrandtia
 nassauensis DSM 44728]
 Length = 431

Score = 176 bits (446), Expect = 6e-42, Method: Compositional matrix adjust.
 Identities = 138/433 (31%), Positives = 215/433 (49%), Gaps = 30/433 (6%)

Query: 15 ISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G V +PGSKS+ +R+L+L A S G + V L + D M+ L+ +G+ V A

Sbjct: 21 VRGRVSIPIGSKSMMSRVLVLTAAASHGASSVAAPLLARDSALMVAGLQAMGIRVVTTDDAL 80

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
 V + P A + G AG MR L A G T+ DG P R+RP+

Sbjct: 81 WMV----HPRAPQGPAAVDC----GLAGTVMRFLPPLAAVAHGPIITF--DGDPYARKRPM 130

Query: 135 GDLVVLGKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
 L+ L LG VD ++ P + G G + GG++ + S SSQ+LS LL++AP

Sbjct: 131 APLLRLALTALGVSVDA--ASESLPFTIQGTGRISGGEITIDASSSSQFLSGLLLSAPRYD 188

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD--DSWDRFYIKGGQKYKSPKNAYVE 251
 G V + S P+V MT+ ++ G + S + W+ ++ GQ + +VE

Sbjct: 189 RGIVLRHQGPVPSPRPHVRMTVDMLRAAGAAVDDSRPNVWE---VEPGQLGG--RAWHVE 243

Query: 252 GDASSASYFLAGAAITGGTVTV-EGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
 D S+A+ FLA A +TGG VTV + TTS GD+ ++ +G + + +T+TG

Sbjct: 244 PDLNSAAPFLAALVTGGEVTVPDWPATTSQPGDL-LRDLFTQLGGRAVLSHDGLTITG- 301

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
 ++ ID ++++ ++ +A V AD P+ +R + R ET+R+ A+ E

Sbjct: 302 -----SGSVRGIDADLSEAGELTPVVAACALADSPSTLRGIGHLRGHETDRLAALTAE 355

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRK 430
 L +LG V E D I P L+ + +DTYDDHRMA A ++ A V + D CT K

Sbjct: 356 LNRLGGDVTETDDGLRIR-PRPLHGSVVDTYDDHRMAQAAAVLGLAVPDVVLSDVACTSK 414

Query: 431 TFPDYFDVLSTFV 443
 T P + + + V

Sbjct: 415 TLPQFPQLWTELV 427

>gb|EFT31959.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
 acnes HL005PA2]

gb|EFT33770.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL005PA3]
Length = 429

Score = 176 bits (446), Expect = 6e-42, Method: Compositional matrix adjust.
Identities = 139/435 (31%), Positives = 220/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++
Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSDGPSVLEGLASRDSYLSAGLQLLGADIQPIGPS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P+E G AG MR L G +V G + RP
Sbjct: 77 VQVMPGLAHPTGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P ++ + G KV + + SSQ++SALL+A+
Sbjct: 126 IAPVLNGLRQLGVEVD---SDRLPFSLDAPDRMCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + SIP++ MT ++ GV SD + ++ G + + +E
Sbjct: 182 PQGIDLRHNGASVPSIPHIAMTCTMLADRGVTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+
Sbjct: 239 DLTNAAVFLAAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGAMVSRVDGSMTIAAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G + L+ +DV++++ ++ +A VA A G + IR VA R ET+R+ A+ EL
Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASLARGSRIRGVAHIRGHETDRLAALHEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLG V++ + IT +KL+ Y DHRMA A +L V + D CT K
Sbjct: 354 KLGVEVQQTDNGLDITGRGADKLHGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVKN 445
T P + + + V+
Sbjct: 414 TMPQFPQMWANLVEE 428

>gb|ADZ12570.1| 5-enolpyruvylshikimate-3-phosphate synthase [Riemerella
anatipestifer RA-GD]
Length = 678

Score = 176 bits (446), Expect = 6e-42, Method: Compositional matrix adjust.
Identities = 133/430 (30%), Positives = 208/430 (48%), Gaps = 42/430 (9%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ + GSKS SNR+L+L L G ++NL N++D + AL +
Sbjct: 17 ISISGSKSESNRLLILQRL-LGDLQINNLSNAQDTQLLQKALYS----- 59

Query: 79 VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
+EV + + +AG AMR LT+ G T +L G RM++RPI LV
Sbjct: 60 -----NDEV-IDIHAGTAMRFLTSYFVIQEGRTT-ILTGSDRMKQRPIAPLV 105

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
LK LGA++ CPP+++ G L +V +S +SSQ++S+LL+ A ++
Sbjct: 106 EALKSLGAEITYLEKEGCPPLKIVG-KKLYKNEVSISAIEVSSQFISLLLVAGFLENGLK 164

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
I ++ + S PY+EMTL+++ G++ E + K VE D SSAS
Sbjct: 165 IALVGHITSRPYLEMTLKMSLDLGIEFEKGTIEVKPLKKELATDNKEYTVESDWSAS 224

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL-EMMGAKVTWTETSVTVTGPPREPFGFR 317
YF + AI V +E TS+QGD ++ + G + + V P ++ +
Sbjct: 225 YFYSLVAIGKKQVALESFKETSMQGDKALVKIYRDFGVETQFQNGERLVLTPIKD--FK 282

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ LK I+++MN PD+A T+ V A I +A+ +VKET+R+VA++ EL K+G
Sbjct: 283 QPLK-INLDMNDPCDIAQTVCVTAAALGVHFIQIEGLATLKVKETDRLVALKNELLKIGLE 341

Query: 378 VEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPD 434
E D I V I TY DHRMAM+F+ A + I D K++P
Sbjct: 342 TEITEDS--IKSARFFQVEEIPCIKTYHDHRMAMSFAPYALVG-DIKIEDASVVEKSYPY 398

Query: 435 YFDVLSTFVK 444
+++ T K
Sbjct: 399 FWEDFKTLK 408

>ref|ZP_06644106.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erysipelotrichaceae
bacterium 5_2_54FAA]
gb|EFE47603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erysipelotrichaceae
bacterium 5_2_54FAA]
Length = 421

Score = 176 bits (446), Expect = 7e-42, Method: Compositional matrix adjust.
Identities = 123/426 (28%), Positives = 203/426 (47%), Gaps = 33/426 (7%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V +P SKS+++R ++ A+L++G +++ N+ S+D+ + ++ LG +E A+
Sbjct: 12 GHVHIPPSKSMRAIICASLAKGRSIIISNVAYSKDIRATIEGMKQLGAHIEV--AEDT 68

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
V + F KE +F +G +R + T+ G R + + +
Sbjct: 69 VTIDGIANFQGLKDKE---IFCNESGSLTRFFIPIFSLCEKPITFTGSGRLLQRPQKVYE 125

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIG---GLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ K L D +GI LP G+ ++ G +SSQ++S LL PL
Sbjct: 126 DIFHEKGLAFQQD-----THGIHQEALPYGEYQIKGDVSSQFISGLLFTLPL 174

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D I I+ S YVE+TL+++E FGV A D I GGQ Y++ N +EGD
Sbjct: 175 EKDSIIRILPPFESRSYVELTLQMLEHFGVHAYFKDEM-TLTIPGGQSYQA-NNYEIEGD 232

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPE 313
S ++F AAI G +TV G S QGD E+L+ GA++ P
Sbjct: 233 YSQLAFFAVYAAIH-GKITVTGVSHASRQGDKAILEILKSFGARIEEV-----PHGY 283

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
F + LK +++ PD+ L V+ +++ G T I + R+KE++R+ A+ EL K
Sbjct: 284 TFYKSELKGTSIDLANCPDLGPILCVLGMYSLGNTIYNAGRLRIKESDRIAAMEEELRK 343

Query: 374 LGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLA-ACAEVPTIRDPGCTRK 431
G ++ D I + + + ++DHR+ MA S+A AC+ TI D K+
Sbjct: 344 FGVTTITSTEDAIFIQGGQDFSCQTTLHGHNDRIVMALSVATACNSCATIEDAQAITKS 403

Query: 432 FPDYFD 437
+P +FD
Sbjct: 404 YPTFFD 409

>ref|YP_001505320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. EAN1pec]
gb|ABW10414.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. EAN1pec]
Length = 459

Score = 176 bits (446), Expect = 7e-42, Method: Compositional matrix adjust.
Identities = 150/459 (32%), Positives = 221/459 (48%), Gaps = 49/459 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE----- 68
+ TV +PGSKS +NR L+LAA ++G + + L S D M ALR LG +V
Sbjct: 18 VRATVTVPGSKSGTNRALVLAADGVSRRLRGALRSRDTVLMAAALRELGATVTDEAAPG 77

Query: 69 -----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG 117
AD+ A VV G PV + + GNAG R A T A G
Sbjct: 78 GAEPGRPGEPGADQGAADIVVTG-----PVGAVRGTAIDCGNAGTVARFTPALATLARG 132

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+ + DG PRMR+RP+ L+ L++LGA +D D P V G G + GG V + S
Sbjct: 133 DVRF--DGDPRMRDRPLTPLLRALRELGAHIDG----DRMPFTVRGTGAVSGGAVTVDAS 186

Query: 178 ISSQYLSALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236

SSQ +S LL+AA G +L S PY++MT+ + GV + D
Sbjct: 187 DSSQLVSGLLLAARFERGATVTHAGHRLPSGPYLDMTVADLRAAGVVVDVDDPTADLLR 246

Query: 237 KGGQKYKS-----PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
GG S P + +E D +SA+ F+A AA+TGG VT+ G ++ Q

Sbjct: 247 AGGTPAASTRRRVRVKPGGPRPLDRVIEPDLNSAAPFVAAAATGGEVITITGWPASTEQPG 306

Query: 285 VKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA 344
++L MG + + VTG R + IDV+++ + A L +A+ A

Sbjct: 307 RMLPDLVAMGCRAELVPEGLRVTTGGGR-----ITGIDVDLSDFGEAAPVLTGLAVLA 359

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDH 404
D P+ +R +A R++ET+R+ A+ +EL +LGA V D I P L +D + DH

Sbjct: 360 DSPSRLRGIAHLRLQETDRLAALASELGRGLGARVTVTDDGLSII-PVPLRGARLDPHADH 418

Query: 405 RMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVLSTFV 443
R+AM +++ A VT+ D T KT PD+ + +T +

Sbjct: 419 RLAMTYAVVGLAVPGVTVDDIATTGKTVPDFARMWTTML 457

>ref|YP_002765629.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus
erythropolis PR4]
sp|C0ZX05.1|AROA_RHOE4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAH32890.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodococcus
erythropolis PR4]
Length = 437

Score = 176 bits (446), Expect = 7e-42, Method: Compositional matrix adjust.
Identities = 143/433 (33%), Positives = 218/433 (50%), Gaps = 44/433 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE--ADKA 72
+ V LPGSKS++NR L+LAAL++G + + L S D M+ ALR LG+ VE D

Sbjct: 18 VDAVVTLPGSKSITNRALILAAALADGPSTITGALRSRDADLMIAALRDLGIGVEEAGDPT 77

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R P+ + + L AG MR L A G + DG + R R

Sbjct: 78 TLRIT-----PGPLRGGEVDCGL---AGTVMRFLPPLAAMADGIVRF--DGDEQARTR 125

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G ++ L+ LGA ++ D P V G G L GG V + S SSQ++S LL++A

Sbjct: 126 PLGTILEALRGLGARIEG---DALPFTVTGTGSLRGGTVTIDASGSSQFVSGLLLSAAA 181

Query: 193 ALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAE-----HSDSWDRFYIKGGQKYKSP 245
V + K + S+P+++MT+ ++ + GV +D+W + P

Sbjct: 182 FEEGVTVVHHDGKPVPSMPHIDMTVEMLRQSGSVVTTTPATGGDADTW-----RVAPGP 233

Query: 246 KNAY---VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
A +E D S+A+ FLA AA+TGGTV+V +++ Q +L MGA VT +

Sbjct: 234 VRAVDWAIPEPLSNATPFLAAAAVTGGTVSVPMPWPSSTTQPGDAIRGILASMGADVTLD 293

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+TV GP + L+ ID++++ + ++ T+A +A A+G + +R +A R ET+

Sbjct: 294 GVLTVRGP-----EKLRGIDIDLHDVGELTPTVAALAALAEGTSHLRGIAHLRGHETD 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTI 422
R+ A+ E+ KLG SV E D I P E L+ +Y DHRMA A ++ V +

Sbjct: 347 RLAALADEINKLGGSVTETDDGLTIVPAE-LHGGQWLSYADHRMATAGAIIGLVVDGVDV 405

Query: 423 RDPGCTRKTFPDY 435
D G T KT P +

Sbjct: 406 DDVGTТАKTLPGF 418

>ref|XP_001019959.1| 3-dehydroquinate synthase [Tetrahymena thermophila]
gb|EAR99714.1| 3-dehydroquinate synthase [Tetrahymena thermophila SB210]
Length = 1559

Score = 176 bits (446), Expect = 7e-42, Method: Composition-based stats.
Identities = 127/408 (31%), Positives = 209/408 (51%), Gaps = 25/408 (6%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
++L GSKS++NR+L+L+AL + + N+L +ED M+ +L+TLG A V
Sbjct: 382 IQLAGSKSITNRVLILSALLDKEIQLQNVLFADTEVMMKSLQTLGACSIQQLDANTVKV 441

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G GG F +D KE +++ N+G + R + + + N + V+ RM+ERPI DL+
Sbjct: 442 KGNGGAFNFQDEKE---IYVNSGTSARFICSMLLLLKPNQSVVIRCCERMKERPIKDLI 498

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L + + P RV GG + ++ ISSQY++ +LMAAP AL V
Sbjct: 499 EALSDF-LNFEYLEKEFYLPFRVTKKYEFKGGDIHINSKISSQYVTGILMAAPYALEPVR 557

Query: 199 IEI--IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA-YVEGDAS 255
+ + +++ S P+++MT +M++FG + + + F I KY PK + Y+E DA+
Sbjct: 558 VILSQTEQITSEPFIQMTFDMMKQFGSNI-YREKQNFNIS-NTKYLPKESYYIEPDAA 615

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPF 315
+ASY +A A + + ++G SLQGD+KF E L +G V + + V + G
Sbjct: 616 TASYDMAWAVLNQKKIIKGFQIHSLLQGDCLKFTEKLVGLGYCVEYNDVGVIIRG----DL 671

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVV--ALFADGPTA--IRDVASWRVKETERMVAIRTEL 371
+K + N D +T ++ AL + + I ++A+ RVKE +R+ A+ L
Sbjct: 672 PQKECTQTTDFDNCTDTFITFGIILAALNNNNQSYKIVNIANQRVKECDRIHALSLNL 731

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTAITD-----YDDHRMAMAFS 411
K G E D I P +K + D+ ++DHR+ MAFS
Sbjct: 732 KKFGIKTIEYDDGIEIFPNKKQLLEQCDSKQSIIIECFNDHRLGMAFS 779

>ref|YP_003541749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanohalophilus
mahii DSM 5219]
gb|ADE36104.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanohalophilus
mahii DSM 5219]
Length = 427

Score = 176 bits (445), Expect = 8e-42, Method: Compositional matrix adjust.
Identities = 148/427 (34%), Positives = 219/427 (51%), Gaps = 27/427 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V P SKS ++R + + +LSE VV L SED + A + LG + +K
Sbjct: 10 VEGEVFAPPSKSYTHRAITIGSLSE-KCVVRRPLISEDTKATIHACKMLGAQINEEKG-- 66

Query: 75 RAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G GK + ED + +GN+G +R +TA + G +L G +R RP
Sbjct: 67 DLFIIEGVKGKPHIPEDV-----IDVGNSGTTLRFMTAVASLVDG--VSILTGDNSLRTRP 119

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
G L+ L LG +V L C P+ V G GL G K+ GSISQ++SALL+A PL
Sbjct: 120 NGPLIEVLHDLGVEVISTLNNGCAPLVVKG--GLKGAIKIDGSISSQFISALLIACPLT 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-EHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ I +L S PYV +TL ++ G + E S+ +F I Q Y + ++ V G
Sbjct: 178 SKSTTLSEIKGELRSKPYVNVTLLEILREAGAEIFEDSNHNIKFIIPPNQDY-NLRDYLVP 236

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSASY LA AA+TG V V+ S QGD+ +L+ MGA ++W + + VTV G
Sbjct: 237 DFSSASYLLAAAMTGSRRVVVKNM-FPSQQGDMAIIGILKQMGAGISWDKDNGRVTVNG- 294

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ LK + V+ PD+ T+AV+ A+G T I + R KET+R+ A+ E
Sbjct: 295 -----RDLKGVVRDAAATPDLVPTIAVLGAVAEGQTVIENAEHVRYKETDRLHAMAVE 347

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTAITDITYDDHRMAMAFSLAACAEVPTVIRDPGCTRK 430
L K+G SV+E D I KL + + + DHR+ MA ++A T+
Sbjct: 348 LKKMGVSVKEDQDKLTIKGG-KLKGSELHGWHDHRIVMALTIAGMVAGDTTVDTAESIFI 406

Query: 431 TFPDYFD 437
++P++FD
Sbjct: 407 SYPNFFD 413

>gb|EGD35333.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga sp.
oral taxon 338 str. F0234]
Length = 447

Score = 176 bits (445), Expect = 9e-42, Method: Compositional matrix adjust.
Identities = 135/427 (31%), Positives = 210/427 (49%), Gaps = 53/427 (12%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+ + GSKS +NR+LLL + V+N S+D M L +
Sbjct: 57 TLNIGGSKSETNRLLLQLCPLSLQ-VENASFSKDSLSMYEGLHS----- 100

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+KE + +G+AG MR LTA A +L G RM+ERPIG L
Sbjct: 101 -----SKEIIN--IGDAGTVMRFLTAYY--AISKRKVILTGSERMQERPIGIL 144

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+QLGA + PP+R+ G L GG + + ISSQ++SALLM AP + +
Sbjct: 145 VDALRQLGASITYLAREGYPLRIEG-KPLLGGTLTIRADISSQFISALLMIAPTfVKGL 203

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ + ++ S PY+ MTL L+ G++A + + + Y SPK VE D SS
Sbjct: 204 SLHLEGEITSFPYLRMTLSLLNELGIEATFEEHTLEVPTPT---ISPKTIIVEPDWSS 259

Query: 257 ASYFLAGAAIT--GGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE- 313
ASYF + A++ G T+++ SLQGD A++ + G K + E + + E
Sbjct: 260 ASYFYSLIALSEVGTTLSSLHYKQDSLQGDRLADIYKTFGVKTLFLEDRIQLVKKKTEI 319

Query: 314 -PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
P N+ PD+A T+AV + + + +KET R+VA++ ELT
Sbjct: 320 PPI-----FSYNLIDTPDIAQTIAVTCFGLGVECFSLGLKTLNIKETNRLVALKEELT 372

Query: 373 KLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEVPTIIRDPGCTRK 430
KL V+ + P ++ N+ AI+ ++DHRMAMAF+ C +VP+TI + K
Sbjct: 373 KLSGEVQISDSEIWPAPCTEITPNI-AINPHNDHRMAMAF-PLCLKVPITITETKVVEK 430

Query: 431 TFPDYFD 437
++P++++
Sbjct: 431 SYPNFEW 437

>ref|YP_004036929.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halogeometricum
borinquense DSM 11551]
gb|ADQ67484.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halogeometricum
borinquense DSM 11551]
Length = 432

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 150/445 (33%), Positives = 216/445 (48%), Gaps = 29/445 (6%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ + P + I G + P SKS ++R +L A TV+ N L S D + A+ G
Sbjct: 2 DVTISPSR-IDGRTRAPPSKSYTHRAILAAGYGGQATVL-NPLVSADTKATMRAVDFAFG 59

Query: 66 SVEADKAAKRAVVVGCGGK--FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ V G G+ P + E N+G MR +TA AA G+ VL
Sbjct: 60 DTDLSADESSLVSGFDGRPEVPADVNC-----NSGTTMRLVTAC--AALGDGLTVL 111

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G +R RP G L+ + LG + P+ V + GG V + G +SSQY+
Sbjct: 112 TGDDSLRSRPQGPLLDVTDLGGRGESTRRNGQAPLVVGD--AMDGGTVSIPGDVSSQYI 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALLMA + ++IE+ +L S PYV++TL L++ FGV+AE + D F + GGQ Y
Sbjct: 170 SALLMAGAVTDEGIDIELETELKSAPYVDITLLELLEFGEAEQ--TADGFSVAGGQSYD 227

Query: 244 SPKNAY-VEGDASSASYFL---AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Y V GD SS SY L A AA G +V VEG S QGD +++ MGA VT
Sbjct: 228 PTGGEYEVPGDFSSISYLLAAGAIAGAAEGSVVVEGA-RPSAQGDAAIVDIVRDMGADV 286

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359

W + +T R L V++ PD+ T+A + ADG T I + R K
Sbjct: 287 WDRDAGELT-----VSRATLTGTTVDVGDTPDLLPTIATLGAVADGDTVIENCEHVRYK 340

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAA-CAE 417
ET+R+ A+ EL K+GASV E D I E V A ++ DHR+ M+ ++A AE

Sbjct: 341 ETDVRSAMADELGKMGASVTEEQDRLTIHGGETDLVGATVEGRHHRIVMSLAIAGLVAE 400

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
T+ +FP++FD + +

Sbjct: 401 GETTVTGAEHVDVSFPNFFDAIESL 425

>ref|YP_003581491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes SK137]
gb|ADD99333.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes SK137]
gb|EFS38047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL074PA1]
gb|EFS48000.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL083PA1]
gb|EFS68323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL007PA1]
gb|EFS71361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL056PA1]
gb|EFT17707.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL053PA1]
gb|EFT19928.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL045PA1]
gb|EFT27781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL005PA1]
gb|EFT52363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL078PA1]
gb|EFT67861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL038PA1]
Length = 429

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 139/435 (31%), Positives = 218/435 (50%), Gaps = 27/435 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PGSKS +NR L+LAALS+G +V++ +L S D + M L+ LG ++

Sbjct: 17 LAGRVTVPGSKSQTNRALVLAALSDGSPVLEGLASRDSYLSAGLQLLGADIQPIGPGS 76

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P+E G AG MR L G +V G + RP

Sbjct: 77 VQVMPGLAHTPGPIE-----CGMAGTVMRFLPVVAALVPGQTRFV--GDEQASRRP 125

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I ++ GL+QLG +VD +D P +N L G KV + + SSQ++SALL+A+

Sbjct: 126 IAPVLNGLRQLGVEVD----SDRLPFSLNAPDRLCGPKVTIDSATSSQFISALLLASARF 181

Query: 194 LGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+++ + S P++ MT ++ GV SD + ++ G + + +E

Sbjct: 182 PQGIDLRHDGASVPSTPHIAMTCAMLADRGTVV-SDEPCHWVVRPGPIHA--LDDVIEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D ++A+ FLA A I GG+VTV G T S Q +F + E MGA V+ + S+T+T

Sbjct: 239 DLTNAAVFLAALIVGGSVTVPGWPTDSTQPGAQFMGIAEKMGMAMVSRVDGSMTITAQ-- 296

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
G + L+ +DV++++ ++ +A VA G + IR VA R ET+R+ A+ EL

Sbjct: 297 ---GWQELRPLDVLHEASELTPVVAASVLRGRSRIRGVAHIRGHETDRLAALEHELA 353

Query: 373 KLGASVEEGPDYCIIT--PPEKLNVT- IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
LG V++ + IT +KL+ Y DHRMA A +L V + D CT K

Sbjct: 354 NLGVEVQQTNDGLDITGRGADKLHGGKFGCYADHRMAHAGALLGLVIDGVELDDITCTSK 413

Query: 431 TFPDYFDVLSTFVK 445
T P + + + V+

Sbjct: 414 TMPQFPQMWANLVVEE 428

>ref|YP_003309207.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sebaldella termitidis
ATCC 33386]
gb|ACZ09276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sebaldella termitidis
ATCC 33386]
Length = 424

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 127/434 (29%), Positives = 223/434 (51%), Gaps = 25/434 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EI + P K + G + +P SKS S+R ++ A+L++G + + NL S D+ ++ G
Sbjct: 2 EIKIIPK-LKGEINIPPSKSYSHRAVIAASLTGDSRIGNLNFSDIQTITTDIMKNFGA 60

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + + G G +E+ + +G +R + + N +DG
Sbjct: 61 VIE--QGEDYLKITGNQGNVTIENN---YIQCNESGSTIR-FIIPIALSRNNGQLTIDG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ ERP + G G P+ + G L ++ G+ISSQ+++
Sbjct: 114 KGKLIERPFDITYYKIFDKQGISYKTTNGK--LPLYIEG--SLKADTFEVEGNISSQFITG 169

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL PL GD EI I L S YV++TL+++E ++ +++D + F IKG Q YK
Sbjct: 170 LLYTLPLLDGDSEIVIKGPLESKGYVDLTLKILEMADIEVKNND-YKSFLIKGNQTYKGF 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ VEGD S +++ A I + + SLQGD E+++ MGA + + ++
Sbjct: 229 -DYTVEGDYSQVAFWIV-AGILSEEINCKNVYKDSLQGDRAIVEIVQRMGANLEINDKNI 286

Query: 306 TVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V P G+ IDV+ + PD+A L V+A ++G T I + R+KE++R+
Sbjct: 287 KVF-----P-GKTKGTVIDVS--QCPDIAPVLTVLAALSEGETRIINAERLRIKESDRIT 338

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
++RTEL KLGA + E D +I ++L +D+++DHR+AMA ++A+ + P+ I
Sbjct: 339 SMRTELNLKLGADIREEGDTLVINGVDELEGGVTVDSDWHDHRVAMALAIASIKCKNPILIT 398

Query: 424 DPGCTRKTFFPDYFD 437
D G RK++P++++
Sbjct: 399 DAGAVRKSYPNFWN 412

>ref|ZP_07089459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
genitalium ATCC 33030]
gb|EFK54772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
genitalium ATCC 33030]
Length = 433

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 142/431 (32%), Positives = 214/431 (49%), Gaps = 31/431 (7%)

Query: 18 TVKLPKSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T +PGSKSL+NR +LAAL++G + + L S D M AL ++G+ D A A
Sbjct: 24 TQVIPGSKSLTNRAYVLAALADGPSTLVGALRSRDTLMESELESMDGVQFTRDGDVTA- 82

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
A ++ G AG MR + A A G ++DG P+ R RP+ +
Sbjct: 83 -----TPGALTGAEVDCGLAGTVMRFVPAVAFAFG--PVLIDGDPQARSRPVSTI 131

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLALGD 196
+ L+ LG VD D P VNG G GG+V++ S SSQ++SALL+A A G
Sbjct: 132 LNALRDLGVHVDG---DSLPTVNGSGSALGGRVEIDASSSSQFVSALLLAGARFERGV 187

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ KL S+P+++MT+ ++ GV E D + + ++ G + +E D S+
Sbjct: 188 QLVHTGGKLPSPHIIQMTVDMVRDAGVTETGD--NEWTVQPGPIAG--RTWMIEPDLN 243

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----SVTVTGPPR 312
A+ FLA AA+TGG VTV + Q +LE MG V+ ++ VTGP
Sbjct: 244 ATPFLAAAAVTGGEVTVFPFWPQETTQAGDAIRGILERMGCDVSLVPNGPAHALKVTGPE- 302

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
G K L+ I ++M+ + ++ T+A A A P+ + +A R ET+R+ A+ E+
Sbjct: 303 ---GGK-LRGISLDMSDIGELTPTVAALAAHATTPSELGTGIAHLRGHETDRLAALSAEIN 358

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTTIRDPGCTRKTF 432
LG +E D IT P L+ +Y DHRMA A ++ VT+ D G T KT
Sbjct: 359 ALGGQCDELDDGLRIT-PAPLHSGTWHSYADHRMATAGAIIGLTVEGVTVEDIGTTAKTL 417

Query: 433 PDYFDVLSTFV 443
P + + S V
Sbjct: 418 PGFEHWMWGMV 428

>ref|YP_004053366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marivirga tractuosa
DSM 4126]
gb|ADR21258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marivirga tractuosa
DSM 4126]
Length = 416

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 134/439 (30%), Positives = 212/439 (48%), Gaps = 61/439 (13%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
++ LP SKS SNR+L++ ALS+G ++NL ++ D ++ L
Sbjct: 18 SINLPSSKSESNNLLVMNALSDBGKIDLNLLSSARDTQTLIKLL----- 60

Query: 78 VVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
E+ E + +AG AMR LTA A N L G RM++RPI L
Sbjct: 61 -----ENENELNTFDVLDAGTAMRFLTAYFAVATKNEV-ALTGTERMKKRPIRIL 109

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
V L+ +GA++ PP+++ K+ + G+ISSQY+SALLM AP +
Sbjct: 110 VNALRSIGAEISYNNEEGFPPLKIKPFQKQISSKISIPGNISSQYISALLMIAPSLPHGL 169

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
EI+I + S PY+ MTL LME G+ ++S + + I+ QKY+ VE D S++
Sbjct: 170 EIKIEPPVFSKPYINMTLGLMELSGI--QYSQNKNTISIQ-YQKYQESSQG-VESDWSAS 225

Query: 258 SYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPF 315
SY+ + A + G V +EG + S QGD E++ G + +T + + E
Sbjct: 226 SYWFSIIAQSEIGKKVFLEGLKSKSFQGDNDIKEIVGNFVSYKFEKTGILL----EKI 280

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
+ ++ K PD+A T+ A + + + S R+KET+R+ A++ EL+K
Sbjct: 281 SSAKNSLLKLDPKKCPDLAQTVLPCAASLNVDMLEMTGLESRLRIKETDRISALQNELSKFN 340

Query: 376 ASVEEGPDYCIITPPEK-----LNVTA-----IDTYDDHRMAMAFSLAACAEVPTIR 423
C +T PEK N A I+TY+DHRMAM F+ A + + I+
Sbjct: 341 -----CKLTEPEKGIWKLDSNNFKAKEGIIETIEDHRMAMGFAPLAL-KTGIQIK 390

Query: 424 DPGCTRKTFPDYFDVLSTF 442
D K++P +++ L F
Sbjct: 391 DIEVVNKSYPSPFWEDLELF 409

>ref|NP_633262.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina mazei
Gol]
sp|Q8PXI0.1|AROA_METMA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAM30934.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosarcina mazei
Gol]
Length = 430

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 151/427 (35%), Positives = 222/427 (51%), Gaps = 27/427 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G V P SKS ++R + LAALS+ + + LL S D + A G +V +K +

Sbjct: 10 IKGEVFAPPSPKSYTHRAITLAALSKEIIHRPLL-SADTLATIRASEMFGAAVRREK--E 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERI 134
++ G GK + D + N+G +R +TA G VL G +R RP

Sbjct: 67 NLIIQSGNGKPGIPDD---VIDAANS GTTLRFMTA IAGLTDG--ITVLTGDSSLRTRPN 120

Query: 135 GDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ L +LGA G + P+ V G G+ G +V++SGSISSQ++SALL+A PLA

Sbjct: 121 GPLLEVLNRLGAKACSTRGNERAPIVVKG--GIKGEVEISGSISSQFISALLIACPLAE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKYKSPKNAYVEG 252
+ II KL S PYV++T+ ++ GVK H+D + +F I G QKY K V G

Sbjct: 179 NSTTSLIIGKLSRPYVDVTIEMLGLAGVKI-HTDDNNGTKFIIPGKQKY-DLKQYTVPG 236

Query: 253 D-ASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS--VTVTG 309
D +S++ A A + G +TV+ S QGD + L+ MGA +TW + VTV G

Sbjct: 237 DFSSASYLLAAAMLEGSEITVKNL-FPSKQGDKVIIDTLKQMGADITWDMEAGIVTVRG 295

Query: 310 PPREFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
GRK LKAI + PD+ T+AV+A A+G + I + R KET+R+ A+ T

Sbjct: 296 -----GRK-LKAITFDAGSTPDLPVTAVLASVAEGTSRIENAEHVRYKETDRLHALAT 348

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
EL K+G S++E D IT L + +DDHR+ M+ ++A +

Sbjct: 349 ELPKMGVSLKEEMDSLITITGG-TLEGAEVHGWDHRIVMSLA IAGMVAGNTIVDTTESVS 407

Query: 430 KTFPDYF 436
++PD+F

Sbjct: 408 ISYPDF 414

>ref|YP_003155352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachybacterium
faecium DSM 4810]
gb|ACU85762.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachybacterium
faecium DSM 4810]
Length = 441

Score = 175 bits (444), Expect = 1e-41, Method: Compositional matrix adjust.
Identities = 134/425 (31%), Positives = 212/425 (49%), Gaps = 16/425 (3%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + V++PGSKSL+ R + LAA ++ +V+ L S D M AL LG +E +

Sbjct: 14 RPVDALVRVPGSKSLTARWMLAAADEPSVLRGALVSRDTRLMDALERLGAVLEVEDG 73

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A + + E V++ G AG MR + G+ + D +R

Sbjct: 74 ALHVTPLPPPAEH---PAEPVEIHTGLAGTVMRFVPMALALHHGDVRFRTGDEA--AFQR 127

Query: 133 PIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L+Q G +V P+ V+G G LPGG+V++ S SSQ++S LL+ A

Sbjct: 128 PMDAVVDVLRQQGVVEVEHGEPRGLPLTVHGTGRLPGRVEVDASASSQFISNLLVAAR 187

Query: 193 ALGDVE-IEIIDKLISIPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNAYV 250
A D+E + + + L S+P+++MT+ + + GV+A H D+ R P +

Sbjct: 188 AETDIELVHVGVELPSLPHIDMTVETLRQAGVEATHQLDAEGRHAWSVRHGAIRPLEVTI 247

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETS SVTVTGP 310
E D S+A FLA A TGGT+ V+ T+ Q + ++L MG +V W E

Sbjct: 248 EPDLSNAGPFLAAAMATGGTIAVDWPETTTQPGDAYRDLLTRMGGEV-WREGRTL CV-- 304

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G L+ ID +M+ M ++ T++ + A+ P+ + VA R ET+R+ A+ TE

Sbjct: 305 ----RGTGTLRGIDADMSAMGELVPTMSALCALAETPSRLTGV AHLRGHETDRLKALATE 360

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
LTK+GA E D I P E L ++Y+DHRMA A ++ + + D G T+K

Sbjct: 361 LTKIGARTSELEDGLEIHPGE-LRGDVFESYEDHRMATAGAIIGLRVPDLRVVDIGTTQK 419

Query: 431 TFPDY 435
T PD+

Sbjct: 420 TLPDF 424

>ref|ZP_02867959.1| hypothetical protein CLOSPI_01799 [Clostridium spiroforme DSM 1552]
gb|EDS74216.1| hypothetical protein CLOSPI_01799 [Clostridium spiroforme DSM 1552]
Length = 426

Score = 175 bits (443), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 121/425 (28%), Positives = 224/425 (52%), Gaps = 25/425 (5%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++P SKSL++R ++ A+L++G + +DN+ S+D+ + A+++LG +E
Sbjct: 10 KLKGKVQVPPSKSLAHRRAIICASLAKGISRIDNIEYSKDIQATIKAMQSLGTKIEK---Y 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+++ F K ++ +G +R + ++ N + G + +RP
Sbjct: 67 NDYLIIDGTSTF----TKNNSEIDCESGSTLRFMIP-ISIVEENKVH-FTGHGNLGKRP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +Q ++ D + V IG L K+ G+ISSQ+++ LL A PL
Sbjct: 121 LDTFYKIFEQ--QNIGYLYKKDILDLYV--IGKLPDHYKIPGNISSQFITGLLFALPLL 176

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD IEI L S Y+++TL+++ ++G+K +++ + F I G Q+Y + ++ VE D
Sbjct: 177 KGDSIIEITSPLESKGYIDLTLQMLNQYGIKIINNN-YQSFIIGNQEYHA-QDYRVEAD 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPRE 313
S A+++L AI G V + SLQGD ++LE MGAK+T V VTG
Sbjct: 235 FSQAIFYLVAGAI-GNDVVLTDNLDSLQGDKATLDILESMGAKITVLGDGVKVTG---- 289

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++L A V+ ++ PDV ++V A G + + + R+KE +R+VA +++ +
Sbjct: 290 ----ENLSATIVDASQCPDVIPVVSVALALATGRSEVINAKRLRIKECDRLVATSSQINE 345

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTIRDPGCTRKTF 432
L +V+E P+ II ++ +Y+DHR+AM ++AA + P+ I + C K++
Sbjct: 346 LSGNVKELPEGMIINGVDEFTGGNCSSYNDRHAMMLAIAATRSIRPIIIDNMECEVEKSY 405

Query: 433 PDYFD 437
P +++
Sbjct: 406 PSFWE 410

>ref|ZP_03929090.1| conserved hypothetical protein [Acidaminococcus sp. D21]
gb|EEH90320.1| conserved hypothetical protein [Acidaminococcus sp. D21]
Length = 425

Score = 175 bits (443), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 131/425 (30%), Positives = 212/425 (49%), Gaps = 22/425 (5%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV P SKS+ +R L+ AAL++G + + ++ S+D+ L LG ++ K
Sbjct: 11 LAGTVTAPSSKSMGHRFLICAALAQGESWIRDVSFSKDIAATRRCLEALGATIMEGPGEK 70

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G+ P + + + G +G +R L G ++ +G + RP+
Sbjct: 71 GRKTYFVKGPQPPHQKSP--LMDCGESGSTLRFLIPLAALDGNFCYNFIGEG--ELGTRPL 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
K+ ++ G++ P+ V G L G + G +SSQ++S LL A PL
Sbjct: 126 TPYETLFKE--ENLHFHYGSRHFPLSVQG--PLKSGHFVVPDGVSSQFISGLLFALPLL 181

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D IEI S YV +TL + FGV D + + GGQ Y+ P + VEGD
Sbjct: 182 QRDSTIEITGSFESQSYVALTSLALSTFGVHV-FQDEPRLYRVLGGQAYR-PYSGSVEGD 239

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPRE 313
S A++FL A+ G +++ G T+SLQGD +L+ MGAK+ S+T+
Sbjct: 240 FSQAFFLVAGALGKG-ISIRGVKTTSSLQGDKAILPILQRMGAKLEEGPESLTI-----H 293

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
P L I ++ + PD+ L+V A A G T I R+KE +R+ A+ +ELTK

Sbjct: 294 P---SSLHGIRIDASDCPDLPILSVAAALAKGTTEIIHAERLRLKECDRLKAMASELTK 350

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTF 432
+GA VEE PD II L+ D+++DHR+AM+ ++AA ++ PV + +K++

Sbjct: 351 MGAHVEERPDGLIIRGVPLMHGAGADSWNDHRVAMSLAIAATRSDGPVILTGSSESVQKSY 410

Query: 433 PDYFD 437
P ++

Sbjct: 411 PQFWQ 415

>emb|CBL34654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium siraeum
V10Sc8a]
Length = 405

Score = 174 bits (442), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 135/433 (31%), Positives = 208/433 (48%), Gaps = 44/433 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65

+I + P K +SG + +P SKS+S+R+L+ AA +GTT +DNLL D+H + AL LG
Sbjct: 2 DIKITPSK-LSGKLIVPPSKSISHRMLICAAFCDGTTIDNLLCEMDLHATINALTALGA 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125

+ + + G P E K V F +G +R + +A G A + G
Sbjct: 61 KINGKDSYDIT---GITRSE--KAAVDCF--ESGSTLRFMIPIFSAFCEAEFT--G 110

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185

++ ERPI L+ + + GA T P R+ G L G G K + GS+SSQ+++
Sbjct: 111 RGKLPERPIAPLIEPMTENGA---VFETLSMPYRIK--GRLNGGKYYIDGSVSSQFITG 164

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245

LL A + D EI + +L S PYV +T+ M++FGV ++ + ++IKGGQKY+ P
Sbjct: 165 LLFALSVLKSDSEIILTTRLESKPYNITIDCMKQFGVWV--CETENGYFIKGGQKYQ-P 221

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305

N VE D S +++FLA A G + + S+QGD ++ E
Sbjct: 222 HNCTVEADMSQSAFFLA-ANCAGSDIELTNLNLNSVQGDKTIVDIAEKFR----- 270

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365

L ID + +PD+ +AV+ F + P I + + R+KE +R+
Sbjct: 271 -----NGGDLSEIDA--SDIPDLVPAIAVMMSFWKEKPCRIINCERLRIKECDRLA 318

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTIRD 424

A + LG + I P E + Y+DHR+AMA ++AA V I+
Sbjct: 319 ATTELINDLGGKAISTENSIEIFPVEAFKGGTVRNYNDHRIAMAGAVAATRSTGEVIK 378

Query: 425 PGCTRKTFPDYFD 437

CT K++P +FD
Sbjct: 379 AECTNKSYPGFFD 391

>ref|ZP_07920257.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
gb|EFV02610.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
Length = 427

Score = 174 bits (442), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 139/449 (30%), Positives = 227/449 (50%), Gaps = 43/449 (9%)

Query: 8 VLQPIKEISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67

+L+P I G + P SKS+S+R+++ AAL++G + V ++L SED+ A+ LG +
Sbjct: 4 ILKP-HPICGEIVAPPSKSVSHRMVMAAALAKGESTVHHVLLSEDLKATCAAMEALGAHI 62

Query: 68 EADKAAKRAVVV---GC-----GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGG 117

E+ ++ V + GC G ++ ++ L AG+ R L
Sbjct: 63 ESAAESRGLVTLTIRGCDRPKAAAGATIYCRESGSTLRFMLPLAGMHARDLH----- 114

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGS 177

+ G R+ ERP+G G + P + +NG GL G L G+
Sbjct: 115 -----ITGEGRLSERPLGPFRNFHTAHGVQWTAPENREL-LTLNG--GLQPGHFLPLGN 166

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+SSQ+++ LL A PL GD I++I ++ S PYV +TL ++ + G+ + S + + I
Sbjct: 167 LSSQFITGLLFALPLLDGDSTIDVITEMESAPYVAITLAVLGQAGIVVDASADFRHYRIA 226

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GGQ Y +P VEGD S A+++LA + G VT G S QGD + + + MG
Sbjct: 227 GGQHY-APGVFTVEGDYSQAAFWLA-IGVLSGPVTCRGLLFDSAQGDARVVDWMREMGGD 284

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWR 357
+T T P R L+ I++N+++ PD+ LAV+A A G + I R
Sbjct: 285 ITRTADGFCAR-PSR-----LRGIEMNVSQCPDLVPVLAVLAAAASGTSRIVGAGRLR 336

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--C 415
+KE++R+ A+ T LT LGA V+E P+ +I L + +++DHR+AMA + A+ C
Sbjct: 337 LKESDRLAAMTTVLTA LGADVKEKPEGLVIRGGRPLKGGRVSSFNDHRVAMALATASTVC 396

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
A PV + +K++P +++ FVK
Sbjct: 397 A-APVVLGDGA EAVQKSY PQFWE--DFVK 421

>ref|YP_001887328.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
B str. Eklund 17B]
sp|B2TQ51.1|AROA_CLOBB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD25121.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
B str. Eklund 17B]
Length = 433

Score = 174 bits (441), Expect = 3e-41, Method: Compositional matrix adjust.
Identities = 131/431 (30%), Positives = 220/431 (51%), Gaps = 30/431 (6%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK P SKS+++R ++ AAL +G + + N+ S+D+ + A+R+LG + K
Sbjct: 10 KLGGEVKTTPPSKSMHRGVICAAALGDGISKIRNINYSDDIIATINAMRSLGAIIT--KED 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF----LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ V+G E K+ ++L +G +R L G++ ++ G +
Sbjct: 68 EYLVHVG----IKSECKKNIELNRTIDCNEGSSTLRFLVPISCFEGSSRFI--GRGNL 121

Query: 130 RERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ G G +R+ GI L G+ KL G ISSQ++S +L
Sbjct: 122 GKRPLDTYYEIFDNQGIKHSYKKGK--LDLRIEGI--LKCGEFKLRGDISSQFISGMLFT 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
PL GD ++ I L S Y+++TL M FG++ +++ F IKG Q YKS +N
Sbjct: 178 LPLLEGDSKVIITTDLESKGYIDLTLSAMSDFGIEI-INNNYREFIIGKNQTYKS-RNYR 235

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+EGD S A++FL A+ V + SLQGD + E+LE M K+ + + G
Sbjct: 236 IEGDYSQAAFFLVADALK-SEVFINDLNLESLQGDKEVIEILERMNMKIKNIDNG--LLG 292

Query: 310 PPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
RE G + ++ ++ PD+ +++ A +G T I +V R+KE +R+ A+ +
Sbjct: 293 IQRENLG-----STIIDGSQCPDIIPVISLAASLCNGRTEIINVGRRLRIKECDRLSAVAS 347

Query: 370 ELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
EL KLGA + E D II + L + ++ DHR+AM ++A+ C E P+ + D
Sbjct: 348 ELNKLGAHIEKEDSLIIDGVKTLKGGVKVWSHKDHRIAMMLAIASTVCME-PIILEDYE 406

Query: 427 CTRKTFPDYFD 437
C K++P +FD
Sbjct: 407 CISKSYPAFFD 417

>ref|ZP_05368127.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia mucilaginosa
ATCC 25296]
gb|EET75609.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia mucilaginosa
ATCC 25296]

Length = 503

Score = 174 bits (440), Expect = 3e-41, Method: Compositional matrix adjust.
Identities = 141/455 (30%), Positives = 220/455 (48%), Gaps = 47/455 (10%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---AD----- 70
V +PGSKSL+NR LLLAAL++ + + L+S D M+ ALR LG +E D
Sbjct: 31 VHIPGSKSLTNRYLLAALADSPSYLRAPLHSRDSALMIEALRQLGAGIELVPTDSPFGP 90

Query: 71 --KAAKRAVVVGCGGKFPVEDAKEE-VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
K V + + A+ V + G AG MR + A G + DG P
Sbjct: 91 DVKVTPLNFVEAHSQAQSDSAQSRVTSIECLAGTVMRFVPALAAALLPGE--FAFDGDP 148

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPP--VRVNGIGGLPGGK---VKLSGSISSQ 181
R+RP+G ++ GL+QLG VDC G + P +R G+ G V++ S SSQ
Sbjct: 149 HARQRPMPGPVLEGLRQLGVQVDCSEQGENALPFVLRSPGLASAEVSEAPVVRIDASTSSQ 208

Query: 182 YLSALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSWSWDRFYIKGG 239
++SALL+ AP L G V + + SIP+++MT+ + + G++ EH S G
Sbjct: 209 FVSALLMLAPRLPQGMVLVHEGSSVPSIPHIQMTVEALRQMGIHQHYPSQGNEAESGE 268

Query: 240 QKYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTV-----EGCGTTSLQGD 284
++ ++ +E D S+A FLA A +TG +VT+ GTT + GD
Sbjct: 269 YRWTVHPGFPFEMTIEPDLNAGPFLAAAVVTGESVTIPHPAPAADSSAGTTQV-GD 327

Query: 285 VKFAEVLEMMGAKVTWTETSTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA 344
+ + E+L +GA+V + E +TVTGP + P G +++ ++A T+A F
Sbjct: 328 M-WRELLPALGAQVRYAEGRLTVTGPALPEGD-----FSFDLSAGGELAPTMAAACAFV 381

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----IDT 400
G + +A R ET+R+ A+ E+ +LG + + D +I P A T
Sbjct: 382 KGRVELTGIAHLRGHETDRLAALAAEINRLGGAHDTADSLVIEAPIATAEAPVLAHT 441

Query: 401 YDDHRMAMAFSLAACAEVPVTIRDPGCTRTKTFPDY 435
YDDHRMA ++ V +++ KT P++
Sbjct: 442 YDDHRMATFAAIIGLRRPNVVQNVATVAKTMPEF 476

>ref|ZP_07800142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium cf.
prausnitzii KLE1255]
gb|EFQ06486.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium cf.
prausnitzii KLE1255]
Length = 423

Score = 174 bits (440), Expect = 3e-41, Method: Compositional matrix adjust.
Identities = 131/437 (29%), Positives = 218/437 (49%), Gaps = 30/437 (6%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ +Q + + GT+ P SKS+++R +L AAL+EG + + NL S+D+ LGA L
Sbjct: 3 VTIQNARPVGGTITAPPSKSMRAVLAALAEGRSHITNLEFSKDISATLGAQAQLCAR 62

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V A AVV G G P+ + + +G +R L + G ++ G
Sbjct: 63 VR--TGADDAVVEGLGHFVPLAAPVDCCE-----SGSTLRFLIPIASLTGQAVSFT--GR 113

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
R+ ERP ++ G L + + G L G+ +L+G++SSQ++S L
Sbjct: 114 GRLMERPQSVYEALYREQG-----LRFEQSAAGLTVEGALTPEYRLAGNVSSQFISGL 167

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L A PL G+ + +I + S Y++MT + FGV++ D + I GGQ Y P
Sbjct: 168 LFALPLLSGNSTLHLIPPVESRSYIDMTRSVQAAGVQSHWLDE-NTLAIPGGQHYH-PC 225

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ VEGD S A++ A GG VT+ G +LQGD ++L GAK T TE ++
Sbjct: 226 DYTVEGDYSQAAPPAVLGAACGG-VTITGLAPETLQGDAAILDILRRCGAKFTQTEAGIS 284

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
F + L +D+++ PD+ L V+ L +G T IR+ R+KE++R+ A
Sbjct: 285 -----FEKAPLHGVDIDLADCPDLGPMLMVLGLLCEGTTVIRNAERLRLKESDRIAA 336

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVT--IDTYDDHRMAMAFS-LAACAEVPVTI 422
+ EL G +E EG + ++L+ A + ++DHR+ M+ + LA +P+T+
Sbjct: 337 MEAELRACGGVLESEGGTITVHGCADRLHAPAGVLHGHNDRVMSLAVLALSTGIPLTV 396

Query: 423 RDPGCTRKTFFPDYFDVL 439
D K++P++F+ +
Sbjct: 397 DDAEAITKSWPNFFFEAI 413

>ref|NP_787695.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tropheryma whipplei
str. Twist]
gb|AAO44664.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tropheryma whipplei
str. Twist]
Length = 486

Score = 174 bits (440), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 127/439 (28%), Positives = 212/439 (48%), Gaps = 36/439 (8%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--DKAAKRA 76
+ +PGSKSL+NR L++AA++ G T + NLL S D + M+ LR +G +E
Sbjct: 62 MSIPGSKSLTNRHLLIAAIIASGETTIHNLLESRTNLMIEGLRRIGCKIEKLNHTGTHDT 121

Query: 77 VVVG----CGGKF-----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ C P + ++ G AG MR L G+ +
Sbjct: 122 GVISPHTCLNDLIQPSDVRIPSKHYTCSTKIDCGLAGTVMRFLPVLAGLCKGSVEFFG 181

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
D + RP+ + L++LG VD D P V+G G + GG ++ + SSQ++
Sbjct: 182 DD--QAIRRPMDGTLHALRKLGVQVD---GDRIPFTVHGRGEIEGGALETTEHSSSQFI 235

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQK 241
S LL++A + ++ I + L S PY++MT+ +M +G+ HSD W K
Sbjct: 236 SGLLLSACRFKNGTLTKHIGNPLPSRPYIDMTVEVMREWGIVNTHSDGVWAVT-----PK 290

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWT 301
+ K+ +E D S+A+ F+ GA +TGG+ T++ + + Q +L GA++T T
Sbjct: 291 ELTGKHITIEPDLNSAAPPFMIGAIVTGGSATIQNWPSKTSQPGKYLEAILPQFGAEITKT 350

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
++TV+G ++ I ++ ++ L +A A+ P+ ++ R ET
Sbjct: 351 ANTITVSG-----TGNTIGIRADLGHIGELVPNLVALATLAETPSVFYNIGHIRYHET 403

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ E++ LG ++ G DY ITP TY DHRMA + ++ +T
Sbjct: 404 DRIEALVNEISSLGGTITAGKDYIKITPTTLTRSGVWKTYKDHRMATSGAIIGLRH-KLT 462

Query: 422 IRDPGCTRKTFFPDYFDVLS 440
I D CT KTFP + D+ S
Sbjct: 463 IEDIECTSKTFPRFADLWS 481

>ref|ZP_07899258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus vortex
V453]
gb|EFU41653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paenibacillus vortex
V453]
Length = 430

Score = 174 bits (440), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 144/435 (33%), Positives = 229/435 (52%), Gaps = 22/435 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++P +++G + SK+ + R LL+AAL+EGT+ + +SED M ++ LG
Sbjct: 2 DVIVRTPKLNIGEIGALSSKNYTTRYLLVAALAEGTSTIYYPAHSESDAMRRICIQLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D+ ++AV+ G G K P D KE L +GNAG +R L VTA T+V
Sbjct: 62 VIEEDE--EKAVITGFG-KSP-RDVKE---LNVGNAGAVLRFLMG-VTALSKEVTFVNTY 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP DL+ L QLG +V+ G P+ + G G GG++ +SG +SSQYLSA
Sbjct: 114 PDSLGLKRPDHLIETLGLGVEVHNEGR--LPITIRG-GHPKGGQLTVSGEVSSQYLSA 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP 245
LL PL D EI + L S + TL ++E+ G+ + ++ + F + GGQ Y++
Sbjct: 171 LLFLTPLLAEDSEITVTGDLKSKVVIGQTLEVLQAGITIDAEDYTFRRVPGGQSYEA- 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
K V+GD ++ LA AA+T VT+ S QG+ +VL M +T +V
Sbjct: 230 KTYTVQGDYPGSAAVLAAAATQSDVTIRNLSEDSKQGERAIIDVLRKMEVPLTHENGNV 289

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G LKA++ + + D + + A+FA+G + +V + R KE +R+
Sbjct: 290 HVE-----GNGLKALEFDGDAATDAVLAMVAAAVFAEGTSRFYNVENLRYKECDRIT 342

Query: 366 AIRTELTKLGASVEEGPDYCIIT-PPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
EL K GA+VEE I+ PE + I+ + DHR+ MA ++ A+ P+ I
Sbjct: 343 DYLNELRKAGANVEERQAEIIVHGRPEGVEGVEINAHFDHRVIMALTVVGLRAQQPIRI 402

Query: 423 RDPGCTRKTFPDYFD 437
+D K++P YFD
Sbjct: 403 KDAHVVAKSYYPQYFD 417

>ref|ZP_07294998.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
hygroscopicus ATCC 53653]
gb|EFL23367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
hygroscopicus ATCC 53653]
Length = 458

Score = 173 bits (439), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 218/435 (50%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---ADK 71
+ TV +PGSKS++NR L+LAAL+ + L S D M ALR +G+ +E +D
Sbjct: 24 VDATVTVPGSKSVTNRGLILAALAAEPGWLRRPLRSRDTLLMADALRAMGVGIEETVSDS 83

Query: 72 AAKRAVVVCGCGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
A G G + + A + +GNAG MR L + A G + DG PR
Sbjct: 84 AFGAGSSSGGGEAWRIIPAGLHGPATIDVGNAGTVMRFLPPVASLADGPVRF--DGDPRS 141

Query: 130 RERPIGLDLVVLGKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
ERP+ ++ L+ LGA +D G P+ V+G G L GG V++ S SSQ++S+LL++
Sbjct: 142 HERPLHGVIDALRALGARIDDD-GRGALPLTVHGGGALDGGPVRIDASASSQFVSSLLLS 200

Query: 190 APLALGDVEIEIIDK-LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK---YKSP 245
AP VE+ I L S+P++ MT+ ++ G + + ++ GG++ +P
Sbjct: 201 APRFNQGVVEVRHIGAAALPSLPHIRMTVDMLRAAGARVDTPEA-----GGEQGVWRVAP 253

Query: 246 -----KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
++ VE D S+A+ FLA A +TGG VT+ + Q + MG
Sbjct: 254 SALLGRDLVVEPDLSNAAPFLAAALVTGGRVTIPDWEHTTQPGDALRRIFTDMGGSCEL 313

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
T+ +T TG R + ID +++++ ++ +A VA AD + +R +A R+ E
Sbjct: 314 TDAGLTFTGTGR-----ITGIDADLHEVGELTPVIAAVALADESVLRGIAHLRLHE 366

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ E+ +LG V E D I P L+ TY+DHR+A A ++ V
Sbjct: 367 TDLRALAKEINELGGEVAETEDGLHIR-PRPLHGGIFHTYEDHRLATAAAVLGLTVEGV 425

Query: 421 TIRDPGCTRKTFPDY 435
I + T KT PD+
Sbjct: 426 QIENVATTAKTLPDF 440

>ref|ZP_04861607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
D str. 1873]
gb|EES92099.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
D str. 1873]
Length = 435

Score = 173 bits (439), Expect = 4e-41, Method: Compositional matrix adjust.

Identities = 117/438 (26%), Positives = 222/438 (50%), Gaps = 42/438 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+SG + +P SKSL++R ++ A LS+G + ++N++ SED+ + + +LG+ ++ D +
Sbjct: 10 ELSGDINIPPSKSLAHRAIISAGLSGDISNIENIIFSEDIKATIRGMESLGEVEIK-DISE 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL----- 123
K+ +D + +G + + + +G +++
Sbjct: 69 KKQ-----DDFNKRTLKVIGRDLVLTRSEIDCSESGSTLRFLIPISLRTC�KV 117

Query: 124 --DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
G ++ RP+ K G G P+ ++G L G+ + G+ISSQ
Sbjct: 118 KFTGKGLVSRPLDVVYSIFKNQGIKYKTSNGK--LPLFIDG--ALKSGEFYVEGNISSQ 173

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+++ L+ P GD +I I +L S Y+++T+ +++FG+K E+ D + F+I+G QK
Sbjct: 174 FITGLMYTLPFLSGDSKIIITTELESKGYIDLTLTKKFGIKIENKD-YKEFFIRGQK 232

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
S N V+GD S ++++ A I G + SLQGD ++++ MG +
Sbjct: 233 SIS-NNYRVQGDQSQAFAWIV-AGILGSNIKTLDLDINSLQGDRVIIDIVKDMGNIKIK 290

Query: 302 ETSVTVTGPPREFFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E + + K I ++ ++ PD+ LAV+ + G T I + R+KE
Sbjct: 291 ENYIETK-----KSKTKGITIDASECPDLVPILAVLGSLSGTTRIINAERLRIKEC 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ A+ TEL K+GA ++E D +I E L +D+++DHR+AM+ ++A+ C E P
Sbjct: 343 DRLKAMATELKKIGADIQELEDGLLIKGREYLGKGTVDSDWHDRIAMSMAIASIKCTE-P 401

Query: 420 VTIRDPGCTRKTFPDYFD 437
+TI++ K++PD+++
Sbjct: 402 ITIKNSEAVNKSYPDFWE 419

>pdb|1P88|A Chain A, Substrate-Induced Structural Changes To The Isolated N-Terminal Domain Of 5-Enolpyruvylshikimate-3-Phosphate Synthase
pdb|1P89|A Chain A, Substrate-Induced Structural Changes To The Isolated N-Terminal Domain Of 5-Enolpyruvylshikimate-3-Phosphate Synthase
Length = 216

Score = 173 bits (439), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 109/224 (48%), Positives = 140/224 (62%), Gaps = 8/224 (3%)

Query: 28 SNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPV 87
SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG+S R ++G GG
Sbjct: 1 SNRALLLAALAHGKTVLTNLLSDDDRHLNALTALGVSYTSLADRTRCEIIGNGGPLHA 60

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDVPRMRERPIGDLVVGLKQLGAD 147
E A E LFLGNAG AMR L AA+ G+ VL G PRM+ERPIG LV L+ GA
Sbjct: 61 EGALE---LFLGNAGTAMRPLAAALCL--GSNDIVLTGEPRMKERPIGHLVDALRLGGAK 115

Query: 148 VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLIS 207
+ + PP+R+ G G GG V + GS+SSQ+L+ALLM APLA D I I L+S
Sbjct: 116 ITYLEQENYPPRLRLQG--GFTGGNVVDVDSVSSQFLTALLMTAPLAPEDTVIRIKGDLVS 173

Query: 208 IPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
PY+++TL LM+ FGV+ E + + +F +KGGQ Y+SP VE
Sbjct: 174 KPYIDITLNLMTKTFGVEIE-NQHYQQFVVGKGGQSYQSPGTYLVE 216

>ref|ZP_06837390.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium ammoniagenes DSM 20306]
gb|EFG81552.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium ammoniagenes DSM 20306]
Length = 424

Score = 173 bits (439), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 133/425 (31%), Positives = 213/425 (50%), Gaps = 33/425 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I T ++PGSKS++NR +LAAL++ +++ N L S D M ALR +G+ +EAD
Sbjct: 17 IQWTQQIPGSKSITNRAFILAALADSPSLRNPLTSRDTELMANALRAVGIGIEADGTDV 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + P E + L AG MR L A G +DG + R RP+
Sbjct: 77 RIT-----PAEITGGSIDCGL--AGTVMRFLPPLAALASGPVE--IDGDEQARVRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ LG DV +D P+ V G GG++ + S SSQ++S LL++AP
Sbjct: 125 STMSQSLRDLGVDS----SDTLPMTVTSTGVPAGGELTIDASGSSQFVSGLLLSAPRYE 180

Query: 195 GDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFY--IKGGQKYKSPKNAYV 250
+ + L S+P+++MT+ ++ + G+ + ++W + + I+GG +
Sbjct: 181 QGITVRHKGGLTPSMPHIDMTVAMLRQAGITVDEGENWWKVHPGTIQGG-----TWN I 233

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGP 310
E D S+A+ FLA A +TGG +TV T+ Q F +++ MGA T + G
Sbjct: 234 EPDLSNATPFLAAALVTGGVLTVDNDWPATTTQPGDAFRHIIQEMGATAEQTPPEYLRAIG- 292

Query: 311 PREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
P GR L+ I+++M+++ ++ T+A +A AD P+ + +A R ET+R+ A+ E
Sbjct: 293 --NPNGR--LQGIELMSQIGELTPTVAALAALADTPSRLTGIAHLRGHETDRLKALAAE 348

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
+ LG +V E D I+ P L+ +Y DHRMA A ++ V I D T K
Sbjct: 349 INN LGGNVTELD DGLEIS-PAPLHGGTWKSYADHRMATAGAIIGLRVEGEIDDIETAK 407

Query: 431 TFPDY 435
T P +
Sbjct: 408 TLPGF 412

>gb|ABZ08445.1| putative EPSP synthase (3-phosphoshikimate
1-carboxyvinyltransferase) [uncultured marine
crenarchaeote HF4000_APKG3B16]
Length = 422

Score = 173 bits (439), Expect = 4e-41, Method: Compositional matrix adjust.
Identities = 122/423 (28%), Positives = 215/423 (50%), Gaps = 22/423 (5%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
EISG + P +KS ++R + LA+L+ +++ N+L S D + + A + G+ + K
Sbjct: 9 EISGKIACPSNKSYPYTHRAIFLASLAIDKSIKILNRSGDTNATINACKNFGVEI---KDV 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ V + + N+G +R TA +A N VL G +++RP
Sbjct: 66 GDDITVTSASVLKLHSNTIDA---ANS GTTIRIATA--ISALANDKIVLTGDSSSLKRP 119

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+ L+ LGA C PP+ V+G + GG+VK+ G+ISSQ++SAL++ AP
Sbjct: 120 MQPLLDALSLGAK--CSSSNGNPPISVSGT--IKGGEVKIPGNISSQFISALMITAPKL 175

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + I KL+S PY++ T+ +M++FGV+ E + + YI Q YK+ + D
Sbjct: 176 ENGLILNIQGLVSKPYIDATITMMKKFGVEVETKTPYKK-YIIEQNYKA-TTLTIPSD 233

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPRE 313
SS + L+ A + G +T++ + Q D ++LE+MG +T + ++ + P +
Sbjct: 234 FSSLALLLSAAVLLGEDLTIQISTGSMPPQADEAIIIDILEIMGVVITLDKNTIKIKSPEKL 293

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G+ +++ PD+ +A++AL P I +V R KET+R+ I EL K
Sbjct: 294 DGGK-----FDLSDSPDLIPAIAAILALKTSKPIEFNVEHARYKETDRIAVIARELAK 346

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
LG V+E D ++ + L +++ +DHR+ MAF +A TI P ++P
Sbjct: 347 LGIKVKEKKDGLVLNNSDNLTGADLNSENDHRLFMAFCIAGMYVGNCTISHPESVEISYP 406

Query: 434 DYF 436

++
Sbjct: 407 NFI 409

>ref|YP_482851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. CcI3]
gb|ABD13122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. CcI3]
Length = 446

Score = 173 bits (439), Expect = 5e-41, Method: Compositional matrix adjust.
Identities = 146/450 (32%), Positives = 227/450 (50%), Gaps = 42/450 (9%)

Query: 10 QPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP++ + V +PGSKS +NR L+LAAL+ GT+ + L S D M G LRTLGL+ V
Sbjct: 25 QPVEAV---VAVPGSKSGTNRALVLAALANGTSRLRGALRSRDTLLMAGVLRTLGLIEVST 81

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ VV G P A + GNAG R A T G+ V DG RM
Sbjct: 82 E--GPDWVVHG---HPTPSAAPTARAECGNAGTVARFTPALATLTRGD--VVFDDGDARM 133

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RERP+ L+ L++LGA++D D P V+G G L GG+V + S SSQ +S LL+A
Sbjct: 134 RERPLTPLLALRELGAIDG---DRMPFTVHGRGRLRGGEVIVDASHSSQLVSGLLLA 189

Query: 190 APLALGDVEIEII---DKLISIPYVEMTLRLMERFGVKA-----HSDSWDRFY 235
+P D + ++ +L S PY++MT+ + G E +D+ R+
Sbjct: 190 SPHY--DTGVTVVHRGSRLLPSAPYLDMTVADLRAAGATVEVDAVCSAAGPVADT--RRWR 246

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
++ G+ + + +E D +SA+ FLA A TGG V + ++ Q ++L MG
Sbjct: 247 VEPGRPTAADRT--IEPDMNSAAFLAAAVATGGRVMISDWPESTEQPGRLLPDLLVAMG 304

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVAS 355
T + +TG G H IDV+++ + A L +A+ AD P+ +R +A
Sbjct: 305 GTARRTSAGLEITG-----AGAVH--GIDVDLSDFGEAAPILTALAVLADSPSRLRGIAH 357

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC 415
R++ET+R+ A+ EL +LGA + D I+ P L+ +D + DHR+AMA+++
Sbjct: 358 LRLQETDRLAALALELGRLGARITVADDGLAIS--PAPLHGARLDPHADHRLAMAYAVVGL 416

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
+ I D T KT PD+ ++ + +
Sbjct: 417 VVPGIVIDDIATTGKTVPDFPEMWTAMLQ 446

>ref|NP_789134.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tropheryma whipplei
TW08/27]
sp|Q83I86.1|AROATROW8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD66871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Tropheryma whipplei
TW08/27]
Length = 443

Score = 173 bits (439), Expect = 5e-41, Method: Compositional matrix adjust.
Identities = 127/439 (28%), Positives = 212/439 (48%), Gaps = 36/439 (8%)

Query: 19 VKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--DKAAKRA 76
+ +PGSKSL+NR L++AA++ G T + NLL S D + M+ LR +G +E
Sbjct: 19 MSIPGSKSLTNRHLLIAAIIASGETTIHNLLESRTDNLMIIEGLRRIGCKIEKLNHTGTHTD 78

Query: 77 VVVG----CGGKF-----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ C P + ++ G AG MR L G+ +
Sbjct: 79 GVISPHCTCLNDLIQPSDVRRIIPSKHYTCSTKIDCGLAGTVMRFLPVLAGLCKGSVEFFG 138

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
D + RP+ + L++LG VD D P V+G G + GG ++ + SSQ++
Sbjct: 139 DD--QAIRRPMDGTLHALRKLGVQVD---GDRIPFTVHGRGEIEGGALETTEHSSSQFI 192

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQK 241
S LL++A + ++ I + L S PY++MT+ +M +G+ HSD W K
Sbjct: 193 SGLLLSACRFKNGTLTKHIGNPLPSRPYIDMTVEVMREWGIVNTHSDGVWAVT-----PK 247

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ K+ +E D S+A+ F+ GA +TGG+ T++ + + Q +L GA++T T
Sbjct: 248 ELTGKHITIEPDLNSAAPPFMIGAIVTGGSATIQNWPSKTSQPGKYLEAILPQFGAEITKT 307

Query: 302 ETSVTVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
++TV+G ++ I ++ + ++ L +A A+ P+ ++ R ET
Sbjct: 308 ANTITVSG-----TGNITGIRADLGHIGELVPNLVALATLAETPSVFYNIGHIRYHET 360

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
+R+ A+ E++ LG ++ G DY ITP TY DHRMA + ++ +T
Sbjct: 361 DRIEALVNEISSLGGITAGKDYIKITPTTLTRSGVWKTYKDHRMATSGAIIGLRH-KLT 419

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I D CT KTFP + D+ S
Sbjct: 420 IEDIECTSKTFPRFADLWS 438

>emb|CBK88194.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium
cylindroides T2-87]
Length = 422

Score = 173 bits (438), Expect = 6e-41, Method: Compositional matrix adjust.
Identities = 120/431 (27%), Positives = 213/431 (49%), Gaps = 36/431 (8%)

Query: 14 EISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SGT+ +P SKS+S+R ++ A+L++G + + NL S+D+ + +R+ G +E K +
Sbjct: 9 KVSGTIAIPASKSISHRAIICASLAQKSTITNLTFKDIETISCMRSFGAKIEVQKNS 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 133
++ GC + D ++ + +G +R L A + TY+ G R+ ERP
Sbjct: 69 --CIEGCN----LFDLQDGI CCDCNESGSTLRFLIPAGALSNKKVTYL--GKGRLLERP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ G+ Q+ D L +R+ G L G ++ G+ISSQ++S LL PL
Sbjct: 121 M-----GIYQIIFDEQKLLFEQSQDAIRIQ--GKLQSGHYQIDGNISSQFISGLLFVLPL 173

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
D + I + S YV++TL +++ FG++ + + +YIKG QKY + + +EG
Sbjct: 174 LDSDSLTLTINEPYESRSYVDLTLDMLKCFGIEIKQDK--NTYYIKGNQKYIA-HDVKIEG 230

Query: 253 DASSASYF--LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S ++F LAG ++T S+QGD ++L G + + +T+
Sbjct: 231 DYSQMAFFGVLAGL---NNSLTCSNMNLSNVQGDKAILDILASAGCSINSKKDFITIHPS 287

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+P K ID ++ PD+ L V+A + + T I + R+KE++R+ A+ E
Sbjct: 288 KLQP-----KTID--LSDCPDLGPILCVLASyceqTTTIINAQRLRMKESDRIEAMEVE 339

Query: 371 LTKLGASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFS-LAACAEVPVTIRDPG 426
L K ++ D I ++ ID+++DHR+ MA CA P I +
Sbjct: 340 LKKWNVDIQTTFDTITIHGKNGYALDDIPIIDSHNDHRIVMAMCVFGLCANTPCIIENAQ 399

Query: 427 CTRKTFPDYFD 437
K++PD+F+
Sbjct: 400 AITKSYPDFFE 410

>ref|ZP_08026066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 178 str. F0338]
gb|EFW10345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 178 str. F0338]
Length = 433

Score = 172 bits (437), Expect = 7e-41, Method: Compositional matrix adjust.
Identities = 138/428 (32%), Positives = 204/428 (47%), Gaps = 28/428 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I V LPGSKS + R L LAA+S+ T + L++ D +GAL +G S A
Sbjct: 13 IDAVVALPGSKQTARALYLAADVSDAPTTIRGALDARDTRLFVGALEQMGASFAPQGGAL 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R P+ + + G AG MR L AA T DG R RP+
Sbjct: 73 RVT-----PMGERPRPAIDCGLAGTVMRFLPP--LAALSRGTTRFDGDAAARARPL 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
L+ L+ +GA V P + G P G + + S SSQ+LSALL+ APL
Sbjct: 123 APLLGALEGMGARVHHEGAPGRLPFTIRGRLRTPPLGAQCAVDASASSQFLSALLLVAPLI 182

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIKGGQKYKSPKN 247
+ + +++S+P+VEMT+R + R G+ E D +W F + SP +
Sbjct: 183 GDPLFVSAPGRVVSMPHVEMTVRALARAGIDIEEVDEAGPVRTWHVFPGR-----PSPGD 237

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E D S+A FLA A +TGG V V G + Q + +L MGA+V + +TV
Sbjct: 238 TDIEPDLSNAGPFLAAAMVTGGRVVRPGWPRATSQPGDAWRAILGHMGARVELGDDGLTV 297

Query: 308 TGPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GP G + ID +M+ + ++ LA + A P+ + +A R ET+R+ A+
Sbjct: 298 EGP-----GAGNYPGIDADMSAVGELTPALAAICASSSPSRLSGIAHLRGHETDRVAAL 352

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGC 427
TEL +LG ++G D C+ P L ++TY+DHRMA ++ V +RD C
Sbjct: 353 ATELNRLLGGDAQDGGD-CLAITPAPLRPGTVETIEDHRMAAFGAVLGLTTAGVGVVDIEC 411

Query: 428 TRKTFPDY 435
T KT P +
Sbjct: 412 TSKTLPGF 419

>gb|AAD13108.1| 5-enolpyruvylshikimate 3-phosphate synthase [Corynebacterium glutamicum]
Length = 498

Score = 172 bits (437), Expect = 7e-41, Method: Compositional matrix adjust.
Identities = 135/437 (30%), Positives = 221/437 (50%), Gaps = 34/437 (7%)

Query: 13 KEISGTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I + +PGSKS++NR L+LAAL+ + + ++L S D M LR+LG+++ +
Sbjct: 89 RPIVSDLAIPGSKSITNRALILAALASTPSTIIDVLRSDTDLMTDGLRSLGITITEEAV 148

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G VE G AG MR L A G + DG P+ R R
Sbjct: 149 DRYRVEPGQLSAGSVE-----CGLAGTVMRFLPPVAAFADGPVHF--DGDPQARVR 197

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAP 191
P+ ++ L+ LG +VD + P VN G +P GG V++ S SSQ++S LL++AP
Sbjct: 198 PMTSILDALRSLGVEVD---NNNLPTVNA-GEVPEGGVVEIDASGSSQFVSGLLLSAP 252

Query: 192 LALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
V ++ + +L S+P++EMT+ ++ G++ E S+ +++ G+ + +
Sbjct: 253 RFKNGVTVKHVGRLSPMPHIEMTVMLRSAGIEIEESE--NQWVVPGEILG--RTWRI 308

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----SVT 306
E D S+A+ FLA AA+TGGT+ + + Q +LE MG +V ++
Sbjct: 309 EPDLSNATPFLAAAATVGGTIKINHWPPIKTQPGDAIRSILERMGEVELVAQGEYDLS 368

Query: 307 VTGPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
VTGP LK I+++M+ + ++ T+A +A A + + +A R ET+R+ A
Sbjct: 369 VTGP-----VALKGIEIDMSDIGELTPTVAALAAALASTESRLTGIAHLRGHETDRLAA 421

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ E+ KLG E D +I P L+ +Y DHRMA A ++ A V + D
Sbjct: 422 LTAEINKLGKCTELKDGLLIE-PASLHGGVWHSYADHRMATAGAIIGLAVDGVQVEDIK 480

Query: 427 CTRKTFPDYFDVLSTFV 443
T KTFP + +V V
Sbjct: 481 TTSKTFPGFENVVEEMV 497

>ref|XP_002773648.1| 3-dehydroquinate synthase, putative [Perkinsus marinus ATCC 50983]
gb|EER05464.1| 3-dehydroquinate synthase, putative [Perkinsus marinus ATCC 50983]

Length = 1978

Score = 172 bits (437), Expect = 8e-41, Method: Compositional matrix adjust.
Identities = 162/481 (33%), Positives = 232/481 (48%), Gaps = 107/481 (22%)

Query: 17 GTVKLPGSKSLSNRILLALLSE---GTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
G ++LPGSKS+SNR L+LAAL+E G V NL SED+ ML AL LG+ V+
Sbjct: 432 GVLELPGSKSISNRALVLAALAEKPGGKCRVFNLTPESEDIRVMLAALSKLGVVDVKYLSEG 491

Query: 74 KRA---VVVGC-GGKFPV--EDAKEEVQ-LFLGNAGIAMRSLTAAV-----TAAGGNATY 121
+ V + C GG + + AK V +++ NAG R +T + T +A
Sbjct: 492 PESGLNVELRCPGGSLLTLLHDTAKAGVTTVWVENAGTVARFITPLLGYLVATCKDPSSAAV 551

Query: 122 VLDGVPRMRERPIGDLVVGKQL--GADVDCFLG--TDCPPVRVNGI----- 164
V+DG RMR RP+ DLV +++ G VD ++G C P+++
Sbjct: 552 VVDGNERMRVRPVEDLVNMQRAFKGVRVD-YVGPTQGCLPLKITKARKRSVADASEGSQ 610

Query: 165 --GGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE----IEIID---KLISIPYVEMT 214
G P G V LS +SSQ++S +L+ + LA G E + + D K +S PY++MT
Sbjct: 611 TSSGFPCTGVDLSSKVSSQFVSGMLLVSSSLARGEEGFTLRLEDTRGGKAVSQPYIDMT 670

Query: 215 LRLMERFGVKA-EHSDSWDRFYIK--GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
R+ME FGVKA +DS R Y K GQK +P VE DAS+ASY LA AA TG +
Sbjct: 671 CRVMEEFQVKAALPETSDGRLYYKVAAGQKLVAPGTyrVEADASAASYPLAIAAATGCEI 730

Query: 272 TV---EGCGTTSLQGDVKF-AEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVN 326
TV + G+ +QG+ F +++L+ MG +
Sbjct: 731 TVNLPYQSLGSRPVQGETLFVSKILKPMGCQ----- 761

Query: 327 MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS--VEEGPDY 384
G + I +VA+ RVKE +R+ A+ + S EE PD
Sbjct: 762 -----GESCITNVANQVRVKECDRIAAMAENINLCFHSKVAEERPDG 802

Query: 385 CII---TP-PEKLNVTADITYDDHRMAMAFSLAACAEVP--VTIRDPGCTRKTFPDYFDV 438
+I +P + L D++DDHR+AMA ++ A P V I P C KTF D++DV
Sbjct: 803 LVIHGGSPVVDGLQSVTTDSHDDHRVAMAIAVLATRFPPEMVCISQPRCQVEKTFSDFDV 862

Query: 439 L 439
L
Sbjct: 863 L 863

>ref|YP_003400659.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Archaeoglobus
profundus DSM 5631]
gb|ADB57986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Archaeoglobus
profundus DSM 5631]
Length = 414

Score = 172 bits (437), Expect = 8e-41, Method: Compositional matrix adjust.
Identities = 139/430 (32%), Positives = 216/430 (50%), Gaps = 38/430 (8%)

Query: 14 EISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+ G P SKS ++R L +ALS + + + L+ +ED L + +G +
Sbjct: 9 EVEGVATPPPSKSYTHRAFLSSALSRHSEIFNPLI-AEDTLATLRCKGIGARFFRHRCF 67

Query: 74 KRAVVVGC---GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ GC G F V ++ ++LF+G + SL+ V+ VLDG +
Sbjct: 68 E---FFGCDEIKSGYFYVNSSGTTLRLFMG-----ILSLSKGVS-----VLDGDESI 111

Query: 130 RERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RP +L L +LGA V F P + V GI L GG VK+ +ISSQ++SALL +
Sbjct: 112 RRRPNLELAKALIKLGAKVKGRDFSAPII-VGGI--LKGGCVKIR-AISSQFVSALLFS 167

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
PLA D E+ +ID + S PY++TL ++E G+K E + FYI+ Q+++ +
Sbjct: 168 LPLAKFDSELRVID-VKSKPYIDVTTLHVLEESGIKLRE--GNTFYIECEQEFR-LRRFD 223

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V D SSASY +A + + G V + G S QGD +++ MG +V W + +
Sbjct: 224 VPADFSSASYLIA-SGVLAGRVELRGV-YDSRQGDKAIVDIVRSMGGEVRWKKEDGVLIA 281

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
E L+ I+V+ PD+ T+AV+ A G T I + R KET R+
Sbjct: 282 EKSE-----LEGIEVDAGDTPDLVPTIAVLGAVAKGRTVIYNAEHLRYKETNRIETTYR 335

Query: 370 ELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
L LG VE+ D +I + +D+Y DHR+AMAF++ VT+++
Sbjct: 336 NLKALGVEVEKRRDGLVIKGG-NIRGGVVDSDYGDHRIAMAFVGLVADKVTVKNAEVVS 394

Query: 430 KTFPDYFDVL 439
+FP++FDVL
Sbjct: 395 VSFPNFFDVL 404

>ref|YP_001137748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium glutamicum R]
sp|A4QC99.1|AROA_CORGB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAF53846.1| hypothetical protein [Corynebacterium glutamicum R]
Length = 430

Score = 172 bits (436), Expect = 8e-41, Method: Compositional matrix adjust.
Identities = 135/435 (31%), Positives = 220/435 (50%), Gaps = 34/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I + +PGSKS++NR L+LAAL+ + + ++L S D M LR+LG+++ + +
Sbjct: 23 IVSDLAIPGSKSITNRALILAAALASTPSTIIDVLRSDTDLMTDGLRSLGITITEEAVDR 82

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G VE G AG MR L A G + DG P+ R RP+
Sbjct: 83 YRVEPGQLSAGSVE-----CGLAGTVMRFLPPVAAFADGPVHF--DGD PQARVRPM 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
++ L+ LG +VD + P VN G +P GG V++ S SSQ++S LL++AP
Sbjct: 132 TSILDALRSLGVEVD----NNNLPTFTVNA-GEVPEGGVVEIDASGSSQFVSGLLLSAPRF 186

Query: 194 LGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
V ++ + +L S+P++EMT+ ++ G++ E S+ +++ + G+ + +E
Sbjct: 187 KNGVTVKHVGRLPSMPHIEMTVDMRLRSAGIEIEESE--NQVWVHPGEILG--RTWRIEP 242

Query: 253 DASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----SVTVT 308
D S+A+ FLA AA+TGGT+ + + Q +LE MG +V ++VT
Sbjct: 243 DLSNATPFLAAAATGGTIKINHWPICKTTPQGDIAIRSILERMGCLEVELVAQGEYDLSVT 302

Query: 309 GPPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
GP LK I+++M+ + ++ T+A +A A + + +A R ET+R+ A+
Sbjct: 303 GP-----VALKGIEIDMSDIGELTPTVAALAAALASTESRLTGIAHLRGHETDRLAALT 355

Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
E+ KLG E D +I P L+ +Y DHRMA A ++ A V + D T
Sbjct: 356 AEINKLGGKCTELKDGLLIE-PASLHGGVWHSYADHRMATAGAIIGLAVDDVQVEDIKTT 414

Query: 429 RKTFFPDYFDVLSTFV 443
KTFP + +V V
Sbjct: 415 SKTFPGFENVWEEMV 429

>ref|YP_062746.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leifsonia xyli subsp. xyli str. CTCB07]
gb|AAT89641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leifsonia xyli subsp. xyli str. CTCB07]
Length = 436

Score = 172 bits (435), Expect = 1e-40, Method: Compositional matrix adjust.
Identities = 134/433 (30%), Positives = 224/433 (51%), Gaps = 23/433 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S +V LPGSKSL+ R L+LAAL++G+++ L+S D M+ ALR+LG+ VE +
Sbjct: 17 VSASVALPGSKSLTARELVLAALADGPSLLRAPLHRSRDSAAAMVEALRSLGVRVE-----E 71

Query: 75 RAVVVGCGGKFPVEDAKE---EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131

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      R   G G F V A+E       + G AG MR +       A G   + D       R
Sbjct: 72 REGSGGFGSDFLVTPAEELLGSTTIECGQAGTVMRFPPIAGLALGPTMF--DADDSARG 129

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+  ++ L+ LG +++   G   P V+G G + GG +++ S SSQ++SALL++A
Sbjct: 130 RPTATIIASRLRGLGVEINDD-GHGALPFTVHGTGTVAGGAIEVDASRSSQFVSALLSAS 188

Query: 192 LALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      +++   ++L S+P++EMT+ +   GV + ++ R+ ++ G   + ++ +
Sbjct: 189 RFENGLDLTHSGERLPSLPHIEMTVAAALAARGVAVDSPET-GRWVVQPGPI--AARDVDI 245

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
      E D S+A+ FLA A +TGG+VT+ G   ++ Q   A +L + GA VT   +TVTGP
Sbjct: 246 EPDLSNAAPFLAAAVVTGGSVTITGWPESTTQVGADLAHLLPLFGATVTKAVDRLTVTGP 305

Query: 311 PREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
      R       ++ I +++   ++A L +A AD P+ I +   ET+R+ A+ E
Sbjct: 306 ER-----IQGIRLDLTTGGELAPALVAIAALADSPSEITGIGHICHHETDRLAALAAE 358

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
      +   G +V E D   + P L   +Y+DHRMA A ++ A V I +   T K
Sbjct: 359 INGFGGAVTELEDGLRVE-PRPLTGGVWRSYEDHRMATAGAI VGLAVEGVEIENVATTAK 417

Query: 431 TFPDYFDVLSTFV 443
      T P + ++ + +
Sbjct: 418 TLPHFTELWARM 430

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>ref|NP_599992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
      glutamicum ATCC 13032]
ref|YP_225054.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
      glutamicum ATCC 13032]
sp|Q9Z470.3|ARO_A_CORGL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB98157.1| 5-enolpyruvylshikimate-3-phosphate synthase [Corynebacterium
      glutamicum ATCC 13032]
emb|CAF19468.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE [Corynebacterium
      glutamicum ATCC 13032]
Length = 430

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Score = 172 bits (435), Expect = 1e-40, Method: Compositional matrix adjust.
Identities = 135/435 (31%), Positives = 220/435 (50%), Gaps = 34/435 (7%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      I   + +PGSKS++NR L+LAAL+   + + ++L S D   M LR+LG+++ + +
Sbjct: 23 IVSDLAIPGSKSITNRALILAAALASTPSTIIDVLRSDTDLMTDGLRSLGITITEEAVDR 82

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      V G   VE       G AG MR L   A G   + DG P+ R RP+
Sbjct: 83 YRVEPGQLSAGSVE-----CGLAGTVMRFLPPVAAFADGPVHF--DGDPQARVRPM 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
      ++ L+ LG +VD   + P VN G +P GG V++ S SSQ++S LL++AP
Sbjct: 132 TSILDALRSLGVEVD----NNNLPFTVNA-GEVPEGGVVEIDASGSSQFVSGLLLSAPRF 186

Query: 194 LGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
      V ++ + +L S+P++EMT+ ++ G++ E S+ +++ + G+   + +E
Sbjct: 187 KNGVTVKHVGGRLPSPHIEMTVDMLRSAGIEIEESE--NQWVVHPGEILG--RTWRIEP 242

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----SVTVT 308
      D S+A+ FLA AA+TGGT+ +   + Q   +LE MG +V   ++VT
Sbjct: 243 DLSNATPFLAAAVTGGTIKINHWPICKTTQPGDAIRSILERMGCLEVELVAQGEYDLSVT 302

Query: 309 GPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      GP       LK I+++M+ + ++ T+A +A A   + + +A R ET+R+ A+
Sbjct: 303 GP-----VALKGIEIDMSDIGELTPTVAALAALASTESRLTGIAHLRGHETDRLAALT 355

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
      E+ KLG   E D +I P L+   +Y DHRMA A ++ A V + D T
Sbjct: 356 AEINKLGGKCTELKDGLLIE-PASLHGGVWHSYADHRMATAGAIIGLAVDGVQVEDIKTT 414

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Query: 429 RKTFFPDYFDVLSTFV 443
KTFP + +V V
Sbjct: 415 SKTFPGFENVWEEMV 429

>ref|YP_003716296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Croceibacter atlanticus HTCC2559]
gb|EAP85908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Croceibacter atlanticus HTCC2559]
Length = 410

Score = 172 bits (435), Expect = 1e-40, Method: Compositional matrix adjust.
Identities = 126/424 (29%), Positives = 212/424 (50%), Gaps = 43/424 (10%)

Query: 16 SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+ ++ + GSKS SNR+L+L AL T+ N+ NS+D + AL+
Sbjct: 12 NASIAVTGSKSESRLILQALYPNLITIT-NVSNSSDDTKVLQKALQ----- 56

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ + + + +AG AMR LTA A N L G RM+ERP+
Sbjct: 57 -----QNQGIVDIHHAGTAMRFLTAYY-ALKANTDVTLTGSKRMKERPMS 100

Query: 136 DLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
LV LK+LGA + PP+ + GI V L+ ++SSQY+SAL++ A
Sbjct: 101 ILVDALKKLGAQITYKTNDGFPPLLIKGITP-EKTSVSLNANVSSQYISALMLVAASLNS 159

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
++I++ ++ S+PY+ MTL L+ R G++ + + I Q + + VE D S
Sbjct: 160 GLDIQKGRVTSVPYINMTLSLLNRVGIRGTFKN--NSITIPPCQSI-ADQIVVVEDSDWS 216

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SASY+ + A++ +++ SLQGD E+ G + +++ ++ + +
Sbjct: 217 SASYYYYSLVALSKNAEISLTSYRQESLQGDSALKEIYTAFGVETLFSNTLL--KK 271

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
K K ++ +++ PD+A T+AV L + + + ++KET+R+ A++TEL KL
Sbjct: 272 TSHKLQKHVEFDLSNTPDIAQTIQIAVTCGLGISCKLTGLHTLKIKETDRLTALKTELYKL 331

Query: 375 GASVEEGPDYCIITPPEKLNVA-IDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
G D + +N A IDTY+DHRMAMAF+ A + +TI D G K++P
Sbjct: 332 GGITIIITNDTLELKATPSVNRNAEIDTYNDHRMAMAFAPLAL-KTDLTINDAGVVSKSYP 390

Query: 434 DYFD 437
+++
Sbjct: 391 TFWE 394

>ref|YP_832132.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter sp. FB24]
gb|ABK04032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter sp. FB24]
Length = 460

Score = 171 bits (434), Expect = 1e-40, Method: Compositional matrix adjust.
Identities = 139/427 (32%), Positives = 213/427 (49%), Gaps = 24/427 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL---SVEADK 71
+ TV +PGSKSL+NR L+LAAL++G + + L+S D M+ ALR LG V +D
Sbjct: 30 VDATVTVPGSKSLTNRYLVLAALADGPSRLRAPLHRSRDSALMIEALRQLGAGIREVHSDG 89

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
A + V + A + + G AG MR + AA N V DG P R+
Sbjct: 90 AFGPDLEV---TPLRADAAATDAAIDCGLAGTVMRFVPP--VAALRNGATVFDGDPHARK 144

Query: 132 RPIGDLVVGLKQLGADVDCFLGT--DCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+G ++ L LG DV GT P V G G + GG + + S SSQ++SALL+
Sbjct: 145 RPMGTIIEALALGVDRADGTPPSALPFTVAGSGHVRGGHLVIDASASSQFVSALLLV 204

Query: 190 APLALGDVEIEIIDKLI-SIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNA 248
+ +E + K + S+ ++ MT+ ++ GV + DS ++ + ++ +

Sbjct: 205 GARFTEGLHLEHVGPVPSLDHINMTVAVLREVGVSVD--DSVPNHVWVAPGRIRA-FDR 261

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A FLA A T GTV + + + Q + +L MGA VT ++TVT

Sbjct: 262 RIEQDLSNAGPFLAAALATRGTVRIPNWPSPTTQVGLWRSILTAMGATVTLDNGLTLVT 321

Query: 309 GPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G P + + ++A T+A + A GP+ + +A R ET+R+ A+

Sbjct: 322 GGP-----EITGADFADTSELAPTVAALCALATGPSRLTGIAHLRGHETDRLAALV 372

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTTIRDPGCT 428
TE+ +LG EE D +I P KL+ + +Y DHRMA A ++ A V + D G T

Sbjct: 373 TEINRLGGDAEETSDGLVIR-PAKLHGGVVHSYADHRMATAGAILGLAVPGVEVEDIGTT 431

Query: 429 RKTFFPDY 435

KT PD+

Sbjct: 432 SKTMPDF 438

>ref|ZP_01201597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium BBFL7]
gb|EAS21015.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Flavobacteria
bacterium BBFL7]
Length = 425

Score = 171 bits (434), Expect = 1e-40, Method: Compositional matrix adjust.
Identities = 137/449 (30%), Positives = 221/449 (49%), Gaps = 59/449 (13%)

Query: 10 QPIKEISGTV--KLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+P+ +S V + GSKS SNR+L+L AL +V NL NS+D +M AL++ +V

Sbjct: 7 KPLNSLSKEVVFITGSKSESRLILKALYPELEIV-NLSNSDDTVHMQEALQSQQSNV 65

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ +G+AG AMR LTA + G + + G

Sbjct: 66 D-----IGHAGTAMRFLTAYYASKEGQVS--ITGSQ 94

Query: 128 RMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RM++RPI LV L+ +GA ++ PP+++NG G + G VKL S+SSQY++AL+

Sbjct: 95 RMQQRPIAVLVDALRSIGAKIEYVNEEGYPPLQING-GHIVGTTVKLDASVSSQYITALM 153

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV-----KAEHSDSWDRFYI 236
+ AP ++IE+I KL S PY+EMT+R ++ GV + + S + I

Sbjct: 154 LIAPSLDKGLKIELIGKLTSRPYIEMTVRHLQSIGVTNNAKQDVDSQKDIQTSSEFIQI 213

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMM 294
K +K + + VE D SSA Y+ + A+ G + ++ S+QGD K +E E

Sbjct: 214 KPLEKIIN-NSLTVESDWSSAGYWSVALQDIGYKLILQYYFKDSVQGDSKLSEYYEAF 272

Query: 295 GAKVTWTETSVTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
G + ++ + + R I +N+ PD A T+ L + +

Sbjct: 273 GVQTSFDNNQLILIKRSHKVAQR-----IVINLVNEPDQAQTIFATCLALGVDAHLTGLH 327

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTATIDTYDDHRMAMAF 410
+ R+KET+R+ A++ ++ SV E I L + IDT+DDHRMAMAF

Sbjct: 328 TLRIKETDRIALKDVGSRFRESVIETQDTITLTCVPLVQYDDPVVIDTFDDHRMAMAF 387

Query: 411 SLAACAEVPTTIRDPGCTRKTFPDYFDVL 439
+ A ++ + I+D G K++P ++D L

Sbjct: 388 APLA-SKTSLLIKDAGVVSXSYQFWDLL 415

>emb|CBK98719.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium
prausnitzii L2-6]
Length = 425

Score = 171 bits (433), Expect = 2e-40, Method: Compositional matrix adjust.
Identities = 136/429 (31%), Positives = 217/429 (50%), Gaps = 30/429 (6%)

Query: 15 ISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I GT+ P SKS+++R +L +AL+EG + ++NL S+D+ L A L V A

Sbjct: 12 IGGTITAPPSKMAHRAVLCSALAEGASHIENLEFSKDISATLSAAGQLCAKVRT--GAD 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
RAVV G G PV + + +G +R L + G T+V G R+ ERP
Sbjct: 70 RAVVEGLGSFLPVSAVDCCE-----SGSTLRFLLPIASLTGQKVTFV--GRGRLMERP- 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L Q + L + P + G L G+ +L+G++SSQ++S LL A PL
Sbjct: 122 QTVYEKLYQ-----EQSLRFEQSPAGLAVEGTLKSGEYELAGNVSSQFISGLLFALPLLA 176

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD + +I + S Y+EMT RFGV++ D + I GGQKY+ P + VEGD
Sbjct: 177 GDSTLHLIPPVESRSYIEMTRAAQRRFGVESRWQDE-NTLLIPGGQKYR-PCDYTVEGDY 234

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A++ A+ GG VT++G +LQGD ++L GA T+ +
Sbjct: 235 SQAAPFAVLGAVQGG-VTLKGLSADTLQGDAAILDILRRCGASFRTTDAGIV----- 285

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
F + L +D+++ PD+ L V+ L +G T IR+ R+KE++R+ A+ EL
Sbjct: 286 FEKAPLHGVDIDLADCPDLGPVLMVLGLLCEGTTTIRNAERLRIKESDRIAAMEAEELRAC 345

Query: 375 GASVE-EGPDYCIITPEKLNVT--IDTYDDHRMAMA-FSLAACAEVPVTIRDPGCTRK 430
G +E +G I + L+ A + ++DHR+ M+ LA A + ++I D +K
Sbjct: 346 GGVLESKGGTTITIHGCADSLHAPAAPLHGHNDHRVMSLAVLALAAGLELSIDDAEAVQK 405

Query: 431 TFPDYFDVL 439
++P +F+ +
Sbjct: 406 SWPHFFFAI 414

>ref|YP_001581882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosopumilus
maritimus SCM1]
sp|A9A231.1|AROANITMS RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABX12444.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosopumilus
maritimus SCM1]
Length = 422

Score = 171 bits (433), Expect = 2e-40, Method: Compositional matrix adjust.
Identities = 124/427 (29%), Positives = 218/427 (51%), Gaps = 22/427 (5%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
+ISG + P +KS ++R + LA+L+ + V+N+L S D + A + G S+E + ++
Sbjct: 9 KISGQIVCPSNKSYPHRAIFLASLAGNGSKVENVLLSADTMATVEACKKFGASIEIENSS 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++V K P++ K ++ N+G +R A+ A+ + L G +++RP
Sbjct: 69 ---IIV---KNPIKFDKIVPEINTENSGTTIR--IASGIASLFSEBITLTGDESLQKRP 119

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+ L +GA G PP+++ G + GG V + G+ SSQ++SALL++APL
Sbjct: 120 MQPLLDALSSIGAQCQSTDGK--PPIKITG--KISGGDVTIPGNFSSQFISALLISAPLT 175

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + I D L+S PY++ T+ M +FGV + + R+ I Q Y + V D
Sbjct: 176 EKGINLSIKDNLVSKPYLDATIAMRKFGVSVQTLIPYKRYNI-SPQVYNA-ATFTVPID 233

Query: 254 ASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SS + L+ A + G ++G QGD F ++LE +G V E + + P +
Sbjct: 234 FSSLALLLSAAVLNGDETVIKGNIGNLPQGDEVFIDILEQLGVTVNIGEDEIKIKSPEKL 293

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
GR +++ PD+ L ++AL ++ P I +V R+KET+R+ EL K
Sbjct: 294 KGRG-----FDLSNSPDLLPPLTLILALNSNPPIEVNVKHARLKETDRIAITSRELVK 346

Query: 374 LGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
LG V+E D I+ E L +++ +DHR+ MAF +A + DP + ++P
Sbjct: 347 LGIKVQENEDGLILESTENLTGAELNSENDHRLFMAFCIAGMYVGNVVTDPESVQVSYP 406

Query: 434 DYFDVLS 440
D+ + ++
Sbjct: 407 DFVEEMN 413

>ref|YP_003089374.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dyadobacter fermentans DSM 18053]
gb|ACT96209.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dyadobacter fermentans DSM 18053]
Length = 411

Score = 171 bits (433), Expect = 2e-40, Method: Compositional matrix adjust.
Identities = 139/442 (31%), Positives = 217/442 (49%), Gaps = 51/442 (11%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+V P + I ++L SKS NR L++ AL+ + + N+ + D ML L +
Sbjct: 5 LVHPPQQPIRAEIQLAASKSECNRALIINALTGFGQSELTNISEARDSQTMLRLLS---- 60

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
DA +V +AG MR LTA A N + G
Sbjct: 61 -----TDAVADVI---DAGTMRFLTAYF--AVTNQKKTMTGT 93

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
PRM ERPIG LV L++LGAD+ PP+++NG ++ + G +SSQY+SAL
Sbjct: 94 PRMCERPILVDALRKLGDITYEKVDGYPPLQLNGFTYSGNNELTMRGDVSSQYISAL 153

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LM AP ++I++ ++ S PY+EMTL M FG+ E+ W+ + PK
Sbjct: 154 LMIAPQLPSGLKIKLEGEVGSRPYIEMTLNQMAHFGI--EYIADWEHNTLTIPPFKYQPK 211

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+E D S ASY+ + A+ V + G SLQGD +++ +G + +T+ V
Sbjct: 212 PYAIESDWSGASYWYSIVALADDAEVELLGLKKDSLQGDSAIVDIMRHLGVESAFTDRGV 271

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+T P + ++ + PD+A T+AVVA ++ + S ++KET+R+
Sbjct: 272 LLTKIPAK-----ASLGWDFTNCPDLAQTVAVVAVKKIRLSLTGIESLKIKETDRVF 324

Query: 366 AIRTELTKLGA---SVEEGPDYCIIT----PPEKLNVTADITYDDHRMAMAFSLAACAEV 418
A++ EL KLGA +E+ Y + T P + V +I TYDDHRMAMAF+
Sbjct: 325 ALQQELKKLGAELTEIEKDHLVEVTTLTDIPTDP--VPSIHTYDDHRMAMAFAPVGMVS- 381

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
+ I++PG K++P Y+ L+
Sbjct: 382 DILIQEPGVVVKSYPGYWKDLA 403

>gb|AAQ84158.1| PlmJK [Streptomyces sp. HK803]
Length = 1003

Score = 171 bits (432), Expect = 2e-40, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 220/435 (50%), Gaps = 25/435 (5%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
IS + +P SK ++R L+LA+L++G + + L ++ V Y + LR GL V+ +
Sbjct: 10 HRISSEILVPNSKYHAHRAILASLADGESRIHGLSDARHVEYTVRLLR--GLGVQLVRE 67

Query: 73 AKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VV G GG + PV+D + G++G + +T A+ N + G R
Sbjct: 68 GDTFVVRGLGGHYRPVQDT-----VSAGSSGTTLYFMTG--LASLSNRAVTITGQKYFRN 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+G L+ L+Q+G ++ DCCPV+V GG+V + G++S Q++S LL+ AP
Sbjct: 121 RVPGLLRALQIGVRLES--ANDCCPVQVRSHRPT--GGEVTIPGTLG--QWISGLLLAP 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G I + D L Y+E+T+ +M +FG++ + W RF + Q + P +
Sbjct: 177 FATGPTTITVSDTLNERTYLELTVAMMRQFGLLEVTVAPDWRFRDVAHQSVR-PTELTLP 235

Query: 252 GDASSASYFLAGAAITGGTVTVEG----CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
D SA++ +A AA+ V + G G + + F ++ MG + + V

Sbjct: 236 PDIGSAAFGIATAALHPSDVLRLGMPSLTGGPADHPEFHFLDIARSMGVPMELDPVAGGV 295

Query: 308 TGPPREPFRGRHLKVIDNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
P LKA+DV+ +PD+ L+ +A FA G + R+VA R+KE++R +

Sbjct: 296 RIQQDAPL----LKAVDVDCRDVDPMLPVLSTLATFAHGSEVFRNVAHTRLKESDR-AGV 350

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
+L +GA +E D +T + L + +Y+DHR+ M+ ++A+ A T+ P

Sbjct: 351 MVQLNSMGAELELSDDTLRVTGVDSLGAELSSYNDRVLM SLAVASSRARGHSTLSYPH 410

Query: 427 CTRKTFPDYFDVLST 441
R ++P + D++++

Sbjct: 411 AYRISYPGFDDMMNS 425

>gb|AAD51963.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
Length = 153

Score = 171 bits (432), Expect = 3e-40, Method: Compositional matrix adjust.
Identities = 88/162 (54%), Positives = 115/162 (70%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+SSQ+L+ALLMAAPLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +

Sbjct: 1 SVSSQFLTALLMAAPLASQDVTISIKGDLVSKPYIDITLHLMKTFGEVDNQ-SYQRFVV 59

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGA 296
+G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA

Sbjct: 60 RGKQQYQSPGDYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRGSVQGDIFADVLEKMG 119

Query: 297 KVTWTETSVTVTGPPREPFRGRHLKVIDNMNMPDVAMTLA 338
VTW + + T R LKAID++MN +PD AMT+A

Sbjct: 120 TVTWGDDFIAC-----RGELKAIDMDMNHIPDAAMTIA 153

>ref|YP_002488440.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter chlorophenolicus A6]
gb|ACL40351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter chlorophenolicus A6]
Length = 475

Score = 170 bits (431), Expect = 3e-40, Method: Compositional matrix adjust.
Identities = 139/433 (32%), Positives = 217/433 (50%), Gaps = 25/433 (5%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLS---VEA 69
+ + TV +PGSKSL+NR L+LAAL++G + + L+S D M+ ALR LG + V

Sbjct: 25 RPVDATVTVPGSKSLTNRYLVALAALADGSPRLRAPLHSRDSVLMIEALRQLGATITEVPG 84

Query: 70 DKAAKRAVVV----GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
D A + V GG+ + A V + G AG MR + GG +T+ DG

Sbjct: 85 DGAFGPDLEVPLQHRGGEGQEDAAGTAVHIDCGLAGTVMRFPPLAALRGGPSTF--DG 142

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGP--PVRVNGIGGLPGGKVKLSGSISSQYL 183
P R+RP+G ++ LK LG V G P V G G + GG + + S SSQ++

Sbjct: 143 DPHARKRPMGTIIIEALKALGVSAEDGGTPASLPFVVEGTGEVRGGHLVIDASASSQFV 202

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SALL+ + +E + K + S+ ++ MT+ ++ GV+ + DS ++

Sbjct: 203 SALLLVGARFTEGLHLEHVGPVPSLDHINMTVAVLRGAGVQVD--DSVPNHVWVSPGPI 260

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
++ + +E D S+A FLA A +GGTV + G + Q + +L MGA+V+ +

Sbjct: 261 RA-FDQQIEQDLSNAGPFLAALASGGTVRIPGWPEQTQQVGDWRSILARMGAEVSLLD 319

Query: 303 TSVTVTGPPREPFRGRHLKVIDNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+TV G +K D ++A T+A + A GP+ + +A R ET+

Sbjct: 320 GVLTVR-----GGTEIKGAD--FADTSELAPTVAALCALATGPSRLSGIAHLRGHETD 370

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI 422
R+ A+ TE+ +LG EE D +I P KL+ + +Y DHRMA A ++ A V +

Sbjct: 371 RLAALVTEINRLGGDAEETSDGLVIR-PAKLHAGVVHSYADHRMATAGAILGLAVEGVQV 429

Query: 423 RDPGCTRKTFPDY 435
D T KT PD+
Sbjct: 430 EDIATTAKTMPDF 442

>ref|ZP_07705928.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dermacoccus sp.
Ellin185]
gb|EFP57731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dermacoccus sp.
Ellin185]
Length = 486

Score = 170 bits (431), Expect = 3e-40, Method: Compositional matrix adjust.
Identities = 152/440 (34%), Positives = 218/440 (49%), Gaps = 34/440 (7%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G +PGSKSL+NR L+LAAL++ +++ L S D M ALR +G+ VE
Sbjct: 44 RPVVGAFSVPGSKSLTNRYLVLAALADDDSLRAPLRSRDTLLMAQALRAMGVQVEDVPG 103

Query: 73 AKRAVVVGCGGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
G + V A + Q+ G AG MR L A G + DG R
Sbjct: 104 DSPE-----GDDWHVTPAPFRGPAQVDCGLAGTVMRFLPPVAALADGPVAF--DGDEHAR 156

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+G ++ L LG +D P V+G G + GG+V+++ S SSQ++SALL++
Sbjct: 157 NRPMGPVLQALADLGVRIDDD--SRRALPFTVHGTGAVTGGRVEVNASTSSQFVSALLLSG 215

Query: 191 PLALGDVEIEIIDK---LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK---S 244
A D + I+ L SIP+++MT+ ++ GV E D D G Y
Sbjct: 216 --ARFDEGVTIVHTGATLPSIPHIDMTVEVLRDAGVIEVGDDVD---ADGRGSYAWSVE 270

Query: 245 PKN-----AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
P + VE D S+A+ FLA AA+TGG V + T + Q VLE MG KVT
Sbjct: 271 PSDIRALDVMVEPDLNAAPFLAAAATGGEVFMADWPTFTTQPGDHIRGVLERMGCKVT 330

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ V GP GR L+ IDV++ + ++ + + ADG + IR VA R
Sbjct: 331 LDRDGLRVRGPEPES---GR--LRGIDVDLTEASELTPVVVALCALADGGSRIIRGVVAHIRGH 385

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
ET+R+ A+ E T +GA V E D +IT P E L+ TYDDHRMAMA ++
Sbjct: 386 ETDRLAALSREFTAIGAQVHETEDGLVITPVPREVLHGGLFHTYDDHRMAMAAAVVGLVV 445

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
+ + + G T KT P +FD
Sbjct: 446 DGIVVENVGTAKTLP-HFD 464

>ref|YP_003274671.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gordonia bronchialis
DSM 43247]
gb|ACY22778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gordonia bronchialis
DSM 43247]
Length = 421

Score = 170 bits (431), Expect = 4e-40, Method: Compositional matrix adjust.
Identities = 143/433 (33%), Positives = 221/433 (51%), Gaps = 27/433 (6%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV+LPGSKS++NR L+LAAL++G + + L S D + MLGAL LG+ V D A +
Sbjct: 13 LDATVELPGSKSITNRALVLAALADGPSTIRGTLRSRDTNLMLGALSALGVGVVRVDPAQE 72

Query: 75 RAVVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V +E A + G AG MR L AA + V DG + R RP
Sbjct: 73 TTV-----SIEPATLHAADIDCGLAGTVMRFLPP--LAALADGPVVFDGDEQARSRP 122

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-AAPL 192
++ L+ LG VD D P V+ G + GG+V + S SSQ++S LL+ AA
Sbjct: 123 QTTILAAALRGLGVVRVDG---DALPFTVHSTGRVTGGEVTIDASGSSQFVSGLLLSAARF 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G V + + S P+++MT+ ++ GV+ + S + D + + G S + VE

Sbjct: 179 DDGLVIWHVGPVPSTPHIDMTVDMLATAGVEVDTSPA-DTWRVAPGP--ISAVDWTVEP 235

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A+ FLA AA+TGGTV V + Q + A+VL MGA V + +++V GP R

Sbjct: 236 DLSNAAFLAAAATGGTVRVYPVVTTPGARIADVLAAMGATVEHLDGTLVSRGPER 295

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
L + +++ + ++ T+A + ADG + + +A R ET+R+ A+ TE+T

Sbjct: 296 -----LSGVTLDLRIDIGELTPTIAALCALADGDSRLSGIAHLRGHETDRLAALTTEIT 348

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTF 432
+LG E D IT L+ ++Y DHRMA A ++ V + D T KT

Sbjct: 349 RLGGVCRETDDGLAIT-GSTLHGGTWESYADHRMATAGAIIGLVTPGVLDVDDVETTTKTL 407

Query: 433 PDYFDVLSTFVKN 445
PD+ ++ ++

Sbjct: 408 PDFPNMWQRMLEQ 420

>gb|ADI07135.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces
bingchenggensis BCW-1]
Length = 464

Score = 170 bits (431), Expect = 4e-40, Method: Compositional matrix adjust.
Identities = 138/441 (31%), Positives = 211/441 (47%), Gaps = 38/441 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS++NR L+LAAL+ + L S D M ALRTL+ +E

Sbjct: 24 VDATVTVPKSGSVTNRGLILAAALAEPLRRPLRSRDTLLMAEALRTLGVGIEETVPDH 83

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-----LGNAGIAMRSLTAAVTAAGGNATYVL 123
G G E E ++ +GNAG MR L A G +

Sbjct: 84 SPGSHGSHGAPGSEGGGEAWRVIPAGLHGPATVDVGNAGTVMRFLPPVAALADGPVRF-- 141

Query: 124 DGVRPMRERPIGDLVVLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG R ERP+ ++ L+ LGA +D G P+ V+G G L GG V++ S SSQ++

Sbjct: 142 DGDKRSHERPLHGVIALDALRALGARIDDD-GRGSLPMTVHGGGALDGGPVRIDASSSSQFV 200

Query: 184 SALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK- 241
SALL++AP VE+ + L S+P++ MT+ ++ G + ++ GG+

Sbjct: 201 SALLLSAPRFNQGVVEVRHVGAALPSLPHIRMTVDMLRAAGAAVDAPEA-----GGEPN 253

Query: 242 --YKSP-----KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
SP ++ VE D S+A+ FLA A +TGG VT+ + Q + M

Sbjct: 254 VWRVSPSALLGRDLVVEPDLNSAAPFLAAALVTGGRVTIPDPWPERTTQPGDSLRRIFTNM 313

Query: 295 GAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
G T+ +T TG R + ID +++++ ++ +A VA AD + + +A

Sbjct: 314 GGACELTDAGLTFTGTGR-----ITGIDADLHEVGELTPVIAAVALADSESTLSGIA 366

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
R+ ET+R+ A+ E+ +LG V E D I P L+ TY+DHR+A A ++

Sbjct: 367 HLRLHETDRLAALAKEINELGGDVTETADGLRIR-PRPLHGGVFHTYEDHRLATAGAVIG 425

Query: 415 CAEVPVTIRDPGCTRKTFPDY 435
V I + T KT PD+

Sbjct: 426 LVVEGVQIENVATTAKTLPDF 446

>ref|YP_003141587.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
ochracea DSM 7271]
gb|ACU93026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
ochracea DSM 7271]
Length = 409

Score = 170 bits (431), Expect = 4e-40, Method: Compositional matrix adjust.
Identities = 136/435 (31%), Positives = 208/435 (47%), Gaps = 55/435 (12%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
L GSKS SNR+L+L AL TV NL ++D + AL + V+

Sbjct: 18 LSGSKSESNRVILQLFPELTV-QNLSTADDTLLQLQALSSHTEVVD----- 64

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
+ +AG AMR LTA G +L G PRM+ERPI LV
Sbjct: 65 -----IHHAGTAMRFLTAYFAIQGKEV-LLTGSPRMKERPINLLVNA 106

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L+QLGAD+ PP+ + G L ++ + G++SSQY SALL+ AP + +
Sbjct: 107 LQQLGADITYTEKEGFPPIYIRG-KKLLINNEIHIQGNVSSQYSSALLLIAPALPNGLTLH 165

Query: 201 IIDKLISIPYVEMTLRLM-----ERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
+ ++ S+PY++MT L+ E+ KA + + N++ VE D
Sbjct: 166 LEGEVTSPLPYLKMTTNLLAHCIGQEQLFKA-----NTIKVNTMNGKNLLHNSWEVESD 219

Query: 254 ASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
SSASY+ A A++ G T+++ + SLQGD + E G ++ +T+
Sbjct: 220 WSSASYWYAFVALSPIGTTLSSLYFKSHSLQGDSALKTIYEFFGVHSSFKGNELTI---- 275

Query: 312 REPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
E K + N+N PD+A T+AV + + + + +KET+R+ A++TEL
Sbjct: 276 -EKVAEPQQKRFEYNLNATPDIAQTIAVTCVAMGLECHLTGLHTLKIKETDRLQALQTEL 334

Query: 372 TKLGASVEEGPDYCIITP-PEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
KLGA V D + P P + +I TY+DHRMAMAF+ + + I D K
Sbjct: 335 RKLGAADVSTTHDSLHLAPCPHLRSGISISATYNDHRMAMAF+PLMLKTNLEIADKEVVSK 393

Query: 431 TFPDYF-DVLSTFVK 444
++P ++ DV VK
Sbjct: 394 SYPSFWHDVAQLTVK 408

>ref|ZP_07865192.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
ochracea F0287]
gb|EFS98653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
ochracea F0287]
Length = 394

Score = 170 bits (430), Expect = 5e-40, Method: Compositional matrix adjust.
Identities = 130/421 (30%), Positives = 201/421 (47%), Gaps = 42/421 (9%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
L GSKS SNR+L+L AL TV NL ++D + AL + V+
Sbjct: 3 LSGSKSESNRVLILQALFPELTV-QNLSTADDTLLLQALTSHTEVVD----- 49

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
+ +AG AMR LTA G +L G PRM+ERPI LV
Sbjct: 50 -----IHHAGTAMRFLTAYFAIQGKEV-LLTGSPRMKERPIHLLVNA 91

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L+QLGAD+ PP+ + G L +V + G++SSQY SALL+ AP + +
Sbjct: 92 LQQLGADITYTEKEGFPPIYIRG-KKLTNNEVHIQGNVSSQYSSALLLIAPALPNGLTLH 150

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGDASSASY 259
+ ++ S+PY++MT L+ + + S + + + N++ VE D SSASY
Sbjct: 151 LEGEVTSPLPYLKMTTNLLAHCIGQEVSFKANTIKVNTMKGKNLLHNSWEVESDWSASY 210

Query: 260 FLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
+ A A++ G T+++ SLQGD + E G ++ +T+ E
Sbjct: 211 WYAFVALSPIGTTLSSLYFKPHSLQGDSALKTIYEFFGVHSSFKGNELTI-----EKVAE 265

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
K + N+N PD+A T+AV + + + + +KET+R+ A++TEL KLGA
Sbjct: 266 PQQKRFEYNLNATPDIAQTIAVTCVAMGLECHLTGLHTLKIKETDRLQALQTELKLGAE 325

Query: 378 VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
V D + P L +I TY+DHRM MAF+ + + I D K++P ++
Sbjct: 326 VSITHDSLHLVPCSHLRSGISISATYNDHRMVMAFT-PLMLKTTLEIADKEVVVSKSYPSFW 384

Query: 437 D 437

Sbjct: 385 H 385

>ref|YP_004014739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. Eu1lc]
gb|ADP78869.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. Eu1lc]
Length = 438

Score = 170 bits (430), Expect = 5e-40, Method: Compositional matrix adjust.
Identities = 146/432 (33%), Positives = 217/432 (50%), Gaps = 30/432 (6%)

Query: 11 PIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P++ + V++PGSKS +NR L+LAA ++G + + L S D M GALR LG+ ++ D
Sbjct: 20 PVRAV---VRVPGSKSGTNRALVLAADGVSRRLGALRSRDTVLMAGALRALGVGIDQD 76

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
++A VV G G+ D + GNAG R A G+ T+ DG PRMR
Sbjct: 77 ESAW--VVRGGLGR---RDGT-PTAIDCGNAGTVARFTPALAALTDGDVTF--DGDPRMR 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ L+ L+ LGA VD D P+ V G GG+ GG V + S SSQ +S LL+AA
Sbjct: 129 HRPLTPLLDALRALGAVVDG----DTMPLVVRGRGGITGGAVTVDASDSSQLISGLLLAA 184

Query: 191 PLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY-KSPK 246
P VE+ + +L S PY++MT+ + G V+ E D D + P
Sbjct: 185 PGYDQGEVSHVGGRLPSGPYLDMTVTDLRAAGATVETEPGDPADPTGKPPTRVTPGPL 244

Query: 247 NAY---VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
AY +E D +SA+ FLA A TGG VT+ + Q +LE MGA T
Sbjct: 245 RAYDRAIEPDLNSAAPFLAAAVATGGEVTIPDWPVTTQPGRMPLPGLLEAMGAHTELTPE 304

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V G L +D ++ + + A L +A+ AD P+ +R +A R++ET+R
Sbjct: 305 GLRVR-----GGDGLHGLDADLGDVGEEAAPVLTALAVLADSPSRLRGIAHLRLQETDR 357

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ +L +LGA + D I P L +D DHR+AM +++ +T+
Sbjct: 358 LGALADQLGRLGADISVTEDGLAIR-PAPLRGARLDPLADHRLAMTYAVVGLRVPGITVD 416

Query: 424 DPGCTRKTFPDY 435
D T KT P++
Sbjct: 417 DIATTGKTVPEF 428

>ref|YP_003362359.1| 5-enolpyruvylshikimate-3-phosphate synthase [Rothia mucilaginosa
DY-18]
dbj|BAI64539.1| 5-enolpyruvylshikimate-3-phosphate synthase [Rothia mucilaginosa
DY-18]
Length = 501

Score = 169 bits (429), Expect = 6e-40, Method: Compositional matrix adjust.
Identities = 139/455 (30%), Positives = 222/455 (48%), Gaps = 47/455 (10%)

Query: 19 VKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---AD----- 70
V +PGSKSL+NR LLLAAL++ + + L+S D M+ ALR LG +E D
Sbjct: 31 VHIPGKSLTNRYLLAALADSPSYLRAPLHSRDSALMIEALRQLGAGIELVPTDSPFGP 90

Query: 71 --KAAKRAVVVGCGGKFPVEDAKEE-VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
K + V + + A+ V + G AG MR + A G + DG P
Sbjct: 91 DVKVTPLSFVEAHSQAQSDSAQSRTVSIIEGLAGTVMRFPALAAALLPGE--FAFDGDP 148

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPP--VRVNGIGGLPGGK---VKLSGSISSQ 181
R+RP+G ++ GL+QLG VDC G + P +R G+ G V++ S SSQ
Sbjct: 149 HARQRPMGPVLEGLRQLGVQVDCEQGENALPFVLRSPGLASAEGVSEAPVVRIDASTSSQ 208

Query: 182 YLSALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++SALL+ AP L G V + + SIP+++MT+ + + G++ + +GG+
Sbjct: 209 FVSALLMAPRLPQGMVLVHEGSSVSIPIHQMTVEALRQMGIEVQEHPNQAEEAEGGE 268

Query: 241 -KYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTV-----EGCGTTSLQGD 284
++ ++ +E D S+A FLA A +TG +VT+ GTT + GD
Sbjct: 269 YRWTVHPCSFPGFEMTIEPDLNAGPFLAAAVVTGESVTIPHPAPAADSSAGTTQV-GD 327

Query: 285 VKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFA 344


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      + + E+L +GA+V + E +TVTGP + P G      +++  ++A T+A  F
Sbjct: 328 M-WRELLPALGAQVRYAEGRLTVTGPAQLPEGD-----FSFDLSAGGELAPTMAAACAFV 381

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----IDT 400
      G + +A R ET+R+ A+ E+ +LG S + D +I      + A      T
Sbjct: 382 KGRVELTGIAHLRGHETDRLAALAAEINRLGGSADHTADSLVIEASIPADAEAEQVLART 441

Query: 401 YDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
      YDDHRMA  ++      V +++      KT P++
Sbjct: 442 YDDHRMATFAAIIGLRRPNVVQNVATVAKTMPEF 476

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>ref|ZP_05401260.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
      QCD-23m63]
ref|ZP_06892619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
      NAP08]
ref|ZP_06903123.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
      NAP07]
gb|EFH07185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
      NAP08]
gb|EFH15523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
      NAP07]
      Length = 437

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Score = 169 bits (429), Expect = 6e-40, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 224/439 (51%), Gaps = 44/439 (10%)

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Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      ++SG VK+P SKS+++R ++ ++LS G + + N+ S+D+ + A+ +LG +E
Sbjct: 10 KLSGDVKIPPSKSIARAVICSSLSNGKSRISNIDFSDDIATIRAMTSLGAIIE----- 64

Query: 74 KRAVVVGCGGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGV 126
      K+ ++ G F E E QL LT +G ++ DGV
Sbjct: 65 KKEDILEISGIFSKEGILNRENQL-----NQPKLTIDCNESGSTLRFLVPISLAFDGV 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDPC-PVRVNGIGGLPGGKVK-----LSGSISS 180
      R IG +G + L + F + + N + + GK+K + G+ISS
Sbjct: 118 KRF----IGRNLGKRPLDITYEIFNRQNIKYSYKENQLDLIISGKLKPDEFVRVKNISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      Q+++ LL P D +I I +L S Y+++TL M+ FG++ ++++ F IKG Q
Sbjct: 174 QFITGLLFILPTLESISKIIITTELESKGYLDLTLSTMKDFGIEI-INNNYKEFIKGSQ 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      YK+ ++ VEGD S +++L+ AI G + + SLQGD + E+L MG ++
Sbjct: 233 TYKA-RDYKVEGDYSQGAFYLSADAI-GEDINILDLKEDSLQGDSEVVEILSRMGMEILR 290

Query: 301 TETSVT-VTGPPREPFRGRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
      + +T L + ++ ++ PD+ L+VVA + G T I + R+K
Sbjct: 291 EGNKIKGITNG-----LNSTLIDASQCPDIIPVLSVVAALSRGKTTIINAGRLRIK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
      E +R+ AI EL+KLGA++EE D II KLN + ++ DHR+AM ++A+C +
Sbjct: 342 ECDRLHAINIELSKLGANIEEKEDSLIIEGVSKLNGGVEVWSHKDHRIAMTLAIASCRCD 401

Query: 418 VPVTIRDPGCTRKTFPDYF 436
      P+ ++D C K++P +F
Sbjct: 402 KPIILKDFECVSKSYPHFF 420

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>ref|YP_003535360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloferax volcanii
      DS2]
gb|ADE04561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloferax volcanii
      DS2]
      Length = 430

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Score = 169 bits (429), Expect = 6e-40, Method: Compositional matrix adjust.
Identities = 142/431 (32%), Positives = 213/431 (49%), Gaps = 26/431 (6%)

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Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      ++G + P SKS ++R +L A S+ V D L+ S D + A+ G SV+ D +

```

Sbjct: 10 VAGRTRAPPSKSYTHRAVLAAGYSDEAVVRDALV-SADTKATMRAVEAFGGSVDCD--GQ 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G GG+ D + N+G MR +T AA G VL G +R RP

Sbjct: 67 TVEVAGFGGRPGTPDDVVNCE---NSGTTMRLVTGC--AALGEGTLVLTGDASLRSRPH 120

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G L+ + L + P+ V G+ GG V++ G +SSQ+++ALLMA +

Sbjct: 121 GPLLDVAFDLDGRAESTRRNGQAPLVVGD--GMTGGTVEIPGDVSSQFITALLMAGAVTE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
+++E+ +L S PYV++TL L+ FGV+A +D+ F + GGQ Y AY V GD

Sbjct: 179 EGIDVELTTELKSSPYVDITLELLADFGVEATRTDAG--FSVPGGQSYAPEGGAYSVPGD 236

Query: 254 ASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
SS SY LA A+ G V +EG S QGD +++ MGA V W E + +

Sbjct: 237 FSSLSYLLAAGAVAGAEGEDVIEGA-RPSAQGDSAIVDIVRDMGATVDWDEDAGELV-- 293

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L V++ PD+ T+AV+ ADG T I + R KET+R+ A+ E

Sbjct: 294 ---VSAADLTGTTVDVGDTPDLLPTIAVLGAIAADGTVIENCEHVRFKETDRVSAMAE 349

Query: 371 LTKLGASVEEGPDYCIITPPE-KLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCT 428
L ++GA+V E D I E L A+D DHR+ M+ ++A A+ TI

Sbjct: 350 LAEMGANVTEQRDLTIHGGETDLVGAADVGRGDHRIVMSLAVAGLVADGETTIAGSEHV 409

Query: 429 RKTFFPDYFDVL 439
+FP++F+ +

Sbjct: 410 DVSFPNFFEAM 420

>ref|YP_001710766.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clavibacter michiganensis subsp. sepedonicus]
emb|CAQ02172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clavibacter michiganensis subsp. sepedonicus]
Length = 487

Score = 169 bits (429), Expect = 6e-40, Method: Compositional matrix adjust.
Identities = 138/422 (32%), Positives = 208/422 (49%), Gaps = 12/422 (2%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV LPGSKSL+NR L+L+AL++ + + + L S D M+ ALR LG +E

Sbjct: 39 LDATVPLPGSKSLTNRELVLALADSPSTLRSPLRSRDLRLMIEALRALGTVIEEVDGGS 98

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G + + + + G AG MR L A G ++ DG P R RP+

Sbjct: 99 ---AFGPDRLITPAELAGGITIECGLAGTVMRFLPPVAALALGPVSF--DGDPSARRRPM 153

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
+ L+ LG DV+ G P + G G +PGG++ + S SSQ++S LL+AAP A

Sbjct: 154 SGTIEALRALGVDVND--GRRALPFSLYGTGEVPGGEIAIDASASSQFVSGLLLAAPRFA 212

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + L S+P++EMT+R + GV E + +I + +E D

Sbjct: 213 QGLRLRHTGETLPSMPHIEMTIRTLAERGTVVVSPEPG--VWIVPPSPIAG-REVRIEPPD 269

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+ FL A + GG V + G + Q A +L GA VT ++ V G P

Sbjct: 270 LSNAAPFLCAALVAGGRVAIPGWPEETTQVGADLAHLPRFGATVTREGGALVVDGGPGPL 329

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G + + +D++++ ++A L +A ADGP+ I + R ET+R+ A+ E+T

Sbjct: 330 AAGGR-ITGVLDLSTGGELAPALVALAALADGPSRITGIGHLRGHETDRLAALAAEITG 388

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
LG SV E D I+ P L+ Y+DHRMA A ++ A V I D G T KT P

Sbjct: 389 LGGSVTELEDGLAIS-PAPLHGGPWRAVEDHRMATAGAIVGLAVPGVEIDDIGTTAKTLP 447

Query: 434 DY 435
++

Sbjct: 448 EF 449

>emb|CBK96585.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium siraeum
70/3]
Length = 405

Score = 169 bits (428), Expect = 7e-40, Method: Compositional matrix adjust.
Identities = 129/425 (30%), Positives = 201/425 (47%), Gaps = 43/425 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SG + +P SKS+S+R+L+ AA +G T +DNLL D+H + AL LG + +
Sbjct: 9 RLSGKLIVPPSKSISHRMLICAAFCGDGITHIDNLLCMDLHATINALTALGAKINGKDGS 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ K V F +G +R + +A G A + G ++ ERP
Sbjct: 69 YDITGTTQPSK-----KAAVDCF--ESGSTLRFMIPISAFGCEAEFT--GRGKLPERP 118

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I L+ + + GA T P +V G L GK + GS+SSQ+++ LL A +
Sbjct: 119 ITPLIKPMTENGA---VFETLSMPYKVKG--KLSGGKYYIDGSVSSQFITGLLFALSVL 172

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D EI + +L S PYV +T+ M++FGV ++ + ++IKGGQKY+ P N VE D
Sbjct: 173 SKDSEIILTTRESKPYVNITIDCMKQFGVG--CETENGYFIKGGQKYQ-PHNCTVEAD 229

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S +++FLA A G + + S+QGD ++ E
Sbjct: 230 MSQSAFFLA-ANCAGSDIELTNLNLNSVQGDKAIVDIAEKFR----- 270

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L ID + +PD+ +AV+ F P I + R+KE +R+ A +
Sbjct: 271 --NGGDLVIDA--SDIPDLVPAIAVMMSFWKKPCRIINCELRRIKECDRLSATELIND 326

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTIRDPGCTRKTF 432
LG + I P E + Y+DHR+AMA ++AA V I+ CT+K++
Sbjct: 327 LGGKAISTENSIEIFPVEAFKGGTVRNYNDHRIAMAGAVAATRSTGEVVIKGAECTKKS 386

Query: 433 PDYFD 437
P +FD
Sbjct: 387 PGFFD 391

>ref|ZP_04448120.1| hypothetical protein BIFANG_03122 [Bifidobacterium angulatum DSM
20098]
gb|EEP20852.1| hypothetical protein BIFANG_03122 [Bifidobacterium angulatum DSM
20098]
Length = 446

Score = 169 bits (428), Expect = 7e-40, Method: Compositional matrix adjust.
Identities = 143/444 (32%), Positives = 219/444 (49%), Gaps = 43/444 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + TV++PGSKSLSNR L+LAAL + LL S D M+ ALRTLGL+ + D+
Sbjct: 16 QPLDATVEIPGSKSLSNRYLILAAALGTQPVRLVGLLRSDTELMNLRNLGVRCDVDEQ 75

Query: 73 AKRAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V V G+F + ++F G AG MR + A G + DG +
Sbjct: 76 SATTVTVTPPANGRF-----RGNTKVFCLAGTVMRFVPLAMFADGPVEF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
RP+ ++ GL QLGA ++ + G T PP V VK+ S SSQ++
Sbjct: 129 ARPMKPVLDGLAQLGAVIE-YHGENGLRPFITPTPTVEER--TSPSVVKIDSSGSSQFI 185

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+ G +E+ +K S+P++ MT+ ++ GV A + + +K G
Sbjct: 186 SGLLLIGSRIPGGLELRHTGEKTPSLPHIRMTVADLQAGVDAIADEQVHVWQVKPG-TV 244

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P++ VE D S+A+ FL A ITGG+V V ++ Q LE MGA+VT+ E
Sbjct: 245 QLPESVTVEPDLSNAAPFLGAALITGGSVRVPNWPQSTTQPGGLLPGYLERMGAEVTFPE 304

Query: 303 TSVTVTGPPREPFGGRKHLK-AIDVNMNKMPPD-----VAMTLAVVALFADGPTAIRDV 353
+ G ++ K + D N+N + D +A +LA + +FAD PT + +
Sbjct: 305 SD-----GIRYCKVSGDGNINGLGDGDLTAAGEIAPSLAAILVFADKPTNMTGI 353

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFS 411
R ET R+ A+ E+T++G E D I P + L+ ++TY DHRMA +
Sbjct: 354 GHLRGHETNRLEALVNEITRVGGKAHELTDGIAIEPVKSGALHGAEMETYADHRMATFAA 413

Query: 412 LAACAEVPVTIIRDPGCTRKTFPDY 435
+ VT+R+ TRKT PD+
Sbjct: 414 MLGLRIEGVTVRNVETTRKTLPDF 437

>ref|YP_872294.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
sp|A0LS98.1|ARO_AACIC1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK52308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
Length = 423

Score = 169 bits (428), Expect = 7e-40, Method: Compositional matrix adjust.
Identities = 143/435 (32%), Positives = 217/435 (49%), Gaps = 32/435 (7%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ V LPGSKS++NR L+LAAL+ T + L + D M+ LR+LG+ + D A
Sbjct: 17 RYDAVHLPKSGKSMNTRALVLAALAEPTAIRGGLRARDTELMMAGLRSLGVGI--DDAG 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V P E + + G AG MR L AA T A G ++ DG PR RERP
Sbjct: 75 DMWLIV-----SPAELRGPAIDCGLAGTVMRFLAAATLATGEVSF--DGDPRRERP 125

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+ L+QLGA++ G PV V G G LPGG + S SSQ++SALL+ AP A
Sbjct: 126 LRPLLDALRQLGAELRDTGGRL--PVTVVGSGHLPGGHCVVDASASSQFVSALLLVAPRA 183

Query: 194 LGDVEIEIIDK-LISIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKSPKNAY 249
V + + + L S+P++ MT+ ++ GV+ +D R I+GG
Sbjct: 184 DTPVTVGHVGRTPSVPHITMTVAMLRERGVAGTGDGSRVQPGPIRGG-----TVQ 236

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S+A+ FLA A +TGG V V + Q ++L MGA+ T +TVTG
Sbjct: 237 IEPDLNSAAPFLAAALVTGGRVRVPDWPMTTQAGDALRDLLTAMGARCELDTGLTVTG 296

Query: 310 PPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P + +D ++ + ++ TLA +A AD P+ R + R ET+R+ A+
Sbjct: 297 GPV-----IHGLDADLRDVSELVPTLAALAAALADRPSTFRGIGHMRGHETDRLAALAA 349

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIIRDPGCTR 429
ELT+LG V D +I P L+ +Y DHRMA ++ + + +
Sbjct: 350 ELTRLGGDVTATDDGLVIR-PRPLHGGVFHSGDHRMATTGAVLGLVIPGIVVENIQTVA 408

Query: 430 KTFPDYFDVLSTFVK 444
KT P + ++ + ++
Sbjct: 409 KTMPTFVELWTGMLR 423

>ref|YP_002906764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
kroppenstedtii DSM 44385]
gb|ACR18221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
kroppenstedtii DSM 44385]
Length = 497

Score = 169 bits (428), Expect = 8e-40, Method: Compositional matrix adjust.
Identities = 139/464 (29%), Positives = 213/464 (45%), Gaps = 49/464 (10%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-- 68
P + ++ TV +PGSKS++NR L+LAAL+ + + L S D M+ ALR +G+S+E
Sbjct: 28 PPRPVATVTIPGSKSMNTRALILAAALASDPSTITGALRSRDTDLMAALRAMGVSIIES 87

Query: 69 -----ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
D +R + G AG MR L A
Sbjct: 88 DSSSGSSSDSSATDNNCRRTPPASLSLLVTPPQLHGATVDCGLAGTVMRFLPPVAALAD 147

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG----- 163
G ++DG P R+RP+ + L+QLG V+ D P+R+ G
Sbjct: 148 G--PVLIDGDPHARKRPLKTMADALRQLGVTVEG---DSLPLRIEGASASSDAHSSTEN 201

Query: 164 -----IG---GLPGGKVKLSGSISSQYLSALLM-AAPLALGDVEIEIIDKLISIPYVEMT 214
+G G G +++ S SSQ++S LL+ AA G L S P++EMT
Sbjct: 202 PNAHVGTTEGPRGRAIRIDASSSSQFISGLLLSAARFTHGITVTHTGATLPSQPHIEMT 261

Query: 215 LRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
+ ++ G+ + + + G+ P +E D S+A+ F+A AA+TGG V +
Sbjct: 262 IDMLRDAGIDVTMPEP-HTWQVAPGEI--QPNRWVIEPDLNATPFMAAAAVTGGRVVIP 318

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKH---LKAIDVNMNMKP 331
T + Q +F +LE MGA + VTGP R L I +++ +
Sbjct: 319 NWPTKTTQPGDQFRTILENMGACHDLVSHDLVVTGPDAPTDRSSSGTGLTGITMDLHDIG 378

Query: 332 DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE 391
++ T+A +A D P+ + +A R ET+R+ A+ T + LG VEE D IIT P
Sbjct: 379 ELTPTIAAALATDTPSHLYGIAHLRGHETDRLHALATNINALGGQVEETDDGLIIT-PA 437

Query: 392 KLNVTAITDYDDHRMAMAFSLAACAEPVVTIRDPGCTRKTTFPDY 435
L+ TYDDHRMA A ++ A V + + T KTFPD+
Sbjct: 438 PLHGDWTPTYDDHRMATAGAVIGLAVAGVRVENIETTSKTFPDF 481

>ref|YP_003681686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nocardiosis
dassonvillei subsp. dassonvillei DSM 43111]
gb|ADH69180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nocardiosis
dassonvillei subsp. dassonvillei DSM 43111]
Length = 448

Score = 169 bits (428), Expect = 8e-40, Method: Compositional matrix adjust.
Identities = 146/429 (34%), Positives = 221/429 (51%), Gaps = 34/429 (7%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA--- 69
+ + + LPGSKS+NR L+LAALSE +V L S D M G+LR LG+ +
Sbjct: 39 RPVRARLSLPGSKSMTNRALVLAALSETPCLVRRPLVSRDSELMAGSLRALGVGITTEGE 98

Query: 70 DKAARAVVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
D A A + G + +GNAG MR + A G T DG PR
Sbjct: 99 DMAVTPAPLRGP-----ASVDVGNAGTVMRFVPPVAALASG--TVEFDGDPR 144

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RERPG+G+L+ L+ LGAD+D G P+ V+G G + GG+V L S SSQ++SALL++
Sbjct: 145 RERPVGELLAALRALGADIDDG-GRGALPMAVHGTGAVHGGVETLDASGSSQFVSALLLS 203

Query: 190 APLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKN 247
V + + S P+++MT+ ++ GV +D SW ++ G S +
Sbjct: 204 GARFTEGVHVRHSGPPVPSQPHLDMTVEMLRAAGVTVSTADNSW---RVEPGPVKVS--D 258

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ETSVT 306
VE D S+A+ FLA A +TGG VT+EG + Q + + MG +V+ + E +T
Sbjct: 259 ITVEPDLNAAAPFLAALVTGGEVTIEGWPEHTSQPGDELRLSFLTRMGGEVSRSPGELLT 318

Query: 307 VTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G GR + ID ++ + ++ T+A VA A P+ + +A R ET+R+ A
Sbjct: 319 LRG-----TGR---ILGIDADLRDVGELTPTVAAVAALATTPSRLTGIAHLRRHETDRIAA 371

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAACAEPVVTIRDPG 426
+ E+ +LG EE PD +I P + +YDDHRMA + ++ A V + +
Sbjct: 372 LAAEINRLGGDAEELPDGLVIN-PRPMRGGVFHSYDDHRMATSGAVIGLAVPGVEVENIA 430

Query: 427 CTRKTTFPDY 435
TRKT PD+
Sbjct: 431 TTRKTLPDF 439

>ref|ZP_00993693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Janibacter sp.
HTCC2649]
gb|EAP99947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Janibacter sp.
HTCC2649]
Length = 432

Score = 169 bits (428), Expect = 8e-40, Method: Compositional matrix adjust.
Identities = 138/432 (31%), Positives = 213/432 (49%), Gaps = 23/432 (5%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ T+ LPSGSKSL+NR L+LAA + G + + + L S D M AL LG+ ++
Sbjct: 15 VAATIDLPGSKSLTNRFVLAAARAGGVSRLRSPLRSRDTLLMAQALGGLGVGIDVDGDD 74

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G + + G AG MR + A G + DG P R RP+
Sbjct: 75 WLVTGP-----EVMGPADIDCGLAGTVMRFVPLAALARGAVRF--DGDPHARTRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G + L+ LG D+D G P V G G + GG V L S SSQ++SALL++AP
Sbjct: 125 GPALDALRHLGVLDLDD--GRGALPFTVRGTGSRGGDVTLTASASSQFISALLLSAPHYD 183

Query: 195 GDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
V I + + S P+++MT+ + G + +++ D + ++ G +P + +E D
Sbjct: 184 QGVTIHHQGEVPSPQHIDMTVEALRDAGADVDDTEA-DTWRVEPGPL--NPLDVQIEPD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+ FLA A +TGG V + + Q + ++L+ MGA V+ +TV+
Sbjct: 241 LSNAAPFLAAALVTGGRVRISSWPQHTTQAGDEIRDILDEMGADVSLGRDGLTVSA---- 296

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+DV+++ ++ +A +A A GP+ IR VA R ET+R+ A+ EL
Sbjct: 297 ---VDGFSGVVDLHDASELTPVVAALAAALAGPSLIRGVAHIRGHETDRLAALARELNA 353

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTTFP 433
LGA+V E D I P L+ T TY DHRM MA ++ A V I D G KT P
Sbjct: 354 LGATVTETADGLHIV-PRPLSPTMFHTYGDHRMVMAGAVIGLAVPGVVIEDVGTVAKTLP 412

Query: 434 DYFDVLSTFVK 445
+ D+ + + +
Sbjct: 413 TFTDLWAHMLGH 424

>ref|YP_003841879.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
ref|ZP_07631033.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
gb|ADL50115.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
Length = 406

Score = 169 bits (427), Expect = 9e-40, Method: Compositional matrix adjust.
Identities = 126/440 (28%), Positives = 218/440 (49%), Gaps = 54/440 (12%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EI + P K++SG V +P SKS+S+R ++ A+L++G ++V N+ S+D+ L + +G+
Sbjct: 2 EITINP-KKLSGKVMVPPSKSVSHRAIICASLAKGKSLVKNIKYSQDIEATLDCMSAMGM 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVT-----AAGGN 118
+ E + + G + +F N ++M + + T A +
Sbjct: 61 TYE--RYEDSLTING-----IDVFNSNGILSMNTRESGSTIRFLIPMALLCS 105

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
T + G ++ +RP+ G + G ++ G L G +++G +
Sbjct: 106 ETVEVTGSEKLMQRPLKPYFDIFDTKGIKYS-YEGN-----KLKLSGKLTSGTYEIGADV 159

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
SSQ++S LL A PL G+ ++I L SI YV++TL +++ FG++ ++D + F IKG
Sbjct: 160 SSQFISGLLFALPLVEGNSIVKITTALESIGYVDLTLDMLKNFGIEIINND-YKEFIK 218

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
Q YK+ + VEGD S A+++ A + G + G S QGD E+L ++

Sbjct: 219 NQSYKA-MDCTVEGDYSQAIFYEV-AKVLGNDIQCLGLNENSSQGD---KEILSIV---- 269

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
E L I +++ +PD+ L V+ F G T I + A R+

Sbjct: 270 -----EKVKNNGLNGIKIDVKDIPDLVPILTTLVLTGTFCKGTTEIYNAARVRI 315

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
KE++R+ + EL KLGA + E PD II KL +D+++DHR+AMA ++A+ E

Sbjct: 316 KESDRLESTTCELRKLGAKITELPDSLIEGTGKLKGGVVDSWNDHRIAMALAIASITICE 375

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
PVTI K++P +++

Sbjct: 376 EPVTITCAESVNKSYPHFWE 395

>ref|ZP_04445584.1| hypothetical protein COLINT_02294 [Collinsella intestinalis DSM 13280]
gb|EEP44796.1| hypothetical protein COLINT_02294 [Collinsella intestinalis DSM 13280]
Length = 438

Score = 169 bits (427), Expect = 1e-39, Method: Compositional matrix adjust.
Identities = 141/434 (32%), Positives = 223/434 (51%), Gaps = 26/434 (5%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SGTV SKS+++RI++ AAL+ G T V D+ + L +G ++

Sbjct: 8 KPLSGTVPAISSKSMARIIIAAALANGVTRVACDITCADIDATIRCLTAIGAKIDPIDG 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V + + A L G +G +R + A G +AT+V G PR+ ER

Sbjct: 68 GFEIHPVLKSLHEHGILRALAGATLDCGESGSTLRFMLPVACALGADATFV--GSPRLGER 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI L L G F G P+R +G + G+ +L G++SSQY+S LL+AAPL

Sbjct: 126 PIAPLTDELMAAGC---TFQGATGLPLRTSGR--MRAGRFELPGNVSSQYISGLLLAAPL 180

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-----WDRFYIKGGQKYKSP 245
GD +I + ++ S PY+ +TL ++ FGVK + F I+ Q Y++P

Sbjct: 181 LDGDTQIAVTGEVESRPYIGLTAVLNAFGVKVIEEGATPGGLPLTVFTTIER-QGYRTP 239

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VEGD S+A+++L+ A+ +VTV G +S+QGD + L + GAK +

Sbjct: 240 GAIAVEGDWSNAAFWSAGALGRHSVTVRGVTSSIQGDRAISAALMLFGAKGQRNARAA 299

Query: 306 TVTGPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV P ++ I++++ +PD+ LA VA A+G T + R+KE +R+

Sbjct: 300 TV-----RP---DNIHGIELDVRDIPDLVPALAAVAACAEGTTRFTGCSRLRIKECDRL 351

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIR 423
AI TEL KLGA+V D +I ++L+ +++ +DHR+AM ++AA CA PV I

Sbjct: 352 AIATELGKLGANVRVDGDALVIEGRDQLDGGVRVNSRNDHRIAMMAAIAAVRCAS-PVEIE 410

Query: 424 DPGCTRKTFPDYFD 437
K++P +F+

Sbjct: 411 GAEAVNKSYPLEFE 424

>ref|ZP_07274174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. SPB78]
gb|EFL02543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp. SPB78]
Length = 443

Score = 168 bits (426), Expect = 1e-39, Method: Compositional matrix adjust.
Identities = 144/445 (32%), Positives = 223/445 (50%), Gaps = 35/445 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV++PGSKS+NR L+LAAL+ + L S D M ALRT+G+ +E +++

Sbjct: 20 VRATVRVPGSKSITNRALVLAALAAEPGWLRPLRSRDTLLMASALRTMGVGIEETVSSE 79

Query: 75 RAVVVGCGGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132

VVG G + V A + + +GNAG MR L T A G + DG PR ER
Sbjct: 80 SCGVVVGAGEAWRVIPAGLRGPATVDVGNAGTVMRFLPPVATLAEGAIRF--DGDPRS YER 137

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L+ LGA +D P+ V G G L GGV++ S SSQ++SALL++AP
Sbjct: 138 PLHGVIDALRALGARIDDG-DRGALPLTVFGSGALDGGKVEVDASSSSQFISALLLSAPR 196

Query: 193 ALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKSPKNA 248
VE+ L S+P++ M++ ++ G + + ++ + + + G ++
Sbjct: 197 FNQGVELRHTGATLPSLPHIRMSVDMLRAVGAQVDEPETGGEPNVVRVTPGALLG--RDL 254

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A FLA A +TGGTVT+ + Q + E+ MG TE +T+T
Sbjct: 255 TIEPDLNAQPFLLAALVTGGTVTIPDWPAGTTQPGDRLREIFTEMGGACELTEAGLTLT 314

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G GR H IDV++ ++ ++ +A VA AD P+ +R VA R+ ET+R+ A+
Sbjct: 315 G-----TGRVH--GIDVDLGEVGETLPGIAAVALADSPSTLRGVAHLRLHETDRLAALT 367

Query: 369 TELTKLGASVEEGPD-----YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP-V 420
E+ +LG V E D C + TA R LA VP V
Sbjct: 368 KEINELGGDVTETADGLHIRRARCTAASSTRTRTTAWP-----RRGQILGLA----VPGV 418

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVKN 445
I + T KT PD+ ++ + + N
Sbjct: 419 GIENVATTAKTLPDFPELWTGMLGN 443

>ref|NP_294820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
radiodurans R1]
gb|AAFL0666.1|AE001959_6 3-phosphoshikimate-1-carboxyvinyltransferase [Deinococcus
radiodurans R1]
Length = 462

Score = 168 bits (425), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 148/434 (34%), Positives = 211/434 (48%), Gaps = 24/434 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++ P +E+ G ++ SK+ + R LL AAL+EG T V + SED ML LR G
Sbjct: 33 DVIVHPARELRGELRAQPSKNYTTRYLLAAALAEGETRVVGVATSEDAEAMLRCLRDWGA 92

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE AV+ G G + + V L GNAG R L V A T+V D
Sbjct: 93 GVEL--VGDDAVIRGFGAR-----PQAGVTLNPGNAGAVARFLMG--VAALTSGTTTFVTDY 144

Query: 126 VPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP GDL+ L++LGA V G P+ V+G + GG V++S SSQY SA
Sbjct: 145 PDSLGRKPQGDLLLEALERLGAWSNDGR--LPISVSGP--VRGGTVEVSAERSSQYASA 200

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ PL +E+ + + S + TL + FGV+A SD R I GGQKY+ P
Sbjct: 201 LMFLGPLLPDGLLELRLTGDIKSHAPLRQTLDTLSDFGVRATASDDLRRISIPGGQKYR-P 259

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V GD ++ L AA+ G V + LQG+ + VL MGA + ++
Sbjct: 260 GRVLVPGDYPGSAAILTAAALLPGEVRLSNLREHDLQGEKEAVNVLREMGADIVREGDTL 319

Query: 306 TVTGPPREPFGKRHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G GR L A+ + + D L A FA+G T +VA+ R+KE +R+
Sbjct: 320 TVRG-----GRP-LHAVTRDGSFTDAVQALTAFAEGDTTWENVATLRLKECDRIS 372

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL--NVTATIDTYDDHRMAMAFSLAAC-AEVPVTI 422
R EL +LG E D +T L +TA D + DHRM M +L A+ P+ I
Sbjct: 373 DTRAELERLGLRARETADSLSVTGSAGLAGGITA-DGHGDHRMIMLLTLLGLRADAPLRI 431

Query: 423 RDPGCTRKTFPDYF 436
RK++P +F
Sbjct: 432 TGAHHIRKSYQFF 445

>sp|Q9RVD3.2|AROA_DEIRA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 439

Score = 168 bits (425), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 148/434 (34%), Positives = 211/434 (48%), Gaps = 24/434 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++ P +E+ G ++ SK+ + R LL AAL+EG T V + SED ML LR G
Sbjct: 10 DVIVHPARELRGELRAQPSKNYTTRYLLAAALAEGETRVVGVATSEDAEAMLRCLRDWGA 69

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE AV+ G G + + V L GNAG R L V A T+V D
Sbjct: 70 GVLE--VGDDAVIRGFGAR-----PQAGVTLNPGNAGAVARFLMG-VAALTSGTTFTVDY 121

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP GDL+ L++LGA V G P+ V+G + GG V++S SSQY SA
Sbjct: 122 PDSLGRKRPQGDLLLEALERLGAWVSSNDGR--LPISVSGP--VRGGTVEVSAERSSQYASA 177

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ PL +E+ + + S + TL + FGV+A SD R I GGQKY+ P
Sbjct: 178 LMFLGPIPLPDGLLELRRLTGDIKSHAPLRQTLDTLSDFGVRATASDDLRRISIPGGQKYR-P 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V GD ++ L AA+ G V + LQG+ + VL MGA + ++
Sbjct: 237 GRVLVPGDYPGSAAILTAAALPGEVRLSNLREHDLQGEKEAVNVLEMGADIVREGDTL 296

Query: 306 TVTGPPPREPFGKRHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G GR L A+ + + D L A FA+G T +VA+ R+KE +R+
Sbjct: 297 TVRG-----GRP-LHAVTRDGSFTDAVQALTAATAAFAEGDTTWNVATLRLKECDRIS 349

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
R EL +LG E D +T L +TA D + DHRM M +L A+ P+ I
Sbjct: 350 DTRAELERLGLRARETADSLSVTGSAGLAGGITA-DGHGDHRMIMLLTLLGLRADAPLRI 408

Query: 423 RDPGCTRKTFPDYF 436
RK++P +F
Sbjct: 409 TGAHHIRKSYPQFF 422

>ref|YP_003653518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobispora bispora
DSM 43833]
gb|ADG89625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobispora bispora
DSM 43833]
Length = 449

Score = 167 bits (424), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 144/424 (33%), Positives = 218/424 (51%), Gaps = 28/424 (6%)

Query: 15 ISGTVKLPKSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL--LSVEADKA 72
+ TV+LPGSKS++NR LLLAAL++G + + L S D M ALR LG L+ + A
Sbjct: 24 VDATVRLPGSKSVTNRALLAALADGPSSIRRALRSRDTLMAAALRALGAELTPSDESA 83

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G P+ + V + +G AG MR + AA + DG P R R
Sbjct: 84 SSVDWTVRPG---PI---RGGVAIDVGLAGTVMRFVPP--VAALADEPVSFDDGPAARRR 135

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G ++ L+ LGA V+ D P V G + GG+V L S SSQ +S LL+A
Sbjct: 136 PMGPILGALRALGAHVEG----DALPFTVRGP--ITGGEVVLDASSSSQMVSGLLLAGAR 189

Query: 193 ALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
V + + S+P++EMT+ ++ + GV + S++ D + ++ G ++ VE
Sbjct: 190 FEKGVTVRHSGPPVPSMPHIEMTVHMLRQAGVAVDDSEA-DVWRVEPGPIRA--RDLTVE 246

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S+A+ FLA A +TG GTVTV + Q + +L MGA VT + V+G
Sbjct: 247 PDLNAAPFLAALVTGGTVTVDPWPERRTTQAGDRLRHLAEMGATVTRVPGGLRVSGSG 306

Query: 312 REPFGKRHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R + I+V+++ + ++ T+A +A ADGP+ I VA R ET+R+ A+ TE+

Sbjct: 307 R-----IAGIEVDLHDVSELTPITIAALADGPSRITGVAHIRGHETDRIAALATEI 359
Query: 372 TKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 431
+LG E D I P L +YDDHRMA A ++ A V + + T KT
Sbjct: 360 NRLGGDARETEDGLEIH-PRPLRGGVFRSYDDHRMATAGAVIGLAVPGVQVENIATTAKT 418
Query: 432 FPDY 435
P++
Sbjct: 419 LPEF 422

>ref|ZP_02693258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Epulopiscium sp.
'N.t. morphotype B']
Length = 428

Score = 167 bits (424), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 128/425 (30%), Positives = 223/425 (52%), Gaps = 26/425 (6%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V++P SKSL++R ++ A+LS G +++ N+ S+D+ + A++ LG +++ + +
Sbjct: 11 LKGEVEIPPSKSLAHRAIICASLSSGESIISNIDYSDDIIATISAVKALGANIKEE--SN 68
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G GK V DA + +G +R T + +V G + +RP+
Sbjct: 69 TLYITIGIQGK-AVNDA---IIDCNESGSTLRFFVPLATLFAESVRFV--GQGNLGRPL 121
Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ ++ D + ++ G + + G ISSQ++S LL A PL
Sbjct: 122 TPFYEIFDKQA--IEYSYEDDELDTIH--GEIKADTFAIRGDISSQFISGLLFALPLLD 177
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D +I + L SI Y+++TL+++E FG+K E+ + ++ F I+G Q YK+ N VEGD
Sbjct: 178 KDSKIVLTTPLESIGYIDLTLQMLEMFGIKVENQN-YETFIIEGKQNYKAI-NYKVEGDF 235
Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A++FLA A+ V V+ S Q D + +L+ +GA+V T T+V
Sbjct: 236 SQAFFLAAGALGNDIV-VKNININSYQADKEVVALLKQIGAEVEITSTTVRAK----- 288
Query: 315 FGRKHLKKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ L I ++ ++ PD+ +A+V G I +VA R+KE +R+ AI EL+KL
Sbjct: 289 --KSKLDNIVMDGSECPDIVPIMALVLALCKGKNEINNVARLRIKECDRLAAINMELSKL 346
Query: 375 GASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTF 432
GA ++E PD I +K N+T + ++ DHR+AM ++AA E V + D C K++
Sbjct: 347 GAKIQELPDSLKIEGVDFNLTKVVS SHKDHRIAMTLAIAATVCENEVILEDYECVSKSY 406
Query: 433 PDYFD 437
P +++
Sbjct: 407 PAFWE 411

>ref|YP_003838341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora
aurantiaca ATCC 27029]
ref|YP_004082701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora sp.
L5]
gb|ADL48765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora
aurantiaca ATCC 27029]
gb|ADU08550.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora sp.
L5]
Length = 433

Score = 167 bits (424), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 139/432 (32%), Positives = 214/432 (49%), Gaps = 27/432 (6%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLSEGTTVVNDNLNSEDVHYMLGALRTLGL--LSVEADKA 72
++ T++LPKSGS++ R L+L AL+ G + + L + D M G LR LG +S+ D
Sbjct: 22 VAATLRLPGSKSMTARALVLGALAGGPSTLARPLRARDTELMAGGLRALGAHMSISDD-- 79
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R +V +P+ + +G AG MR L A G T+ DG P R R
Sbjct: 80 -DRWLVR---PYPLAG---PAHVDVGLAGTVMRFLPPVAGLAAGRVT--DGDPHARTR 129

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP- 191
P+G L+ L+ LG +D P V V G G + GG V + S SSQ +S LL+AAP
Sbjct: 130 PLGPLIGALRTLGVRIIDAPPAGSLPLV-VLGAGRVTTGGDVVIDASASSQLVSGLLLAAPR 188

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G V + S P++ MT++++ G + + D + ++ G S + +E
Sbjct: 189 FDRGVVVRHEGPPVPSAPHLRMTVQMLRAAGAAVDDTTP-DVWTVPEGP--LSGRGWEIE 245

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S A+ F A A +TGG VT++G +SLQ + E+L MG +V+ +TV
Sbjct: 246 PDLGSAAPFFFAALVTGGEVTLQGWPRSSLQPVEQLRELLHRMGGEVSLGTDGLTVR--- 302

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
G ++ +D +++ + ++ L + L ADGP+ + + R ET+R+ A+ E
Sbjct: 303 ----GTGTVRGLDADLSDVGELTPVLTALTLLADGPSRLTGIGHIRGHETDRVTALAKEF 358

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
T LGA + E D I P L TY DHRMA A ++A A + + D CT KT
Sbjct: 359 TALGADITETRDGLDIR-PRPLRGGTFRITYADHRMAHAAVAGLAVPGIEVDDVACTSKT 417

Query: 432 FPDYFDVLSTFV 443
P++ + S V
Sbjct: 418 MPEFPALWSGMV 429

>ref|YP_004223355.1| 5-enolpyruvylshikimate-3-phosphate synthase [Microbacterium
testaceum StLB037]
dbj|BAJ73475.1| 5-enolpyruvylshikimate-3-phosphate synthase [Microbacterium
testaceum StLB037]
Length = 449

Score = 167 bits (424), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 134/433 (30%), Positives = 213/433 (49%), Gaps = 23/433 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---ADK 71
+ TV +PGSKSL+NR L+LAA+++G ++ L+S+D M+ ALR LG+ +E D
Sbjct: 26 VDATVTVPGSKSLTNRELVLAAIADGPGMLHAPLHSDDSVRMVEALRALGVGIEEVATDS 85

Query: 72 AAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
++V F + + G AG MR + A G+
Sbjct: 86 PFGPDLLVTPPASF-----AGDTTVDCGQAGTVMRFVAPLAGLARGDVAVTAH--ESALH 138

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+G ++ L+ +G D+D G P V G G + GG+V++ S SSQ++S LL+AAP
Sbjct: 139 RPMGAMISALRDVGVDIDDG-GHWALPFTVRGHGHVRGGEVEIDASQSSQFVSGLLLAAP 197

Query: 192 -LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+G + +L SIP+++MT+ + G+ E + G + K+ +
Sbjct: 198 RFDVGLHLRHVGSRLPSIPHIDMTVEALGHRGIHVERPSVGEWIVPAGPVRA---KDVAI 254

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 310
E D S+A+ FLA A +TGGTV+V G S Q A++L MGA+V+ ++TV+
Sbjct: 255 EPDLSNAAPFLAAAMVTGGTVSVTGWPLHSTQPGALLADILSEMGARVSRRGGTLTVSAG 314

Query: 311 PREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R + ++++++ ++A TL +A FADGPT + + R ET+R+ A+
Sbjct: 315 DR-----IVGLELDLSATGELAPTLFGLAAFADGPTTLHGIGHIRGHETDRIAALVGN 367

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
L LG E D I P+ L + DHR+A +L V I D G T K
Sbjct: 368 LRSLGGEAHELEDGIRIV-PQPLRGGEWKAHHDHRLATTGALIGLRVPGVEIDDIGTTAK 426

Query: 431 TFPDYFDVLSTFV 443
T P + + T +
Sbjct: 427 TLPQFAGLWRTML 439

>ref|ZP_03505661.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli Brasil 5]
Length = 358

Score = 167 bits (424), Expect = 2e-39, Method: Compositional matrix adjust.
Identities = 132/392 (33%), Positives = 204/392 (52%), Gaps = 44/392 (11%)

Query: 4 AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ ++ P + +SG PGSKS++NR LLLA L++GT+ + L S+D YM ALR +
Sbjct: 5 AKLTIIPPGRPLSGRAMPPGSKSITNRALLLAGLAKGTSRLTGALKSDDTRYMADALRAM 64

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++++ + VV G G P + LFLGNAG A R L AA G T ++
Sbjct: 65 GVAID-EPDDTTFVVTGSGRLMP-----PKAPLFLGNAGTATRFLAAAAALVDG--TVIV 116

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
DG MR+RPIG LV ++ LG DV G CPPV V G G ++ + G +SSQY+
Sbjct: 117 DGDEHMRKRPIGPLVEAMRTLIGIDVSAETG--CPPVTVRGTGRFEADRILIDGGLSSQYV 174

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQ 240
SALLM A V+IE++ + I ++ Y+++T M+ FG + E + +W R G
Sbjct: 175 SALLMMAAGDRPVDIELVGEDIGALGYIDLTTAAMKAFGARVEKTSFVTW-RVEPTG-- 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y++ + +E DAS+A+Y A ++ G + + Q D K E +
Sbjct: 232 -YRA-ADFVIEPDASAATYLAEEVLSDGQIDLGVPNDAFTQPDAKAYETIA----- 281

Query: 301 TETSVTVTGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
R P HL A +++ ++M D T+AV+A F + P +A+ RVKE
Sbjct: 282 -----RFP---HLPA-EIDGSQMQDAVPTIAVLAAFNETPVRFGIANLRVKE 325

Query: 361 TERMVAIRTELTKL--GASVEEGPDYCIITPP 390
+R+ A+ T L + G +VE+G + + + P
Sbjct: 326 CDRIRALSTGLNNIREGLAVEQGDDELIVHSDP 357

>ref|YP_001311640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
sp|A6M254.1|ARO_A_CLOB8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR36684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
Length = 435

Score = 167 bits (423), Expect = 3e-39, Method: Compositional matrix adjust.
Identities = 127/434 (29%), Positives = 223/434 (51%), Gaps = 34/434 (7%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+P SKS+++R ++ AAL +G + V N+ S+D+ + A+ +LG + +
Sbjct: 10 KLSGEVKIPPSKSMRAVICAALGDGVSKVTNIDYSDDIIATIEAMSSLGAKITKKEDY 69

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLVDGVPRMRER 133
+ KE+ + +G +R L + DGV R R
Sbjct: 70 LEVYGINSPENIKANSVKEQRTIDCNESGSTLRFLVPIAA-----LFDGVNRFVGR- 120

Query: 134 IGDVLVVLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLSGSISSQYLSALL 187
G+L G + L F +GI G L G+ K+ G+ISSQ+++ LL
Sbjct: 121 -GNL--GKRPLDTYYKIFDEQGIKYSYKDGILDLKTEGKLKAGEFKMEGNISSQFITGLL 177

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
PL GD +I I ++ S Y+++TLR ++ FGV+ +++++ F IKG Q YKS +
Sbjct: 178 FTLPLLDGDSKIVITTEMESKGYIDLTLRAIKDFGVEI-INNNYEEFIKGNQIYKSI-D 235

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VEGD S A++F A++ V + SLQGD + ++L+ MG K+ + +
Sbjct: 236 YRVEGDYSQAFFFCADALSSNIV-LNDLKLDSLQGDKEVIDILQRMGLKLNNKDNLIG 294

Query: 308 TGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ LK+ ++ ++ PD+ +++VA ++G T I + R+KE +R+ A+
Sbjct: 295 SASL-----GLKSTIIDGSQCPDIIPVSVLVAALSEGTTIINAGRLRIKECDRLAAV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKL--NVTADTYDDHRMAMAFSLAA--CAEVPVTIR 423
+EL KLGA + E + II ++L NV + ++ DHR+AM ++A+ C E + ++

Sbjct: 348 TSELNKLGAKEEKEEGLIEGVKELKGNV-EVWSHKDHRIAMTMAIASTMCKE-RIILK 405

Query: 424 DPGCTRKTFFPDYFD 437

D C K++P ++D

Sbjct: 406 DYECVSKSYQFWD 419

>ref|YP_843454.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosaeta thermophila PT]
sp|A0B7Z0.1|AROA_METTP RecName: Full=Probable 3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK14814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanosaeta thermophila PT]
Length = 421

Score = 167 bits (423), Expect = 3e-39, Method: Compositional matrix adjust.
Identities = 152/431 (35%), Positives = 218/431 (50%), Gaps = 28/431 (6%)

Query: 17 GTVKLPGSKSLSNRILLALAALSEGTTVVNDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76

GTV P SKS ++R +L+ ALS+ V L+ S D + A G V+ +

Sbjct: 12 GTVCAPPSKSYTHRAVLITALSDSGCVHRPLI-SADTRATISACDAFGADVKLRGDSLEI 70

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136

V + P E V L N+G +R ++A G VL G +R RP G

Sbjct: 71 QGVSGAPRTP-----ENVIDVL-NSGTTLRFMSAVAALTDG---AVLTGDSSIRSRPNP 121

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196

L+ L +LGA+ G D P+ + G L GG L GS+SSQ+LSALL+A PL+ G+

Sbjct: 122 LLKALNELGAFAFSIRGNDRAPLVIRGR--LRGGSTSLDGSVSSQFLSALLIACPLSSGE 179

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256

I I +L S PY EMTL ++ + G AE D F ++GGQ Y+ + V GD SS

Sbjct: 180 TTISIKGELKSRPYAEMTLDIRKAG--AEICTDGDIFMRGGQSYRLAET-VPGFDFSS 236

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETS--VTVTGPPREP 314

ASY LA AA G+ TVEG S QGD ++L MGA+V+W S V V+G

Sbjct: 237 ASYPLA-AAALAGSATVEGL-FPSRQGDSAIVDILREMGAEVSWDMESGEVRVSG----- 289

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374

L+ +++ ++ PD+ TLAV+ A+G T I++ R KET+R+ A+ EL K+

Sbjct: 290 ---ADLRGREIDASQTPDLVPTLAVLGAVAEGRTVIKNAEHVRHKETDRIHAMAVELKKM 346

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTFFPD 434

GA++ E PD I + L+ + Y DHR+ MA +LA I ++P

Sbjct: 347 GANIRERPDGLEIDGGD-LHGADLHGVDHRIVMALTLAGIVAGDTRIDTAESVDVSYPG 405

Query: 435 YFDVLSTFVKN 445

+F+ + N

Sbjct: 406 FFEDMRRLGAN 416

>ref|ZP_05271942.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile QCD-66c26]
ref|ZP_05322336.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile CIP 107932]
ref|ZP_05356183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile QCD-76w55]
ref|ZP_05384950.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile QCD-97b34]
ref|ZP_05397282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile QCD-37x79]
ref|YP_003214779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile CD196]
ref|YP_003218223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile R20291]
ref|ZP_07406684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile QCD-32g58]
emb|CBA63357.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile CD196]

emb|CBE04506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
R20291]
Length = 437

Score = 167 bits (423), Expect = 3e-39, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 225/439 (51%), Gaps = 44/439 (10%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+P SKS+++R ++ ++LS G + + N+ S+D+ + A+ +LG +E
Sbjct: 10 KLSGDKVIPPSSKMAHRAVICSSLSNGKSRIISNIDFSDDIATIRAMTSLGAIE----- 64

Query: 74 KRAVVVGCGGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGV 126
K+ ++ G F E E QL LT +G ++ DGV
Sbjct: 65 KKEDILEISGIFSKEGILNRENQL-----NQPKLTIDCNESGSLRFLVPISLAFDGV 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVK-----LSGSISS 180
R IG +G + L + F + + N + + GK+K + G+ISS
Sbjct: 118 KRF----IGRGNLGRPLDTYYEIFDRQNIKYSYKENQLDLIISGKLKPDEFVRVKGNISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+++ LL P D +I I +L S Y+++TL ++ FGV+ ++++ F IKG Q
Sbjct: 174 QFITGLLFILPTLESISKIIITTELESKGYLDLTSTIKDFGVEI-INNNYKEFIKGNQ 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+ ++ VEGD S +++L+ AI G +++ SLQGD + E+L MG ++
Sbjct: 233 TYKA-RDYKVEGDYSQGAFLSADAI-GEDISILDLKEDSLQGDSEVVEILSRMGMEILR 290

Query: 301 TETSVT-VTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ +T L + ++ ++ PD+ L+VVA + G T I + R+K
Sbjct: 291 EGNKIKGITNG-----LNSTLIDASQCPDIIPVLSVVASLSIGRTTIINAGRLRIK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
E +R+ AI EL+KLGA++EE D II KLN + ++ DHR+AM ++A+C +
Sbjct: 342 ECDRLHAINVELSKLGANIEEKEDSLIIEGVSKLNGGVEVWSEKDHRIAMTLAIASCRCD 401

Query: 418 VPVTIRDPGCTRKTFPDYF 436
P+ ++D C K++P +F
Sbjct: 402 KPIILKDFECVSKSYPHFF 420

>ref|YP_659044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloquadratum walsbyi
DSM 16790]
sp|Q18F09.1|AROA_HALWD RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAJ53455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haloquadratum walsbyi
DSM 16790]
Length = 432

Score = 167 bits (423), Expect = 3e-39, Method: Compositional matrix adjust.
Identities = 141/430 (32%), Positives = 207/430 (48%), Gaps = 31/430 (7%)

Query: 22 PGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAAKRAVVVG 80
P SKS ++R +L A + T++D L+ S D + A+ G +VE D+ + G
Sbjct: 17 PPSKSYTHRAILAAGYGDSATIIDPLI-SADTQATMRAIEAFGGTVEHVDE--NHIEITG 73

Query: 81 CGGK--FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G+ P + E N+G R + A A G VL G +R RP G L+
Sbjct: 74 FNGRPRPTPTDIINCE-----NSGTTTRLVAACGALADG--LCVLGTGDESLRSRPHGPLL 125

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
++ L + P+ V GG V + G ISSQY++ALLMA + + ++
Sbjct: 126 EAIETLDGRGESTRRNGQAPLIVGD--AFQGGSVAPGDISSQYITALLMAGAVTVDGID 183

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGDASSA 257
I + +L S PYV++T+ L+ F V E + D F + GGQ Y Y V GD SS
Sbjct: 184 ITLETTELKSAPYVDITVELLSAFDVTVER--TADGFAVPGGQSYTPTDGTYYVPGDFSSI 241

Query: 258 SYFLAGAAITGGTVT--VEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SY LA A+ +EG S QGD E+++ MG +V W + +T P

Sbjct: 242 SYLLAAGAVAATADGAVIIEGA-HPSAQGDSAIVEIIQSMGGQVAWDRNAGELTVPA--- 297

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
L I V++ MPD+ T+A + ADG T I + R KET+R+ A+ TEL +

Sbjct: 298 ---ASLTGITVDVGNMPDLLPTIATLGAIADGDTVINNCEHVRYKETDRVSAMATELGAM 354

Query: 375 GASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKT 432
GASV E D I E L+ T ++ + DHR+ M+ ++AA AE TI D +F

Sbjct: 355 GASVTEKHDQLTIHGGETTSLGTHVEGHGDHRIVMSLAIALAAEGETTISDSSEDVDVSF 414

Query: 433 PDYFDVLSTF 442

P +F+ LS

Sbjct: 415 PSFFESLSAL 424

>ref|YP_001088340.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
630]

sp|Q187E3.1|AROA_CLOD6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

emb|CAJ68705.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
630]

Length = 437

Score = 167 bits (422), Expect = 4e-39, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 224/439 (51%), Gaps = 44/439 (10%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+P SKS+++R ++ ++LS G + + N+ S+D+ + A+ +LG +E

Sbjct: 10 KLSGDVKIPPSKSMRAVICSSLSNGKSRISNIDFSDDIIATIRAMTSLGAIIE----- 64

Query: 74 KRAVVVGCGGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGV 126
K+ ++ G F E E QL LT +G ++ DGV

Sbjct: 65 KKEDILEISGIFSKEGILNRENQL-----NQPKLTIDCNESGSTLRFLVPISLAFDGV 117

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDGP-PVRVNGIGGLPGGKVK-----LSGSISS 180
R IG +G + L + F + + N + + GK+K + G+ISS

Sbjct: 118 KRF----IGRGNLKGKPLDITYEIFDRQNIKYSYKENQLDLIISGKLPDEFKRVKGNISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+++ LL P D +I I +L S Y+++TL ++ FGV+ ++++ F IKG Q

Sbjct: 174 QPITGLLFILPTLESDSKIIITELESKGYLDLTLSTIKDFGVEI-INNNYKEFIKGNQ 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+ ++ VEGD S +++L+ AI G +++ SLQGD + E+L MG ++

Sbjct: 233 TYKA-RDYKVEGDYSQGAFLSADAI-GEDISILDKEDSLQGDSEVVEILSRMGMEILR 290

Query: 301 TETSVT-VTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ +T L ++ ++ PD+ L+VVA + G T I + R+K

Sbjct: 291 EGNKIKGITNG-----LNGLTLDASQCPDIIPVLSVVASLSIGKTTIINAGRLRIK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
E +R+ AI EL+KLGA++EE D II KLN + ++ DHR+AM ++A+C +

Sbjct: 342 ECDRLHAINVELSKLGANIEEKEDSLIIEGVSKLNGGVEVWSHKDHRIAMTLAIASCRCD 401

Query: 418 VPVTIRDPGCTRKTFTPDYF 436

P+ ++D C K++P +F

Sbjct: 402 KPIILKDFECVSKSYPHFF 420

>ref|ZP_05351032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
ATCC 43255]

Length = 437

Score = 167 bits (422), Expect = 4e-39, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 224/439 (51%), Gaps = 44/439 (10%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+P SKS+++R ++ ++LS G + + N+ S+D+ + A+ +LG +E

Sbjct: 10 KLSGDVKIPPSKSMRAVICSSLSNGKSRISNIDFSDDIIATIRAMTSLGAIIE----- 64

Query: 74 KRAVVVGCGGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGV 126
K+ ++ G F E E QL LT +G ++ DGV
Sbjct: 65 KKEDILEISGIFSKEGILNRENQL-----NQPKLTIDCNESGSTLRFLVPISLTFDGV 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVK-----LSGSISS 180
R IG +G + L + F + + N + + GK+K + G+ISS
Sbjct: 118 KRF----IGRGNLGRPLDTYYEIFDRQNIKYSYKENQLDLIISGKLPDEFVRVKNISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+++ LL P D +I I +L S Y+++TL ++ FGV+ ++++ F IKG Q
Sbjct: 174 QFITGLLFILPTLESISKIIITTELESKGYLDLTSTIKDFGVEI-INNNYKEFIIKGNQ 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+ ++ VEGD S +++L+ AI G +++ SLQGD + E+L MG ++
Sbjct: 233 TYKA-RDYKVEGDYSQGA FYLSADAI-GEDISILDLKEDSLQGDSEVVEILSRMGMEILR 290

Query: 301 TETSVT-VTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ +T L ++ ++ PD+ L+VVA + G T I + R+K
Sbjct: 291 EGNKIKGITNG-----LNGTLIDASQCPDIIPVLSVVASLSIGKTTIINAGRLRIK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
E +R+ AI EL+KLGA++EE D II KLN + ++ DHR+AM ++A+C +
Sbjct: 342 ECDRLHAINVELSKLGANIEEKEDSLIEGVSKLNGGVEVWSHKDHRIAMTLAIASCRCD 401

Query: 418 VPVTIRDPGCTRKTFPDYF 436
P+ ++D C K++P +F
Sbjct: 402 KPIILKDFECVSKSYPHFF 420

>ref|ZP_07991977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
variable DSM 44702]
Length = 427

Score = 167 bits (422), Expect = 4e-39, Method: Compositional matrix adjust.
Identities = 142/424 (33%), Positives = 211/424 (49%), Gaps = 24/424 (5%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKS++NR LLL+AL++G + + L S D M ALRT+G +V D
Sbjct: 15 VTATVSVPGSKSITNRALLLSALADGPSEITGALQSRDTQLMADALRTMGTTVVTD--GD 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P + EVQ G AG +R L A A G+ + G + RP+
Sbjct: 73 NITVT-----PGDLHGGEVQ--CGLAGTVLRFLPAVAALADGDVWF--HGDREAQARPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APL 192
G + L+ LGA V P P V G GG+ GG+V + S SSQ++S LL+A A
Sbjct: 123 GTTLESLEALGATVKTSDDPGNPLPFAVTGHGGIRGGEVHIDASASSQFVSGLLLAGARF 182

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G + + D + S P++EMT++++ GV + S++R+ + G ++ VE
Sbjct: 183 DEGVTVVHVGDAVPSQPHIEMTVQMLRAAGTVTD--VSFNRWTVHPGPVRG--RHWAVEP 238

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPP 311
D S+A+ FL+ AA+TGG V V + Q +F VLE MGA V T T +
Sbjct: 239 DLSNATPFLSAAAVTGGEVVRWDPAQTTPGDQFRAVLEDMGATVDLATHTGELIV--- 295

Query: 312 REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R G L I +M+ + ++ T+A + A G + + +A R ET+R+ A+ EL
Sbjct: 296 RGAAGGA-LTGITWMDHDIGELTPTVAALCALAKGRSHLYGIAHLRGHETDRLAALAEAL 354

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 431
T LG V + D +I P L+ TY DHRMA A ++ V + D T KT
Sbjct: 355 TGLGCGVSQTADGLVID-PAPLHGGLWHTYADHRMATAGAILGLVTEGVQVEDITTTTKT 413

Query: 432 FPDY 435
P +
Sbjct: 414 LPGF 417

>ref|ZP_02184530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Carnobacterium sp.
AT7]

gb|EDP68657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Carnobacterium sp.
AT7]
Length = 417

Score = 167 bits (422), Expect = 4e-39, Method: Compositional matrix adjust.
Identities = 118/430 (27%), Positives = 216/430 (50%), Gaps = 35/430 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV +P SKS+++R ++ A+L+ G + + N+ S+D+ + +R+ G + D
Sbjct: 11 LNGTVTVPPSKSMAHRAVICASLAAGRSTIKNIQLSDDILATIEGMRSFGAIFDYDDQTL 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G AKE + +G +R L T G ++ G + +RP+
Sbjct: 71 TIDGIRNG-----TAKESRTINCNESGSTLRFLIPLATLFTGETHFI--GQGHGKRPL 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ A + +++++ G L G ++ G ISSQ+++ +L+ PL
Sbjct: 123 EPYQ---ELFDAQSLHYHQATTENQLSVAGSLTPGIYEMRGDISSQFITGMLLTPLLA 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD ++I L S Y+++TL +++ FG+ E + F IKG Q Y SP++ VEGD
Sbjct: 180 GDSVLQITTHLESKGYIDLTLVLQSGILIEQEEDGQVFRKQQAAY-SPRDYTVEGDY 238

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A+++L+ A+ G + V G + SLQGD +L+ + +E
Sbjct: 239 SQAFAWLSANAL-GNKLLVSGLDSDSLQGDQAIVSILDTLSDGSNDSE----- 285

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ ID ++PD+ +A+VA + G T I ++ R+KE++R+VA + ELT L
Sbjct: 286 -----RVID--GAQVPDIIPVVALVAALSKGKTKIINLERLRIKESDRLVATQKELTAL 337

Query: 375 GASVEEGPDYCIITPEKLN-VTAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTF 432
GA +E D +I +L+ + ++ DHRMAM ++A+ +E P+ I+D C +K++
Sbjct: 338 GAQIEIVEDSLLEIEGVSRLSGGQQVWSHKDHRMAMMLAIASTVSEEPHDKTDCKVKSX 397

Query: 433 PDYFDVLSTF 442
P++++
Sbjct: 398 PNFWETFQQL 407

>ref|ZP_04605604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora sp.
ATCC 39149]
gb|EEP71534.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micromonospora sp.
ATCC 39149]
Length = 433

Score = 167 bits (422), Expect = 4e-39, Method: Compositional matrix adjust.
Identities = 138/429 (32%), Positives = 210/429 (48%), Gaps = 27/429 (6%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 75
T++LPGSKS++ R L+L+AL+ G + + L + D M G LR LG +S+ D R
Sbjct: 25 TLRLPGSKSMTARALVLSALASGPSTLAGPLRARDTELMAGGLRALGAHMSITDD---DR 81

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V P+ + +G AG MR + A G T+ DG P+ R RP+G
Sbjct: 82 WLVR----PHPLAG---PAHVDVGLAGTIRFVPPVAGLAEGRVTF--DGDQPQARTRPLG 132

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LAL 194
L+ L+ LG V+ T P+ V G G + GG+V + S SSQ +S LL+AAP
Sbjct: 133 PLIDALRSLGVRVES-ATGSLPLTVFGTGSVAGGEVVIDASASSQLVSGLLLAAPRFDR 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G V + + S P++ MT++++ G + D + ++ G + +E D
Sbjct: 192 GVVVRHVGPVPSPAPHLRMTVQMLRAAGAAVDDGTP-DVVVVEPGPLTG--RGWEIEPDL 248

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A F A A +TGG VT+ +S Q + +L+ MG +V T +TV G
Sbjct: 249 SGAVPFFAAALVTGGEVTLRSWPRSSAQPVQLRTLQRMGGEVNLTGGLTVRG----- 303

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G H ID +++ + ++ L +A+ AD P+ VA R ET+R+ A+ E L

Sbjct: 304 TGVVH--GIDADLSDVSELTPALTALAMLADSPSRFTGVVAHIRGHETDRIAALAREYLGL 361
Query: 375 GASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTTFPD 434
GA + E D I P L+ A TY DHRMA A ++ A + + D CT KT P+
Sbjct: 362 GADLTESADGLEIR-PRPLHGAFRTYHHRMAHAAAVTGLAVPGIELDDVSCTSKTMPE 420
Query: 435 YFDVLSTFV 443
+ + S V
Sbjct: 421 FPRLWSAMV 429

>ref|ZP_02423949.1| hypothetical protein ALIPUT_00064 [Alistipes putredinis DSM 17216]
gb|EDS04193.1| hypothetical protein ALIPUT_00064 [Alistipes putredinis DSM 17216]
Length = 416

Score = 166 bits (421), Expect = 5e-39, Method: Compositional matrix adjust.
Identities = 126/433 (29%), Positives = 213/433 (49%), Gaps = 27/433 (6%)

Query: 11 PIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G P SKS + R L + L+EGT+ + N+ +D + + LG V
Sbjct: 6 PPGRVRGICIPPCSKSYAQRALAASLLAEGTSRLHNIEFCDDTRSAIRCIEALGARVR-- 63
Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +R + + GG P D +L++G +G++ R T + V +G +
Sbjct: 64 RTGERTLEID-GGLSPAGD-----RLYVQSGSLSTRLFTPIASLCDTPIGVVGEGP--LL 115
Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
R ++ L+ LG V D P+ + G + GG+V++ G +SSQ+++ LL+A
Sbjct: 116 HRSFRTMIRTLRALGVRV--HNRNDHLPLHIQG--PIRGGEVQIEGLVSSQFITGLLLAL 171
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P+A + I + +IS PY+++T+ ERFG++ H D + FY+ GGQ+Y+ P +
Sbjct: 172 PIAEEETTIH-VPHVISTPYIDITIDTAERFGIEILHKD-YKEFYVAGGQRYR-PAEFEI 228
Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
E D S+A++ L A+ G VT+ S Q D L GA V ++TV
Sbjct: 229 ESDWSAAAFLLVAGAV-AGEVTIRNLSVLSRQADTAVMTALVRAGASVIDEGDTITVAHR 287
Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
P L+A + + P + LA +A A+G + I+ + KE R +IR E
Sbjct: 288 P-----LQAFSFDATQCPGLFPALAAALASAEGTSVIKGTSLRLENKEGNRAESIREE 339
Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTR 429
KLG V+ + + ++ + ++DDHR+AM+ ++AA A+ PV I +P C
Sbjct: 340 YAKLGIEVDLDEEDTMKIRGGIRGGHVHSHDDHRIAMSLAVAALNADTPVVIENPACVA 399
Query: 430 KTFPDYFDVLSTF 442
K+FPD+F+ L +
Sbjct: 400 KSFPDFFERLESL 412

>ref|YP_886256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
smegmatis str. MC2 155]
gb|ABK72540.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
smegmatis str. MC2 155]
Length = 443

Score = 166 bits (421), Expect = 5e-39, Method: Compositional matrix adjust.
Identities = 139/426 (32%), Positives = 217/426 (50%), Gaps = 27/426 (6%)

Query: 15 ISGTVKLPKSKSLNRIILLAL--SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ TV +PGSKSL+NR L+LAAL S+GT+ + L S D M+ A+RTLG++V+ A
Sbjct: 22 VDATVTVPGSKSLTNRALILAAALATSQGTSTISGALRSRDTLMEIAIRTLGVTVDISAA 81
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G P DA + L AG +R + AA ++ DG + R R
Sbjct: 82 DPTELTV-HGSIEPATDATVDCGL----AGTVLRFVPP--VAALSRSSVTFDGDEQARSR 134
Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-AP 191
PI L+ GL++LG +D D P V G G + GG V++ S SSQ++S LL++ A
Sbjct: 135 PIAPLLDGLRRLGVRLDG----DGLPFTVRGTGTVSGGTVEIDASGSSQFVSGLLLSGAG 190

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G + + S P+V MT+ ++ GV+ + S + +R+ + G N +E
Sbjct: 191 FENGLTIVHTGVSVPSPAPHVAMTVAMLRDAGVEVDDSSVA-NRWQVNPGPVAARSWN--IE 247

Query: 252 GDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S+++ FLA A +TGGTV + G T S+Q E+L +G V + + VTG
Sbjct: 248 PDLSNSTPFLAAALVTGGTVRIAGWPVTSIQPADTILELLATVGGSVREADGHLEVTGA- 306

Query: 312 REPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA-DGPTA-IRDVASWRVKETERMVAIRT 369
+ +++ + ++A T+A +A A +G T+ +R +A R ET+R+ A+ T
Sbjct: 307 -----HEYGGFEADLHDVGELAPTVAALAAALAKEGSTSQLRGIAHLRGHETDRLAALT 360

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E+ LG E D +IT L+ +Y DHRMA A ++ V + + T
Sbjct: 361 EINGLGGDCRETDDGLLIT-ARPLHGGTWSYADHRMATAGAIVGLRVPGVVVENIETTA 419

Query: 430 KTFPDY 435
KT PD+
Sbjct: 420 KTLPDF 425

>ref|ZP_03782667.1| hypothetical protein RUMHYD_02118 [Blautia hydrogenotrophica DSM 10507]
gb|EEG48998.1| hypothetical protein RUMHYD_02118 [Blautia hydrogenotrophica DSM 10507]
Length = 426

Score = 166 bits (421), Expect = 5e-39, Method: Compositional matrix adjust.
Identities = 136/425 (32%), Positives = 214/425 (50%), Gaps = 24/425 (5%)

Query: 15 ISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V+ SKS+++R + AAL+E + V SED+ + L +G+ K+
Sbjct: 10 LGGSVRAIPSKSMAHRHFIAAALAEAPSRVVCPSGMSSEDIKATMDCLEAMGVMFNRKKSEY 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ K+ A E ++L +G +R L V A G + +G R+ +RP+
Sbjct: 70 E--VMSETKKWSA-GADEALKLPCKESGSTLRFLLPVVAALGIKVEFHEEG--RLPQRPL 124

Query: 135 GDLVVGKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
L L++ G C L P+R G L G ++ G+ISSQ+++ LL A PL
Sbjct: 125 SPLYEELQKHG---CRLSPQGVTPRLCQG--KLEAGIYEIPGNISSQFITGLLFALPLL 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD EI + L S YV+MTL+++++GV ++ + F I GGQ Y + ++ +EGD
Sbjct: 179 KGDSEIRLTSALASARYVDMTLQVLKQYGVVVSCTE--EGFQIPGGQSYLAQQSVQIEGD 236

Query: 254 ASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+++L AA+ G +TV S QGD K ++L+ MGAKV + TVT P R
Sbjct: 237 WSNAAFWLTAAM-GKKITVTCLDENSTQGDKKILDILKRMGAKVEQRDWEATVT-PER- 293

Query: 314 PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L D++ +PD+ LA A + G T I + R+KE++R+ ++ L
Sbjct: 294 -----LDGTDIDAGDIPDLVPILAAAAVSRGKTRIYNAGRLRLKESDRLSVSQVLNG 347

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRM-AMAFSLAACAEVPTIRDPGCTRKTF 432
LG V E D IT E+L +D DHR+ MA A E PV I K++
Sbjct: 348 LGGQVRELEDGLEITGRERLAGGRVDAAGDHRIAMMAVAAMVCENPVEICGAQAVNKS 407

Query: 433 PDYFD 437
P +F+
Sbjct: 408 PGFFE 412

>ref|ZP_07908824.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii ATCC 51333]
gb|EFU79617.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii ATCC 51333]
Length = 463

Score = 166 bits (421), Expect = 6e-39, Method: Compositional matrix adjust.

Identities = 140/454 (30%), Positives = 216/454 (47%), Gaps = 50/454 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-----A 69
+ G V+LPGSKSL R LLL+A+ + + +L + D M+ ALR+LG +
Sbjct: 15 VFGAVRLPGSKSLSALELLLSAIGDAEANLTGVLFAFRTDLMVQALRSLGAVIAPWPPVV 74

Query: 70 DKAARKRAVVVGCGKFPVEDAKE-----EVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
D+ + + P +DA V + G AG MR + A A G +V
Sbjct: 75 DQPVQIKPLSQLWTGAPAQDASGGPSGGVPVTVDCGLAGTVMRFIPALAVAGRAVRFVA 134

Query: 124 DGVPRMRERPIGDLVVLKQLGADVD-----CFLGTDCPPVRVNGIGGLPGGKVKLSG 176
D + RP+ L+ L QLGA ++ F T PP PG +V +
Sbjct: 135 DS--QANARPMRPLLDALVQLGARIEYESPDGGVFPYTIYPPE-----RPGAETVDA 186

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHE--SDSWDR 233
+ SSQ++S+LL+AAPL I L S+P++EMT++ + + G+ E SD
Sbjct: 187 TASSQFISLLLAAPLFPDGTIRSKTVALPSLPHIEMTMQCLSQHGITVEQGIGSDDGKP 246

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
F+ + ++ ++E D S+A FLA I GG ++V ++Q + ++L +
Sbjct: 247 FWNVVSEPVFG-QDVFIEPDLSNAGPFLALVGIAGGRISVPAWPARTMQAGAAWLQILPL 305

Query: 294 MGAKVTWTETSTVTVTGPFPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
MG V W +TV+ P L+ +D + + + ++ T+A +A FA+G + IR +
Sbjct: 306 MGLHVEWNCGLTVSRP-----GPLQLDADFSVAGELVPTVAALAAFAEGTSHIRGL 358

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGP-DYCIIT----PPEKLNVTDAID-----TY 401
R ET+R+ A+R ELT +G S E P D +IT P + ID +Y
Sbjct: 359 QHLRGHETDRLEALRAELTAIGISCEITPEDDLVITGKPVTPSWRDTPTIDAKPLLLHSY 418

Query: 402 DDHRMAMAFSLAACAEPVPTIRDPGCTRKTFPDY 435
DHR+A F PV I D G T KT PD+
Sbjct: 419 QDHRLA-TFGALLGLYPVQIDDIGATTKTLPDF 451

>ref|YP_001222059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clavibacter
michiganensis subsp. michiganensis NCPPB 382]
emb|CAN01363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clavibacter
michiganensis subsp. michiganensis NCPPB 382]
Length = 487

Score = 166 bits (420), Expect = 6e-39, Method: Compositional matrix adjust.
Identities = 142/429 (33%), Positives = 209/429 (48%), Gaps = 26/429 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV LPGSKSL+NR L+L+AL++ + + L S D M+ ALR+LG +E
Sbjct: 39 LDATVPLPGSKSLTNRELVLALADSPSTLRAPLRSRDLRLMIEALRSLGTVIEE----- 93

Query: 75 RAVVVGCGGKF-----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
V GG F P E A V + G AG MR L A G ++ DG P
Sbjct: 94 ----VDGGGAFGPDLRITPAELAG-GVTIECGLAGTVMRFLPPVAALALGPVSF--DGDP 146

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
R RP+ + L+ LG DV+ G P + G G +PGG++ + S SSQ++S LL
Sbjct: 147 SARRRPMSTIEALRALGVVDNDD-GRRALPFSLYGTGEVPGGEIAIDASASSQFVSGLL 205

Query: 188 MAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+AAP A G L S+P++EMT+R + GV + + ++ +
Sbjct: 206 LAAPRFAQGLRLRHTGATLPSMPHIEMTIRTLAERGVVVSPEPG--LWVVPSSPIAG-R 262

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+E D S+A+ F A A + GG V + G + Q A +L GA VT ++
Sbjct: 263 EVRIEPDLSNAPFFFAALVAGGRVAIPGWPEETTQVGADLAHLPRFGATVTREGDALV 322

Query: 307 VTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V G P G + + +D++++ ++A L +A ADGP+ I + R ET+R+ A
Sbjct: 323 VDGGPGLAAGGR-IPGVLDLSTGGELAPALVALAALADGPSRITGIGHLRGHETDRLAA 381

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEPVPTIRDPG 426
+ E+T LG SV E D I P L+ Y+DHRMA A ++ A V I D
Sbjct: 382 LAAEITGLGGSVTELDGLAIE-PAPLHGGPWRAYEDHRMATAGAIVGLAVPGVEIDDIC 440

Query: 427 CTRKTFPDY 435
T KT P++
Sbjct: 441 TTAKTLPEF 449

>ref|YP_002785524.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus deserti
VCD115]
gb|ACO45770.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
deserti VCD115]
Length = 446

Score = 166 bits (420), Expect = 6e-39, Method: Compositional matrix adjust.
Identities = 146/440 (33%), Positives = 215/440 (48%), Gaps = 24/440 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++V+ P++E+ G V+ SK+ + R LL AAL+EG T V + SED H ML L G
Sbjct: 17 DVVVHPVRELRGDVRAGPSKNYTTRYLLAALAEGETRVVG VATSEDAHMLRCLTDWGA 76

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E V+ G G + V L GNAG R L V A + T V D
Sbjct: 77 GIE--HIGDDVVIRGFCAA-----PRAGVTNLPGNAGAVARFLMG-VAALTRDITLVTDH 128

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP GDL+ L++LGA V G PV ++G + GG V++S SSQY SA
Sbjct: 129 PDSLGRRPQGDLLAALERLGARVSSNEGR--LPVTISGP--VRGGVVEVSAERSSQYASA 184

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP 245
L+ APL G +++ + ++ S + TL + FG++A SD R I GGQ+Y+ P
Sbjct: 185 LMFLAPLLPGGLDLRLTGQIKSHAPLRQTLDTLAAFGIRASASDDLRSRVQIPGGQRYQ-P 243

Query: 246 KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V GD ++ LA AA+ G V + LQG+ + +VL MGA + ++
Sbjct: 244 GRVLVPGDYPGSAALLAAAALLPGEVRLSNLRENDLQGEREAVDVLREMGADIHREGDTL 303

Query: 306 TVTGPPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
V G + L+A++ + + D L A A+G T +V + R+KE +R+
Sbjct: 304 IVRGG-----QTLRAVNRDGDGFTDAVQALTAALAAGTTTWHNVYTLRLKECDRIS 356

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
R EL +LG E D +T ++ VTA D + DHRM M +L AE PV I
Sbjct: 357 DTRRELERLGLQARETEDSLSVTGAAQIAGGVTA-DGHGDHRMIMLLTLLGLRAEAPVRI 415

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
RK++P +F L +
Sbjct: 416 TGAHHRKSYPQFFAHLHSL 435

>ref|ZP_05329984.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium difficile
QCD-63q42]
Length = 437

Score = 166 bits (420), Expect = 7e-39, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 223/439 (50%), Gaps = 44/439 (10%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+P SKS+++R ++ ++LS G + + N+ S+D+ + A+ +LG +E
Sbjct: 10 KLSGDVKIPPSKSMRAVICSSLSNGKSRISNIDFSDDIATIRAMTSLGAIIE----- 64

Query: 74 KRAVVVGCGGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV-----LDGV 126
K+ ++ G F E E QL LT +G ++ DGV
Sbjct: 65 KKEDILEISGIFSKEGILNRENQL-----NQPKLTIDCNESGSTLRFLVPISLAFDGV 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVK-----LSGSISS 180
R IG +G + L + F + + N + + GK+K + G+ISS
Sbjct: 118 KRF----IGRNLGKRPLDYYEIFDRQNIKYSYKENQLDLIISGKLKPDEFVRVKNISS 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+++ LL P D +I I +L S Y+++TL ++ FGV+ ++++ F IKG Q
Sbjct: 174 QFITGLLFILPTLESDSKIIITTELESKGYLDLTLSTIKDFGVEI-INNNYKEFIKGNQ 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK+ ++ VEGD S +++L+ AI G +++ SLQGD + E+L MG ++
Sbjct: 233 TYKA-RDYKVEGDYSQGA FYLSADAI-GEDISILDLKEDSLQGDSEVVEILSRMGMEILR 290

Query: 301 TETSVT-VTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ +T L ++ ++ PD+ L+VVA + G T I + R+K
Sbjct: 291 EGNKIKGITNG-----LNGTLIDASQCPDIIPVLSVVASLSIGRTTIINAGRLRIK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
E +R+ AI EL KLGA++EE D II KLN + ++ DHR+AM ++A+C +
Sbjct: 342 ECDRLHAINVELNKLGANIEEKEDSLIIEGVSKLNGGVEVWSHKDHRIAMTLAIAASCRCD 401

Query: 418 VPVTIRDPGCTRKTFPDYF 436
P+ ++D C K++P +F
Sbjct: 402 KPIILKDFECVSKSYPHFF 420

>ref|ZP_02028886.1| hypothetical protein BIFADO_01332 [Bifidobacterium adolescentis
L2-32]
gb|EDN83042.1| hypothetical protein BIFADO_01332 [Bifidobacterium adolescentis
L2-32]
Length = 449

Score = 166 bits (420), Expect = 7e-39, Method: Compositional matrix adjust.
Identities = 139/443 (31%), Positives = 214/443 (48%), Gaps = 31/443 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ TV +PGSKSLSNR L+LAAL + LL S D M+ ALR LG+ E D+
Sbjct: 19 KPLNATVVVPGSKSLSNRYLILAAALGHRPVRVLVGLLRSDTELMMDALRALGVRCEIDEQ 78

Query: 73 AKRAVVVCGCGKFPVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V P D + ++F G AG MR + A G + DG +
Sbjct: 79 VDTTVTV-----VPPSDGRFHGGTKVFCGLAGTVMRFVPLAMFADGPVAF--DGDEQAY 131

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
RP+ ++ GL+QLGA ++ + G T PP V+ V + S SSQ++
Sbjct: 132 ARPMKPVLDGLEQLGACIE-YHGEEGRLPFTITPPQTVSQCA--EPSMVSIDSSGSSQFI 188

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+ G +E+ +K S+P++ MT+ + GV+ ++D R +
Sbjct: 189 SGLLLIGSRVPGGLELHHTGEKTPSLPHIRMTVADLHGSGVRV-NADEHARVWTVQPGAV 247

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P+ VE D S+A+ FL A I GGTV V ++ Q LE MGA E
Sbjct: 248 QLPETVTVEPDLSNAAPFLGAALIAGGTVRVPHWPESTTQPGMPLPGYLERMGA-----E 302

Query: 303 TSVTVTGPPR--EPFGRKHLKAI-DVMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
S V R E G H+ + D ++ ++A +LA + +FAD PT + + R
Sbjct: 303 ISFPVIDDVRYCEVTGNHVSGLGDFDLTAAGEIAPSLAAILVFADKPTRMIGIGHLRGH 362

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAE 417
ET R+ A+ E+T++G + E PD ITP +L + ++TY DHRMA ++
Sbjct: 363 ETNRLEALANEITRVGGAAHELPGLEITPVSANRLRPSVMETYADHRMATFAAMLGLRI 422

Query: 418 VPVTIRDPGCTRKTFPDYFDVLS 440
+ +++ T KT P++ D+ +
Sbjct: 423 KGIQVKNVATTAKTLPNFVDLWN 445

>ref|YP_003726593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanohalobium
evestigatum Z-7303]
gb|ADI73797.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methanohalobium
evestigatum Z-7303]
Length = 427

Score = 166 bits (419), Expect = 8e-39, Method: Compositional matrix adjust.
Identities = 148/432 (34%), Positives = 216/432 (50%), Gaps = 35/432 (8%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G + P SKS ++R + + +LS +T+ LL S D + A G ++E K
Sbjct: 9 KLHGELYAPPSKSYTHRAITIGSLSHQSTIHRPLL-SADTEATIRACEMFGANIE--KKN 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ + G G V + +V+ N+G +R +TA T G VL G +R RP
Sbjct: 66 NKLEINGIDGAPHVPEDVIDVE----NSGTTLRFM TALATLTDG--VTVLTGDRSVRTRP 119

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
G L+ L+ LG DV P+ V G GL G K+ GSISSQ++SALL+A PL
Sbjct: 120 NGPLLEVLQNLGVDVDFSTRNNGRAPLVVKG--GLKGAITKIDGSISSQFVSALLIACPLT 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG----VKAHSDSWDRFYIKGGQKYKSPKNAY 249
+ I +L S PYV++T ++E+ G V H+ +F I QKY K
Sbjct: 178 NNSTTLSEIKGELKSKPYVDITTEIIEKAGCEIFVDKNHN---TKFIIPAKQKY-DLKEYT 233

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS--VTV 307
V GD SSASY LA AA+TG VTV+ S QGDVK ++LE MGA + W + V+V
Sbjct: 234 VPGDFSSASYLLAAAAMTGSKVTVKNL-FPSKQGDVKIIDILEQMGANIHWDKDKGDVSV 292

Query: 308 TGPPREPFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G L I V++ PD+ T+AV+ A G T IR+ R KET+R+ A+
Sbjct: 293 NNGD-----LNGITVDLGASPDLPFTIAVLGTVAKGTTVIRNAEHVRYKETDRIHAM 344

Query: 368 RTETLTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
EL K+G V+E D + +K NV + DHR+ MA ++A T+
Sbjct: 345 ANELQKMGIKVKEEKDRLTVNNGNLKANVYG---WHDHRIVMALTIAGLIAGDTTVDTA 401

Query: 426 GCTRKTFPDYFD 437
++P++F+
Sbjct: 402 ESVFISYPNFFE 413

>ref|YP_003982923.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia dentocariosa
ATCC 17931]
gb|ADP39489.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia dentocariosa
ATCC 17931]
Length = 507

Score = 166 bits (419), Expect = 9e-39, Method: Compositional matrix adjust.
Identities = 141/442 (31%), Positives = 219/442 (49%), Gaps = 32/442 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S +++PGSKSL+NR LLLAAL++ + + L+S D M+ AL LG E +
Sbjct: 61 MSARMRIPGSKSLTNRYLLAALADSPSRLRAPLHSRDSALMISALEALGAQFERIETGS 120

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ A V++ G AG MR + A G+ Y DG P+ R+RP+
Sbjct: 121 EFGPDLLITPLNLASAPPMVKIDCGLAGTVMRFVPALAAALLPGD--YNFDGDPQARKRPM 178

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIG-----GLPGGKVKLSGSISSQYLSALL 187
L GL+QLGA ++ D P ++ G G P ++ + S SSQ++SALL
Sbjct: 179 AALCDGLRQLGARIERSGNDSDVDTLPFTLHSPGLAAASGTP-AEIFIDASASSQFVSALL 237

Query: 188 MAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AP L G + + SIP++EMTL+ + GV+AE D + + S
Sbjct: 238 LIAPRLPQGLTIHHRGNAVPSIPHIEMTLQTLRDLGVRAEAVA--DEYAWRIFPGTISGF 295

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGC-----GTTSLQGDVKFAEVLEMMGAK 297
+ VE D S+A FLA A +TG +VT+ G GTT QG ++ +L +G
Sbjct: 296 DITVEPDLSNAGPFLAAAMVTGNSVTIPGWPAPTADGSPGTT--QGGDEWRTILPRLGGA 353

Query: 298 VTTWTETSVTVTGPPREPFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWR 357
V ++ S+TVTGP E R L ++ N+ ++A T+A + D P+ + + R
Sbjct: 354 VEFSSNGSLTVTGP--EDITR--LSGVFENLQTAGELAPTVAALVALLDSPSTLTGIGHLR 409

Query: 358 VKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKL--NVTADITYDDHRMAMAFSLA 413
ET+R+ A+ TE+ +LG EE D ++ P +L + + TY+DHR+A ++
Sbjct: 410 GHETDRLAALVTEINRLGGLAEETADGIHVLPRVRLPQDSPVTVQTYEDHRVATFAAVI 469

Query: 414 ACAEVPVTIRDPGCTRKTFPDY 435
E V I + T KT P +
Sbjct: 470 GLHEPGVRIENVQTTAKTLPQF 491

>ref|YP_003284025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blattabacterium sp.
(Blattella germanica) str. Bge]
gb|ACY40415.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blattabacterium sp.
(Blattella germanica) str. Bge]
Length = 385

Score = 166 bits (419), Expect = 9e-39, Method: Compositional matrix adjust.
Identities = 115/351 (32%), Positives = 194/351 (55%), Gaps = 18/351 (5%)

Query: 98 LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP 157
+ +AG AMR LT+ G VL G RM+ERPI LV L++LG+++ P
Sbjct: 36 IHHAGTAMRFLTSYFAIQEGKEI-VLTGSERMKERPISVLVEALRELGEISYLEKRGYP 94

Query: 158 PVRVNGIGGLPGGKVKLSGSISSQYLSAL-LMAAPLALGDVEIEIIDKLISIPYVEMTLR 216
P+++ G + GKG+ + ISSQY+S+L L+A+ +G ++I + + SIPY++MT
Sbjct: 95 PIKILG-KKILGGKIDIDAKISSQYISSLMLIASQFKIG-LKIHKLGNITSIPYIKMTFD 152

Query: 217 LMERFGVKAHSDSWDRFYIK-GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVE 274
L+ G+K SW+ I ++ K K ++E D SSASY+ + AAI+ + +T+
Sbjct: 153 LLTLAGIKT---SWEEIIHHPKRNKGKVFHIESDWSSASYYYMAAISQSHITLS 208

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVA 334
SLQGD + A + + T+ + +V +T + F K K I++N+NK PD+A
Sbjct: 209 SYNNESSLQGDREVASIYDKNFGITTFDKNV-MTLKKLNFCEK--KFIELNLNKTDPDIA 265

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI-ITPPEKL 393
T+ V +++ + + ++KET+R++A++ EL K G + D C+ IT +
Sbjct: 266 QTIVVTCAALGIKCSLKGLETLKIKETDRLLALKEELLKFGV-ITNITDSCLEITDFSRK 324

Query: 394 NVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLST 441
+ + I TY DHRMAM+FS + I DP +K++P++++ L +
Sbjct: 325 KINSFIKIKTYQDHRMAMSFSTFGLCSSFLQIEDPNVVKSYPNFWDNLR 375

>ref|ZP_03567874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium rimae ATCC
49626]
gb|EEE18111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium rimae ATCC
49626]
Length = 438

Score = 166 bits (419), Expect = 9e-39, Method: Compositional matrix adjust.
Identities = 127/439 (28%), Positives = 209/439 (47%), Gaps = 38/439 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
E+SG+++ SKS ++R + AA ++G T + S+D+ + L TLG
Sbjct: 8 HELSGSIRSVAKSEAHRSFICAAFADGITDITCHTASKDIDATIACLETLAGHFAKTSK 67

Query: 73 AKRAVVVGCGGKFPVEDAKE-----EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
R P++ K L G + +R L V A G ++G
Sbjct: 68 GYRVS-----PIKQPKRVLFNLRFDLNCGESASTLRFLLPLVCALGRKVELHVEGT 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ L GA + D P+ V+G + GG L G+ISSQ++S L
Sbjct: 120 --LAHRPLTPFYEELVSHGARLS---PEDSYPLSVSG--QIKGGYFVLPGNISSQFVSG 172

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIKGGQ 240
LMAAPL D+E+ + + + S PY+++T ++ +FGV E + + RFY+
Sbjct: 173 LMAAPLMEQDLEVLVTEPVESAPYIDLTCVLAKFGVGVEKTHVTENDTEYLRFYVSDNV 232

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+Y++P VEGD S+A+++L A+ G V V S QGD L ++GA+V+
Sbjct: 233 RYQTPGLLEVEGDWSNAAFWLTAGAL-GSGVEVTDLNMQSKQGDRTILAALSLVGARVSR 291

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
++ HL+AI +N+ PD+ LA+VA FA+G + V R+KE
Sbjct: 292 HGSTAAAM-----YDHLRAIQLNVADTDLVPPLAIVAAFAEGTSKFSQVQRLRLKE 343

Query: 361 TERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
++R+ +I ++ LG EG D +I L+ ++D DHR+ M ++AA A
Sbjct: 344 SDRLQSTIAAISALGGRAYIEGDDTLVIEGHGSLDGGSDVGDSDHRIVMMAVAASFANN 403

Query: 419 PVTIRDPGCTRKTFPDYFD 437
P T+ K++P +F+
Sbjct: 404 PTTVTTHAEAIKSYPAFFE 422

>ref|YP_001360961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kineococcus radiotolerans SRS30216]
gb|ABS02697.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kineococcus radiotolerans SRS30216]
Length = 449

Score = 166 bits (419), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 148/436 (33%), Positives = 217/436 (49%), Gaps = 43/436 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV----- 67
+ V +PGSKSL+NR L++AAL+E +++ L S D M+ ALR LG V
Sbjct: 29 LDAVVAVPGSKSLTNRYLVVAALAERPSSLRGLASRDITLLMVDALRLLGADVAEGGRDA 88

Query: 68 ----EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
AD + V G ++ G AG MR L AA
Sbjct: 89 PGVDPADWVVRPGPVTGG-----ARIDCGLAGTVMRFLPP--VAALAEPEPVHF 134

Query: 124 DGVRPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG-IGGLPGGKVKLSGSISSQY 182
DG R RERP+G ++ GL+QLGA VD G P V G GGL GG V++ S SSQ+
Sbjct: 135 DGDDRARERPMGAVLDGLRQLGALVDDG-GRGLLPFSVQGPAGGLRGGPVRIDASASSQF 193

Query: 183 LSALLMAAPLALGDVEIEIIDK---LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+SALL+ A +E++ + + S P+V MT+ ++ GV + S + R++++ G
Sbjct: 194 VSALLLVG--ARTREGLELVHEGPPVPSEPHVRMTVEVLRDVGVVVDDS-TPGRWFVEAG 250

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ +P + VE D S+A FLA AA+ GG V V G ++ Q +VL+ MGA+V
Sbjct: 251 EI--NPLDVQVEPDLNAGPFLAAAAGGRVVRVPGWPQSTTQAGDLLRDVLDQMGAEVN 308

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ V G L ID++++ ++A + +A A PT +R +A R
Sbjct: 309 LDREGLVVEG-----TGELYGIDLDLHEAGELAPVITALAALASSPTRLRGIAHLRGH 361

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
ET+R+ A+ TE+ LG EE D ++ P L+ TY DHRMA A +L
Sbjct: 362 ETDRLKALVTEVNALGGQAEETIDGLLVPRPLHGGVFRTYADHRMATAGALLGLTVPG 420

Query: 420 VTIRDPGCTRKTFPDY 435
V + D TRKT PD+
Sbjct: 421 VLVEDVATTRKTLPDF 436

>ref|YP_952599.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium vanbaalenii PYR-1]
sp|A1T5Z3.1|AROAMYCVP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM12593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium vanbaalenii PYR-1]
Length = 446

Score = 166 bits (419), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 138/429 (32%), Positives = 214/429 (49%), Gaps = 30/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALS--EGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
+ TV +PGSKS +NR L+LAAL+ +G++ + L S D M+ AL+ LG+ VEA D
Sbjct: 13 VHATVTVPGSKQTNRALVLAALAVPQGSSTISGALRSRDTLMSALQGLGVVVEAPDT 72

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSL--TAAVTAAGGNATYVLDGVPRM 129
+ G K ++ G AG +R + AA+T T DG +
Sbjct: 73 DGSDGTELTVSGALA---PKAGARIDCGLAGTVLRFVPPVAALT----TETVTFDGDEQA 125

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RPI L+ GL+ LG +D D P V G G + GG V++ S SSQ++S LL++
Sbjct: 126 RARPIAPLLDGLRALGVAIDG---DGLPFSVRGQGSVRGGTVEIDASGSSQFVSGLLLS 181

Query: 190 -APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G + + S P++ MT+ ++ GV+ + S + DR+ + G + ++
Sbjct: 182 GAAFTGELTVVHTGGAVPSAPHIAMTVSMLRDAGVEVDDSA--DRWRVAPGPI--AARHW 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VE D S+A FLA A I+GGTV V G T S Q +L +G++V + + V
Sbjct: 239 AVEPDLSNAVPFLAAAVISGGTVRVGTWPTVSTQPAATILSLLTSLGSEVRQGNHLEVQ 298

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMVA 366
G IDV++ + ++A ++A +A A + +R +A R ET+R+ A
Sbjct: 299 -----GATSYDGDIDVLDRLDVGELAPSVAAAMAALASPGSVSRLRGIAHLRGHETDRLAA 351

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
+ EL +LG EE D +IT +++ +Y DHRMA A ++ V + D G
Sbjct: 352 LSAELNRLGGQCEETDDGLVIT-ARQMHGGVWRSYADHRMATAGAIVGLRVPGVEVEDIG 410

Query: 427 CTRKTFPDY 435
T KT PD+
Sbjct: 411 TTAKTLPDF 419

>gb|ADX73645.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter
phenanthrenivorans Sphe3]
Length = 462

Score = 166 bits (419), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 138/431 (32%), Positives = 214/431 (49%), Gaps = 28/431 (6%)

Query: 13 KEISGTVKLPKSKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLS---VEA 69
+ ++ TV +PGSKSL+NR L+LAAL++G + + L+S D M+ ALR LG + V
Sbjct: 25 RPNATVTVPGSKSLTNRYLVLAALADGPSRLRAPLHSRDSALMVQALRQLGATITEVPG 84

Query: 70 DKAACKRAVVVGCGKFPVED--AKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D A + V P++ A ++ G AG MR + AA N V DG P
Sbjct: 85 DGAFGPDLEV-----VPLDPGAASSVTRIDCGLAGTVMRFVPP--LAALRNGASVFDGDP 137

Query: 128 RMRERPIGDLVVLKQLGADVDCFLG--TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
R+RP+G ++ LK LG V G P V G G + GG + + S SSQ++SA
Sbjct: 138 HARKRPMGTIIEALKALGVAVTSEEGTTPSSLPFLVEGTGEVRGGHLVVDASASSQFVSA 197

Query: 186 LLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LL+ + +E + K + S+ ++ MT+ ++ GV + DS ++ ++
Sbjct: 198 LLLVGARFTEGLHLEHVGPVPSLDHINMTVSVLRGAGVAVD--DSVPHWVVSPPGPIRA 255

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ +E D S+A FLA A + GTV + G + Q + +L MGA V+ +
Sbjct: 256 -FDQRIEQDLSNAGPFLAAALASHGTVRIPGWPEETQQVGDWLRSILTRMGADVSLRDGV 314

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+TVTG P +K D ++A T+A + AD P+ + +A R ET+R+
Sbjct: 315 LTVTGGPT-----IKGAD--FADTSELAPTVAALCALADAPSRLSGIAHLRGHETDRL 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
A+ E+ +LG EE D +I P KL+ + +Y DHRMA A ++ A V + D
Sbjct: 366 AALVAEINRLGGDAEETSDGLVIR-PAKLHAGVVHSYADHRMATAGAILGLAVEGVQVED 424

Query: 425 PGCTRKTFPDY 435
T KT PD+
Sbjct: 425 IATTAKTMPDF 435

>gb|AAD51957.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
gb|AAD51958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
gb|AAD51959.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
gb|AAD51962.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
gb|AAD51965.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella

pneumoniae]
gb|AAD51966.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAD51967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47853.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47855.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
Length = 153

Score = 165 bits (418), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 85/162 (52%), Positives = 113/162 (69%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+SSQ+L+ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +
Sbjct: 1 SVSSQFLTALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ-SYQRFVV 59
Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA
Sbjct: 60 RGKQQYQSPGDYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIFADVLEKMG 119
Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLA 338
VTW + + T LKA+D++MN +PD AMT+A
Sbjct: 120 TVTWGDDFIAC-----HGELKAVDMDNMNHPDAAMTIA 153

>gb|AAD51960.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
gb|AAG47850.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
Length = 153

Score = 165 bits (418), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 85/162 (52%), Positives = 113/162 (69%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+SSQ+L+ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +
Sbjct: 1 SVSSQFLTALLMTAPLAPQDTVIIKGDVSKPYIDITLHLMKTFGVEVDNQ-SYQRFVV 59
Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA
Sbjct: 60 RGKQQYQSPGDYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIFADVLEKMG 119
Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLA 338
VTW + + T LKA+D++MN +PD AMT+A
Sbjct: 120 TVTWGDDFIAC-----HGELKAVDMDNMNHPDAAMTIA 153

>ref|YP_002834221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium aurimucosum ATCC 700975]
ref|ZP_06043040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium aurimucosum ATCC 700975]
gb|ACP32283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium aurimucosum ATCC 700975]
Length = 434

Score = 165 bits (417), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 132/442 (29%), Positives = 215/442 (48%), Gaps = 31/442 (7%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69

Q +S T ++PGSKS++NR L+LAAL++ +++ N L S D M AL+ +G+ +
Sbjct: 16 QSTGPLSWTQEVPGSKSMTNRALILAAALADSPSIIYNPLVSRDITLMKEALKAMGVGISE 75

Query: 70 DKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
R P E V G AG MR L A G V+DG P
Sbjct: 76 WGPLRLVT-----PGLHGATVD--CGLAGTIMRFLPPVAALADG--PVVIDGDPYA 123

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R+RP+ + L++LG D++ D P+ + G G +V + S SSQ++S LL+A
Sbjct: 124 RKRPMSTMTTALRELGV DIEG---DNLPLSITPHGIPEGA EVTIDASASSQFVSGLLLA 179

Query: 190 APLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ + + S P++ MT+ ++ GV S+ D + ++ G+ +
Sbjct: 180 GARYRNGISVRHEGGTVPSQPHILMTICMLREAGVHVLASE--DNWVVRPGKIEG--REW 235

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS---- 304
Y+E D S+A+ FLA AA++GG+V++ + Q F +LE MGA+V + +
Sbjct: 236 YIEPDLSNATPFLAAAASVSGSVSILNWPEETTQPGDSFRGILEQMGAQVEYVPQAPCQD 295

Query: 305 --VTVTGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ VTGP G L+ +D++M + ++ T+A + A P+ + +A R ET+
Sbjct: 296 PYLQVTGPTEE---GLAGLRGVLDMDIGELTPTVAALCALASTPSTLTGIAHLRGHETD 352

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
R+ A+ TE+ LG +V E D IT P L+ +Y DHRMA A ++ A V +
Sbjct: 353 RLAALATEINALGGNVTELDGLRIT-PAPLHGGQWHSYADHRMATAGAIIGLAVDGEV 411

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
D T KT P + + +
Sbjct: 412 EDIDTTSKTLPGFAKMWEAMIH 433

>ref|YP_003343719.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptosporangium
roseum DSM 43021]
gb|ACZ90976.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptosporangium
roseum DSM 43021]
Length = 425

Score = 165 bits (417), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 144/430 (33%), Positives = 214/430 (49%), Gaps = 36/430 (8%)

Query: 13 KEISGTVKLPKSKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV----E 68
+ + +V LPSKSKS++NR LLLAAL++G V L S D M ALR LG ++ E
Sbjct: 13 EPVRASVPLPGSKSVTNRALLLAALADGPGTVRLALRSRDADLMADALRALGATMTPSNE 72

Query: 69 ADKAARAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ A+ G GG ++ +G AG MR + + G + DG
Sbjct: 73 GASSVDWAITPGPVAGG-----ARIDVGLAGTVMRFVPPMAALSDGEVFF--DGD 120

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
P R+RP+G ++ L+ LGA+VD D P V G L GG+V L S SSQ+LS L
Sbjct: 121 PHARKRPMGTILAAALRALGAEVD---NDALPFTVRGP--LTGGEVTLASGSSQFLSGL 174

Query: 187 LM-AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ AA G + S P++ MT++++ FGV+ + S+ D + ++ G
Sbjct: 175 LLTAARFEKGLTVRHAGPPIPSQPHIRMTVQMLREFGVRVDDSEP-DVWRVEPGPIRA-- 231

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
++ VE D S+A+ FL A +TGGTVTV + + Q + ++L MGA V +
Sbjct: 232 RDTFTEPDLNSAAPFLCAAMVTGGTVTVDPWPSETTQPGDQLRQLLADMGASVERVPGGL 291

Query: 306 TVTGGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+VTG R + I ++ + ++ T+A +A AD P+ I VA R ET+R+
Sbjct: 292 SVTGTGR-----VGGIAADLRDVAELTPTIAAALADSPSRISGVAHIRGHETDRLA 344

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ E+ LG V E D I P L TYDDHRMA A ++ A V + +
Sbjct: 345 ALAAEINGLGGDVSETEDGLEIR-PRPLTGGVFHTYDDHRMATAGAVIGLAVPGVQVENI 403

Query: 426 GCTRKTFPDY 435
T KT P++

Sbjct: 404 ATTGKTLPEF 413

>ref|YP_003161758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Jonesia denitrificans
DSM 20603]
gb|ACV09455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Jonesia denitrificans
DSM 20603]
Length = 446

Score = 165 bits (417), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 141/428 (32%), Positives = 210/428 (49%), Gaps = 30/428 (7%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSL+NR LLLAAL+ T + L S D M+ ALR LG +
Sbjct: 24 LTATVTVPKSGSKSLNRHLLAALAAEPTTIHGALRSRDSQLMITALRALGADITESADGT 83

Query: 75 RAVVVGCGGKFPVEDAKE--EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V P+ ++ + G AG MR L A T G T ++DG + R
Sbjct: 84 TITVT-----PLTQGANVGDTITDCGLAGTVMRFLPIAATLVKG--TILIDGDEGAKVR 135

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-AAP 191
P+ ++ L+ LG ++ G D P ++ GG+ GG + + S SSQ++S LL+ AA
Sbjct: 136 PMSPILEALEDLGVEITRHNG-DFLPFTMHPTGGVTGGHLDVDASGSSQFVSGLLLTAAAR 194

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS--DSWDRFY--IKGGQKYKSPKN 247
G + D+L SIP++ MT ++ GV A S +W I+GG
Sbjct: 195 FTNGLTLHHVGDRLPSIPHIAMTCVDLNDLGVTAHTSAPGTWTVAAGPIRGG-----T 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E D S+A+ F+A A I GG+VT+ +T+ Q E MGA+ T + +T+
Sbjct: 248 ITIEPDLSNATPFMAAALIHGGSVTIPAWPSTTTQPGGLAPSFFERMGARCTIDDAGLTI 307

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
TG G HL +++ ++A T A +A AD PT I +A R ET+R+ A+
Sbjct: 308 TG-DGTVHGLAHL-----DLAAGELAPTFAALAALADSPTEIHGIAHLRGHETDRLAAL 361

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
E+ +LG S ++ D IIT P L+ TY DHRMA A ++ V + +
Sbjct: 362 SAEINRLGGSCQQTDDGLIIT-PAPLHEGIFHTYHDHRMATAGAILGLRVAGVEVENIDT 420

Query: 428 TRKTFPDY 435
T KT PD+
Sbjct: 421 TAKTLPDF 428

>ref|YP_004070625.1| 5-enolpyruvylshikimate-3-phosphate synthase [Thermococcus
barophilus MP]
gb|ADT83402.1| 5-enolpyruvylshikimate-3-phosphate synthase [Thermococcus
barophilus MP]
Length = 403

Score = 164 bits (416), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 144/441 (32%), Positives = 220/441 (49%), Gaps = 45/441 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I + P+K + G ++ P SKS ++R L L LSEG T ++N L D L A+R G
Sbjct: 2 IEITPVKTLDGKIRAPPSKSYTHRALFLGLLSEGKTKIENPLICTDTLATLNAVRAFGAR 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ + V G+ VE AK + F +G R A G + V+DG
Sbjct: 62 ADWN-----FVSSGE--VEPAK--INAF--ESGTTARLAIGIGALADGRS--VIDGK 106

Query: 127 PRMRERPIGDLVVGLKQLGADVDC--FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+R+RP+ L+ L LG FL PVRV G G + V++ GSISSQ+++
Sbjct: 107 ESLRKRPMEPLRLALNDLGVKTQSNGLF-----PVRVFG-GEIREDYVRVDGSISSQFIT 160

Query: 185 ALL-MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
ALL + A + L IE+++ +S PY+E+TLR ++ VK E D F++ G K
Sbjct: 161 ALLILGAKVGLS---IEVLNP-VSKPYLEITLRTLKWANVKVERDDGI--FHVHQGVK-- 212

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303

+ + GD SSAS+FL AI G V VEG +Q D ++L GA++ +
Sbjct: 213 -ADHFSIPGDYSSASFFLVAGAI-F-GKVRVEGLDKEDVQADKLILDLLREFGAEIRTKGD 270

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
 V V R L +V+ PD+ LAV+ +++G T +R R KE++R
Sbjct: 271 YVEVE-----RDELVGQEVDCRDFPDLFPILAVLGAYSEGKTVLR-AKHLRYKESDR 321

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
 + + L K+GA V+E D II+ E L T ++ +DHR+AMA ++AA A+ I
Sbjct: 322 IRTMALNLAKMGAKVKELDDGLIISKSE-LRGTVLNPQNDHRIAMALTIAALGAKGKSLI 380

Query: 423 RDPGCTRKTFPDYFDVLSTFV 443
 + C K++P++F L +
Sbjct: 381 LNERCVEKSYPNFFKDLRGLI 401

>gb|AAD51961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
Length = 153

Score = 164 bits (416), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 85/162 (52%), Positives = 113/162 (69%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
 S+SSQ+L+ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +
Sbjct: 1 SVSSQFLTALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ-SYQRFVV 59

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGA 296
 +G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA
Sbjct: 60 RKGQYQSPGQYLVVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIFADVLEKMG 119

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLA 338
 VTW + + T LKA+D++MN +PD AMT+A
Sbjct: 120 IVTWGDDFIAC-T-----HGELKAVDMDMNHIPDAAMTIA 153

>ref|YP_716153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia alni ACN14a]
emb|CAJ64639.1| 3-phosphoshikimate 1-carboxyvinyltransferase 2
(5-enolpyruvylshikimate-3-phosphate synthase 2) (EPSP synthase 2) (EPSPS 2) [Frankia alni ACN14a]
Length = 439

Score = 164 bits (416), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 140/430 (32%), Positives = 209/430 (48%), Gaps = 31/430 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
 + ++ V +PG+KS +NR L+LA L+ GT+ + L S D M G LR LG + D
Sbjct: 24 RPVTAVVPVPGAKSGTNRALVLATLANGTSRLRGALRSRDTLLMAGVLRALGAEISTD-- 81

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
 +V A+ E GNAG R A T G+ + DG RMR+R
Sbjct: 82 GPDWIVRPAPTTRLAAGARAEC---GNAGTVARFTPALATLREGDVAF--DGDARMRDR 135

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
 P+ L+ L++LGAD+D D P V G G LPGA+V + S SSQ +S LL+AAP
Sbjct: 136 PLTPLLALRLGADIDG---DRMPFTVVRGRRLPGGEVTVDASDSSQLVSGLLLAAPR 191

Query: 193 ALGDVEIEIIDK---LISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKYKSP 245
 D + ++ + L S PY++MT+ + G V +D R+ ++ G+ +
Sbjct: 192 Y--DAGVTVVHRGTRLPSGPYLDMTVADLRAAGAVVDVAPPAGDSRRWRVPEGELTAA- 248

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
 + +E D +SA+ FLA A TGG V V + Q +L MGA T +
Sbjct: 249 -DRAIEPDMNSAAAFLAAALATGGRVVVPDWPEATEQPGRMLPTLLAAMGATTERTAAAGL 307

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
 V+G + IDV++ + A L +A+ AD P+ +R + R++ET+R+V
Sbjct: 308 AVSG-----GGGIHGIDVDLGDGFGEAAPVLTALAVLADSPSRLRGIGHLRLQETDRLV 360

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
 A+ EL LGA + D I P L +D DHR+AMA+++ + I D

Sbjct: 361 ALAQELGSLGARITVTDDGLAIE-PAPLRGARLDPRADHRLAMAYAVVGLVVPGLVDDI 419

Query: 426 GCTRKTFPDY 435

T KT PD+

Sbjct: 420 ATTGKTVPDF 429

>ref|ZP_03010719.1| hypothetical protein BACCOP_02601 [Bacteroides coprocola DSM 17136]
gb|EDV00313.1| hypothetical protein BACCOP_02601 [Bacteroides coprocola DSM 17136]
Length = 357

Score = 164 bits (416), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 117/348 (33%), Positives = 180/348 (51%), Gaps = 26/348 (7%)

Query: 101 AGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVR 160

AG AMR LTA + A G T+++ G RM++RPI LV L+ LGADV+ PP+R

Sbjct: 17 AGTAMRFLTAFL--AVGEGTHIITGTQRMQQRPI SILVNLRALGADVEYAGNEGFPLR 74

Query: 161 VNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMER 220

+ G L +V L G++SSQY+SALLM P +++ + +++S PY+++TL+LM

Sbjct: 75 IVG-RKLVNSEVTLPGNVSSQYISALLMIGPALTNGLKLTLTGEIVSRPYIDLTLKLMRD 133

Query: 221 FGVKAEHSDSW---DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGC 276

FG +W ++ +K Q Y++ YVE D S+ASY+ A++ TV + G

Sbjct: 134 FGANV----AWISENQLEVK-PQPYQAVP-YYVESDWSAASYWEICALSEQATVCLPGL 187

Query: 277 GTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--TGPPREPFGRKHLKAIDVNMNKMPPDVA 334

S QGD + A + E +G + + E VT+ TG K ++ + PD+A

Sbjct: 188 FRESPQGDSEVARLFEQLGVETVYGEREVTLRKTG-----KITARMEYDFVNQPDLA 239

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL- 393

T V P + S ++KET+R+ A+ E+ KLG + E + E+

Sbjct: 240 QTFVVTCAVMGIPFRFSGLSLQKIKETDRIALIAEMKKLGYLITESEGSVLSWNGERCT 299

Query: 394 --NVTADITYDDHRMAMAFSLAACAEVPTTIRDPGCTRKTFPDYFDVL 439

IDTY+DHRMAMAF+ + I P K++P Y++ L

Sbjct: 300 PDTSPCIDTYEDHRMAMAFAPVCIRLQDIYINHPQVVTKSYPHYWENL 347

>gb|AAG47852.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella pneumoniae]
Length = 153

Score = 164 bits (416), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 85/162 (52%), Positives = 113/162 (69%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236

S+SSQ+L+ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +

Sbjct: 1 SVSSQFLTALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGEVDNQ-SYQRFVV 59

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGA 296

+G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA

Sbjct: 60 RGKQQYQSPGDYLVVEGDASSASYFLAAGAIKGGTVKIGRNSVQGDIFADVLEKMG 119

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLA 338

VTW + + T LKA+D++MN +PD AMT+A

Sbjct: 120 TVTWGDDFIAC-T-----HGELKAVDMDMNHIPDAAMTIA 153

>ref|ZP_08023913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dietzia cinnamea P4]
gb|EFV91534.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dietzia cinnamea P4]
Length = 415

Score = 164 bits (415), Expect = 3e-38, Method: Compositional matrix adjust.
Identities = 143/441 (32%), Positives = 211/441 (47%), Gaps = 60/441 (13%)

Query: 19 VKLPGSKSLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAA----- 73

V +PGSKSL+NR L LAAL++G + + L S D M+GALR+LG +E+

Sbjct: 5 VVVPKSKSLTNRALPLAALADGPSRLTGTLSRDTLDMIGALRSLGARIESPSTLGSDD 64

Query: 74 -----KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

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                R  VV C                      G AG MR +      A G +T+ D
Sbjct: 65  TDLITPGPLRGGVVQC-----GLAGTVMRFPPIAALATGPSTF--D 105

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184
          G P R RP  ++ L+ LGA++D      + P V+G G L GG+V++ S SSQ++S
Sbjct: 106  GDPAARVRPQSTVLDALRALGAEIDG---ERLPFTVSGTSLRGGRVEMDASASSQFVS 161

Query: 185  ALLMAAPLALGDVEIEII---DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
          LL++A A D ++++      + S P++EMTL ++ GV E      + G
Sbjct: 162  GLLLSA--ARFDEGVDLVHVGASPVPSGPHIEMTLAMLRESGVTVEQTPSSWRVVPVPG-- 217

Query: 241  KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
          + + VE D S+A+ FLA AA+TGGTV V      T+ Q      ++L MGA VT
Sbjct: 218  -PIAAVDRVVEPDLNATPFLAAAATVGGTVRVPHWPATTTQPGDAIRDILRAMGASVTL 276

Query: 301  -----TETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
          ++ V GP R      L +D +++ + ++ T+A +      ADGP+ + +A
Sbjct: 277  EIADGADHGTLLVVVGPSR-----LSPVDRDLSAVGELTPTVAALCALADGPSRLTGIA 329

Query: 355  SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA 414
          R ET+R+ A+ EL +G V E D I+ P L      Y DHRMA A ++
Sbjct: 330  HLRGHETDRLLAALAE LGAVGCGVTELDGGLAIS-PAPLRGAPWRAYADHRMATAGAIVG 388

Query: 415  CAEVPVTIRDPGCTRKTTFPDY 435
          V + D GCT KT P +
Sbjct: 389  LVVPGVEVDDIGCTSKTLPGF 409

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>ref|YP_003985678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gardnerella vaginalis
ATCC 14019]
gb|ADP38655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gardnerella vaginalis
ATCC 14019]
Length = 460

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Score = 164 bits (415), Expect = 3e-38, Method: Compositional matrix adjust.
Identities = 142/454 (31%), Positives = 221/454 (48%), Gaps = 41/454 (9%)

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Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
          ++ TV +PGSKSLSNR L+LAAL + V+ LL S D M+ AL G+ ++
Sbjct: 23  LNATVNIPGSKSLSNRYLILAAALGKKPVVLKGLLRSDTELMINALSVFVGKCDLSCDG 82

Query: 75  RAVVV--GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
          + V      G F V+D      + G AG MR +TA A N      DG + R
Sbjct: 83  TTCVICPPKNGVFSVDDC---AVVNCGLAGTVMRFVTALALFA--NNCVKFDGDEQAYAR 137

Query: 133  PIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIG-----GLPGGKVKLSGSI 179
          P+ ++ GL+QLGA + + G      + PP + G      +++ S S
Sbjct: 138  PMKPVLDGLEQLGAKI-VYHGKVGFLPFSVIPKNLESYGINDAQNSCNRVIRIDSSSS 196

Query: 180  SQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYI 236
          SQ++SALL+ A      G ++IE I KL S+P+++MT+ + + G V S W +
Sbjct: 197  SQFISALLLIASRVPGGLQIEHIGSKLPSMPHIQMTMEDVRKAGGVVDMPESGVW---RV 253

Query: 237  KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
          K      P      VE D S+A+ F+ A I GG V +      + Q      +LE MGA
Sbjct: 254  KE-HDLTLPHEVVVEPDLNAAFFIGAALIAGGCVKIPNWPLKTTQPGGLLPGILEQMGA 312

Query: 297  KVTWTET-----SVTVTGPPREPFGGRKH-LKAIDVNMNKMMPDVAMTLAVVALFADGPTAI 350
          K+ + +      ++ VTG      G+ H +K++D +      +VA ++A + FAD + +
Sbjct: 313  KIVFEHRSDSSTLCVTGS-----GKIHAIKSLD--LAAAGEVAPSIAAILAFADSVSEL 365

Query: 351  RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAF 410
          R +A R ET R+ AI TEL ++G EE D I P + ++ I+TY DHRMA
Sbjct: 366  RGAHLRGHETNRLSAIVTELNRVGIGAEELDDGIRIIPSKNMHGEVIETYADHRMATFA 425

Query: 411  SLAACAEVPVTIRDPGCTRKTTFPDYFDVLSTFVK 444
          S+      +++++ TRKT PD+ + + +K
Sbjct: 426  SMLGLRISNISVKNIAATRKTLPDFPTMWNMLK 459

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>ref|ZP_07666535.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gardnerella vaginalis

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ATCC 14018]
Length = 456

Score = 164 bits (414), Expect = 3e-38, Method: Compositional matrix adjust.
Identities = 142/454 (31%), Positives = 221/454 (48%), Gaps = 41/454 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSLSNR L+LAAL + V+ LL S D M+ AL G+ ++
Sbjct: 19 LNATVNIPKSGKSLSNRYLILAAALGKKPVVLKGLLRSDTELMINALSVFGVKCDLSLSCDG 78

Query: 75 RAVVV--GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 132
+ V G F V+D + G AG MR +TA A N DG + R
Sbjct: 79 TTICVIPPKNVFSVDDC---AVVNCGLAGTVMRFVTALALFA--NNCVKFDGDEQAYAR 133

Query: 133 PIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIG-----GLPGGKVKLSGSIS 179
P+ ++ GL+QLGA + + G + PP + G +++ S S
Sbjct: 134 PMKPVLDGLEQLGAKI-VYHGKVGFLPFSVIPKNLESYGINDAQNSCNNRVIRIDSSSS 192

Query: 180 SQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYI 236
SQ++SALL+ A G ++IE I KL S+P+++MT+ + + G V S W +
Sbjct: 193 SQFISALLLIASRVPGGLQIEHIGSKLPSPHMQMTMEDVRKAGGVDMPESGVW---RV 249

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
K P VE D S+A+ F+ A I GG V + + Q +LE MGA
Sbjct: 250 KE-HDITLPHVEVVEPDLSNAAPFIGAALIAGGCVKIPNWPLKTTQPGGLPGILEQMGA 308

Query: 297 KVTWTET-----SVTVTGPPREPFGGRKH-LKAIDVNMNKMPPDVAMTLAVVALFADGPTAI 350
K+ + + ++ VTG G+ H +K++D + +VA ++A + FAD + +
Sbjct: 309 KIVFEHRSDDSTLCVTGS-----GKIHAIKSLD--LAAAGEVAPSIAAILAFADSVSEL 361

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
R +A R ET R+ AI TEL ++G EE D I P + ++ I+TY DHRMA
Sbjct: 362 RGIAHLRGHETNRLSAIVTELNRVGIGAEELDDGIRIIPSKNMHGEVIETYADHRMATFA 421

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
S+ +++++ TRKT PD+ + + +K
Sbjct: 422 SMLGLRISNISVKNIAATTRKTLPDFPTMWNMLK 455

>gb|EFR56629.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alistipes sp. HGB5]
Length = 414

Score = 164 bits (414), Expect = 3e-38, Method: Compositional matrix adjust.
Identities = 136/433 (31%), Positives = 211/433 (48%), Gaps = 33/433 (7%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + GT+ P SKS + R L + L E T+V+ N+ D L + TLG V
Sbjct: 6 PSGRVKGTLPKPSKSYAQRALAASLLCEETSVLNRNIEFCSDSLQCIETLGARV--T 63

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + + GG P + L +G +G++ R T + G T ++G +
Sbjct: 64 RIGEETLSIE-GGLRP-----QGHTLRVGESGLSTRLFTPIASLCGTPIT--IEEGTLL 115

Query: 131 ERPIGDLVVGLKQLGA---DVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RP+ ++ L+ LG D FL P V G + GG+V + GS+SSQ+++ L+
Sbjct: 116 RRPMEEMIGPLRTLGVVRVDNNGGFL-----PFEVRG--PIRGGEVDVDGSVSSQFITGLM 168

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A PLA D I + +S PY++MT+ RFGV+ H+D ++ FYI+GGQ+Y SP
Sbjct: 169 LALPLARHDTTTHV-RSAVSTPYLDMTIDTAARFGVEICHND-YEEFYIEGGQRY-SPAC 225

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+EGD S+A+ L A+ G VTV S Q D L GA V SVT
Sbjct: 226 LSIEGDWSAAAMLLVAGAV-AGEVTVRNISMLSKQADTAVCTALVRAGAAVINEADSVTT 284

Query: 308 TGPPREPFGGRKHLKADVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
P L + + PD+ LA +A ADG + IR + KE+ R AI
Sbjct: 285 ISRP-----LHGFEDATNCPDLFPALAAALAAADGVSTIRGTSRLHKESNRAEAI 336

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
R E K+G V+ + + K+ + ++DDHRMAM+ +++A + +TI +

Sbjct: 337 REEYAKVGIEVDISEEDVMRIRGGKIRPARVSSHDDHRMAMSMMAVSALRCDGQITIENAE 396

Query: 427 CTRKTFPDYFDVL 439

C K++P +F+ L

Sbjct: 397 CVAKSYPGFFEDL 409

>ref|ZP_07756778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Megasphaera
micronuciformis F0359]
gb|EFQ05104.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Megasphaera
micronuciformis F0359]
Length = 427

Score = 163 bits (413), Expect = 4e-38, Method: Compositional matrix adjust.
Identities = 137/436 (31%), Positives = 212/436 (48%), Gaps = 27/436 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

+VL P K++SG + +P SKS +R L+ AAL++G ++V N+ SED+ L+ G

Sbjct: 2 NLVLTP-KKLSGILAVPSSKSAGHRELICAAALADGKSLVKNITPSEDLEATCRVLQAFGA 60

Query: 66 SVEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+VE R V GG P + ++ G +G +R L G TY

Sbjct: 61 TVETVSHEDGRLTVAVTGGLRPQTGS---LRADCGESGSTVRFLIPVGLLTGMKITYT-- 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLS 184

G R+ ERP+ + + G D P+ V G L GG +L G++SSQ+ +

Sbjct: 116 GRGRLPERPLDPFLNIFDN--KKIAYTKGKDSLPLTVKG--RLKGGIYELPGNVSSQFFT 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYK 243

LLMA PL D ++ + S Y+ +TL + R G+ E D Y I+G Q Y+

Sbjct: 172 GLLMALPLLPPDSVLQSTTVVESESYINITLDCLRRHGIYVEKER--DGLYLIRGRQAYR 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303

+ + VEGD S A+++L G I G TV ++G S QGD +E M ++ +

Sbjct: 230 TGEYP-VEGDFSQAAPFLVGG-IIGDTVELKGLSNNSTQGDRTTVVSFIESMRGRIERS-G 286

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363

SV P R + +++ PD+ LAV+ F+ G T I + A R+KE +R

Sbjct: 287 SVLRAVPSRT-----TGLTIDVKDCPDLPALAVLGTFSQGITRIVNGARVRLKECDR 339

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVT 421

+ A+ EL +GA V E D II L + ++DHR+AMA ++A+ C +T

Sbjct: 340 IHAMTHELNSIGAKVRETGDGLIIEGVSSLTGGRVQAWNDHRIAMALAMASQRCTG-KLT 398

Query: 422 IRDPGCTRKTFPDYFD 437

I C RK++P ++

Sbjct: 399 IEAECVRSYPSFWQ 414

>gb|AAD51964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Klebsiella
pneumoniae]
Length = 153

Score = 163 bits (413), Expect = 4e-38, Method: Compositional matrix adjust.
Identities = 85/162 (52%), Positives = 112/162 (69%), Gaps = 9/162 (5%)

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYI 236

S+SSQ+L+ALLM APLA D I I L+S PY+++TL LM+ FGV+ ++ S+ RF +

Sbjct: 1 SVSSQFLTALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKTFGVEVDNQ-SYQRFVV 59

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296

G Q+Y+SP + VEGDASSASYFLA AI GGTV V G G S+QGD++FA+VLE MGA

Sbjct: 60 CGKQQYQSPGDYLVVEGDASSASYFLAAGAIIKGGTVKVTGIGRNSVQGDIFADVLEKMG 119

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLA 338

VTW + + T LKA+D++MN +PD AMT+A

Sbjct: 120 TWTWGDDFIAC-----HGELKAVDMDMNHIPDAAMTIA 153

>dbj|BAJ47896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Caldiarchaeum subterraneum]

dbj|BAJ47961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Caldiarchaeum subterraneum]
dbj|BAJ49518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Caldiarchaeum subterraneum]
Length = 429

Score = 163 bits (413), Expect = 5e-38, Method: Compositional matrix adjust.
Identities = 137/436 (31%), Positives = 210/436 (48%), Gaps = 33/436 (7%)

Query: 15 ISGTVKLPKSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V+ P SKS ++R+ LA+L T + L S D + A + LG + A
Sbjct: 11 LKGVVEAPPSKSYTHRVFSLASLCTEKTTHITPLISRDTQATINAAKMLGAEIVEKPGAY 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A+ +F D +V N+G +R T T T VL G +R RP+
Sbjct: 71 TAL---GRRQFKTPDNIIDVM---NSGTTLRITYTGLATLVEKGYT-VLTGDESIRRRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L Q+GA+ G P+ V G G G K+ G SSQY+++LL+ A
Sbjct: 123 AQLLEALHQIGAECWSTRNGSAPIIVKG-GNRITGTAKIKGEDESSQYVTSLLLTGLAAH 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKNAY---- 249
GD+EI++ ++L+S PYV+ T++++E FG + W R SP+ +
Sbjct: 182 GDIEIQVTEELVSKPYVDATVKMVEVFGGEIRRRGYEWFV-----SPQELHGVEF 232

Query: 250 -VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
V GD SSA++ +A A +T G VT++ T Q D K E++++ G++ T+T + V
Sbjct: 233 TVPGDFSSAAFIIAAAHLTQGHVTIKNLSTRYPQADEKIVEIKLYGSEATFTSEGLVVE 292

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G GR H A +V + PD+ AV+A DG T I VA R+KE++R+
Sbjct: 293 G-----GRNHADA-EVVLRDAPDLLPVTAVIAAVNDGQTRIHGVAHARLKESDRIALTA 345

Query: 369 TELTKLGASVEEGPDYCIIT-PPEKLNVTATIDTYDDHRMAMAFS-LAACAEVPVTIRDPG 426
EL KLG VEE D +I P A+D + DHR+ MAF+ L E + ++
Sbjct: 346 AELRKLGEVEELADGLLIHGNPRIKGGVAVDGHDHRLFMAFTVLGLTLEKGLIVKGAE 405

Query: 427 CTRKTFPDYFDVLSTF 442
++P + LS
Sbjct: 406 SADVSYPAFLQDLSKL 421

>ref|ZP_06559559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Megasphaera genomosp.
type_1 str. 28L]
gb|EFD94495.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Megasphaera genomosp.
type_1 str. 28L]
Length = 426

Score = 163 bits (413), Expect = 5e-38, Method: Compositional matrix adjust.
Identities = 124/427 (29%), Positives = 196/427 (45%), Gaps = 21/427 (4%)

Query: 17 GTVKLPKSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +++P SKS+ +R L+ AALS GT+ V + S+D+ L L+ LG+ + D
Sbjct: 12 GAIRVPSSKSMGHRHLICAALSRGTSTVQGVSPSQDIEATLRILQALGVRIHTDTDGTHC 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
GG D V G +G +R L +G ++ G R+ ERP+
Sbjct: 72 TYTVTGGMRSFADT---VLCDAGESGSTLRFLPLAVWSGNTTRFI--GRGRLPERPLQP 126

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ + P+ V+G+ G L G++SSQ+ S LL PL G+
Sbjct: 127 YYSIFQ--AQHIAFHRENGSLPLTVHGV--FHPGTYVLPGNMSSQFFSGLLFMLPLLRGN 182

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
E+ + S Y+ +TL + G++ + D ++I+G Q Y++ A VEGD S
Sbjct: 183 SELRSTTPIESAGYALATLDCLAAHGEVQRQAE-DGYFIRGEQSYRAGSYA-VEGDYSQ 240

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPFPREPFG 316
A+++LA + G V +G S QGD +L+ MGA + +V
Sbjct: 241 AAFWLAAGTLQG-RVCKGLQPRSRQGDKAIISLLQAMGANLHVVDGTVRAE----- 291

Query: 317 RKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L I ++ PD+ LA +A A G T + A R+KE +R+ A+ EL KLGA
Sbjct: 292 TSSLHGIAADVADCPDLVPVLAALATQAQGVITYLYHAARVRLKECDRLHAMTVLQKLGA 351

Query: 377 SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS-LAACAEVPVTIRDPGCTRKTFFPDY 435
+EE PD I L + + DHR+AMA + LAA E P+ + +K++P +
Sbjct: 352 HIEETPDSLRIVGKTSLRGGRVYAWRDHRIAMALAVLAASCEAPLQLEGAEEAVQKSYQF 411

Query: 436 FDVLSTF 442
+ T
Sbjct: 412 WQDFQTL 418

>ref|ZP_01308785.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri str. Hc (Homalodisca coagulata)]
ref|YP_001597999.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri GWSS]
gb|EAT14083.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri str. Hc (Homalodisca coagulata)]
gb|ABS30603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri GWSS]
Length = 413

Score = 163 bits (413), Expect = 5e-38, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 213/435 (48%), Gaps = 60/435 (13%)

Query: 14 EISGTVKLPKSGKSLSNRILLALAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I+G V + GSKS SNR L+L AL ++N+ NS+D + AL +
Sbjct: 12 DINGNVNITGSKSESNRFLILKALYPDIIELENISNSDDTFILKKAL-----FS 60

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
K+ ++ + ++G AMR LTA + N +L G RM+ERP
Sbjct: 61 KKKLIN-----IKHSGTAMRFLTAFFSIKE-NREVILTGSYRMQERP 101

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV LK+LG ++ PP+R+ G L GG++ + +ISSQY+SAL++ A
Sbjct: 102 ISVLVETLKKLGGNIFYEKKNGYPPLRIIG-KKLLGGEINIDANISSQYISALMLIASKF 160

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
++I + +K+ SI Y++MTL++++ G+ W+ K+K +E
Sbjct: 161 ENGLKIYLSNKTISISYIKMTLKVLLKLGIN-----LWNKNIIYIKKIKFKKKIKITIES 216

Query: 253 DASSASYFLAGAAITG-GTVTVEGCGTTSLSQGDVKFAEVLE-MMGAKVTWTETSVTVTGP 310
D SSASY+ + A++ + ++ ++QGD + + + K + + +
Sbjct: 217 DWSSASYYSLSVALSKTADLNLKFFNKKNIQGDSIISNIYKNFFNVKTLFKNNEINL--- 273

Query: 311 PREPFGKRLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ L +ID+++N PD+A T+ V +R + + ++KET+R+ A++ E
Sbjct: 274 --KKLIDIDLNSIDIDLNSTPDIAQTIVVTCTGLKIKCVLRGLETLIKIKETDRLNALKNE 331

Query: 371 LTKLGASVEEGPDYCIITPP--EKLNVTAID-----TYDDHRMAMAFSLAACAEVPVT 421
L+KLG IIT E LN I TYDDHRMAM+FS P++
Sbjct: 332 LSKLGVK-----SIITNSSIELLNFEIKKEIYIYTYDDHRMAMSFSTLGII-YPI 383

Query: 422 IRDPGCTRKTFFPDYF 436
I + K++P+++
Sbjct: 384 ILNYNVSKSYPNFW 398

>ref|YP_604470.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
geothermalis DSM 11300]
sp|Q1IZN3.1|AROAEIDG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF45301.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
geothermalis DSM 11300]
Length = 440

Score = 163 bits (413), Expect = 5e-38, Method: Compositional matrix adjust.
Identities = 146/437 (33%), Positives = 214/437 (48%), Gaps = 24/437 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++ P+ E+ G ++ SK+ + R LL AAL+EG T V SED ++ LR G
Sbjct: 10 DVLVHPVSELRGELRAQPSKNYTTTRYLLAALAEGETRVVGAATSEDAEALIRCLRAWGA 69

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V D+ + VV G G + + L GNAG R L V A + T+V D
Sbjct: 70 DV--DRVGEDVVVRGFGAH-----PRAGMTLNPNGAGAVARFLMG-VAALTDTTTFVTDY 121

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP GDL+ L++LGA V G PV ++G + GG+V++S SSQY SA
Sbjct: 122 SESLGRRPQGDLLAALERLARGVSSRNQ--LPVTLSGP--VRGGRVEVSAQRSSQYASA 177

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ PL +++ + ++ S + TL + FG++A S R I GGQ Y+ P
Sbjct: 178 LMFLGPLLPDGLDLRLTGEIKSHAPLRQTLDTLAAFLQARASADLTRITIPGGQAYR-P 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V GD ++ L AA+ G VTV LQG+ + VL MGA + V
Sbjct: 237 GRVLVPGDYPGSAALLVAAALLPGEVTVTNLREGDLQGEREALNVLAMGADLVREGDRV 296

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
TV G GR L A+ + + D L A FA G T +VA+ R+KE +R+
Sbjct: 297 TVRG-----GRP-LHAVTRDGSFTDAVQALTAFAFGTTTWENVATLRLKECDRI 349

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
R EL +LG + E D IT +++ ++TA D + DHRM M +L AE P+ I
Sbjct: 350 DTRRELERLGLTATETADSLITGADRIPLDLTA-DHGHGHRMIMLLTLLGLRAEAPLRI 408

Query: 423 RDPGCTRKTFPDYFDVL 439
RK++P +F L
Sbjct: 409 TGAHHRKSYPLFFRHL 425

>ref|ZP_07670058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erysipelotrichaceae
bacterium 3_1_53]
gb|EFP62886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erysipelotrichaceae
bacterium 3_1_53]
Length = 420

Score = 163 bits (412), Expect = 6e-38, Method: Compositional matrix adjust.
Identities = 119/426 (27%), Positives = 202/426 (47%), Gaps = 28/426 (6%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG V +P SKS+++R ++ AAL++GT+V+ N+ S+D+ + ++ LG + ++ +
Sbjct: 11 SGHVAIPPSKSMARAIICAALAQGSTSVIKNVAYSQDIKTTIAGMQQLGADIRMEE--DQ 68

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ G F V+ + ++F +G +R + T+ G R+ +RP
Sbjct: 69 VTITGIQ-DFTVQ---QKEVFCCESGSLRFFIPIFSLCNQEITFT--GQGRMLQRPQK 121

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+ L F D + + L G + L G +SSQ++S LL P+
Sbjct: 122 ----VYEDLFHSQSLFFEQDASGITIRE--RLRPGDITLKGDVSSQFISGLLFTPLMLKE 175

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
D I I+ S YV++TL+++E FGV +D +I G QKYK+ + +EGD S
Sbjct: 176 DSTIHILPPFESRSYVDLTLQMLETFGVHTSFTDEL-TIHIPGNQKYKAADYS-IEGDYS 233

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
++F AAI +T+ G S QGD K +L+ G + E +
Sbjct: 234 QLAFFAVLAANND-LTITGVHHNSRQGDKKILSILKDFGVHMEEVENGYHIYK----- 286

Query: 316 GRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
R H A+D + PD+ L V+A+++ G T I + R+KE++R+ A+ EL K
Sbjct: 287 SRLHGNVD--LADCPDLGPILTVLAMYSNGNTHIYNAGRLRIKESDRIEAMEQELRKFH 344

Query: 376 ASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFP 433
+ + I+ T + ++DHR+ MA S+AA C+ TI K++P
Sbjct: 345 VDIHSTENEIFISGGTDYTCDELSAHNDHRIVMALSAASCSNSICTIEGAQAINKSYP 404

Query: 434 DYFDVL 439

+FD L
Sbjct: 405 TFFDDL 410

>ref|YP_003687978.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(phosphoenolpyruvate:3-phosphoshikimate5-O-(1-carboxyvinyl)-transferase) (EPSP synthase)
[Propionibacterium freudenreichii subsp. shermanii
CIRM-BIA1]
emb|CBL56542.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(phosphoenolpyruvate:3-phosphoshikimate5-O-(1-carboxyvinyl)-transferase) (EPSP synthase)
[Propionibacterium freudenreichii subsp. shermanii
CIRM-BIA1]
Length = 450

Score = 163 bits (412), Expect = 6e-38, Method: Compositional matrix adjust.
Identities = 133/430 (30%), Positives = 204/430 (47%), Gaps = 31/430 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS NR L+LAAL +G + + L ++ D+ M+ ALR LG ++ A +
Sbjct: 32 LHATVHVPGSKSEGNRALVLAALGDGPSTITGLPDARDIRLMIAALRGLGTIAPGDAHE 91

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G P+ A + G AG MR + G +V D R ERPI
Sbjct: 92 VTVHPG-----PLHAATAPID--CGLAGTVMRFVPLAALVAGTTRFVGDD--RAAERPI 142

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ GL+QLGA +D P + L G +V + S SSQ++S LL+AA
Sbjct: 143 APLLEGLRQLGAATS----SDAIPFDLTAPDELGTGHEVSIDASASSQFISGLLLAAAAP 198

Query: 195 GDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+++ + S P+++MT+ ++ R GV+ + R+ ++ G + + +E D
Sbjct: 199 QGIDLMHTGATVPSAPHIDMTIAMLARHGVRVAQPERGRRWVVEGSMIRAA--DERIEPD 256

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
++A+ FL ITGG+V V S Q VL MGA T T
Sbjct: 257 LTNAAVFLIAGVITGGSVAVADWPRRTQPGALIGPVLARMGAATGAGRATAT----- 311

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
R L+ ++++ ++ ++A +A+ A G T IR V R ET+R+ AI TELT+
Sbjct: 312 --HRDDLQGAELDLRPASELTCSVAALAVAARGTTTIRGVGHIRGHETDRIAAIATELTR 369

Query: 374 LGASVEEGPDYCIIT----PPEKLNVTAD----TYDDHRMAMAFSLAACAEVPVTIRDP 425
+G V E PD I ++L+ + D Y DHRMA +L + + D
Sbjct: 370 VGVDVAELPDGLRIEGMAGRLDQLHPSTGDLFRCYADHRMAHLGALIGLMVPGIRLDDV 429

Query: 426 GCTRKTFPDY 435
G T KT PD+
Sbjct: 430 GSTTKTMPDF 439

>ref|ZP_06425502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptostreptococcus
anaerobius 653-L]
gb|EFD04619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptostreptococcus
anaerobius 653-L]
Length = 454

Score = 163 bits (412), Expect = 6e-38, Method: Compositional matrix adjust.
Identities = 127/456 (27%), Positives = 228/456 (50%), Gaps = 42/456 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLS----EGTTVDNLLNSEDVHYMLGALR 61
+I ++P K++ G++ +P SKS+++R+++ A+L+ + T ++N+ S+D+ +GA+R
Sbjct: 2 DIRIRP-KKLCGSINIPPSKMAHRMIICASLATLSCDHDTNIENIAMSDDILATIGAMR 60

Query: 62 TLGLSVEAD---KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-- 116
+LGL +E D R V G G A + + + G +G +R + ++
Sbjct: 61 SLGLEIEKDLLEGGRYRLKVSIGIDSRNDGLADDYLTIDCGESGSTLRFIIPILSVFAKR 120

Query: 117 -GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
G Y LD R+ +RP+ L + G D + D + + G+ G ++

Sbjct: 121 YGLVNYRLDTRGRLLQRPLDPYFDILDREGIDYNI----DGTSLYIRGMKGFSQSSYEID 176

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
G ISSQ++S LL + PL D +I I ++L S YV+MTL + ++G++ E+ D + F

Sbjct: 177 GGISSQFISGLLFSLPLMDFDTDIVIKNRLESRGYVDMTLDALYKYGIEVENID-YKTFK 235

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMG 295
IKG Q YK P A VEGD S A++FL A+ G V ++G SLQ D + ++++

Sbjct: 236 IKGNQSYK-PVKASVEGDYSQAFFLVANAL-GNKVQIKGLDPGSLQLDKEIVDIIDRYD 293

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
K E AI ++ +PD+ ++++A P+ I V

Sbjct: 294 -KYYCNEGGDRCIASDL-----AIGIDATNIPDIVPIMSLLATNYKYPISKISGVER 343

Query: 356 WRVKETERMVAIRTELTKLGASVE-----EGPDYCIITPPEKLN-----VTAIDTYD 402
R+KE++R+ A ++L LG +E E I ++ N +D++

Sbjct: 344 LRIKESDRLQATSSQLRILGKDIEIIGEKEETSLLINGNLDGRNKDQSTGDDYYLVDSFK 403

Query: 403 DHRMAMAFSLAA-CAEVPVTIIRDPGCTRKTFFPDYFD 437
DHR+AM ++AA ++ + I+D K++P+++D

Sbjct: 404 DHRIAMTLAIAATVSDKDLVIKDAHVVSKSYPNFWD 439

>ref|YP_001135951.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium gilvum
PYR-GCK]
sp|A4TFB8.1|AROAMYCGI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP47163.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium gilvum
PYR-GCK]
Length = 446

Score = 163 bits (412), Expect = 6e-38, Method: Compositional matrix adjust.
Identities = 139/428 (32%), Positives = 221/428 (51%), Gaps = 31/428 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALS--EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ TV +PGSKS +NR L+LAAL+ EG++ + L S D M+GAL TLGLSV A +

Sbjct: 16 VHA TVTVPGSKSQTNRALVLAALAAREGSSRISGALRSRDTLDMIGALETGLSVAASDS 75

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSL--TAAVTAAGGNATYVLDGVPRMR 130
+ V G P +A+ + L AG +R + AA++A T DG + R

Sbjct: 76 DPADLTV-SGTLAPAAEARVDCGL----AGTVLRFVPPIAALSA----QTVTFDGDGEQAR 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMA- 189
RPI L+ GL+ LG D+D D P V G G + GG V++ S SSQ++S LL++

Sbjct: 127 SRPIAPLLDGLRTLGVDDIDG----DGLPFAVRGTGTVAGGTVEIDASGSSQFVSGLLLSG 182

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G + D + S P++ MT+ ++ GV+ + S + DR+ + G ++

Sbjct: 183 AAFTDGLTIVHTGDSVPSAPHIAMTVSMLRDAGVEVDDS-APDRWRVSPGP--IGARDWV 239

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S++ FLA A ++GG V + G T S+Q ++L + +V + + V

Sbjct: 240 IEPDLSNSVPFLAAAVVSGGAVRITGWPTVSIQPADTILKILAGLNGEVRKGSYSLEVQ- 298

Query: 310 PPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMVAI 367
G + IDV++ + ++A ++A +A AD + +R +A R ET+R+ A+

Sbjct: 299 -----GATNYGGIDVDLRDVGELAPSVAAAMALADPGSVSRLRGIAHLRGHETDRLAAL 352

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIIRDPGC 427
TE+ +G EE D +IT E ++ +Y DHRMA A ++ + + D G

Sbjct: 353 STEINGIGGQCEETEDGLVITARE-MHGGTWSSYADHRMATAGAIIGLRVPGIEVEDIGT 411

Query: 428 TRKTFFPDY 435
T KT PD+

Sbjct: 412 TAKTLPDF 419

>ref|ZP_07526056.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptostreptococcus
stomatis DSM 17678]
gb|EFM64781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptostreptococcus

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stomatis DSM 17678]
Length = 471

Score = 162 bits (411), Expect = 7e-38, Method: Compositional matrix adjust.
Identities = 138/462 (29%), Positives = 230/462 (49%), Gaps = 54/462 (11%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLG---- 64
      PI+E+          SKS  +R L+ A+L++G + +      SED+   + AL  +G
Sbjct: 20 NPIREVEAI----SSKSFIHRALICASLAQGRSTISYKGLSEIDIMATISALEVMGAKIYI 75

Query: 65 ----LSVEADKAAKRAVVVGCGGKFP--VEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGG 117
      ++VEA A  + +G G      D K E  +      +G +R L  T+
Sbjct: 76 EEDWMTVEAIPADNMHSIGSKGNHDHISSDGKYGEKIVDCRESGSTLRMLLPLATSLSD 135

Query: 118 NATYVLGDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVVRV-NGIG---GLPGGKV- 172
      + Y+  G  + RPI DL  L+Q G  +      +D P+ + N IG  + K+
Sbjct: 136 D--YIFTGRHGLMTRPIDDLTQALRQAGFSI----SSDSLPIEIRNRIGRKRDIIEPKKIS 189

Query: 173 --KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
      ++ G ISSQY+S LL+A PL  G + ++++DKL S PY+++T +M FGV+ E  DS
Sbjct: 190 DFQIRGDISSQYISGLLLAGPLMDGKLRVDVMDKLESKPYIDLT KDVMSLFGVEVEEYDS 249

Query: 231 W-----DR-----FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
      DR      + IK GQ YKS K      E D S+A +FLA A+  G + V
Sbjct: 250 RESLADGDRNRIIKTYSIKPGQAYKSNK-IKAESDWSNAGFFLAIGALFRG-IRVLNLDL 307

Query: 279 TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLA 338
      S QGD + E+L+ GA++ ++ + V  R+P      +++N+  PD+  LA
Sbjct: 308 ESSQGDKRIIEILKEYGARLVVKDSYIEVLPGQRKP-----LNLNIADTPDMLPILA 359

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT 396
      ++A+FA+G ++  + R+KE++R+ ++ + + LGA      II+      +KL V
Sbjct: 360 ILAVFAEGESSFTGIDRLRIKESDRIESVISMVECLGACACLGKKNLIISGRDRKKLPVY 419

Query: 397 AIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTTFPDYFD 437
      ++++DHR+ MA S+AA  + + I      K++P +FD
Sbjct: 420 RVNSFNDHRIVMASSIAASLLDGQLIEGAEAVNKSYPYTFD 461

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>ref|ZP_01946380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
      'MSU Goat Q177']
ref|ZP_02219938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
      334]
ref|YP_002305636.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
      CbuK_Q154]
sp|B6J892.1|AROAX_COXB1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|EAX32956.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
      'MSU Goat Q177']
gb|EDR35049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
      334]
gb|ACJ20491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
      CbuK_Q154]
      Length = 438

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Score = 162 bits (411), Expect = 7e-38, Method: Compositional matrix adjust.
Identities = 141/436 (32%), Positives = 219/436 (50%), Gaps = 29/436 (6%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P + +SG + +PG KS+S+R +LLAA++EG T VD  L  D  M+ AL+ +G S++
Sbjct: 7  PSQGLSGEICVPGDKSISHRAVLLAAIAEGQTQVDGFLMGADNLAMVSALQQMGASIQVI 66

Query: 71 KAAKRAVVVGCGG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGP 127
      +      VV G G  + P E      L  GN+G A+R L+  + AG      VL G
Sbjct: 67 EDENILVVEGVGMTGLQAPPE-----ALDCGNSGTAIRLLSGLL--AGQPFNTVLTGDS 118

Query: 128 RMRERPIGDLVVGKQLGADVDCFLGTDCPPVVRVNGIGLPGGKVKLSGSISSQYLSALL 187
      ++ RP+ ++  L  +GA +D      + PP+++ G  L G  +L  + S+Q  S LL
Sbjct: 119 SLQRRPMKRIIDPLTLMGAKIDST--GNVPPLKIYGNPRLTGIHYQLPMA-SAQVKSCLL 175

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Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G I P + T RL++ F + + GG K K+ +
Sbjct: 176 LAGLYARGKTCIT-----EPAPSRDHTERLLKHFYTLQKDKQS--ICVSGGGLKA-ND 227

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ GD SSA++F+ A IT G+ + C + +L+MMGA + T +
Sbjct: 228 ISIPGDISSAAFFIVAATITPGS-AIRLCRVGVNPNTRLGVINLLKMMGADIEVTHYTEKN 286

Query: 308 TGPPREPFGRK-HLK AIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK ID+ +++P D L + A A G T +RDVA RVKET+R
Sbjct: 287 EEPTADITVRHARLKGIDIPDQVPLTIDEFPVLLIAAVAQGKTVLRDVAELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L KLG + E PD II L +++YDDHR+AMAF++A A+ PV I
Sbjct: 347 IAAMVDGLQKLGIAAESLPDGVIIQ-GGTLEGGEVNSYDDHRIAMAFVAGTLAKGPVRI 405

Query: 423 RDPGCTRKTFFPDYFDV 438
R+ + +FP++ ++
Sbjct: 406 RNCNVKTSFPNFVEL 421

>ref|YP_003543344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri DMIN]
gb|ADE35480.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri DMIN]
Length = 413

Score = 162 bits (411), Expect = 7e-38, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 213/435 (48%), Gaps = 60/435 (13%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+I+G V + GSKS SNR L+L AL ++N+ NS+D + AL +
Sbjct: 12 DINGNVNITGSKSESNRFLILKALYPDIIELENISNSDDTFILKKAL-----FS 60

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
K+ ++ + ++G AMR LTA + N +L G RM+ERP
Sbjct: 61 KKKLIN-----IKHSGTAMRFLTAFFSIKE-NREVILTGSYRMQERP 101

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV +K+LG ++ PP+R+ G L GG++ + +ISSQY+SAL++ A
Sbjct: 102 ISVLVETIKKLGGINIFYEKKNGYPPLRIIG-KKLLGGEINIDANISSQYISALMLIASKF 160

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
++I + +K+ SI Y++MTL+++++ G+ W+ K+K +E
Sbjct: 161 ENGLKIYLSNKTISISYIKMTLKVLLKLGINV---LWNKNIIYIKKIKFKKKIKITIES 216

Query: 253 DASSASYFLAGAAITG-GTVTVVEGCGTTSLQGDVKFAEVLE-MMGAKVTWTETSVTVTGP 310
D SSASY+ A++ + ++ ++QGD + + + K + + +
Sbjct: 217 DWSSASYYSVALSKTADLNLKFFNKKNIQGDSIISNIYKNFFNVKTLFKNNEINL--- 273

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ L +ID+++N PD+A T+ V +R + + ++KET+R+ A++ E
Sbjct: 274 --KKLIDIDLNSIDIDLNSTPDIAQTIVVCTGLKIKCVLRGLETLKIKETDRLNALKNE 331

Query: 371 LTKLGASVEEGPDYCIITPP--EKLNVTA-----IDTYDDHRMAMAFSLAACAEVPVT 421
L+KLG IIT E LN I TYDDHRMAM+FS P++
Sbjct: 332 LSKLGVK-----SIITNSSIELLNFEIKKKEIYISTYDDHRMAMSFSTLGII-YPI 383

Query: 422 IRDPGCTRKTFFPDYF 436
I + K++P+++
Sbjct: 384 ILNYNVVSXSYPNFW 398

>ref|YP_004078450.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
Spyr1]
gb|ADU00616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
Spyr1]
Length = 446

Score = 162 bits (411), Expect = 8e-38, Method: Compositional matrix adjust.
Identities = 139/428 (32%), Positives = 221/428 (51%), Gaps = 31/428 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALS--EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ TV +PGSKS +NR L+LAAL+ EG++ + L S D M+GAL TLGLSV A +
Sbjct: 16 VHATVTVPGSKSQTNRALVLAALAAREGSSRISGALRSRDTLMIGALETTLGLSVAASDS 75

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSL--TAAVTAAGGNATYVLDGVPRMR 130
+ V G P +A+ + L AG +R + AA++A T DG + R
Sbjct: 76 DPADLTV-SGTLAPAAEARVDCGL----AGTVLRFVPPIAALSA----QTVTFDGDEQAR 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA- 189
RPI L+ GL+ LG D+D D P V G G + GG V++ S SSQ++S LL++
Sbjct: 127 SRPIAPLLDGLRTLGVLDIDG----DGLPFAVRGTGTVAGGTVEIDAGSSSQFVSGLLLSG 182

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G + D + S P++ MT+ ++ GV+ + S + DR+ + G ++
Sbjct: 183 AAFSTDGLTIVHTGDSVPSAPHIAMTVSMLRDAGVEVDDS-APDRWRVSPGPIGA--RDWV 239

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S++ FLA A ++GG V + G T S+Q ++L + +V + + V
Sbjct: 240 IEPDLNSNVPFLAAAVVSGGAVRITGWPTVSIQPADTILKILAGLNGEVRKGSSYLEVQ- 298

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMVAI 367
G + IDV++ + ++A ++A +A AD + +R +A R ET+R+ A+
Sbjct: 299 -----GATNYGGIDVDLRDVGELAPSVAAAMALADPGSVSRLRGIAHLRGHETDRLAAL 352

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGC 427
TE+ +G EE D +IT E ++ +Y DHRMA A ++ + + D G
Sbjct: 353 STEINGIGGCETEEDGLVITARE-MHGGTWSSYADHRMATAGAIIGLRVPGIEVEDIGT 411

Query: 428 TRKTFPDY 435
T KT PD+
Sbjct: 412 TAKTLPDF 419

>ref|YP_875152.1| 5-enolpyruvylshikimate-3-phosphate synthase [Cenarchaeum symbiosum
A]
gb|ABK76848.1| 5-enolpyruvylshikimate-3-phosphate synthase [Cenarchaeum symbiosum
A]
Length = 414

Score = 162 bits (410), Expect = 9e-38, Method: Compositional matrix adjust.
Identities = 132/422 (31%), Positives = 209/422 (49%), Gaps = 26/422 (6%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+ GTV P SKS ++R++ LA+LSEGT+ + N+L+SED + A R G + D
Sbjct: 5 ELRGTVSCPPSKSYTHRMVFLASLSEGTSRRIKLNHSEDAEATMRACRGFGADITED--G 62

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G P + + + N+G +R A AGG + + G +++RP
Sbjct: 63 SDLVIRGNPEVKPAD-----IDVANS GTTIRIAAAVAALAGGRSN--MTGDSSIQKRP 113

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G L+ L+ +GA C PP+ V G + GG + G +SSQ++SALLMAAPL
Sbjct: 114 MGPLLEALEAIGAR--CVSEEGSPPLSVEGP--IQGGAASIRGDVSSQFISALLMAAPLT 169

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
VE+ I + +S PY+ T+ M +FGV+ + ++ ++ G YK V D
Sbjct: 170 PMGVELSITGEPVSRPYIGATISAMAKFGVQVVAADHKKYGVRPG-GYKG-TEVVVPPD 227

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+ S LA + +TG + +E + QGD F +LE +G + + + + PPR
Sbjct: 228 YSTLSLLLAASVLTGDLGLEIEAENS DLPQGDKAFLGILEQLGVTLRPGK-RIATSSPPR- 285

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L ++ PD+ L+++AL D I +V R+KET+R+ + EL K
Sbjct: 286 -----LNGGTFDLGDTPLDPLPPLSILALKCD-RMEIVNVGHARLKETDRIGILCRELGK 338

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
LG +EE D +I L+ +D DHR+ MAF +A IRD ++P
Sbjct: 339 LGLDIEERKDGMLIRTGGGLHGAELDEPGDHRLFMAFCIAGMHLGDCVIRDTDSVAVSYP 398

Query: 434 DY 435
+
Sbjct: 399 GF 400

>ref|YP_001069689.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
JLS]
sp|A3PWC1.1|AROA_MYCSJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABN97198.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
JLS]
Length = 438

Score = 162 bits (410), Expect = 9e-38, Method: Compositional matrix adjust.
Identities = 134/429 (31%), Positives = 214/429 (49%), Gaps = 34/429 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALS--EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ T+ +PGSKS +NR L+LAAL+ +GT+ + L S D M+GAL+TLG VE+
Sbjct: 16 VHATLTIPGSKSQTNRALVLAALATPQGTSTISGALRSRDTLMIGALQTLGFDVES--- 72

Query: 73 AKRAVVVGCGGKFPVEDAKEEV---QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
VG V ++ G AG +R L AA T DG +
Sbjct: 73 -----VGTDSDLRVGGGLAPAAGARVDCGLAGTVLRFLPP--VAALSTETVEFDGDEQA 124

Query: 130 RERPIGLDVLVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RPI L+ GL+ LG +D D P RV G G + GG V++ S SSQ++S L+++
Sbjct: 125 RARPIAPLLAGLQSLGVRIDG---DGLPFRVRGEGSVAGGTVEIDASASSQFVSGLMLS 180

Query: 190 APLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
L + I + + S P+V MT+ ++ GV+ + +++ +R+ ++ G+ + ++
Sbjct: 181 GALFRDGLTIVHTGESVPSAPHVAMTVSMLRDAGVEVDDTET-NRWTVRPGRV--AARHW 237

Query: 249 YVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A FL+ ++GG V V G S Q +LE +GA V +E+ + V
Sbjct: 238 TIEPDLNNAVPFLSAGVVSGGAVRVTVGWPVAVSTQPAAAIMAILEKVGAVVRQSESYLEVQ 297

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVMATLAVVALFAD--GPTAIRDVASWRVKETERMVA 366
G + + DV+++ + ++ +A +A A + +R VA R ET+R+ A
Sbjct: 298 -----GTRQYQGFVDVLDHVGELTPAVAALAAVATPGAVSRLRGVAHLRGHETDRLAA 350

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTVIRDPG 426
+ E+ LG EE D +IT L+ +Y DHRMAMA ++ V I D
Sbjct: 351 LSAEINGLGGQCEETADGLVIT-AAPLHGGVWHSYADHRMAMAGAIVGLRTPGVEIEDIA 409

Query: 427 CTRKTFPDY 435
T KT P++
Sbjct: 410 TTAKTLPEF 418

>ref|YP_003938566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum S17]
gb|ADO52992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum S17]
Length = 476

Score = 162 bits (410), Expect = 1e-37, Method: Compositional matrix adjust.
Identities = 141/444 (31%), Positives = 211/444 (47%), Gaps = 25/444 (5%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D
Sbjct: 43 LNATVTIPGSKSLSNRYLILAAALGAKPVTLVGLLSRDTLMMGALSALGVRCIDIDPEND 102

Query: 75 RAVVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V V P E + V ++ G AG MR + A +A DG + R
Sbjct: 103 TTVTV-----TPPESGRFSGNVGVYCGLAGTVMRFVPGALALFA--DAPVRFDDGDDQAYAR 155

Query: 133 PIGDLVVGLKQLGADVDCF----LGTDCPPVRVNG---IGGLPGGKVKLSGSISSQYLS 184
P+ ++ GL+QLGA V+ L P R +G G KV + S SSQ++S
Sbjct: 156 PMQPVLDGLEQLGARVEYHGEHGRLPFTITPPRHDGEQADDGSAAAKVSIDSSGSSQFIS 215

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
 LL+ G +E+ +K S+P++ MT+ + A +D R + G +
 Sbjct: 216 GLLLIGSRLPGGLELRHTGEKTPSLPHIRMTVADVNGASGNAT-ADEESRVVRVGHAAALQ 274

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
 P+ VE D S+A+ FL A I GGTV V + Q LE MGA+V++ E
 Sbjct: 275 LPERVVVEPDLSNAAPFLGAALIAGGTVRVPHWPAETTQPGGLLPGYLERMGARVSFPPEE 334

Query: 304 SVTVTGPPREPFGFRKHLKAI-DVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
 E G H+ + D ++ ++A +LA + FAD PT + + R ET
 Sbjct: 335 DGVRYC---EVSGDGHVHGLGDFDLTAAGEIAPSLAAILAFADAPTRMLGIGHLRGHETN 391

Query: 363 RMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
 R+ A+ TE+T++G E D IT P E+L+ +++Y DHRMA ++ A V
 Sbjct: 392 RLEALVTEITRIGGEARELEDGIEITPVPVERLHGEVMESYADHRMATFAAMIGLAVPGV 451

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
 I + TRKT PD+ + + ++
 Sbjct: 452 RIVNVETTRKTLPDFVGMWTGMLE 475

>ref|YP_002307523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermococcus
 onnurineus NAl]
 gb|ACJ16626.1| 5-enolpyruvylshikimate-3-phosphate synthase [Thermococcus
 onnurineus NAl]
 Length = 402

Score = 162 bits (410), Expect = 1e-37, Method: Compositional matrix adjust.
 Identities = 137/439 (31%), Positives = 221/439 (50%), Gaps = 42/439 (9%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
 +++P+ E++G V+ P SKS ++R LA L+EG + V L S+D L A+R G S
 Sbjct: 3 VIIRPVGEVTEVEEAPPSKSYTHRAYFLALLAEGRSKVKRPLVSDDTLATLNIRAIFGAS 62

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
 VE + +++ K DA E +G R A + GG +T ++G
 Sbjct: 63 VEGE-----SIIPPEWPKGAFIDAHE-----SGTTARIALAVASIGGGEST--VNGG 107

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
 R+RERP G+LV L++ GA+++ + P+RV G L V++ S SSQ+ +AL
 Sbjct: 108 RRLRERPFGEVLVRLRKAGAEIEG---ERLPLRVIG-RNLRRRDVEVDASTSSQFATAL 162

Query: 187 LMAAPLALGDVEIEI-IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
 L+ V +E+ I + +S PY+E+T R ++ FG + +D FYI+ G S
 Sbjct: 163 LIIG---AKVGMEVLIKRSVSRPIYEVARTLKAFGADFR-EGFD-FYIEPGITGTS- 215

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
 V GD SSAS+FLA A+ G V + +Q D + L GA+V V
 Sbjct: 216 --FTVPGDYSSASFFLAAGALY-GRVKIRNLDPKDVQADRAIIDALREFGAEVVRVGRNYV 272

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
 + L+ ++++ + PD+ LAVVA +A+G + +R R KE++R+
 Sbjct: 273 EAE-----KGELRGVEMDCSDFPDLPVLAVVASAEGRSVLR-ARQLRFKESDRVR 323

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRD 424
 A+ L+++G V E PD I + +T++DHR+AMA +AA A I +
 Sbjct: 324 AMAVNLSRMGIRVRELPDGLEIEGG-RPKGGQFETFNDHRIAMAMVVAALGARGESVIPE 382

Query: 425 PGCTRKTFPDYFDVLSTFV 443
 G K++P +F+ L V
 Sbjct: 383 TGSVSKSYPGFNDLRLRV 401

>ref|YP_003373856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gardnerella vaginalis
 409-05]
 gb|ADB14644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gardnerella vaginalis
 409-05]
 Length = 461

Score = 162 bits (410), Expect = 1e-37, Method: Compositional matrix adjust.
 Identities = 139/435 (31%), Positives = 218/435 (50%), Gaps = 23/435 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--D 70
++ +++PGSKSLSNR L+LAAL + V+ LL S D M+ AL T G+ E+ +
Sbjct: 29 HQLKAYIEVPGSKSLSNRYLILALALGTSVVLQGLLRSDTELMINALSTFGVRCESLNE 88

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
K V+ G F V D E ++ G AG MR + A A N DG +
Sbjct: 89 DGTKLRVIPPEDGIFRVPDPAE---VYCGLAGTVMRFVAAALALFA--NKAVRFDGDKQAY 143

Query: 131 ERPIGDLVVGLKQLGADV-----DCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RP+ ++ GL+QLGA V + FL T PP I V++ S SSQ++S
Sbjct: 144 ARPMKPVLDGLEQLGARVKYHEEGFLPFTITPPSVEFKINNFSEKIVQIDSSSSSQFIS 203

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQK 241
ALL+ G +E++ I D L S+P++ MT+ + + G V + W ++K K
Sbjct: 204 ALLLIGSRIPGGLELKHIGDTLPSMPHIRMTMDDICKAGGIVNMTSNAMW---HVKE-SK 259

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+E D S+A+ FL + I GG+V++ +S Q +LE M AKV++
Sbjct: 260 INLANVVTIEPDLNAAAPFLGASLIAGGSVSIPNWPFSSTQPGGLLPGILETMCAKVSFE 319

Query: 302 ETSVTVTGPPPREPFGRKHLKAID-VNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+TS E G +KAI ++++ ++A ++A + FADGP+ + +A R E
Sbjct: 320 KTSDDAGIMHVESDGA--IKAIPYLDLSAAGEIAPSAAILAFADGPSELHGIAHLRGHE 377

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
T R+ A+ EL ++G +E D I P ++ ++TY DHRMA ++ +
Sbjct: 378 TNRLQALVNELNRVGIGAKELEDGIRIEPSNHHMGEVMEYADHRMATFAAMLGLRIENI 437

Query: 421 TIRDPGCTRKTFPDY 435
I++ TRKT PD+
Sbjct: 438 RIKNISTTRKTIPDF 452

>ref|ZP_06927588.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gardnerella vaginalis
AMD]
gb|EFH27149.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gardnerella vaginalis
AMD]
Length = 453

Score = 162 bits (410), Expect = 1e-37, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 218/435 (50%), Gaps = 23/435 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--D 70
++ +++PGSKSLSNR L+LAAL V+ LL S D M+ AL T G+ E+ +
Sbjct: 21 HQLKAYIEVPGSKSLSNRYLILALALGTSVVLQGLLRSDTELMISALSTFGVRCESLNE 80

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
K V+ G F + D E ++ G AG MR + A A N DG +
Sbjct: 81 DGTKLRVIPPEDGVFRIPDPAE---VYCGLAGTVMRFVAAALTLFA--NKAVRFDGDKQAY 135

Query: 131 ERPIGDLVVGLKQLGADV-----DCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RP+ ++ GL+QLGA V + FL T PP + I V++ S SSQ++S
Sbjct: 136 ARPMKPVLDGLEQLGARVKYHEEGFLPFTITPPAIESRINDFSEKIVQIDSSSSSQFIS 195

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQK 241
ALL+ G +E++ I D L S+P++ MT+ + + G V + W ++K K
Sbjct: 196 ALLLIGSRIPGGLELKHIGDTLPSMPHIRMTMDDICKAGGVNMTSNAMW---HVKE-SK 251

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+E D S+A+ FL + I GG+V++ +S Q +LE M AKV++
Sbjct: 252 IALSDTVTIEPDLNAAAPFLGASLIAGGSVSIPNWPFSSTQPGGLLPGILEKMCACVSFE 311

Query: 302 ETSVTVTGPPPREPFGRKHLKAID-VNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+TS E G +KAI ++++ ++A ++A + FADGP+ + +A R E
Sbjct: 312 KTSDDAGIMHVESDGS--IKAIPYLDLSAAGEIAPSAAILAFADGPSELHGIAHLRGHE 369

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
T R+ A+ EL ++G +E D I P ++ ++TY DHRMA ++ +
Sbjct: 370 TNRLQALVNELNRVGIGAKELEDGIRIEPSNHHMGEVMEYADHRMATFAAMLGLRIENI 429

Query: 421 TIRDPGCTRKTFFPDY 435
I++ TRKT PD+
Sbjct: 430 RIKNISTTRKTIPDF 444

>ref|ZP_07456280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium ATCC 27679]
ref|ZP_07695387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium JCVIHMP022]
gb|EFM41447.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium ATCC 27679]
gb|EFO78430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium JCVIHMP022]
Length = 450

Score = 162 bits (409), Expect = 1e-37, Method: Compositional matrix adjust.
Identities = 135/439 (30%), Positives = 208/439 (47%), Gaps = 22/439 (5%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ TV +PGSKSLSNR L+LAAL + LL S D M+ ALR LG+ E D A
Sbjct: 19 KPLNATVVVPGSKSLSNRYLILAAALGSAPVRLVGLLRSDTELMDALRALGVRCEIDAA 78

Query: 73 AKRAVVVCGCGKFPVEDA-KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V V P D + ++F G AG MR + A G + +G +
Sbjct: 79 TDTTVTV---VPPANDRFRGNTKVFCLAGTVMRFVPLAMFADGPVDF--EGDEQAYA 132

Query: 132 RPIGDLVVGLKQLGADVDCF-----LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
RP+ ++ GL+QLGA ++ L P V+ V + S SSQ++S L
Sbjct: 133 RPMKPVLDGLQQLGATIEYHGEGRLPFTITPPTVDPAAARATPSVVSIDSSGSSQFISGL 192

Query: 187 LMAAPLAGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ G +E+ +K S+P++ MT+ + GV + + + ++ G + P
Sbjct: 193 LLVGSRVPGGLELHHTGEKTPSLPHIRMTVADLRGSGVSVQADEEARVWTVRPG-AVQLP 251

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETS 304
VE D S+A+ FL A I GGTV V + Q LE MGAKV++ +E
Sbjct: 252 NAVTVEPDLNNAAPFLGAALIAGGTVRVPHWPENTTQPGGLLPGYLERMGAKVSFPSENG 311

Query: 305 VTVTGPPREPFRGRKHLKAI-DVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ E G H+K + D ++ ++A +LA V +FAD PT + + R ET R
Sbjct: 312 IRYC---EVRGDGHKGLGDFDLTAAGEIAPSLA AVLVFAD EPTRLMGIGHLRGHETNR 367

Query: 364 MVAIRTELTKLGASVEEGPDYCIITP--PEKLNVT AIDTYDDHRMAMAFSLAACAEVPVT 421
+ A+ E+ ++G E D I P E L + ++TY DHRMA ++ +
Sbjct: 368 LEALVNEIKRIGGEARELSDGLEIVPVSSENLKPSEMETYADHRMATFAAMLGLRIKGIQ 427

Query: 422 IRDPGCTRKTFFPDYFDVLS 440
+ + T KT PD+ ++ +
Sbjct: 428 VHNVATTAKTLPDFVNWN 446

>dbj|BAJ30694.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Kitasatospora setae KM-6054]
Length = 439

Score = 162 bits (409), Expect = 1e-37, Method: Compositional matrix adjust.
Identities = 137/430 (31%), Positives = 207/430 (48%), Gaps = 25/430 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS +NR L+LAAL++G V L S D M LR LG++VE A
Sbjct: 15 VDATVTIPGSKSATNRALVLAALADGPGWVRRPLRSRDSQLMADGLRALGVTVEETVNAA 74

Query: 75 RAVVVCGCGK-----FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
G GG P E ++ +GNAG MR L A G + DG PR
Sbjct: 75 SG---GTGGGEAWRVIPAERLLGPARVDVGNAGTVMRFLPPLAALADGPVHF--DGDPRS 129

Query: 130 RERPIGDLVVGLKQLGADVDCFGLTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
ERP ++ L+ LGA +D G P+ V+G G L GG V++ S SSQ++SALL++
Sbjct: 130 HERPQHGVIDALRVLGARIDG-GRGGFPLTVHGTGALDGGPVEVDASSSSQFISALLS 188

Query: 190 APLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKA---EHSDSWDRFYIKGGQKYKSP 245

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      A      VEI      + S+P++ MT+ ++ + G +      E      D + + G
Sbjct: 189 AARFQHGVEIRNTGGSVPSLPHIRMTVDMVRKAGGQVDAPEGDGGEKDVWRVTPGALIG-- 246

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      ++ VE D S+A+ F A A TGG VTV      + Q + E+ MG +T+ +
Sbjct: 247 RDLVVEPDLNSAAPPFAAALATGGRVTVRDPWRHTYQPGDQLREIFTAMGGSCEFTDEGL 306

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
      TG +      + I+ +++ + ++ +A VA A + + +A R+ ET+R+
Sbjct: 307 EFTGTGK-----ISGIEADLHDVGELTPVIAAVALAGSESHLYGIAHLRLHETDRLA 359

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
      A+ E+ LG V E D I P L+ TY+DHR+A A ++ V + D
Sbjct: 360 ALAREINALGGVDTETEDGLRIR-PRPLHGGVFHTYEDHRLATAAAVLGLLVGVLVEDV 418

Query: 426 GCTRKTFPDY 435
      T KT PD+
Sbjct: 419 ATTAKTLPDF 428

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>ref|ZP_02918899.1| hypothetical protein BIFDEN_02218 [Bifidobacterium dentium ATCC
27678]
ref|YP_003360463.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium Bdl]
gb|EDT46367.1| hypothetical protein BIFDEN_02218 [Bifidobacterium dentium ATCC
27678]
gb|ADB09639.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
dentium Bdl]
Length = 450

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Score = 162 bits (409), Expect = 1e-37, Method: Compositional matrix adjust.
Identities = 135/440 (30%), Positives = 209/440 (47%), Gaps = 24/440 (5%)

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Query: 13 KEISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++ TV +PGSKLSNR L+LAAL + LL S D M+ ALR LG+ E D A
Sbjct: 19 KPLNATVVVPGSKLSNRYLILAAALGSVPVRLVGLLRSDTELMMDALRALGVRCEIDAA 78

Query: 73 AKRAVVV--GCGGKFVPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      V V G+F + ++F G AG MR + A G + DG +
Sbjct: 79 TDTTVTVVPPADGRF-----RGNTKVFCLAGTVMRFVPGLAMFADGPVDF--DGDEQAY 131

Query: 131 ERPIGDLVVGLKQLGADVDCF-----LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      RP+ ++ GL+QLGA ++ L P V+ V + S SSQ++S
Sbjct: 132 ARPMPKPVLDGLQQLGATIEYHGEEGRLPFTITPPTVDPAAARATPSVVSIDSSGSSQFISG 191

Query: 186 LLMAAPLALGDVEIEII-DKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      LL+ G +E+ +K S+P++ MT+ + GV + + + ++ G +
Sbjct: 192 LLLVGSRVPGGELHHTGEKTPSLPHIRMTVADLRGSGVSVQADEEARVWTVRPG-AVQL 250

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TET 303
      P VE D S+A+ FL A I GGTV V + Q L+ MGAKV++ +E
Sbjct: 251 PNAVTVPEPDLNSAAPFLGAALIAGGTVRVPHWPENTTQPGGLPGYLKRMGAKVSFLSEN 310

Query: 304 SVTVTGPPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      + E G H+K + D ++ ++A +LA V +FAD PT + + R ET
Sbjct: 311 GIRYC----EVRGDGHIKGLGDFDLTAAGEIAPSLAAVLVFADEPTRMLGIGHLRGHETN 366

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
      R+ A+ E+ ++G E D I P E L + ++TY DHRMA ++ +
Sbjct: 367 RLEALVNEIKRIGGEARELSGLEIVPSSSENLPSEMETYADHRMATFAAMLGLRIKGI 426

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
      + + T KT PD+ ++ +
Sbjct: 427 QVHNVAATAKTLPDFVNMWN 446

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>ref|ZP_02456732.1| bifunctional prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Burkholderia pseudomallei 9]
Length = 149

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Score = 161 bits (408), Expect = 1e-37, Method: Compositional matrix adjust.

Identities = 82/146 (56%), Positives = 101/146 (69%), Gaps = 8/146 (5%)

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
GA VT + + V G G H L ID++ N +PD AMT+AV ALFADGP+ +R+
Sbjct: 1 GANVTMGDDWIEVRG-----IGHDHGRLAPIDMDFNLIPDAAMTIAAALFADGPSTLRN 55

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTI-IDTYDDHRMAMAFS 411
+ SWRVKET+R+ A+ TEL K+GA+VEEG DY ++TPP +L A IDTYDDHRMAM FS
Sbjct: 56 IGSWRVKETDRIAAMATELRKVGATVEEGADYLVVTPPAQLTPNASIDTYDDHRMAMCFS 115

Query: 412 LAACAEVPTVIRDPGCTRKTFPDYFD 437
L + VPV I DP C KTFPDYFD
Sbjct: 116 LVSLGGVPVRINDPKCVGKTFPDYFD 141

>ref|YP_001538880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora arenicola
CNS-205]
gb|ABV99889.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora arenicola
CNS-205]
Length = 433

Score = 161 bits (408), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 130/432 (30%), Positives = 206/432 (47%), Gaps = 23/432 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S T++LPGSKSL+ R L+L+ L+ G + + L + D M LR +G+ + +
Sbjct: 22 VSTTLRLPGSKSLTARALVLSGLATGPSTLARPLRARDTELMADGLRAMGVHMSISDDER 81

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P+ + +G AG MR L A G T+ DG P+ R RP+
Sbjct: 82 WLVR-----PHPLAG---PAHVDVGLAGTVMRFLPPVAGLADGQITF--DGDPPQARLRPL 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
G L+ L +LG + T P+ V G G + GG+V + S SSQ +S LL+AAP
Sbjct: 132 GPLLDALSRLGVRITTP-PTGSLPLTVLGGGQIRGGEVVIDASASSQLVSGLLLAAPHFD 190

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G V + + S P++ MT+ ++ G + + D + ++ G + +E D
Sbjct: 191 RGVVVRHVGPVPVPSAPHLRMTVHMLRSAGAAVDDTAP-DVWTVPEPGLAG--RGWEIEPD 247

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S A F A A +TGG VTV G S+Q + +L+ MG +V+ + +TV
Sbjct: 248 LSGAVPFFAAALVTGGEVTVTGWPGGSVQPVVERLRGLLQAMGGEVSLSTAGLTVR----- 302

Query: 314 PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G L + +++ + ++ L +A+ AD P+ +A R ET+R+ ++ E T
Sbjct: 303 --GTGALHGLTADLSVSELTPALTALAMLADSPSRFTGIAHIRGHETDRITSLAREFTA 360

Query: 374 LGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFP 433
LGA + E D I P L +TY DHRMA A ++ A + + D CT KT P
Sbjct: 361 LGADLTEFHDGLAIR-PRPLRSGVFETYHDHRMAHAAAITGLAVPGIELSDVACTSKTMP 419

Query: 434 DYFDVLSTFVKN 445
++ + S V
Sbjct: 420 EFPALWSAMVTG 431

>ref|ZP_05902570.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia
hofstadii F0254]
gb|EEX73483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia
hofstadii F0254]
Length = 433

Score = 161 bits (408), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 127/441 (28%), Positives = 224/441 (50%), Gaps = 38/441 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
++GT+++P SKS S+R ++ AAL+E + +DNL S D+ + G + +
Sbjct: 10 LNGTIEIPPSKSYSHRAVIAAALAENKDNRKSKIDNLKFSVDITTTDIMENWGAKINRE 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130


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      +++      ++G GKK      +D  + VQ      +G  +R L      + DG  ++
Sbjct: 70  ESSLE--IIGNGGKVVPKD--KYVQC--NESGSTIRFLIP--IGITDENELIFDGKGKLV 121

Query: 131  ERPIGDLVVGLKQLGADVDCFLGTDPC--PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      +RP+      + G      F  +      P+ VNG  L  G  ++ G+ISSQ+++ LL
Sbjct: 122  DRPLDSYYRIFDKQG----IFYKNENGKLPILTUNG--KLKAGNYEIDGNISSQFITGLLY 175

Query: 189  AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      A PL  GD ++ I  L S  Y+++TL +++  G++  +++ +  F IKG Q YK P +
Sbjct: 176  ALPLLDGDSKLTINKNLESKYIDLTLLEILKLAGIEIVNNN-YKSPDIKGNQIYK-PFDY 233

Query: 249  YVEGDASSASYFLAGAAITGGTVTVEGC---GTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      VEGD S  ++++  I+      C      SLQGD +  E++E MGA +  +  V
Sbjct: 234  TVEGDYSQVAFWIVAGIISANKDNEVKCLHVNKNSLQGDREIIEIVERMGADIEIFDNYV 293

Query: 306  TVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
      V  P  +      K  +++++ PD+  L V+  ++G T I +  R+KE++R+
Sbjct: 294  LVR-PSK-----TKGTVIDISQCPDIGPILTVLGALSEGETRIINGERLRIKESDRIT 345

Query: 366  AIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
      +I+TEL KLGA+V E  D  II  E      ++ ++DHR+AM+ ++A+  E  +  +
Sbjct: 346  SIKTELNKLGANVAEEGDSLIIQGVVEFTGGVTVNAWNDHRIAMSLAIASTRCEKEIILE 405

Query: 424  DPGCTRKTFFPDYFDVLSTFVK 444
      +  RK++P ++D  FVK
Sbjct: 406  EAESVRKSYPHFWD---DFVK 423

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>ref|ZP_05631302.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
      gonidiaformans ATCC 25563]
ref|ZP_07914369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
      gonidiaformans ATCC 25563]
gb|EFS28839.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
      gonidiaformans ATCC 25563]
Length = 408

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Score = 161 bits (408), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 118/432 (27%), Positives = 209/432 (48%), Gaps = 50/432 (11%)

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Query: 14  EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      + G VK+P SKS  +R ++ A+ S+  +V+DN+ S+D+  L  ++ LG  +E
Sbjct: 7  HLKGVKIPSSKSYCHRYIIAASFSSKESVLDNVSMSSDDIKSTLEIVKKLGAKIEQ---K 63

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT-AAVTAAGGNATYVLDGVPRMRER 132
      + ++  K  + D KE +  F  +  +R L  ++T      Y  +P+  R
Sbjct: 64  NQTFIIQ---KKSICDKKEPLYFFCSASASTLRFLIPISITNPRKVFFYKGHNLPK---R 117

Query: 133  PIGDLVVGLK-----QLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
      P+      L+      Q  + D +  D      G L  GK  ++G++SSQ+++AL
Sbjct: 118  PLSPFFPILEASHVSFQTKGEKDLICIQLD-----GQLKSGKYEIAGNVSSQFITAL 168

Query: 187  LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      L A PL  GD EI I+  L S  Y+EMTL ++E+F ++  +  + FYI G Q Y+S
Sbjct: 169  LFALPLLEGDSEISILGNLESRAYIEMTLVDLEKFQIQIFRTK--NTFYIPGNQIYQSYS 226

Query: 247  NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      + +EGD S A++FL  ++ G  + ++G  S Q D  E+L M+  T  E  +
Sbjct: 227  TS-IEGDYSQAFFLVANSL-GNQIIQGLSQESKQADY---EILSMIKKLETKKEDEIL 281

Query: 307  VTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
      V      ++ ++ PD+  L++ A  G T I+++  ++KE +R+ A
Sbjct: 282  V-----LDGSQCPDIVPILSLRAALTPGKTMIQNIERLKIKECDRLHA 324

Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLA-ACAEVPVTIRDP 425
      L  +LGA V E      L  ++ ++ DHRMAM  ++A +C +  +  + D
Sbjct: 325  TAEILNLGAKVIEHTASLEFDGVSHLIGNSVSSFGDHRMAMMIAIASSCCQGEIILDDG 384

Query: 426  GCTRKTFFPDYFD 437
      C  K++P++++
Sbjct: 385  NCVSKSYPNFWE 396

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>ref|YP_003970881.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Bifidobacterium
bifidum PRL2010]
gb|ADP35844.1| AroA 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum PRL2010]
Length = 476

Score = 161 bits (408), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 140/444 (31%), Positives = 211/444 (47%), Gaps = 25/444 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSLSNR L+LA L + LL S D M+GAL LG+ + D
Sbjct: 43 LNATVTIPGSKSLSNRYLILAVLGAKPVTLVGLLRSDTELMMGALSALGVRCDIDPEND 102

Query: 75 RAVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V V P E + V ++ G AG MR + A +A DG + R
Sbjct: 103 TTVTV-----TPPESGRFSGNVGVYGLAGTVMRFVPLALFA--DAPVRFDDQAYAR 155

Query: 133 PIGDLVVGLKQLGADVDCF----LGTDCPPVRVNG---IGGLPGGKVKLSGSISSQYLS 184
P+ ++ GL+QLGA V+ L P R +G G KV + S SSQ++S
Sbjct: 156 PMQPVLDGLEQLGARVEYHGEHGRLPFTITPPRHDEQADDGSAAAKVSIDSSGSSQFIS 215

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
LL+ G +E+ +K S+P++ MT+ + G A +D R + G +
Sbjct: 216 GLLLIGSRLPGGLELRHTGEKTPSLPHIRMTVADVNGAGGNAT-ADEESRVVRVGHAAALQ 274

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P+ VE D S+A+ FL A I GGT V + Q LE MGA+V++ E
Sbjct: 275 LPERVVVEPDLSNAAPFLGAALIAGGTVRVPHWPVETTQPGGLLPGYLERMGARVSFPPEE 334

Query: 304 SVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
E G H+ + D ++ ++A +LA + FAD PT + + R ET
Sbjct: 335 DGVRYC---EVSGDGHVHGLGDFDLTAAGEIAPSLAAILAFADAPTRMLGIGHLRGHETN 391

Query: 363 RMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TE+T++G E D IT P E+L+ +++Y DHR+A ++ A V
Sbjct: 392 RLEALVTEITRIGGEARELEDGIEITPVPVERLHGEVMEASYADHRIATFAAMIGLAVPGV 451

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
I + TRKT PD+ + + ++
Sbjct: 452 RIVNVETTRKTLPDFVGMWTGML 475

>ref|ZP_06417370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. EUN1f]
gb|EFC79823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Frankia sp. EUN1f]
Length = 457

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 155/451 (34%), Positives = 221/451 (49%), Gaps = 41/451 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS +NR L+LAAL++G + + L S D M ALR LG V A
Sbjct: 24 VRATVAVPGSKSGTNRALVLAALADGVSRLRGLRSDTLMAAALRNLAQV--DAPG 81

Query: 75 RAVVVGCGGK-----FPVEDAKEEV-QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A G GG PV + + GNAG R A T A G+ + DG PR
Sbjct: 82 TATDPGPGGADLVVAGPVGAIHGGLASIDCGNAGTVARFTPALATLAKGDVHF--DGDPR 139

Query: 129 MRERPIGDLVVGLKQLGADVDCFGLTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
MRERP+ L+ L++LGA +D D P V G GG+ GG V + S SSQ +S LL+
Sbjct: 140 MRERP+LPLLAALRELGARIDG----DRMPFTVRGGGIAGGAVTVDASTSSQLVSGLLL 195

Query: 189 AAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWD 232
AA G +L S PY++MT+ + GV H D S
Sbjct: 196 AASRFERGATVTHAGHRLPSGPYLDMTVADLRAAGVTV-HVDVPGPGDRPAGMADAASIR 254

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLE 292
R+ ++ G +P + +E D +SA+ FLA A TGG VT+ G + Q E+L
Sbjct: 255 RWRVEPGGP--APLDRVIEPDLNSATAFLAAAVATGGQVTIPGWPAPTEQPGRLLELLV 312

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352

MGA+ + VTG R + ID +++ + A L +A+ AD P+ +R
Sbjct: 313 AMGAEEQRPEGLRVTGGGR-----IAGIDADLSDFGEAPVLTGLAVLADSPSRLRG 365

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
+A R++ET+R+ A+ +EL KLGA + D I P L +D + DHR+AM F++
Sbjct: 366 IAHLRLQETDRLAALASELGKLGARITVTDDGLRID-PVPLRGARLDPHADHRLAMTFAV 424

Query: 413 AACAEVPVTIIRDPGCTRKTFPDYFDVLSTFV 443
A VTI D T KT PD+ + ++ +
Sbjct: 425 VGLAVPGVTIDDIATTGKTVPDFARMWTSML 455

>ref|ZP_04664941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis CCUG 52486]
gb|EEQ54968.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis CCUG 52486]
Length = 445

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 139/443 (31%), Positives = 214/443 (48%), Gaps = 23/443 (5%)

Query: 13 KEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKLSNRYLILAAALGSKPVTILIGLLRSRDTLMMGALEALGVRCDDVSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPLATLPAAQAQVSIDSSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + + P
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE MGAKV++ T+
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQMGAQVSFP----TI 303

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 DGVRYCEVTGDGTVRGLGTFDLTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP-VTI 422
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P + +
Sbjct: 364 ALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPDIEV 422

Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
+ TRKT PD+ + S ++
Sbjct: 423 INVATTRKTLPDFVGMWSGMLRQ 445

>ref|ZP_03646185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum NCIMB 41171]
Length = 476

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 206/435 (47%), Gaps = 25/435 (5%)

Query: 15 ISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKLSNR L+LA L + LL S D M+GAL LG+ + D
Sbjct: 43 LNATVTVTPGSKLSNRYLILAVLGAKPVTLVGLLSRDTLMMGALSALGVRCDDIDPEND 102

Query: 75 RAVVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 132
V V P E + V ++ G AG MR + A +A DG + R
Sbjct: 103 TTVTV-----TPPESGRFSGNVGVYCGLAGTVMRFVPGALFA--DAPVRFDDQAYAR 155

Query: 133 PIGDLVVGLKQLGADVDCF-----LGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLS 184
P+ ++ GL+QLGA V+ L P R +G G KV + S SSQ++S

Sbjct: 156 PMQPVLGDGLEQLGARVEYHGEHGRLPFTITPPRHDGKQADDGSAAKVSIDSSGSSQFIS 215

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
LL+ G +E+ +K S+P++ MT+ + A +D R + G +

Sbjct: 216 GLLLGISRLPGGLELRHTGEKTPSLPHIRMTVADVNGASGNAT-ADEESRVWRVGHAAALQ 274

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P+ VE D S+A+ FL A I GGTV V + Q LE MGA+V++ E

Sbjct: 275 LPERVVVEPDLSNAAPFLGAALIAGGTVRVPHWPAETTQPGLLPGYLERMGARVSFPPEE 334

Query: 304 SVTVTGPPREPFGGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
E G H+ + D ++ ++A +LA + FAD PT + + R ET

Sbjct: 335 DGVRYC---EVSGDGHVHGLGDFDLTAAGEIAPSLAAILAFADAPTRMLGIGHLRGHETN 391

Query: 363 RMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPV 420
R+ A+ TE+T++G E D IT P E+L+ +++Y DHRMA ++ A V

Sbjct: 392 RLEALVTEITRIGGEARELEDGIEITPVVERLHGEVMSYADHRMATFAAMIGLAVPGV 451

Query: 421 TIRDPGCTRKTFPDY 435
I + TRKT PD+

Sbjct: 452 RIVNVETTRKTLPDF 466

>ref|ZP_05616981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_5R]

ref|ZP_07922727.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_5R]

gb|EFS20753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_5R]

Length = 408

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 117/432 (27%), Positives = 209/432 (48%), Gaps = 50/432 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G VK+P SKS +R ++ A+ ++ +V+DN+ S+D+ L ++ LG +E

Sbjct: 7 HLKGKVKIPSSKSYCHRYIIAASFACKESVLDNVMSDDIKSTLEIVKKLGAKIEQ---K 63

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT-AAVTAAGGNATYVLDGVPRMRER 132
+ ++ K + D KE + F + +R L ++T Y +P+ R

Sbjct: 64 NQTFIIQ---KKSIIYDKKEPLYFFCSESASTLRFLIPISITNPRKVFFYKGHNLPK---R 117

Query: 133 PIGDLVVGLK-----QLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
P+ L+ Q + D + D G L GK +++G++SSQ+++AL

Sbjct: 118 PLSPPFFPILEASHVSFQTKGEKDLCIQLD-----GQLKSGKYEIAGNVSSQFITAL 168

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L A PL GD EI I+ L S Y+EMTL ++E+F ++ + + FYI G Q Y+S

Sbjct: 169 LFALPLLEGDSIEISILGNLESRAYIEMTLDVLEKFQIQIFRTK--NTFYIPGNQIYQSYS 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +EGD S A++FL ++ G + ++G S Q D E+L M+ T E +

Sbjct: 227 TS-IEGDYSQAFFLVANSL-GNQIIQGLSQESKQADY---EILSMIKKLETKKEDEIL 281

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V ++ ++ PD+ L++ A G T I+++ ++KE +R+ A

Sbjct: 282 V-----LDGSQC PDIVPILSLRAALTPGKTMIQNIERLKIKECDRLHA 324

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLA-ACAEVPVTIRDP 425
L +LGA V E L ++ ++ DHRMAM ++A +C + + + D

Sbjct: 325 TAEILNLQLGAKVIEHTTSLEFDGVSHLIGNSVSSFGDHRMAMMIAIASSCCQGEIILDDG 384

Query: 426 GCTRKTFPDYFD 437
C K++P++++

Sbjct: 385 NCVSKSYPNFWE 396

>ref|ZP_07802215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum NCIMB 41171]

gb|EFR50149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
bifidum NCIMB 41171]

Length = 452

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 140/435 (32%), Positives = 206/435 (47%), Gaps = 25/435 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSLSNR L+LA L + LL S D M+GAL LG+ + D
Sbjct: 19 LNATVTIPGSKSLSNRYLILAVLGAKPVTTLVGLLRSDTELMMGALSALGVRCIDIDPEND 78

Query: 75 RAVVVGCG--GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V V G+F V ++ G AG MR + A +A DG + R
Sbjct: 79 TTVTVTPPESGRF-----SGNVGVYCGLAGTVMRFVPGALFA--DAPVRFDDQAYAR 131

Query: 133 PIGDLVVGLKQLGADVDCF-----LGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLS 184
P+ ++ GL+QLGA V+ L P R +G G KV + S SSQ++S
Sbjct: 132 PMQPVLDGLEQLGARVEYHGEHGRLPFTITPPRHDKQADDGSAAKVSIDSSGSSQFIS 191

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
LL+ G +E+ +K S+P++ MT+ + A +D R + G +
Sbjct: 192 GLLIGSRLPGGLELRHTGEKTPSLPHIRMTVADVNGASGNAT-ADEESRVVRVGHAAALQ 250

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
P+ VE D S+A+ FL A I GGTV V + Q LE MGA+V++ E
Sbjct: 251 LPERVVVEPDLNAAPFLGAALIAAGTVRVRPHWPAETTPQGGLLPGYLERMGARVSFPPEE 310

Query: 304 SVTVTGPPREPFGFRKHLKAI-DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
E G H+ + D ++ ++A +LA + FAD PT + + R ET
Sbjct: 311 DGVRYC---EVSGDGHVHGLGDFDLTAAGEIAPSLAAILAFADAPTRMLGIGHLRGHETN 367

Query: 363 RMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ TE+T++G E D IT P E+L+ +++Y DHRMA ++ A V
Sbjct: 368 RLEALVTEITRIGGEARELEDGIEITPVPVERLHGEVMESYADHRMATFAAMIGLAVPGV 427

Query: 421 TIRDPGCTRKTFPDY 435
I + TRKT PD+
Sbjct: 428 RIVNVEITRKTLPDF 442

>ref|ZP_06265222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyramidobacter
piscolens W5455]
gb|EFB91510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyramidobacter
piscolens W5455]
Length = 421

Score = 161 bits (407), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 139/429 (32%), Positives = 215/429 (50%), Gaps = 32/429 (7%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++SGT+ SKS +R+L+ AAL + + S+D+ + LR LG + A
Sbjct: 8 RKLSGTIAAIPSKSHVHRLICAALGNRPATLPCRVSQDIEATVRCLRALGAGI----A 63

Query: 73 AKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+V+ P++ +A +L G +G R +T A G A + L G ++
Sbjct: 64 VGGSVIA---VTPLDRNASGAAELDPGESGSTYRFMTPLAAALGRKARFTLRG--KLSS 117

Query: 132 RPIGDLVVGLKQLGADVDCFGLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ DL +++ GA V GTD P V G L G+ +L G++SSQ+ + LL A P
Sbjct: 118 RPMDDLWNEMERHGA-VITGKGDHPVVE---GRLTAGRYRLPGAVSSQFFTGLLFALP 172

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L G+ + I D+L S YV+MTL + FG+ S DRF + G Q+Y +P E
Sbjct: 173 LLEGNSRVLIADRLSAGYVDMTLAALAAFGIAVGRSA--DRFSVSGAQRVYTPAKLRAE 230

Query: 252 GDASSASYFL-AGAAITGGTVTVVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
GD S+A+++L AGAA G + V G SLQGD AE+L MGA+++ S+ P
Sbjct: 231 GDWSNAAFWLCAGAA--GAKLAVTGLTRPSLQGDSVVAELLRRMGAEISIAAGDSIAAA-P 287

Query: 311 PREPFGFRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ L+ +++ PD+ LAV A G TAI +V R+KE++R+ ++
Sbjct: 288 AK-----LRETCIDVGDTPLDLPALAVAAAAGKRTAIANVGRLRLKESDRVASVCGA 340

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
L LG + +I L +D DHR+AM + A+ C+E VTI
Sbjct: 341 LNALGGHAVPDGNCILIDGCGSLRGGIVDACGDHRIAMLGAAASVLCSET-VTITGAEAV 399

Query: 429 RKTFFPDYFD 437
K++P +FD
Sbjct: 400 DKSYPGFDD 408

>ref|ZP_06982068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroidetes oral
taxon 274 str. F0058]
gb|EFI16533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroidetes oral
taxon 274 str. F0058]
Length = 406

Score = 160 bits (406), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 126/436 (28%), Positives = 215/436 (49%), Gaps = 47/436 (10%)

Query: 12 IKEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++EI + LP SKS+ NR+L++ A++ G ++D +D+ G R L ++ +
Sbjct: 10 VEEIGNPISLPASKSIVNRLLIIEAIT-GKKILDQ---KDIS--CGDTRVLAELSSPT 62

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
K ++ +G AMR LTA ++ G +VL+G RM
Sbjct: 63 TRK-----YIEQSGTAMRFLTAFLSIRKGEE-FVLEGDERMSA 99

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+G LV L++LGAD++ D P+++ G G L GG +++ GS SSQY+SAL++ AP
Sbjct: 100 RPYGALVDALRRLGADIEYLQHEDYLPKIRG-GSLHGGTIEIDGSQSSQYVSALMLIAP 158

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G + I II K S+PY+ +T +M + GV E + S I Q PK VE
Sbjct: 159 TLEGLRLI-IIRKPSSLPYILLTADVMRQMGVCVEMTGS---TISIPQSEYRPKKISVE 213

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D S+A ++ A ++ T+ + T S Q D + + G +++S+ +
Sbjct: 214 ADFSAAVFWYALFIVSPRQTMELRNLTTESRQPDRIVTIAHDFGVTTTHCSDSSLILGKE 273

Query: 311 PREPFGRKHL-KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+H+ K ++ ++ PD+ L V+ + +A+ R+KE++R+ A+
Sbjct: 274 -----SVRHIPKVEYDLRHTPDIMPVLTMCCMLGVEFVLSGLANLRIKESDRIGAMVE 328

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
EL K ++ D P + +T IDT+ DHR+AMAF+L + +TI P
Sbjct: 329 ELAKCRYMLQATDDTVRWPHLQTEITKPVTTIDTHSDHRIAMAFALLR-EQRDITILSPE 387

Query: 427 CTRKTFPDYFDVLSTF 442
K++P+++ L+ F
Sbjct: 388 VVEKSYPNFWHDLAAF 403

>ref|ZP_03324214.1| hypothetical protein BIFCAT_00999 [Bifidobacterium catenulatum DSM
16992]
gb|EEB22028.1| hypothetical protein BIFCAT_00999 [Bifidobacterium catenulatum DSM
16992]
Length = 463

Score = 160 bits (406), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 136/448 (30%), Positives = 215/448 (47%), Gaps = 35/448 (7%)

Query: 13 KEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + TV +PGSKSLSNR L+LAAL + LL S D M+ ALR+LG+ E D+
Sbjct: 33 KSLDATVVVPGSKSLSNRYLILAALGHCPVRLVGLLRSDTELMMDALRSLGVRCEIDEQ 92

Query: 73 AKRAVVVGCGGKFPVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V P D + ++F G AG MR + A G + DG +
Sbjct: 93 VDTTVTV-----VPPSDGRFHGGTKVFCGLAGTVMRFVPLAMFADGPVDF--DGDEQAY 145

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
RP+ ++ GL+QLGA ++ + G T PP V+ V + S SSQ++
Sbjct: 146 ARPMKPVLDGLEQLGACIE-YHGEGRLPFTITPPQTVSQCA--EPSVVSIDSSGSSQFI 202

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+ G +E+ +K S+P++ MT+ + GV+A ++D R +
Sbjct: 203 SGLLLIGSRVPGGLELHHTGKTPSLPHIRMTVADLHGSGVRA-NADEHARVWTVQPGAV 261

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P+ VE D S+A+ FL A I GGT V ++ Q LE MGA++++
Sbjct: 262 QLPETVTVEPDLSNAAPFLGAALIAGGTVRVPHPPESTTQPGLLPGYLERMGAEIFPV 321

Query: 303 TS----VTVTGPPREPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWR 357
VTG R + + D ++ ++A +LA + +FAD PT + + R
Sbjct: 322 IDGVRYCEVTGDGR-----VSGLGDFDLTAAGEIAPSLAAILVFADAPT RMLGIGHLR 374

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAAC 415
ET R+ A+ E+T++G E PD I P +N+ ++TY DHRMA ++
Sbjct: 375 GHETNRLKALVNEITRVGGDARELPDGLAIPVPMNLKPAEMETYADHRMATFAAMLGL 434

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSFV 443
+ +++ T KT PD+ ++ + +
Sbjct: 435 KINGIQVKNIATTAKTLPDFANMWTNML 462

>ref|NP_819558.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
493]
sp|Q83E11.1|AROA_COXBU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAO90072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
493]
Length = 438

Score = 160 bits (406), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 140/436 (32%), Positives = 218/436 (50%), Gaps = 29/436 (6%)

Query: 11 PIKEISGTVKLPGSKSLNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + +SG + +PG KS+S+R +LLAA++EG T VD L D M+ AL+ +G S++
Sbjct: 7 PSQGLSGEICVPGDKSISHRAVLLAAIAEGQTQVDGFLMGADNLAMVSALQQMGASIQVI 66

Query: 71 KAAKRAVVVGGCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VV G G + P E L GN+G A+R L+ + AG VL G
Sbjct: 67 EDENILVVEGVGMTGLQAPPE-----ALDCGNSGTAIRLLSGLL--AGQPFNTVLTGDS 118

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
++ RP+ ++ L +GA +D + PP+++ G L G +L + S+Q S LL
Sbjct: 119 SLQRRPMKRIIDPLTLMGAKIDST--GNVPPLKIYGNPRLTGIHYQLPMA-SAQVKSCLL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G I P + T RL++ F + + GG K K+ +
Sbjct: 176 LAGLYARGKTCIT----EPAPSRDHTERLLKHFYTLQKDKQS--ICVSGGGKLKA-ND 227

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ GD SSA++F+ A IT G+ + C + +L+MMGA + T +
Sbjct: 228 ISIPGDISSAAFFIVAATITPGS-AIRLCRVGNPTRLGVINLLKMMGADIEVTHYTEKN 286

Query: 308 TGPPREPFGRK-HLK AIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK ID+ +++P D L + A A G T +RD A RVKET+R
Sbjct: 287 EEPTADITVRHARLKGIDIPDPVPLTIDEFPVLLIAAAVAQKTVLRDAAELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L KLG + E PD II L +++YDDHR+AMAF++A A+ PV I
Sbjct: 347 IAAMVDGLQKLGAESLPDGVIIQ--GGTLEGGEVNSYDDHRIAMAFVAGTLAKGPVRI 405

Query: 423 RDPGCTRKTFPDYFDV 438
R+ + +FP++ ++
Sbjct: 406 RNCNDNVKTSFPNFVEL 421

>ref|YP_001160527.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora tropica
CNB-440]
gb|ABP56149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinispora tropica
CNB-440]

Length = 433

Score = 160 bits (406), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 134/434 (30%), Positives = 212/434 (48%), Gaps = 31/434 (7%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S T++LPGSKSL+ R L+L+ L+ G + + L + D M LR +G V +
Sbjct: 22 VSTTLRLPGSKSLTARALVLSGLATGPSTIARPLRARDTELMANGLRAMGAHVSISDDER 81

Query: 75 RAV----VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V +VG + +G AG MR L A G T+ DG P+ R
Sbjct: 82 WLVRPHPLVG-----PAHIDVGLAGTVMRFLPPVSGGLADGRITF--DGDPQAR 127

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+G L+ L++LG + P+ V G G + GG+V + S SSQ +S LL+AA
Sbjct: 128 QRPLGLPLLDALRLGVRITSPASGSL-PLTVLGS GTIRGGEVVIDASASSQLVSGLLAA 186

Query: 191 P-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P G V + + S P++ MT++++ G + + D + ++ G +
Sbjct: 187 PHFDRGVVRHVGPVPVPSAPHLRMTVQMLRAGAAIDDTTP-DVWTVPEGPLTG--RGWE 243

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S A F A A +TGG VTV G S+Q + +L+ MG +V+ + T +TV G
Sbjct: 244 IEPDLSGAVPFFAAALVTGGEVTVTGWPGGSVPVERLRGLLQAMGGEVSLSTTGLTVRG 303

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
G H + +++ + ++ L +A+ AD P+ +A R ET+R+ A+
Sbjct: 304 -----TGSVH--GLTADLSDVSELTPALTALAMLADSPSRFTGIAHIRGHETDRISALAR 356

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTR 429
E + LGA + E D I P L+ +TY DHRMA A +A A + + D CT
Sbjct: 357 EFSALGADLTESHDLAIR-PRPLHGGVFETYHHRMAHAAAIAGLAVPGIELSDVACTS 415

Query: 430 KTFPDYFDVLSTFV 443
KT P++ + S V
Sbjct: 416 KTMPEFPALWSAMV 429

>ref|ZP_07453845.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium yurii
subsp. margaretiae ATCC 43715]
gb|EFM39696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium yurii
subsp. margaretiae ATCC 43715]
Length = 417

Score = 160 bits (406), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 218/429 (50%), Gaps = 40/429 (9%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG ++ SKS+++R ++ +ALS + + S+D+ L A+ LG+ + D A
Sbjct: 9 LSGKIQAITSKMAHRQIICSALSADSTLFIPIIDISDDICTLSAVENLGIKLIKDAYI 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-----GVPRM 129
R + K + D +E +G +R + A +LD G R+
Sbjct: 69 R--LSPTNKKSELFDCRE-----SGTTLRFMLTI-----APSILDICHTGRGRL 111

Query: 130 RERPIGLDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
ERPI ++ L+ C + +D P+ + +V+++ +ISSQ++S LL++
Sbjct: 112 PERPINQIIDILRS----PKCEVSSDKLPLTIKN--KFEFTEVEIAANISSQFISGLLIS 165

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+ L DV I+++ S YV+MT+ +M R+G+ E + ++I+ Q+Y SPK
Sbjct: 166 SVLQKDDVHIKVVGDFESKSYVDMTVDVMRRYGI--EIIEDKSYFIRKNQRYISPKNV 223

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S++++FL AI G VT+ G SLQ D + E++E GA+V E +TV+
Sbjct: 224 IEKDWSNSAFFLTAGAI-GAPVTLCLNPNLSLQSDKRIIEIENFGARVDMDEDEITVSK 282

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ I+V+M+++PD+ L+V+A G + + R+KE++R+ A
Sbjct: 283 DKSD-----VIEVDMSQIPDLLPILSVLACATKGTSRFYNNRRLRLKESDRIYASCR 334

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCT 428
+ LG + E D II +L +D+++DHR+AM+ ++A+ + V I+
Sbjct: 335 MIKALGGNAVEKDDIELIEGRGRLRGTTVDSFNDHRIAMSAIASIICDDDDVIKGENAV 394

Query: 429 RKTFFPDYFD 437
K++P +F+
Sbjct: 395 NKSYPKFFE 403

>ref|ZP_03709874.1| hypothetical protein CORMATOL_00689 [Corynebacterium matruchotii
ATCC 33806]
gb|EEG27837.1| hypothetical protein CORMATOL_00689 [Corynebacterium matruchotii
ATCC 33806]
Length = 378

Score = 160 bits (405), Expect = 4e-37, Method: Compositional matrix adjust.
Identities = 115/352 (32%), Positives = 183/352 (51%), Gaps = 23/352 (6%)

Query: 99 GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCP 158
G AG MR + A G+ + DG R+RP+ ++ GL+ LG V D P
Sbjct: 41 GLAGTVMRFVPLAALADGDVFF--DGDEHARQRPMPKGILDGLRALGISVQG---DSLP 94

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRL 217
+V+G G GG V+++ S SSQ++S LL+AAP A G I + L S+P++EMT+ +
Sbjct: 95 FKVSGNGSPMGGMVEINASSQFVSGLLLAAPRFAQGKITVRHIGETLPSMPHIEMTVHM 154

Query: 218 MERFGVKAHSDSWDRFY----IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
+ + G + + ++ I+GG VE D S+A+ FLA AA+TG TV V
Sbjct: 155 LRQAGASVDTTAYQWSVTPGPIRGV-----VRVEPDLSNATPFLAAAVTGSTVQV 207

Query: 274 ECGGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDV 333
+ TT+ Q +LE MG V+ T++ +TVTGP +P L+ I+++M+ + ++
Sbjct: 208 KDWPTTTTQPGDAIRNILERMGCTVSLTSDTLTVTGP--KP---GSLQGIEIDMSDIGEL 262

Query: 334 AMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
T+A +A A P+ + +A ET+R+ A+ TE+TK+G E PD I P L
Sbjct: 263 TPTVAAMATIAKSPSTLTGIAHLHGHTDRLQALATEITKIGGQCSELPDGLAIKPSGSL 322

Query: 394 NVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
+ TYDDHRMA ++ + + + T KT P + + + V+
Sbjct: 323 HGAHWSTYDDHRMATTAIGLVAPGIKVENIETTAKTLPGFDRMWADMVQE 374

>ref|ZP_03742913.1| hypothetical protein BIFPSEUDO_03494 [Bifidobacterium
pseudocatenulatum DSM 20438]
gb|EEG70476.1| hypothetical protein BIFPSEUDO_03494 [Bifidobacterium
pseudocatenulatum DSM 20438]
Length = 446

Score = 160 bits (405), Expect = 4e-37, Method: Compositional matrix adjust.
Identities = 138/446 (30%), Positives = 213/446 (47%), Gaps = 31/446 (6%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + TV +PGSKSLSNR L+LAAL + LL S D M+ ALR LG+ E D+
Sbjct: 16 KTLDATVVVPGSKSLSNRYLILALALGHRPVRLVGLLRSDTELMDALRALGVRCEIDEQ 75

Query: 73 AKRAVVVCGGKFPVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V P D + ++F G AG MR + A G + DG +
Sbjct: 76 VDTTVTV-----VPPSDGRFHGGTKVFCGLAGTVMRFVPLAMFADGPVDF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
RP+ ++ GL+QLGA ++ + G T PP V+ V + S SSQ++
Sbjct: 129 ARPMKPVLDGLQLGACIE-YHGEGRLPFTITPPQTVSQCA--EPSVVSIDSSGSSQFI 185

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+ G +E+ +K S+P++ MT+ ++ GV+A ++D R +
Sbjct: 186 SGLLLIGSRVPGGLELHHTGKTPSLPHIRMTVADLQSGSVRA-NADEHARVWTVQPGAV 244

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P+ VE D S+A+ FL A I GGTV V ++ Q LE MGA E
Sbjct: 245 QLPETVTVPEPDLASNAAPFLGAALIAAGTGVVRVPHWPESTTQPGGLLPYLEHMGA-----E 299

Query: 303 TSVTVTGPPR--EPFGRKHLKAI-DVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
S V R E G H+ + D ++ ++A +LA + +FAD PT + + R
Sbjct: 300 ISFPVIDGVRYCEVTGSSHINGLGDFDLTAAGEIAPSLAAILVFADKPTRMLGIGHLRGH 359

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAACAE 417
ET R+ A+ E+T++G E D I P N+ ++TY DHRMA ++ +
Sbjct: 360 ETNRLEALVNEITRVGGEARELADGLEIVPVNPKAKMETYADHRMATFAAMLGLSI 419

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSSTFV 443
+ +++ T KT PD+ ++ + +
Sbjct: 420 NGIQVKNIATTAKTLPDFANMWTNML 445

>ref|YP_002303912.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
CbuG_Q212]
sp|B6J1D9.1|AROA_COXB2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACJ18767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
CbuG_Q212]
Length = 438

Score = 160 bits (404), Expect = 4e-37, Method: Compositional matrix adjust.
Identities = 140/436 (32%), Positives = 218/436 (50%), Gaps = 29/436 (6%)

Query: 11 PIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + +SG + +PG KS+S+R +LLAA++EG T VD L D M+ AL+ +G S++
Sbjct: 7 PSQGLSGEICVPGDKSISHRAVLLAAIAEGQTQVDGFLMGADNLAMVSALQQMGASIQVI 66

Query: 71 KAAKRAVVVGGCGG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VV G G + P E L GN+G A+R L+ + AG VL G
Sbjct: 67 EDENILVVEGVGMTGLQAPSE-----ALDCGNSGTAIRLLSGLL--AGQPFNTVLTGDS 118

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
++ RP+ ++ L +GA +D + PP+++ G L G +L + S+Q S LL
Sbjct: 119 SLQRRPMKRIIDPLTLMGAKIDST--GNVPPLKIYGNPRLTGIHYQLPMA-SAQVKSCLL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G I P + T RL++ F + + GG K K+ +
Sbjct: 176 LAGLYARGKTCIT----EPAPSRDHTERLLKHFYHTLQKDKQS--ICVSGGGKLKA-ND 227

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ GD SSA++F+ A IT G+ + C + +L+MMGA+ F T +
Sbjct: 228 ISIPGDISSAFFIVAATITPGS-AIRLCRVGNPTRLGVINLLKMMGADIEVTHYTEKN 286

Query: 308 TGPPREPFGGRK-HLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK ID+ +++P D L + A A G T +RD A RVKET+R
Sbjct: 287 EEPTADITVRHARLKGIDIPDQVPLTIDEFPVLLIAAAVAQKTVLRDGAELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L KL+ E PD II L +++YDDHR+AMAF++A A+ PV I
Sbjct: 347 IAAMVDGLQKLGAIAESLPDGVIIQ--GGTLEGGEVNSYDDHRIAMAFVAGTLAKGPVRI 405

Query: 423 RDPGCTRKTFPDYFDV 438
R+ + +FP++ ++
Sbjct: 406 RNCDNVKTSFPNFVEL 421

>emb|CBK70704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum F8]
Length = 445

Score = 160 bits (404), Expect = 5e-37, Method: Compositional matrix adjust.
Identities = 142/446 (31%), Positives = 211/446 (47%), Gaps = 29/446 (6%)

Query: 13 KEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKSLSNRYLILAAALGSKPVTIIGLLRSRDTLMMGALEALGVRCDVDSA 75

Query: 73 --AKRAVVVGGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130

Sbjct: 76 V G+F V +F G AG MR + A G + DG +
TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+

Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPPATLPAAQAQVSIDSSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + + P

Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--- 304
VE D S+A+ FL A I GGTV V T+ Q LE MGAKV++

Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGLLPGYLEQMGAQVSFPTIDGVR 307

Query: 305 -VTVTGPPREPFGFRKH-LKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
VTG G H L D+ ++A +LA + +FAD T + + R ET

Sbjct: 308 YCEVTGD-----GTVHGLGTFDLTAA--EIAPSLAAILVFADKSTDMVGIGHLRGHETN 360

Query: 363 RMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVP- 419
R+ A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P

Sbjct: 361 RLEALVNEIRRVGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPD 419

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVN 445
+ + + TRKT PD+ + S ++

Sbjct: 420 IEVINVATTRKTLPDFVGMWSGMLRQ 445

>ref|YP_001112510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
reducens MI-1]
sp|A4J3N2.1|ARO_A_DESRM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABO49685.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
reducens MI-1]
Length = 429

Score = 159 bits (403), Expect = 6e-37, Method: Compositional matrix adjust.
Identities = 142/456 (31%), Positives = 224/456 (49%), Gaps = 48/456 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+V+ P+K++ G V +PG KS+S+R +++ AL++G T V N L ED + LR +G+

Sbjct: 2 ELVINPVKKLRGNVSVPGDKSISHRAVMVGALAQQGITEVSNFLMGEDCLATVKCLRAMGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLD 124
S+E K + G G ++ +E L GN+G R L + AG T ++

Sbjct: 62 SIEGPTNGKLLIY-GVG---LQGLREPADLLDTGNSGTTTRLLMGIL--AQQPFTSIIT 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLG---TDCPPVRVNGIGGLPGGKVK----LSGS 177
G +++RP+ + L+ +GA FLG + P+ V G GK+K S

Sbjct: 115 GDQSLKKRPMARVTKPLQDMGAS---FLGRNQNNLLPMAVQG-----GKLPIDFHSPV 165

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S+Q SA+L A A G + + +S + E R+++ FG + E + R IK

Sbjct: 166 ASAQVKSAVLFAGLFAEG--YTSVTEPAVSRDHSE---RMLKAFGAEVEVNQTVR--IK 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
G + K K V GD SSA++ + AAI G+ +T++G G + + EVL+ MGA

Sbjct: 219 GLPQLKGMK-ITVPGDISSAAFLMVAAAILPGSDITIQGVGINPTRDGI--LEVLRQMGA 275

Query: 297 KVTWTETSVTVTGPPREPFGFRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPT 348
+ + + EP G +K ++ + ++ D +AV A +A G T

Sbjct: 276 GIEIMHSRLQ---GGEVPVDIRIKGAELQGTLSGPIIPLIDEIPIIAVAAAYARGTT 331

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAM 408
IRD + +VKE+ R+ ++ EL K GA+VEE D II L+ +Y DHRMAM

Sbjct: 332 VIRDASELKVKESNRISVVRELKFGATVEELSDGLIIQGGTPLSGAVCQSYGDHRMAM 391

Query: 409 AFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTFV 443
A ++A A T I C +FP + DVL +

Sbjct: 392 AMAVAGLAASGQTLIEQADCIPVSFPGFSDVLKEVI 427

>ref|ZP_03391386.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
sputigena Capno]
gb|EEB65536.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Capnocytophaga
sputigena Capno]
Length = 416

Score = 159 bits (403), Expect = 6e-37, Method: Compositional matrix adjust.
Identities = 129/430 (30%), Positives = 210/430 (48%), Gaps = 47/430 (10%)

Query: 15 ISG-TVKLPGSKSLSNRILLLAALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SG T++L GSKS SNR LLL A + NL ++D + AL++
Sbjct: 11 VSGKTLQLSGSKSESNRALLQAFFPELQI-KNLSTADDTLLLRALQS----- 58

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+E + + +AG AMR LTA G +L G RM+ERP
Sbjct: 59 -----KEATIDIHAGTAMRFLTAYFATQVGREV-LLTGSARMKERP 99

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I LV L++LGAD+ PP+ + G+ L +V++ G +SSQ+LSALL+ A
Sbjct: 100 IHLLVEALQRLGADIRYGERDGFPPLYIKGVA-LSKKEVRIRGDVSSQFLSALLLIASSL 158

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP-KNAY--V 250
+ + + +L S+PY++MT+ ++ + W+ +K P KN V
Sbjct: 159 PNGLTLILEGELTSMPLYKMTVSFLQY--CLGKEVVQWEGNVLVKVASHINKPLKNNIWEV 216

Query: 251 EGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
E D SSASY+ + A++ G +T+ SLQGD E+ + G T+ +++ +
Sbjct: 217 ESDWSSASYWFSFVALSPIGTQLTLTHFKEDSLQGDSALPELYKHFGVSTTFKGSTMKI- 275

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
E H +++ +N PD+A T+AV AL + + + +KET+R+ A++
Sbjct: 276 ----EKTALPHPIRLELQLNDTPDIAQTIAVTALGLGLEANLSGLHTLKIKETDRLQALQ 331

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
TE+ KLGA V + + L I TY+DHRMAMAF+ + P+ I +
Sbjct: 332 TEMIKLGAENVITDESHLASCNHLREGVPIATYNDHRMAMAF-PLMLKTPIVIENTKEV 390

Query: 428 TRKTFPDYFD 437
K++P +++
Sbjct: 391 VSKSYPAFWE 400

>ref|YP_003661054.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JDM301]
gb|ADH00224.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JDM301]
Length = 445

Score = 159 bits (403), Expect = 7e-37, Method: Compositional matrix adjust.
Identities = 139/438 (31%), Positives = 211/438 (48%), Gaps = 23/438 (5%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKA--AKR 75
TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 21 TVTVPGSKSLSNRYLILAAALGSKPVTLIGLLRSRDTLMMGALEALGVRCVDVSATDTTV 80

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 135
V G+F V +F G AG MR + A G + DG + RP+
Sbjct: 81 TVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPNVF--DGDEQAYARPMK 133

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLMAAPLA 193
++ GL+QLGA VD P + LP + ++S S SSQ++S LL+ +
Sbjct: 134 PVLGDLEQLGATVDYHGEVGRLPFTITPPATLPAAQVVSIDSSGSSQFISGLLLISSKL 193

Query: 194 LGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G + + +K S+P++ MT+ + G E +D R + + + P VE
Sbjct: 194 PGGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSKVTVPE 252

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A+ FL A I GGTV V T+ Q LE MGA+V++ T+ G

Sbjct: 253 DLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQMGAEVSFQ----TIGGVRY 308

Query: 313 -EPFGRKHLKAIADV-NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
E G ++ + ++ ++A +LA + +FAD PT + + R ET R+ A+ E

Sbjct: 309 CEVTGDGIVRGLGTFDLTAAGEIAPSLAAILVFADKPTDMVGIGHLRGHETNRLEALVNE 368

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVP-VTIRDPGC 427
+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P + + +

Sbjct: 369 IRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPDIEVINVAT 427

Query: 428 TRKTFPDYFDVLSTFVKN 445
TRKT PD+ + S ++

Sbjct: 428 TRKTLPDFVGMWSGMLRQ 445

>gb|ADL20421.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudotuberculosis 1002]
Length = 424

Score = 159 bits (402), Expect = 7e-37, Method: Compositional matrix adjust.
Identities = 131/436 (30%), Positives = 211/436 (48%), Gaps = 30/436 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S V +PGSKS++NR L+L+AL++ + + L+S D M AL+ LG V + ++

Sbjct: 14 VSAVTVTPGSKSMTNRALVLSALADSPSHIKGALHSRDTLMTALQALGTDVRSHDSSS 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P+ + L AG MR + A G + DG P+ R RP+

Sbjct: 74 LVV----NPVPLHGGTVDCGL---AGTVMRFVPPVAALAQGTTEF--DGDPQARTRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L+ +G V D P ++ GG + + S SSQ++S LL+AAP

Sbjct: 123 NQILDALRGIGVQVH---GDALPFSISSSETPHGGSIDIDASSSSQFVSGLLLAAPCYR 178

Query: 195 GDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + I KL SIP++EMT+ ++ GV+ + S GG S + +E D

Sbjct: 179 DGLTVRHIGGKLPISIPHIEMTVDMLSAGVQVDDSSSENQWTVHPGG---ISGRTWEIEPD 235

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT---ETSVTVTG 309
S+A+ FLA AA+TGGTVT+ G + Q +L MG V++ ++ VTG

Sbjct: 236 LSNATPFLAAAAVTGGTVTIPGWPQRTTQAGDSIRSILSSMGCDVSFITYNGSNALQVTG 295

Query: 310 PPREPFGKHLKAIADVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P L I ++M+ + ++ T+A +A A P+ + +A R ET+R+ A+

Sbjct: 296 P-----SDGLNGICLMSDIGELTPTVAALAALAATPSELSGIAHLRGHETDRLKALSD 349

Query: 370 ELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E+ ++G EE D IT P L +Y DHRMA A ++ + + + T

Sbjct: 350 EINRIGGHCEELADGLRIT-PRPLRAGTWHSYADHRMATAGAIVGLVVPGRIVENIATTA 408

Query: 430 KTFPDYFDVLSTFVKN 445
KT PD+ ++ S V +

Sbjct: 409 KTLPDFENIWSAMVSD 424

>ref|NP_696144.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum NCC2705]
gb|AAN24780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum NCC2705]
Length = 455

Score = 159 bits (402), Expect = 8e-37, Method: Compositional matrix adjust.
Identities = 141/445 (31%), Positives = 209/445 (46%), Gaps = 27/445 (6%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A

Sbjct: 26 QPLNATVTPGSKSLSNRYLILAALGSKPVTLLIGLLRSRDTLMMGALEALGVRCDVDSA 85

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +

Sbjct: 86 TDTTVTVTPPVSGRF-----HGNVNVCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 138

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 139 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPPATLPAAQAQVSIDSSGSSQFISGLLL 198

Query: 189 -AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
++ L G +K S+P++ MT+ + G E +D R + + + P
Sbjct: 199 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 257

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--- 304
VE D S+A+ FL A I GGT V T+ Q LE MGAKV++
Sbjct: 258 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGLLPGYLEQMGAQVSFPTIDGVR 317

Query: 305 -VTVTGPPREPFGFRKH-LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
VTG G H L D + ++A +LA + +FAD T + + R ET
Sbjct: 318 YCEVTGD-----GTVHGLGTFD--LTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETN 370

Query: 363 RMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
R+ A+ E+ ++G + EE PD I P E L+ ++TY DHRMA ++ +
Sbjct: 371 RLEALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMATFAAMLGLRIPDI 430

Query: 421 TIRDPGCTRKTFPDYFDVLSSTFVKN 445
+ + TRKT PD+ + S ++
Sbjct: 431 EVINVATTRKTLPDFVGMWSGMLRQ 455

>ref|ZP_03976086.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 55813]
gb|EEI81380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 55813]
Length = 445

Score = 159 bits (402), Expect = 8e-37, Method: Compositional matrix adjust.
Identities = 137/442 (30%), Positives = 211/442 (47%), Gaps = 21/442 (4%)

Query: 13 KEISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKLSNRYLILAALGSKPVTLIIGLLRSRDTLMMGALEALGVRCDVDSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGLALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPPATLPAAQAQVSIDSSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + + P
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGT V T+ Q LE MGAKV++ T+
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGLLPGYLEQMGAQVSFP----TI 303

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 DGVRYCEVTGDGTVRGLGTFDLTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA ++ + +
Sbjct: 364 ALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMATFAAMLGLRIPDIEVI 423

Query: 424 DPGCTRKTFPDYFDVLSSTFVKN 445
+ TRKT PD+ + S ++
Sbjct: 424 NVSTTRKTLPDFVGMWSGMLRQ 445

>ref|YP_003782930.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudotuberculosis FRC41]
gb|ADK28323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium

pseudotuberculosis FRC41]
gb|ADL10018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudotuberculosis C231]
gb|ADO25810.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudotuberculosis I19]
Length = 471

Score = 159 bits (402), Expect = 9e-37, Method: Compositional matrix adjust.
Identities = 131/436 (30%), Positives = 211/436 (48%), Gaps = 30/436 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+S V +PGSKS++NR L+L+AL++ + + L+S D M AL+ LG V + ++
Sbjct: 61 VSAVTVTPGSKSMTNRALVLSALADSPSHIKGALHSRDTDLMTALQALGTDVRSHDSSS 120

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P+ + L AG MR + A G + DG P+ R RP+
Sbjct: 121 LVV----NPVPLHGGTVDCGL---AGTVMRFVPPVAALAQTTEF--DGDPQARTRPM 169

Query: 135 GDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L+ +G V D P ++ GG + + S SSQ++S LL+AAP
Sbjct: 170 NQILDALRGIGVQVH---GDALPFSISSSETPHGGSIDIDASSSSQFVSGLLLAAPCYR 225

Query: 195 GDVEIEII-DKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYSKPNAYVEGD 253
+ + I KL SIP++EMT+ ++ GV+ + S GG S + +E D
Sbjct: 226 DGLTVRHIGGKLPISIPHIEMTVMLRSAGVQVDDSSSENQWTVHPGG---ISGRTWEIEPD 282

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT---ETSVTVTG 309
S+A+ FLA AA+TGGTVT+ G + Q +L MG V++ ++ VTG
Sbjct: 283 LSNATPFLAAAATVGGTVTIPGWPQRTTQAGDSIRSILSSMGCDVSFITYNGSNALQVTG 342

Query: 310 PPREFPGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P L I ++M+ + ++ T+A +A A P+ + +A R ET+R+ A+
Sbjct: 343 P-----SDGLNGICLMSDIGELTPTVAALAALAATPSELSGIAHLRGHETDRLKALSD 396

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E+ ++G EE D IT P L +Y DHRMA A ++ + + + T
Sbjct: 397 EINRIGGHCEELADGLRIT-PRPLRAGTWHSYADHRMATAGAIVGLVVPGIRVENIATTA 455

Query: 430 KTFPDYFDVLSTFVKN 445
KT PD+ ++ S V +
Sbjct: 456 KTLPDFENIWSAMVSD 471

>ref|ZP_06977445.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gardnerella vaginalis
5-1]
gb|EFH70976.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gardnerella vaginalis
5-1]
Length = 461

Score = 159 bits (402), Expect = 9e-37, Method: Compositional matrix adjust.
Identities = 138/441 (31%), Positives = 217/441 (49%), Gaps = 35/441 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEA--D 70
++ +++PGSKSLSNR L+LAAL + V+ LL S D M+ AL T G+ E+ +
Sbjct: 29 HQLKAYIEVPGSKSLSNRYLILAALGTSVVLQGLLRSDTDLMINALSTFGVRCESLNE 88

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
K V+ G F V D E ++ G AG MR + A A N DG +
Sbjct: 89 DGTKLRVIPPEDGVFRVPDNAE---VYCGLAGTVMRFVAALALFA--NKAVRFDGDKQAY 143

Query: 131 ERPIGDLVVGLKQLGADV-----DCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RP+ ++ GL+QLGA V + FL T PP I V++ S SSQ++S
Sbjct: 144 ARPMKPVLDGLQLGARVKYHEEGFLPFTITPPSVEFKINNFSEKIVQIDSSSSSQFIS 203

Query: 185 ALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQK 241
ALL+ G +E++ I D L S+P++ MT+ + + G V + W ++K K
Sbjct: 204 ALLLIGSRIPGGLELKHIGDTLPSMPHIRMMDICKAGGSVNMTSNAMW---HVKE-SK 259

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+E D S+A+ FL + I GG+V++ +S Q +LE M AKV +
Sbjct: 260 INLANVVTIEPDLNAAPFLGASLIAGGSVSIPNWPFSSTQPGGLLPGILEKMKAKVNFE 319

Query: 302 ETSVTVTGPPREPFGGRKH-----LKAID-VNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
+T + G H +KAI +++++ ++A ++A + FADGP+ + +A
Sbjct: 320 KTG-----DDAGIMHVESDSAIAIPYLDLSAAGEIAPSIAAILAFADGPSELHGIA 371

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R ET R+ A+ EL ++G +E D I P ++ ++TY DHRMA ++
Sbjct: 372 HLRGHETNRLQALVNEINRVGIGAKELEDGIRIEPSNHMHGEVMEYADHRMATFAAMLG 431

Query: 415 CAEVPVTIRDPGCTRKTFPDY 435
+ I++ TRKT PD+
Sbjct: 432 LRIENIRIKNISTTRKTIPDF 452

>ref|ZP_07940937.1| EPSP synthase [Bifidobacterium sp. 12_1_47BFAA]
gb|EFV38096.1| EPSP synthase [Bifidobacterium sp. 12_1_47BFAA]
Length = 445

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 143/446 (32%), Positives = 211/446 (47%), Gaps = 29/446 (6%)

Query: 13 KEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKLSNRYLILAAALGSKPVTILIGLLRSRDTLMMGALEALGVRCDVDSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPPATLPSAQVSISSGSSQFISGLLL 188

Query: 189 -AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
++ L G +K S+P++ MT+ + G E +D R + + + P
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLSQGDVKAFAEVLEMMGAKVTTWTETS--- 304
VE D S+A+ FL A I GGTV V T+ Q LE MGAKV++
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQMGAQVSPFTIDGVR 307

Query: 305 -VTVTGPPREPFGGRKH-LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWVRVKETE 362
VTG G H L D+ ++A +LA + +FAD T + + R ET
Sbjct: 308 YCEVTGD-----GTVHGLGTFDLTAAG--EIAPSLAAILVFADKSTDMVGIHGLRGHETN 360

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP- 419
R+ A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P
Sbjct: 361 RLEALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPD 419

Query: 420 VTIRDPGCTRKTFPDYFDVLSFVKN 445
+ + + TRKT PD+ + S ++
Sbjct: 420 IEVINVATTRKTLPDFVGMWSGMLRQ 445

>ref|ZP_03806226.1| hypothetical protein PROPEN_04628 [Proteus penneri ATCC 35198]
gb|EEG83857.1| hypothetical protein PROPEN_04628 [Proteus penneri ATCC 35198]
Length = 172

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 72/126 (57%), Positives = 94/126 (74%)

Query: 317 RKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWVRVKETERMVAIRTELTKLGA 376
R LK ID++MN +PD AMT+A ALFA+G T IR++ +WRVKET+R+ A+ EL K+GA
Sbjct: 42 RGILKGIDMDMNTIPDAAMTIATTALFAEGETVIRNIYNWRVKETDRLAAMAAELQKVGA 101

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
VEEG DY + PP++L I+TY+DHR+AM FSL A ++ P+TI DPGCT KTFPDYF
Sbjct: 102 IVEEGHDYLVKIPPKQLTTADIETYNDHRIAMCFSLVALSDTPTITILDPGCTAKTFPDYF 161

Query: 437 DVLSTF 442
+ L T

Sbjct: 162 EKLETL 167

>ref|YP_004220402.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JCM 1217]
dbj|BAJ66310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JCM 1217]
Length = 445

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 143/446 (32%), Positives = 211/446 (47%), Gaps = 29/446 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKSLSNRYLILAAALGSKPVTLLGLLRSDTDLMMGALEALGVRCVDVSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPNVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRLPFTITPPATLPQAQVVSIDSSGSSQFISGLLL 188

Query: 189 -AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
++ L G +K S+P++ MT+ + G E +D R + + + P
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS--- 304
VE D S+A+ FL A I GGTV V T+ Q LE MGAKV++
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGTVRVHPWETTTQPGGLLPQYLEQMGAKVSFPTIDGVR 307

Query: 305 -VTVTGPPREPFGGRKH-LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
VTG G H L D+ ++A +LA + +FAD T + + R ET
Sbjct: 308 YCEVTGD-----GTVHGLGTFDLTAAG--EIAPSLAAILVFADKSTDMVGIGHLRGHETN 360

Query: 363 RMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVP- 419
R+ A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P
Sbjct: 361 RLEALVNEIRRVGGAEEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPD 419

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVKN 445
+ + + TRKT PD+ + S ++
Sbjct: 420 IEVINVATTRKTLPDFVGMWSGMLRQ 445

>ref|ZP_03930554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerococcus
tetradius ATCC 35098]
gb|EEI82734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerococcus
tetradius ATCC 35098]
Length = 430

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 122/429 (28%), Positives = 222/429 (51%), Gaps = 31/429 (7%)

Query: 14 EISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLN--SEDVHYMLGALRTLGLSVEADK 71
EI G +K SKSL +R ++L+ +++ ++ +N SED+ L + LG + +
Sbjct: 15 EIKGKMKSIPSKSLHLRAIILSGIAKDREIILEQVNTISEDIEATLTICIEKGAKTKVEG 74

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ R +G K +V+L +G +R L V+ AT +D +R+
Sbjct: 75 DSIRITSLG-----NIKKSKVELHCKESGTTLRLLPLVSTFSKEAT--VDCSEGLRK 125

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI +L+ L++ G + P+ ++G + K+SG ISSQY+S LL+ +
Sbjct: 126 RPIRELIETLEESG----LYFKEKGFPINISG--NVTDFFKISGDISSQYVSGLLLLSS 179

Query: 192 LALGDVEIEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ-KYKSPKNAYV 250
L I + KL S YV +T++++ FG+ + F I GG+ + PK +
Sbjct: 180 LLDQRSSIYLTTLKESRAYVNITIKVLRDFGIIVNELEEG-VFEIYGGDRILPPKEYQI 238

Query: 251 EGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS SVTVTGP 310

EGD S+A++FL G + G ++ + G S QGD K ++L+ GA +T ++ ++
Sbjct: 239 EGDWSNAAFFLVGGCL-GDSIKMSGLNLESSQGDKKIVQILKKAGAILTCSDDFISSN-- 295

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R HL + +V+ ++ PD+ L+VVA + G + ++ ++KE+ R+ +
Sbjct: 296 -----RSHLNSFEVDFSETPDLFPILSVVAALSKGQSILKGGERLKLKESNRIESTFQM 349

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
L LGA V++ D II E L+ +++++DHR+ M+ ++A+ C E PV+I + G
Sbjct: 350 LKSLGADVKKREDGLIIQGKEILDGGIVNSFNDHRIVMSVTMASIRCKE-PVSIVNAGAV 408

Query: 429 RKTFFPDYFD 437
K++P++F+
Sbjct: 409 NKSYPNFFE 417

>ref|YP_181207.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides
ethenogenes 195]
sp|Q3Z992.1|AROA_DEHE1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW40208.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides
ethenogenes 195]
Length = 420

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 135/426 (31%), Positives = 200/426 (46%), Gaps = 25/426 (5%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS + R L+ AA + G + + + L ++D L LG+ + D A+
Sbjct: 12 GEIAVPSSKSYTIRGLIAAAQANGQSRISPLAADDTLASRQVLSGLGIDINTDAEAESEW 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G K P + LF + +R ++A V A +L G MR RP+
Sbjct: 72 QLTGNTFKKPAGN-----LFCRESAATLRFMSA-VCARLPFECRLLAGHSLMR-RPMLP 123

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L QLQ +++ T + G G + KV L G+ISSQY+SAL++ AP
Sbjct: 124 LIQALHQLGIEIETRGNNTV----IKG-GEITRSKVSPLGNISSQYVSALMLMAPACKSG 178

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+EI + S+PY++MT + +E FG+KA S W I Q Y P VEGD SS
Sbjct: 179 LEIHLATPPASLPYLKMTKQTLESFGIKAYTSIDWQEISIP-PQPYL-PARYRVEGDWSS 236

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
AS FLA AI + + T S Q D + L MGA+V + V V+ P
Sbjct: 237 ASSFLALGAI-AAPLFISNLDTESFQADRIMIKFLSEMGAEVESGQNVVKVSPKP----- 290

Query: 317 RKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L AI ++ D+ LA+ A A G + + V R+KE+ R+ A+ L+ +G
Sbjct: 291 ---LTAIQADLTHSIDLLPALAITAACAKGQSILSGVRQARIKESNRIRAVSQGLSAMGI 347

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEPVVTIRDPGCTRKTFPDYF 436
+V E D II ID+ DHR+AMAF I + C KT+PD++
Sbjct: 348 NVTEEDRLIIEGGMPRGAE-IDSLGDHRIAMAFGALGAVTGETCISEAECVSKTYPDFW 406

Query: 437 DVLSTF 442
L +
Sbjct: 407 QKLESL 412

>ref|YP_004000333.1| aroA [Bifidobacterium longum subsp. longum BBMN68]
gb|ADQ03467.1| AroA [Bifidobacterium longum subsp. longum BBMN68]
Length = 445

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 139/443 (31%), Positives = 213/443 (48%), Gaps = 23/443 (5%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKSLSNRYLILAALGSKPVTLIIGLLRSRDTLMMGALEALGVRCDVDSA 75

Query: 73 --AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVSVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRPLPFTITPPATLPAAQAQVSIDSSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI--EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + + P
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPRAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE MGAkv++ T+
Sbjct: 248 VTVEPDLNSAAPFLGAAIAGGTVRVVPHWPETTTQPGGLLPGYLEQMGAKVSFP----TI 303

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 DGVRYCEVTGDTVRGLGTDLTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPEKLNVTADITYDDHRMAMAFSLAACAEVP-VTI 422
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P + +
Sbjct: 364 ALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPDIEV 422

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 445
+ TRKT PD+ + S ++
Sbjct: 423 INVSTTRKTLPDFVGMWSGMLRQ 445

>ref|YP_002379387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothecae sp. PCC
7424]
sp|B7KLE7.1|AROACYP7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACK72519.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothecae sp. PCC
7424]
Length = 448

Score = 159 bits (401), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 126/438 (28%), Positives = 215/438 (49%), Gaps = 25/438 (5%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R L+L A+++G T++ LL ED H R +G + K
Sbjct: 28 LTGKITIPGDKSISHRALMLGAIAQGETI IKGLLLGEDPHSTAKCFRAMGAEISPLNTDK 87

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V G G + + +E V + GN+G MR L + A+ + + G +R RP
Sbjct: 88 -IIVKGIG----LGNLQEPVDVLDAGNSGTTMR-LMLGLLASHPERFFTVTGDSSLSRSP 141

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+Q+GA + P+ ++G P + I+S + + ++ A L+
Sbjct: 142 MSRVIKPLQQMGAQIWGRKQNSLAPLAISGQSLQP---IHYHSPIASAQVKSICILLAGLS 198

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + + + +S + E R+++ FG E + G + + V GD
Sbjct: 199 V-EGKTTVTPEALS RDHSE---RMLKAFGANLEIDPQTHSVTVMGPSRLTG-QTVIVPGD 253

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L AG+ + G + +E G + + EVLEMMGA +T +TG P
Sbjct: 254 ISSAAFVWLVAGSIVPGSDLLIENVGINPRTGI--LEVLEMMGADLTLLNQR-EITGEPV 310

Query: 313 EPFGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
KH LKA ++ + +P D LAV A+FA G T IRD RVKE++R+ +
Sbjct: 311 ADIRVKHSQKACTISGDIVPRLIDEIPILAVAFAVQGGTTVIRDAQELRVKESDRLAVM 370

Query: 368 RTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
EL ++GA + E PD IT P L + +D+Y DHR+AM+ ++AA A TI
Sbjct: 371 ACENLQMGAKITELPDGLEITGPVSLKGSQVDSYTDHRIAMSLAIAALNASHSTTIHRAQ 430

Query: 427 CTRKTFPDYFDVLSTFVK 444

++P++ L +
Sbjct: 431 AAASYSPEFITTLQQLCQ 448

>emb|CBL17641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus sp.
18P13]
Length = 416

Score = 158 bits (400), Expect = 1e-36, Method: Compositional matrix adjust.
Identities = 133/423 (31%), Positives = 209/423 (49%), Gaps = 33/423 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV +P SKS ++R L+ AAL++GT+ + NL +SED+ +GAL+ +G + +
Sbjct: 10 LEGTVSIPASKSAHRALICALAKGTSRLTNLSDSEDIATIGALQQMGAKIT--RTGS 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G +E + + L G +G +R L A G T + G R+ RP+
Sbjct: 68 SVTVTGI-----LEPPTQPITLDCGSGSTLRFILPVAAALGLTCTIIGKG--RLPYRPL 120

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L + G + P+ ++G L G +L G +SSQYL+ LL+A PL
Sbjct: 121 DAYLRELPKKGISIQPERQDALLPLHMSG--KLQSGVFQLEGDVSSQYLTGLLLALPLLE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD +E+ L S PYV+MT L+ + GV E + + + I GG Y P + +EGD
Sbjct: 179 GDSRLELTSPLESAPYVDMTAALLRQAGVPTEKTP--EGYRIPGGGVYH-PLSLAIEGDY 235

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A++FL A+ G V V+G G S QGD K E+L ++ +T+ + +G
Sbjct: 236 SQAFFLTANAL-GSHVRVDGLGENSCQGDRIKIVEILR----ELCYTKENTIASG----- 285

Query: 315 FGRKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ V +PD+ L V+A P+ I R+KE++R+ AI L +
Sbjct: 286 -----LSVYAADIPDLVPVLTVLACLCKGKPSRIYGAKRLRLKESDRLAIAAALNAI 337

Query: 375 GASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFP 433
G V + D I P D+ DHR+AM+ ++AA + PVTI RK++P
Sbjct: 338 GGQVSQTFEDGLEIQPIAAFTGTTADSCGDHRIAMSLAVAATRSTAPVTILGAEAVRKSYP 397

Query: 434 DYF 436
D++
Sbjct: 398 DFW 400

>ref|ZP_07879918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 180 str. F0310]
gb|EFU61458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 180 str. F0310]
Length = 451

Score = 158 bits (400), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 138/435 (31%), Positives = 205/435 (47%), Gaps = 40/435 (9%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+ TV +PGSKS++ R L LAA+ E ++V L + D AL +G +E A A
Sbjct: 15 VDATVAIPGSKSITARALYLAAGVGEAPSLVTGALEARDTRLFADALEVMGARIEDAGDGA 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYVLDGVPRMRE 131
R + P + E L AG MR L AA++A + DG +
Sbjct: 75 LRVTPM----SLPPRGRIEGL----AGTVMRFLPPLAALSAE----ETLFDGDKQAYA 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAA 190
RP+G L+ L ++GA V P + G P G + + S SSQ+LSALL+ +
Sbjct: 123 RPLGPLLDALVRMGASVTYHGERGHLFPFSIRGLRTPPLGAQAVDASSSSQFLSALLLV 182

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRF--YIKGGQK 241
PL + + + S+P+VEMTL + G+ E D +W F +GG+
Sbjct: 183 PLVGDPLFVSAPGPVPSMPHVEMTLASLAGAGIDLEVVDQAQDLSTWHVFPSPRPGGE- 241

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC-GTTSLQGDVKFAEVLEMMGAKVTW 300
VE D S+A FLA A ITGG V + G T+ GD + +L MGA +T

Sbjct: 242 -----IVVEPDLNAGPFLAAAMITGGRVRIPAWPGATTQAGDA-WRALLGHMGATITL 294

Query: 301 TETSVTVTGPPREPFGKRLKKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E +T+TGP G + I M ++ ++ TLA + +A P+ + +A R E

Sbjct: 295 DEEGLTLTGP-----GAGNYPGIKATMAEVGELTPTLAAICAYASTPSHLSGIAHLRGHE 349

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
T+R+ A+ E+ + G EE D +IT P L+ I +Y DHRMA ++ +

Sbjct: 350 TDRLAALVAEINRAGGQAEETEDGLVIT-PRPLHAAQIRSYADHRMATFGAILGLITPGI 408

Query: 421 TIRDPGCTRKTFPDY 435
T+ D CT KT P +

Sbjct: 409 TVDDITCTSKTLPGF 423

>ref|ZP_07148087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
resistens DSM 45100]
Length = 429

Score = 158 bits (399), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 133/429 (31%), Positives = 204/429 (47%), Gaps = 42/429 (9%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV- 77
V +PGSKS++NR L+LAAL+ G + ++ L S D M+ +LR LG + D V

Sbjct: 19 VHIPGSKSITNRALILAALANGPSTINGALLSRDTELMMSLRQLGTEIRVDGTTIHIVP 78

Query: 78 -----VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
VV C G AG MR + A G + DG + R

Sbjct: 79 EPKLTGGVVHC-----GLAGTVMRFVPPVAALAEGTVEF--DGDVQAR 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGP--PVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+RP+ + L+ LGADV+ + D P P ++G G L GG+V + S SSQ++S LL

Sbjct: 120 KRPMATTLDSLRLGADVET-VSDDNPDGLPFLIHGRGHLDGGEVSIDASASSQFVSGLL 178

Query: 188 MAAPLALGDVEIEIII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+A V ++ + + L S P+VEMTL ++ GV+ E S++ + ++ G

Sbjct: 179 LAGARFERGVRVKNVGNALPSQPHVEMTLEMLRLAGVQVE--TSFNEWTVEPGPIAGRTW 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
N VE D S+A+ F+A AA TGG V + T+ Q +F +L+ MG + +

Sbjct: 237 N--VEPDLNATPFFMAAAAATGGNVRIGNWPQTTTQPGDQFRVLLDDMGVNCEYHAHDSS 294

Query: 307 VTGPPREPFGKRLKKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ E G LK I +M+ + ++ T+ +A AD + + +A R ET R+ A

Sbjct: 295 L-----EVHSGSGELKGITWMDHIGELTPTVVALAALADSRSHLYGIAHLRGHETNRLAA 349

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ + LG V+E D II P L +Y DHRMA A ++ + + D

Sbjct: 350 LSANINALGGRVQETEDGLIID-PAPLRGGQWASYADHRMATAGAIIGLCVEGIEVEDID 408

Query: 427 CTRKTFPDY 435
T KT P +

Sbjct: 409 TTAKTLPGF 417

>ref|ZP_08010275.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coprobacillus sp.
29_1]
gb|EFW05597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coprobacillus sp.
29_1]
Length = 425

Score = 158 bits (399), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 113/436 (25%), Positives = 212/436 (48%), Gaps = 45/436 (10%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ G V +P SKS+++R ++ A+L+ G +++ ++ S+D+ + A++ LG +

Sbjct: 8 KKLKGKVNVPKSKMAHRAIICASLARGKSIIRHIEYSKDIEATISAMKALGTMI----- 62

Query: 73 AKRAVVVCGGKFPVEDAKE--EVQLFLGN-----AGIAMRSLTAAVTAAGGNATYV 122
F +D E F+ N +G +R + N +

Sbjct: 63 -----FQYDDYLEIDGTTTFMRNMCDIDCHESGSTLRFMVPIISIVCEANVHFT 110

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G R+ +RP+ Q ++ D + + G L G+ ++ G +SSQ+
Sbjct: 111 --GQGRLLGKRPLDVIYKIFDQ--QNIGYLYQEDVLDLYIKG--RLKAGEFEIPGDVSSQF 164

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S LL A PL G+ +I I L S Y+++TL+++E++GV E+ + + F I GGQ Y
Sbjct: 165 ISGLLFALPLLDGNSKIMITSPLESKYIDLTQLMLEQYGVHIENKN-YQEFIIHGGQIY 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P + YVE D S A+++L A+ G V +EG ++ QGD + ++LE MG ++
Sbjct: 224 Q-PCDYVEADFSQAAYFLVAGAL-GNDVVLEGLNLSTHQGDKEAIDILERMGCQLIAKN 281

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ L A ++ ++ PD+ +A+ ++G T I ++ R+KE +
Sbjct: 282 DGYQIYPGI-----LTATTIDGSCPDIIPIVIALACALSEGVTIENIGRLRIKECD 333

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVT 421
R+ A + +LG +E + II + L + +Y+DHMMAM ++A+ V
Sbjct: 334 RLSATVEVINQLGGIAKEEENAMIEGVKTLQGGKVSSYNDRMMAMEIASTVCHHQVV 393

Query: 422 IRDPGCTRKTFPDYFD 437
I + C K++P +++
Sbjct: 394 IDNKDCVEKSYPSFWE 409

>ref|YP_638530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
MCS]
ref|YP_937382.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
KMS]
sp|Q1BCB0.1|AROAMCSS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A1UCN4.1|AROAMCSS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG07474.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
MCS]
gb|ABL90592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium sp.
KMS]
Length = 438

Score = 158 bits (399), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 133/426 (31%), Positives = 211/426 (49%), Gaps = 28/426 (6%)

Query: 15 ISGTVKLPKSKSLNRIILLAAALS--EGTTVDNLLNSDVHYMLGALRTLGLSVEADKA 72
+ T+ +PGSKS +NR L+LAAL+ +GT+ + L S D M+GAL+TLG VE+
Sbjct: 16 VHATLTIPGSKSQTNRALVLAALATPQGTSTISGALSRDITLMIGALQTLGFDVESAGT 75

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
V G ++ G AG +R L AA T DG + R R
Sbjct: 76 DSDLRVGGG-----LGPAAGARVDCGLAGTVLRFLPP--VAALSTETVEFDGDEQARAR 127

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI L+ GL+ LG +D D P RV G G + GG V++ S SSQ++S L+++ L
Sbjct: 128 PIAPLLAGLQALGVRIDG----DGLPFRVRGEGSVAGGTVEIDASASSQFVSGMLLSGAL 183

Query: 193 ALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+ I + + S P+V MT+ ++ GV+ + + + +R+ ++ G + ++ +E
Sbjct: 184 FRDGLTIVHTGESVPSAPHVAMTVSMLRDAGVEVDDTKT-NRWTVRPGPV--AARHWTIE 240

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTESTSVTVTGPP 311
D S+A FL+ ++GG V + G S Q +LE +GA V TE+ + V
Sbjct: 241 PDLNNAVFPFLSAGVVSAGAVRITGWPVAVSTQAGAIMAILEKVGAVVRQTESYLEVQ--- 297

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMVAIRT 369
G + + DV+++ + ++ +A +A A + +R VA R ET+R+ A+
Sbjct: 298 ----GTRQYQGFVDVLDHVGELTPAVAALAAVATPGAVSRLRGVAHLRGHETDRLAALSA 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E+ LG EE D +IT L+ +Y DHRMAMA ++ V I D T

Sbjct: 354 EINGLGGQCEETDDGLVIT-AAPLHGGVWHSYADHRMAMAGAIVGLRTPGVEIEDIATTA 412

Query: 430 KTFPDY 435

KT P++

Sbjct: 413 KTLPEF 418

>ref|ZP_07747176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mucilaginibacter
paludis DSM 18603]
gb|EFQ77027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mucilaginibacter
paludis DSM 18603]
Length = 473

Score = 158 bits (399), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 140/474 (29%), Positives = 227/474 (47%), Gaps = 54/474 (11%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSED-----VH 54
A I+ + K +SGT++L GSKS NR L++ ALS+G V N+ ++ D VH
Sbjct: 3 ANIIISKATKTLSTGTIQLTSGKSECNRALIIEALSCKGKVKVLNISDAADAVTLAAVLKVH 62

Query: 55 YMLGALRTLGLSVEADKAAKRAVVVGC GG-----KFPVEDAKEEV 94
+ + ++ R G + P D
Sbjct: 63 SPWSIVHSQAVADREPSTIDRQPPTMDHGPSTMDRQPPTMDHRLSTIDRQPPTMDHGPST 122

Query: 95 QLF--LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFL 152
+ +G AG AMR LTA + N ++ G RM++RPIG LV +++LGA +D +
Sbjct: 123 MDYVDIGPAGTAMRFLTAYLPLLDKN--IIITGTRKMQRPPIGILVDAMRKLGAIDYQV 180

Query: 153 GTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LALGDVEIEIIDKLISIPYV 211
PP++++ ++ + G+ISSQY++ALL+ AP L LG + +EI +L S PYV
Sbjct: 181 NEGFPPQLIHSGFQQKTDRISIKGNISSQYITALLLIAPSLPLG-LTLEIEGELTSKPYV 239

Query: 212 EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITG-GT 270
EMTL ++++ G++ +WD I + + VE D S+ASY+ A AA+
Sbjct: 240 EMTLAMLQQVGIGQ---HTWDDNNIHIANQPFKETSILVEPDWSAASYWYIAALCDEAE 295

Query: 271 VTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMK 330
+ + SLQGD E++ G + + V + + P RK + +
Sbjct: 296 LFLPALTPYSLQGDVITEIMANFGITSQFKDGGVHLQKEAK-PILRKIF-----DFKEC 349

Query: 331 PDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV-EEGPDYCIITP 389
PD+A T+ VV + + ++KET+R+ A++ EL K+G + E+G Y +
Sbjct: 350 PDLAQTIVVCAALGHDAFTTGLETLKIKETDRVAALQNELAKIGVKLTEKGQVYKLDSC 409

Query: 390 ----PEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFPDYFDVL 439
PEK+ I TY+DHRMAMAF+ A V + +P K++P ++ L
Sbjct: 410 EKQIPEKVT---IRTYEDHRMAMAFAPLALVVPQVEVEEPQVVEKSYPAFWSDL 460

>emb|CAK45651.1| unnamed protein product [Aspergillus niger]
Length = 1031

Score = 158 bits (399), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 109/283 (38%), Positives = 156/283 (55%), Gaps = 16/283 (5%)

Query: 169 GGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAH 227
GG++ L+ +SSQY+S+LLM AP A V ++++ K IS PY++MT +M FG+ +
Sbjct: 3 GGQINLAAKVSSQYVSSLLMCAPYAKEPVTCLKLVGGKPISQPYIDMTTAMMRSFGIDVKK 62

Query: 228 SDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKF 287
S + + Y +Y +P VE DASSA+Y LA AAITG T TV G+ SLQGD +F
Sbjct: 63 STTEEHTYHIPQGRYVNPAYMVESDASSATYPLAIAAITGTTCTVPNIGSKSLQGDARF 122

Query: 288 A-EVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADG 346
A +VL MG V T++S TVTG P G +V+M M D +T +V+A A G
Sbjct: 123 AVDVLRLPMGCTVEQTDSTTVTGAP----GGVLRPLPNVDMPEMTDAFLTASVLAAVARG 178

Query: 347 -----PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----A 397
T I +A+ RVKE R+ A++ EL K G E D I ++ ++
Sbjct: 179 DGSNHTTRIYGIANQRVKECNRIKAMKDELAKFGVVCREHDDGIEIDGIDRTSLRQPAGG 238

Query: 398 IDTYDDHRMAMAFS-LAACAEVPTIRDPGCTRKTFPDYFDVL 439
+ YDDHR+A +FS L+ I + C KT+P ++D L
Sbjct: 239 VFCYDDHRVAFSFSVLSLVTPQSTLILEREKVGTWPGWWSL 281

>ref|ZP_06141949.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus
flavefaciens FD-1]
Length = 416

Score = 157 bits (398), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 127/427 (29%), Positives = 210/427 (49%), Gaps = 41/427 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGT--TVVDNLLNSEDVHYMLGALRTLGLSVE-ADK 71
+ G V++P SKS ++R ++ AALS + +V+ + S+D+ LGA+ G E DK
Sbjct: 10 LKGRVEIPSSKSCAHRALICAAALSSDSEPSVLGSGISFSKDIETLGAMEAFGAKWEMTDK 69

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G G + A+ ++ + +G +R + A G + ++ G R+ +
Sbjct: 70 ESGTVTVWGIG---TDRAEGKLSIDCNESGSLRFVIPIAAALGYDTEFI--GRGLRPQ 123

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI + ++LG F + P ++G L GK ++ G++SSQ+++ LL A P
Sbjct: 124 RPID---IYTRELGRKGITFNYNNTMPFDISG--QLTSGKYEIEGNVSSQFITGLLFALP 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L GD EI + L S PYV++T+ M+RFGV + +++ + IKGGQ+Y S + VE
Sbjct: 179 LLEGDSIEILTSHLESRPYVDITIDTKRFGVVIDETET--SYTIKGGQRYHS-HSERVE 235

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S A++F AI G + + S+QGD + +T V G
Sbjct: 236 GDYSQAFAFFCVANAI-GSEIELGNLSPDSVQGDKRI-----TSITADILKDGVIGSF 286

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
RE + + +PD+ L+V+A + G + I + R+KE++R+ L
Sbjct: 287 RE-----DCSDIPDLVPILSVLAAYGSGESVIYNAERLRIKESDRLETTAAML 334

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
+G V D II P +KL +D DHR+ MA ++AA C+ V I
Sbjct: 335 NGIGGDVTVTDDGLIIRPTDKLTGGKVDGCGDHRIVMAAVALGCSG-DVIITGAEAVE 393

Query: 430 KTFPDYF 436
K++PD+F
Sbjct: 394 KSYPDFF 400

>ref|ZP_06757803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp.
6_1_27]
gb|EFG24918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp.
6_1_27]
Length = 422

Score = 157 bits (398), Expect = 3e-36, Method: Compositional matrix adjust.
Identities = 121/427 (28%), Positives = 208/427 (48%), Gaps = 31/427 (7%)

Query: 16 SGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+GT+ +K+ ++R L+ AAL+ ++ + S+D+ + +LR LG V + +
Sbjct: 10 TGTIASIPAKAHRAHALICAALANSSSTILLSRTSKDIDATMDSLRLGLAHVYEN---K 66

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
V V G A ++ + +G +R L V A+ N V D R+ +RP+
Sbjct: 67 VVTVTPG-----PAPKGYVVPHESGTTLR-LLLPVAASICNEVNV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + G+ L GG+ + G +SSQ+ S LL+AAP G
Sbjct: 119 PMLGEMKAHGV---FSQDKPPFTMTGL--LQGGQFSMVGDVSSQFFSGLLLAAP-QCG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS----WDRFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FGV +H+ + + F + +K N +E
Sbjct: 172 GATITSTPLQSSDYVTLTTTMDADFVTVDHPTARGTVQESFTVTANATFKGQSNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311

GD S+ + ++ AA+TG +T+ G S+Q D + +V+E G +TW + ++TV+G
Sbjct: 232 GDWSNTAIWMVAAAMTGPITITGMNQNISIQADRRIMQVIESSGCTITWDDMNITVSGRA 291

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P I ++ +MPD+ +A +A G ++ + A R+KE++R+ + +
Sbjct: 292 SKP-----IHADLEQMPDMLPVMMAALACSIQGESEFVNGARLRLKESDRLETVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A +E PV ++D K
Sbjct: 344 RDLGGTVREDGDDLYIIGSGILKGGQGDVCVNDHRLVMAGTLMALISETPVILQDSEAITK 403

Query: 431 TFPDYFD 437
++PD+F+
Sbjct: 404 SYPDFFE 410

>ref|YP_003411129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geodermatophilus
obscurus DSM 43160]
gb|ADB76758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geodermatophilus
obscurus DSM 43160]
Length = 422

Score = 157 bits (397), Expect = 3e-36, Method: Compositional matrix adjust.
Identities = 138/430 (32%), Positives = 211/430 (49%), Gaps = 38/430 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ V LPGSKSL+ R L+LAAL++G + + L + D M ALR LG+ V D+ +
Sbjct: 14 VDAVVALPGSKSLTARALVLAALADGPSRLVRPLRARDTDLMAAALRALGVRV--DEVGE 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPI 134
V + P E + G AG +R L A G +DG PR+ ERP
Sbjct: 72 DWAVTPRALRGPAE-----VDAGLAGTVLRFLLPPVAALADGPVR--VDGDPRLHERPN 122

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L+ LG VD G P V+G G + GG V + S SSQ +S LL+AA
Sbjct: 123 AGLIAALRDLGVRVDDD-GRGRAPFTVHGTGRVVRGGAVTVDASESSQIVSGLLLAARFD 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-----SPKNA 248
V++ + + S+P+VEMT+ + GV ++ G+ ++ + ++
Sbjct: 182 EGVDLALAGGVPSMPHVEMTVESLRERGVD-----VVRTGRGWRVAPGPVAAARDE 231

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A+ FLA A +TGG VT+ + Q + +L MGA V T + VT
Sbjct: 232 VLEPDLNAAPFLAAALVTGGRVTIIRDWPAETTQPGGRLDALLGAMGAHVERTGEGRLVT 291

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G ++ + ++ ++ ++ LA + ADG + + V R ET+R+ A+
Sbjct: 292 -----GSGTVRPLVADLGEVGELTPVLAALCALADGTSRLTGVGHLRGHETDRLQALD 344

Query: 369 TELTKLGASVEEGPDYCIITP-PEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPG 427
LT +GA VE+ PD +ITP P + + +Y DHRM A ++ A V +RDPG
Sbjct: 345 EVLTSVGARVEQLPDGLVITPGPHR--AARLGSYADHRMVHAAVLGLAVEGVEVRDPGA 402

Query: 428 TRKTFPDYFD 437
KT PD+ D
Sbjct: 403 VSKTLPDFVD 412

>ref|ZP_04598887.1| hypothetical protein VEIDISOL_00288 [Veillonella dispar ATCC 17748]
gb|EEP66222.1| hypothetical protein VEIDISOL_00288 [Veillonella dispar ATCC 17748]
Length = 422

Score = 157 bits (397), Expect = 3e-36, Method: Compositional matrix adjust.
Identities = 130/427 (30%), Positives = 206/427 (48%), Gaps = 31/427 (7%)

Query: 16 SGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 75
+GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V +
Sbjct: 10 TGTIASIPAKAHARALICAALATSPSTILLSRTSKDIDATMDSLRLGLGAHV---VYEN 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIG 135
+V G P AK V +G +R L V A+ N V D R+ +RP+

Sbjct: 66 KIVTVTSGPAP---AKGNV--VPHESGTTLR-LLLPVAASICNDVDV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + G L GG+ + G +SSQ+ S LL+AAP +G

Sbjct: 119 PMLSEMKAHGV---FSQDKPPFTMTG--HLQGGQFSMVGDVSSQFFSGLLLAAP-QIG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHS---DSWDRFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FGV+ EH+ D + F + G + N +E

Sbjct: 172 LSTITSTPLQSSDYVTLTTETMRNFGVEVEHTLPDTEINEAFTVPFGASFIGRDNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S+A+ ++ A +TG +T+ G S+Q D + +V+ G V W +VTVTG

Sbjct: 232 GDWSNAAIWMVAAGMTGRPITITGMNKNVQADRRIMQVMIDAGCDVIWGMNVTVTGRA 291

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P I ++ +MPD+ +A +A G +A A R+KE++R+VA+ +

Sbjct: 292 SKP-----IHADLEQMPDMLPVMAALACISGESAFVKGARLRLKESDRLVAVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A +E PVT++D K

Sbjct: 344 RDLGGTVREDGDDLYIIGSGILKGGQGDVNDHRLVMAGTLMALISENPVTLKDSEAITK 403

Query: 431 TFPDYFD 437
++PD+F+

Sbjct: 404 SYPDFFE 410

>ref|YP_002470344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis AD011]
gb|ACL29768.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis AD011]
gb|ADC85990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis BB-12]
Length = 462

Score = 157 bits (397), Expect = 3e-36, Method: Compositional matrix adjust.
Identities = 132/459 (28%), Positives = 220/459 (47%), Gaps = 47/459 (10%)

Query: 15 ISGTVKLPKSKSLSNRIILLAAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74
I TV +PGSKSLSNR L+LAALS ++ LL S D M+GAL+ LG++ + D

Sbjct: 20 IDATVTIPGSKSLSNRFLILAALSRLKVRRIEGLLRSDTELMGALKALGVAFQEDATEP 79

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V V P E ++F G AG MR + A G + DG + RP+

Sbjct: 80 TTVTV-----IPPAEGFTGNTEVFCGLAGTVMRFVPLTLFAKGPVRF--DGDEQAYARPM 133

Query: 135 GDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
G ++ G++QLGA ++ F G T PPV++ + G P KV++ S SSQ++S LL

Sbjct: 134 GPVLEGRQLGARIE-FEGEEGHLPTVTPPVQLGNLKGKP-QKVRIDSSASSQFISGLL 191

Query: 188 M-AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
+ + L G + +L S+P++ MT ME H + R +I + +

Sbjct: 192 LIGSRLPDGLILEHTGVQLPSMPHIRMT---MEDVDAAGGHIEMPQRGRWIVDHAELQMA 248

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ VE D S+A+ FL A I G+V + + Q +L GA S+

Sbjct: 249 AHVVVEPDLSNAAPFLGAALIASGSRIPNWAHTTQPGGFLPHILHRFGA-----SI 301

Query: 306 TVTGPPR-----EPFGRKHLKAIDV-----NMNMPDVAMTLAVVALFADGP 347
T+ G P E F + ++V +++ + ++ ++A +A+FA+ P

Sbjct: 302 TLGGEFPNEVNDCECFDDYNGILEVSSDGVIEGLGECDLAIGEITPSIAAIAVFANAP 361

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHR 405
+ + + R ET R+ A+ TE+ ++G+ +E + I P + ++ ++TY DHR

Sbjct: 362 SVLVGIGHLRGHETNRLEALATEINRVGSDAQEEAELSIAPVARDLMHGAVMETYADHR 421

Query: 406 MAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
MA ++ A + + + TRKT PD+ + + ++

Sbjct: 422 MATFAAMLGLAIDGIEVTNVETTRKTIPDFVGMWNGMLR 460

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>ref|ZP_02962867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis HN019]
ref|YP_002968397.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis Bl-04]
ref|YP_002969964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis DSM 10140]
gb|EDT89744.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis HN019]
gb|ACS46335.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis Bl-04]
gb|ACS47902.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis DSM 10140]
gb|ADG33527.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis V9]
Length = 448
```

Score = 157 bits (397), Expect = 3e-36, Method: Compositional matrix adjust.
Identities = 132/459 (28%), Positives = 220/459 (47%), Gaps = 47/459 (10%)

```
Query: 15  ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I TV +PGSKSLSNR L+LAALS ++ LL S D M+GAL+ LG++ + D
Sbjct: 6 IDATVTIPGSKSLSNRFLILALLSRKPVRIEGLLRSDTELMGALKALGVAFQEDATEP 65

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V V P E ++F G AG MR + A G + DG + RP+
Sbjct: 66  TTVTV----IPPAEGFTGNTEVFCGLAGTVMRFVPLTLFAKGPVRF--DGDEQAYARPM 119

Query: 135  GDLVVLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
G ++ G++QLGA ++ F G T PPV++ + G P KV++ S SSQ++S LL
Sbjct: 120  GPVLEGRQLGARIE-FEGEEGHLPTFTVTPPVQLGNLKGKP-QKVRIDSSASSQFISGLL 177

Query: 188  M-AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
+ + L G + +L S+P++ MT ME H + R +I + +
Sbjct: 178  LIGSRLPDGLILEHTGVQLPSMPHIRMT---MEDVDAAGGHIEMPQRGRWIVDHAELQMA 234

Query: 246  KNAYVEGDASSASYFLGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ VE D S+A+ FL A I G+V + + Q +L GA S+
Sbjct: 235  AHVVVEPDLSNAAPFLGAALIASGSRIPNWPAAHTTQPGGFLPHILHRFGA-----SI 287

Query: 306  TVTGPPR-----EPFGRKHLKAIDV-----NMNMPDVAMTLAVVALFADGP 347
T+ G P E F + ++V +++ + ++ ++A +A+FA+ P
Sbjct: 288  TLGGEPFNEVNDCECFDDYNGILEVSSDGVIEGLGECDSAIGEITPSIAAIAVFANAP 347

Query: 348  TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHR 405
+ + + R ET R+ A+ TE+ ++G+ +E + I P + ++ ++TY DHR
Sbjct: 348  SVLVGIGHLRGHETNRLEALATEINRVGSDAQEEAELSIAPVARDLMHGAVMETYADHR 407

Query: 406  MAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
MA ++ A + + + TRKT PD+ + + ++
Sbjct: 408  MATFAAMLGLAIDGIEVTNVETTRKTIPDFVGMWNGMLR 446
```

```
>ref|YP_001424881.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
Dugway 5J108-111]
sp|A9KCT5.1|ARO_A_COXBN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS76509.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii
Dugway 5J108-111]
Length = 438
```

Score = 157 bits (396), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 139/436 (31%), Positives = 216/436 (49%), Gaps = 29/436 (6%)

```
Query: 11  PIKEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + +SG + +PG KS+S R +LLAA++EG T VD L D M+ AL+ +G S++
Sbjct: 7 PSQGLSGEICVPGDKSISQRAVLLAAIAEGQTQVDGFLMGADNLAMVSALQQMGASIQVI 66

Query: 71  KAAKRAVVVGCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VV G G + P E L GN+G A+R L+ + AG VL G
Sbjct: 67  EDENILVVEGVGMTGLQAPPE-----ALDCGNSGTAIRLLSGLL--AGQPFNTVLTGDS 118
```

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
++ RP+ ++ L +GA +D + PP+++ G L G +L + S+Q S LL
Sbjct: 119 SLQRRPMKRIIDPLTLMGAKIDST--GNVPPMKIYGNPRLTGIHYQLPMA-SAQVKSCLL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G I P + T RL++ F + + GG K K+ +
Sbjct: 176 LAGLYARGKTCIT----EPAPSRDHTERLLKHFYHTLQKDKQS--ICVSGGGKLA-ND 227

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ GD SSA++F+ A IT G+ + C + +L+MMGA + T +
Sbjct: 228 ISIPGDISSAFFIVAATITPGS-AIRLCRVGVNPTRLGVINLLKMMGADIEVTHYTEKN 286

Query: 308 TGPPREPFGRK-HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK ID+ +++P D L + A A G T +RD A RVKET+R
Sbjct: 287 EEPTADITVRHARLKGIDIPDQVPLTIDEFPVLLIAAAVAQKTVLRDAAELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L KLG + E PD II L +++YDDHR+AMAF++A A+ V I
Sbjct: 347 IAAMVDLQKLGLIAAESLPDGVIIQ--GGTLEGGEVNSYDDHRIAMAFVAGTLAKGSVRI 405

Query: 423 RDPGCTRKTFPDYFDV 438
R+ + +FP++ ++
Sbjct: 406 RNCNPKTSFPNFVEL 421

>ref|ZP_02444898.1| hypothetical protein ANACOL_04233 [Anaerotruncus colihominis DSM
17241]
gb|EDS08908.1| hypothetical protein ANACOL_04233 [Anaerotruncus colihominis DSM
17241]
Length = 416

Score = 157 bits (396), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 139/426 (32%), Positives = 208/426 (48%), Gaps = 39/426 (9%)

Query: 17 GTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G + P SKS ++R L+ AALS V + S D+ L LR +G++ ++
Sbjct: 13 GKLAAPPKSAHRAALCAALSAMPCRVFPVAASSDMRATLRVLRAMGVNWTQEEN---- 68

Query: 77 VVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
VV G + A+E +G +R L A G A + G R+ ERP+G
Sbjct: 69 TVVFEGASW---QAREPFDCL--ESGSTLRFLLPVAAALGLPAAFTGGG--RLPERPLGA 121

Query: 137 LVVGLKQLG-ADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
L+ ++ G A D L P ++G L G+ L G +SSQ++S LL A PL G
Sbjct: 122 LMEQMRAGHVAFS DGR-----PFSISGR--LAAGRYTLPGDVSSQFISGLLFALPLVEG 174

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYVEGDA 254
D EI + L S YV+MTL + + G++ ++S W + GGQ Y+S + VE D
Sbjct: 175 DSEIVLTSPLQAGYVDMTLEALAQSGIRVSRTEGQWQ---VPGGQAYRSGERT-VEADW 230

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A+++L AGAA GG V + G S QGD +++ GA+++ P
Sbjct: 231 SNAAFWLCAGAA--GGDVRLTGLRDGSAQGDRAVFDLIGQFGAQISRANVTRCAHAP-- 286

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L I ++ +PD+ LAV A FA G T I + R+KE++R+ + L
Sbjct: 287 -----LHGIRIDAGPIPDLPILAVTAFAAQGDTEIYNAGRLRIKESDRLSTVAALLRD 340

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRK 431
LG SV+E PD I TA D +DHR+ M+ ++A C E PV IR K+
Sbjct: 341 LGGSVDEYPDLRTHGGGLRGGTA-DGANDHRVMSAAIAGMFCRE-PVLIRGAEAVHKS 398

Query: 432 FPDYFD 437
+PD+F+
Sbjct: 399 YPDFFE 404

>ref|ZP_06826700.1| short-chain-fatty-acid-CoA ligase [Streptomyces sp. SPB74]
gb|EDY45390.1| short-chain-fatty-acid-CoA ligase [Streptomyces sp. SPB74]
Length = 995

Score = 157 bits (396), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 221/437 (50%), Gaps = 27/437 (6%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++G V +P SK ++R L+LA+L+EG + V L ++ V Y + LR LG+ + +
Sbjct: 10 HQLTGEVLVPNSKYHAHRALILASLAEGVSRVHGLSDARHVQYTVQLLRGLGVKITTE-- 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G GG++ A + G++G + + + + + T + G R R
Sbjct: 68 GDTFVVHGLGGRYRPRRAA---VSAGSSGTTLYFMIGLASLSDRDVT--VTGQKYFRRR 121

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G L+ L+Q+G D DCPVVRV GG V+++G++S Q++S L++ AP
Sbjct: 122 PVGPLLTALRQMGVGADS--ADDCPPVRVAARRP-SGGHVRIAGTLS-QWISGLILLAPF 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE+ +L Y+E+T+ +M +FG+ S+ W RF ++ GQ + +
Sbjct: 178 ATGRTTIEVEGELNERSYLELTVAMMRQFGLAVTVSEDWRRFDVEPGQSAVA-TELTLP 236

Query: 253 DASSASYFLAGAAITGGTVTVGCGGTTSLQG-----DVKFAEVLEMMGAKVTWTETSVT 306
D SA++ +A AA+ V ++G T L+G + F ++ MG + E +
Sbjct: 237 DIGSAAFGIAAAALHPSDVLLKGM--TRLEGGPADHPEFHFLDIARAMGVPMELDEAAGG 294

Query: 307 VTGPPREFFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V P LK ++V+ +PD+ L+ + FA G + ++A R+KE++R A
Sbjct: 295 VRIRQEAPM---LKGVEVDCRDVPMPLPILSTLGSFAYGESVFHNIAHTRLKESDRAAA 350

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ +L +G +E D + E L + +++DHR+ M+ ++A+ A T+ P
Sbjct: 351 M-LQLNAMGGDELDGDALVRVGVEGLVGAKLSSFNDRHVLMSLAVASSRARGHSTLTYP 409

Query: 426 GCTRKTFFPDYFDVLSTF 442
R ++P Y D ++T
Sbjct: 410 NAYRISYPAYLDAMNTL 426

>ref|YP_377334.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9902]
sp|Q3AXB7.1|AROASYN9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB26290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9902]
Length = 437

Score = 157 bits (396), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 142/444 (31%), Positives = 207/444 (46%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+PG KS+S+R LL A++EGTT ++ LL +ED LR +G+ + +A K
Sbjct: 15 LQGRVKVPGDKSISHRSLLFGAIAEGTTTIEGLLPAEDPISTAACLAMGVGITPIEAGK 74

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G D +E Q L GN+G MR + + G +VLDG +R R
Sbjct: 75 IVTVEGVG-----LDGLQEPQHILDCGNSGTTMRLMLGLLAGRAGR-HFVLDGDASLRRR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+ + L +GADV + P+ V G L G+I S+Q SA+
Sbjct: 129 PMRRVQGPLASMGADVRGRDNGNLAPLAVQG-----TTLRGTIVGTPVASAQVKSAL 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSP 245
L+AA A D +I+ S + E R++ FG E R +K G
Sbjct: 181 LLAALTA--DGPTTVIEPSQSRDHSE---RMLRAFANLEVGEMGRHISVKPGATLHG- 234

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA+++L AGA + G +T+E G + EVL+ MGA +
Sbjct: 235 QTVVVPGDISSAAFVWAGALVPGSDLTIENTVGLNPTR--TGILEVLDQMGANIEIVHPR 292

Query: 305 VTVTGPPEPFRGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V G P KH LK MP D L+V A F DG + I + RVK

Sbjct: 293 -DVAGEPVGDLRVKHGPKLPFQFGEEIMPRLVDEVPILSVAACFCDGESRISGASELRVK 351

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
ET+R+ + +L +GA +EE D I L TA+D+ DHR+AM+ ++AA A

Sbjct: 352 ETDRLAVMARQLKAMGAEIEEHEDGMTIRGGRPLRGTLALDSETDHRVAMSMAIAALMASG 411

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
P T+ ++P ++D L+

Sbjct: 412 PSTLARSEAAAVSYPTFWDDLARL 435

>ref|YP_463398.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-C]
sp|Q2IMC8.1|AROA_ANADE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABC79961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-C]
Length = 440

Score = 157 bits (396), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 144/437 (32%), Positives = 208/437 (47%), Gaps = 39/437 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R LL ALS G T V LL++EDVH A+ LG
Sbjct: 18 LRGAIEVPDGKSIHRSLLFGALSTGETRVTGLLDAEDVHSTRKAVEALG----- 67

Query: 75 RAVVVGCGGKF---PVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A+V GG+ P +E + GN+G ++R LT ++ G VL G +R
Sbjct: 68 -AIVREEGGEVVVTPPATLREP GDVIDCGNSGTSRLRLTGVL SGVPG--LSVLTGDASLR 124

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ ++ L+ +GA++ G PPV V G G L G + L + S+Q SA+L+A
Sbjct: 125 RRPVRRVIDPLRAMGANLSARDGDRLPVVRG-GPLRGARQVLPVA-SAQVKSAILLAG 182

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G E +++ S + E LR M GV + S + + V
Sbjct: 183 LFAEG--ETTVEPEKSRDHTERMLRGM---GVPVKVSG----LEVSVAARPAGGRVDV 233

Query: 251 EGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVITVTG 309
GD SSA++FL GAA + G VTV G + +VL MGA V W V G
Sbjct: 234 PGDISSAAFFLCGAAALPGSEVTVRNLGVNETR--TGLLDVLRAMGADV-WLANLREVAG 290

Query: 310 PPREFPGRK--HLKAIDVNMNKMPPDVAMTLAVV--ALFADGPTAIRDVASWRVKETERM 364
PR + L+A ++ +P + L VV A A G T IRD RVKE++R+
Sbjct: 291 EPRADVTVRADRLATEIRGATIPRLIDELPVVMVMATQARGRTVIRDAKELRVKESDRL 350

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTI 422
A+ L + GA +E D C I P L + T DHR+AM+ ++A C PV +
Sbjct: 351 AAMGETLARAGARIELYEDGCAIEGPTPLRGVEVTRLDHRIAMSMAVAQLFCGGEPVVL 410

Query: 423 RDPGCTRKTFPDYFDVL 439
D C +FP +F +L
Sbjct: 411 DDVACVATSFPSFFRLL 427

>ref|ZP_05613250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium
prausnitzii A2-165]
gb|EEU98347.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium
prausnitzii A2-165]
Length = 424

Score = 156 bits (395), Expect = 5e-36, Method: Compositional matrix adjust.
Identities = 133/442 (30%), Positives = 216/442 (48%), Gaps = 38/442 (8%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++V++ + ++G + P SKS+++R +L AAL++GT+ + +L S+D+ LGA L
Sbjct: 2 DVVVKRARPVAGRIAAPP SKSMAHRAVLCAALAKGTSHLHHLAFSKDISATLGAAGRLCA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V + AVV G G PV+ + + +G +R L + G T+ G

Sbjct: 62 RVTTGE--NDAVVEGLGRFLPVDAPVDCCE-----SGSTLRFLIPLASLTGQEVFTFT--G 112

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
R+ ERP +Q G + G D R+ G L G+ +L+G++SSQ++S

Sbjct: 113 RGRLMERPQSVYKTLYQQQGLRFE--QGAD----RLTVEGALTPGEYELAGNVSSQFISG 166

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL A PL G + +I + S Y++MT + FGV++ D + I GGQ Y P

Sbjct: 167 LLFALPLLGGTSTLHLIPPVESRSYIDMTRAVQHAFGVESRWLDE-NTLEIPGGQHLYL-P 224

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ VEGD S A++ A+TGG V + G +LQGD E+L GA+ T T V

Sbjct: 225 GDYTVGEDYSQAAPPAVLGAVTGG-VAITGLSEETLQGDAAILEILRRCGARFTRTGQGV 283

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
F + L D+++ PD+ L V+ L +G T IR+ R+KE++R+

Sbjct: 284 V-----FEKAPLHGTDIDLADCPDLGPVLMVLGLLCEGTTVIRNAERLRIKESDRIE 335

Query: 366 AIRTELTKLGASVE-EGPDYCI-----ITPPEKLNVTATIDYDDHRMAMAFSLAACAEV 418
A+ TEL G +E EG I + PE+ + ++DHR+ M+ ++ A A

Sbjct: 336 AMETELRACGGQLESEGGTITIHCAGALHAPEQ---PLSGHNDHRVVMSLAVLALAAG 391

Query: 419 PVT-IRDPGCTRKTFPDYFDVL 439
I K++PD+ + +

Sbjct: 392 LALPISGAEEAVAKSWPDFLEAI 413

>ref|YP_003800841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Olsenella uli DSM
7084]
gb|ADK67961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Olsenella uli DSM
7084]
Length = 440

Score = 156 bits (395), Expect = 5e-36, Method: Compositional matrix adjust.
Identities = 139/445 (31%), Positives = 214/445 (48%), Gaps = 33/445 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I + P ++G+++ SKS ++R+L+LAAL+ TT +D +S+D+ + L LG

Sbjct: 2 DITIHP-HALTGSIRAVASKSAHRLVLALAPTNTNDCNSSDDIEATVSCLEALGA 60

Query: 66 SVEADKAAKRAVVVGC--GGK--FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ + R + C GG FP A+ L G +G +R L A G A

Sbjct: 61 RIARTRVGFRVKPLPCRTGGDQGF---ARSGAVLDCGESGSTLRFLLPVGCALG--AQM 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G R+ RP+ L L GA + ++ + + G L GG + G +SSQ

Sbjct: 116 RLTGHGRLASRPLSPLYEELVAHGARL-----SEKGRPLEVAGKLRGGSFFIPGDVSSQ 170

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA----EHSDSWDR---- 233
Y S LLMAAPL G I + + + S PY+++TL + FGV+ E D

Sbjct: 171 YASGLLMAAPLEGPSTIVVGEPISRPYIDVTLEALRDFGVEVACAREAGAGGDVRRSV 230

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
F + + SP A VEGD S+++++LA AA+ GG V VEG S QGD L

Sbjct: 231 FTVPAAQLASPGTAVVEGDWSNSAFWLAAAAM-GGDVAVEGLRMDSPQGDRAVLALAA 289

Query: 294 MGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
GA+V TS HL+ ++++ +PD+ LA VA A+G T I

Sbjct: 290 FGARVRRGGTSAACA-----HDHLQGRITIDVSDIPDLVPLA AVASIAEGSTRIVGA 341

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLA 413
A R+KE++R+ + L LGA + D ++ L+ +D +DHR+AM ++A

Sbjct: 342 ARLRLKESDRLETVCAALALGADIRVEADGLAVSGRPTLSGGEVDAANDHRIAMMAAIA 401

Query: 414 ACAEV-PVTIRDPGCTRKTFPDYFD 437
A TI C K++P +F+

Sbjct: 402 AAHATGSTTIHGAECVSKSYPRFFE 426

>ref|ZP_03945961.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium
vaginale DSM 15829]

ref|ZP_07665284.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium vaginae DSM 15829]
gb|EEI85157.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium vaginae DSM 15829]
Length = 450

Score = 156 bits (395), Expect = 6e-36, Method: Compositional matrix adjust.
Identities = 134/454 (29%), Positives = 213/454 (46%), Gaps = 41/454 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+V+QP + GTV SKS+++R+L+LAA + ++ S+D+ + L LG
Sbjct: 2 NVVIQP-HGLQGTVSAIASKSMAHRLILAASTSAIVDINCSSTSDDIQATIECLEALGA 60

Query: 66 SVEADKAAKRAVVVGCCKFPVEDAKEE-----VQLFLGNAGIAMRSLTAAVT 113
+ R + + + D K V L G +G +R + V
Sbjct: 61 CITRTTLGYRVRGMFFASQSSSLADTKAAFTDNSSATGDTPTVILNCGESGSTLRFMLPVVA 120

Query: 114 AAGGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKV 172
A G +A V G R+ RP+ L L G CFL P+ + G L GG
Sbjct: 121 ALGKHAYLV--QGRLATRPLEPLYSELCAHG----CFLSEQGAFFLEIKG--KLSGGVF 172

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
+ G++SSQY+S LL+AA +A +EI + S YV+MT+ +++FG+ + +D
Sbjct: 173 HIPGNVSSQYISGLLLAAGIAHLHLEIIVSKPFESKSYVKMTIDALQQQFGINVAQTQEYD 232

Query: 233 -----RFYIKGGQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD 284
RF + Q P+ + VEGD S A ++L AA+ G + + G TS QGD
Sbjct: 233 DQQQEFIRFVSDE-QTSLSLPRQSLTVEGDWSGAGFWLCAAAL-GNPLRMSGLSLTSSQGD 290

Query: 285 VKFAEVLMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA 344
L GA+ T + + V G K L+ + ++ + D+A LA +A FA
Sbjct: 291 KAILACLAFAFGARTQKTASYIEV-----GSKALRPATLPLDDIVDLAPPLAALACFA 342

Query: 345 DGPTAIRDVASVRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDH 404
+G T + + R+KE++R+++I T L +GA + D I L ++ + DH
Sbjct: 343 NGTTKLTHASRLRLKESDRILSITTTLQNMGADISSDADTYIHGHGMLTGGEVECFRDH 402

Query: 405 R-MAMAFSLAACAEVPTIRDPGCTRKTFPDYFD 437
R MA AA A+ P TIR C RK++P +F+
Sbjct: 403 RIAMMATIAAAYAQHPTTIRGAECVRKSYPTFFE 436

>ref|YP_002132567.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter sp. K]
sp|B4ULJ1.1|AROANASK RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACG71438.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter sp. K]
Length = 440

Score = 156 bits (395), Expect = 6e-36, Method: Compositional matrix adjust.
Identities = 146/434 (33%), Positives = 208/434 (47%), Gaps = 33/434 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R LL ALS G T V LL++EDVH A+ LG +V D+ A+
Sbjct: 18 LRGAIEVPGDKSISHRSLLFGALSTGETRVTLGLDAEDVHSTRRAVEALGATVR-DEGAE 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 133
VVV P +E + GN+G ++R LT ++ G VL G +R RP
Sbjct: 77 --VVV----TPPATLREP GDVIDCGNSGTSRLRLTGVLGVPVPG--LSVLTGDASLRRRP 127

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ +GAD+ G PPV V G G L G + L S+Q SALL+A A
Sbjct: 128 VRRVIDPLRVMGADLSARDGDRLPVVRG-GPLRGAR-HLLPVASQVKSALLLAGLFA 185

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E +++ S + E LR M GV S + + V GD
Sbjct: 186 --DGETAVVEPEKSRDHTERMLRGM---GVPVRVSG---LEVSVSAARPAGGRVDVPGD 236

Query: 254 ASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPR 312

SSA++FL GAA + G VTV G + +VL MGA V + V G PR
Sbjct: 237 ISSAAFFLCGAAALPGSEVTVRN LGVNETR--TGLLDVLRAMGADVRLADLR-EVAGEPR 293

Query: 313 EPFGRK--HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ L+ ++ +P D + V+A A G T IRD RVKE++R+ A+

Sbjct: 294 ADVTVRADRLEGTEIRGATIPRLIDELPAVMVMATQARGRTVIRDAKELRVKESDRLAAM 353

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L + GA +E D C I P L + T DHR+AMA ++A C PV + D

Sbjct: 354 GETLARAGARIELFEDGCAIDGPTPLRGVEVTRLDHRIAMAMAVAQLFCGGEPVVLDDV 413

Query: 426 GCTRKTFFPDYFDVL 439
C +FP +F +L

Sbjct: 414 ACVATSFPGFFRL 427

>ref|YP_002490631.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-1]
sp|B8J8W7.1|AROANAD2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACL63565.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-1]
Length = 440

Score = 156 bits (394), Expect = 7e-36, Method: Compositional matrix adjust.
Identities = 144/434 (33%), Positives = 207/434 (47%), Gaps = 33/434 (7%)

Query: 15 ISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R LL ALS G T V LL++EDVH A+ LG +V + A

Sbjct: 18 LRGAIEVPGDKSISHRSLFGALSTGETRVAGLLDAEDVHSTRRAVEALGATVRTEGAE- 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VVV P +E + GN+G ++R LT ++ G VL G +R RP

Sbjct: 77 --VVV-----TPPATLREPGDVIDCGNSGTSRLRLTGVLSGVPG--LSVLTGDASLRRRP 127

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ +GA++ G PPV V G G L G + L S+Q SALL+A A

Sbjct: 128 VRRVIDPLRVMGANLSARDGRLPPVVVRG-GALRGAR-HLLPVASAQVKSALLLAGLFA 185

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G E +++ S + E LR M GV + S + + V GD

Sbjct: 186 EG--ETTVEPEKSRDHTERMLRGM---GVPVKVSG---LEVSVSAAARPAGGRVDVPGD 236

Query: 254 ASSASYFLAGAA-ITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++FL GAA + G VTV G + +VL MGA V V G PR

Sbjct: 237 ISSAAFFLCGAAALPGSEVTVRN LGVNETR--TGLLDVLRAMGADVRLANLR-EVAGEPR 293

Query: 313 EPFGRK--HLKAIDVNMNKMPPDVAMTLAVV---ALFADGPTAIRDVASWRVKETERMVAI 367
+ L+ ++ +P + L VV A A G T IRD RVKE++R+ A+

Sbjct: 294 ADVTVRADRLEGTEIRGATIPRLIDELPVVMVMATQARGRTVIRDAKELRVKESDRLAAM 353

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L++ GA +E D C I P L + T DHR+AM+ ++A C PV + D

Sbjct: 354 GETLSRAGARIELFEDGCAIDGPTPLRGVEVTRLDHRIAMSMAVAQLFCGGEPVVLDDV 413

Query: 426 GCTRKTFFPDYFDVL 439
C +FP +F +L

Sbjct: 414 ACVATSFPSFFRL 427

>ref|YP_004170224.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
maricopensis DSM 21211]
gb|ADV66559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deinococcus
maricopensis DSM 21211]
Length = 445

Score = 156 bits (394), Expect = 7e-36, Method: Compositional matrix adjust.
Identities = 142/434 (32%), Positives = 202/434 (46%), Gaps = 22/434 (5%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

++ + P+ + GT+ SK+ + R LL AAL+EG T V + SED +L LR G
Sbjct: 16 DVTVHPVAALRGTLHAQPSKNYTTRYLLAAALAEGPTRVHGVATSEDAEALLRCLRDWGA 75

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ D + A+V G G + V L GNAG R L A V + T V D
Sbjct: 76 HIALD--GEDALVTGFGAH-----PRPGVTLNPGNAGAVARFLMA--VALLTQSTTLVTDY 127

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP GDL+ L LGA V G PV V+G + GG V++S SSQY S
Sbjct: 128 AESLGKRPQGDLEALHALGATVTSTTEGR--LPVTVSGP--VVGGPVQVSAERSSQYASG 183

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ AAPL +++ + + S + TL+ + FGV S R I GGQ Y++P
Sbjct: 184 LMFAAPLLPNGLDLHLTGDKVSHAPLRQTLQTLRTFTFTASADLRTVTIPGGQTYRAP 243

Query: 246 KNAY-VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
A V GD ++ LA AA+ G V V LQG+ +VL MGA+V S
Sbjct: 244 GGAVRVPGDYPGSAAILAAAVRPGEVRLNLLADDLQGERAAVDVLRDMGAQVWRDGDG 303

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V G L+A+ + + D L A A G T +VA+ R+KE +R+
Sbjct: 304 VVVQ-----GGAPLRALTRDGAFTDAVQALTAASAQGVTTWENVATLRLKECDRI 356

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAAC-AEVPVTI 422
R L +G E D +T + +D Y DHRM M +L A+ P+T+
Sbjct: 357 SDTRALASIGVHATETHDSLVTGAAHIPGGVIVDGYGDHRMIMMLTLLGLRADAPITV 416

Query: 423 RDPGCTRKTFPDYF 436
RK++P +F
Sbjct: 417 TGAHHVRKSYPGFF 430

>ref|ZP_01467675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
BL107]
gb|EAU71568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
BL107]
Length = 437

Score = 156 bits (394), Expect = 7e-36, Method: Compositional matrix adjust.
Identities = 142/446 (31%), Positives = 208/446 (46%), Gaps = 39/446 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+PG KS+S+R LL A++EGTT ++ LL +ED LR +G+S+ +A +
Sbjct: 15 LQGRVKVPGDKSISHRSLLFGAIAEGTTTIEGLLPAEDPISTAACLAMGVSIPIEAGQ 74

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G D +E L GN+G MR + + G +VLDG +R R
Sbjct: 75 LVTVEGVG-----LDGLQEPDHILNCGNSGTTMRLMLGLLAGRAGR-HFVLDGDASLRRR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+ + L +GADV + P+ V G L G+I S+Q SA+
Sbjct: 129 PMRRVQGPLASMGADVGRDSCGNLAPLAVQG-----TTLRGTIIVGTPVASAQVKSAL 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSP 245
L+AA A D +I+ S + E R++ FG E R +K G
Sbjct: 181 LLAALTA--DGPTTVIEPSQSRDHSE---RMLRAFGANLEVGGEMGRHISVKPGATLHG- 234

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA+++L AGA + G +T+E G + EVL+ MGA +
Sbjct: 235 QTVVVPGDISAALFVAGALVPGSDLTIENTVGLNPTR--TGILEVLDMGANGIEIVNPR 292

Query: 305 VVTGTGPPREPFGGRKH--LKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V G P KH LK MP D L+V A F DG + I A RVK
Sbjct: 293 -DVAGEPVGDLRVKHGPLKPFQFGEEIMPRLVDEVPLSVAACFCDGESRISGAELRVK 351

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEV 418
ET+R+ + +L +GA +EE D I L+ TA+D+ DHR+AM+ ++AA A
Sbjct: 352 ETDRLAVMARQLKAMGAIEIEHDDGMTIRGGRPLHGTALDSETDHRVAMSMVAALMANG 411

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
P T+ ++P ++D L +

Sbjct: 412 PSTLARSEAAVSYPTFWDDLRLHR 437

>ref|ZP_04624289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia kristensenii
ATCC 33638]
gb|EEP91177.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Yersinia kristensenii
ATCC 33638]
Length = 127

Score = 156 bits (394), Expect = 7e-36, Method: Compositional matrix adjust.
Identities = 71/121 (58%), Positives = 91/121 (75%)

Query: 320 LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
++ ID++MN +PD AMT+A ALFADGPT IR++ +WRVKET+R+ A+ TEL K+GA VE
Sbjct: 1 MQGIDMDNMNHPDAAMTIATTALFADGPTTIRNIYNWRVKETDRLSAMATELRKVGAEVE 60

Query: 380 EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
EG DY + PP +L I TY+DHRMAM FSL A ++ VTI DP CT KTFPDYF+ L
Sbjct: 61 EGQDYIRVVPPTQLIAAEIGTYNDHRMAMCFSLVALSQTQVTILDPKCTAKTFPDYFEQL 120

Query: 440 S 440
+
Sbjct: 121 A 121

>ref|ZP_08114716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
nigrificans DSM 574]
gb|EGB21839.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
nigrificans DSM 574]
Length = 434

Score = 156 bits (394), Expect = 7e-36, Method: Compositional matrix adjust.
Identities = 144/453 (31%), Positives = 217/453 (47%), Gaps = 44/453 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
E+ + IK++ G +PG KS+S+R ++L AL+ GTT V+N L ED + R LG+
Sbjct: 7 ELTINQIKQLKGETAVPGDKSISHRAVMLGALARGTTRVENFLTGEDCLSTVRCFRALGV 66

Query: 66 SVEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVL 123
VE D VG G +E V + GN+G R + + AG + ++
Sbjct: 67 PVEGPDNGCLTIQGVGLNG-----LQEPVTILDAGNSGTTTRLMLGIL--AGQSFCSII 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP---PVRVNGIGGLPGGKVK----LSG 176
G + RP+ + L +GA F+G D P+ + G G++K S
Sbjct: 119 TGDASLSRRPMARVTTPLAGMGAK---FIGRDNNNLLPLAIRG-----GQLKPLNYQSP 169

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L+A A G E + + IS + E R+++ FG A+ I
Sbjct: 170 VASAQVKSAILLAGLFAQG--ETSVTEPTISRDHTE---RMLKSFG--ADIKQEGTTVTI 222

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
KG + K + V GD SSA++ + AAI G+ VT+ G G + EVL+ MG
Sbjct: 223 KGRPELKG-RQVVVPGDISAFLMVAAILPGSEVTIRGVGNPTRDG--LLEVLKNMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAI 350
+V G P K L+ +++ N +P D +AV A A G T I
Sbjct: 280 GQVELLNLR-DQCGEPVADIRVKGSDLQGTEISGNLIPRLIDEIPIIAVAAACARGTTVI 338

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
RD A +VKE+ R+ + ELTKLGA+VEE PD II + L +D++ DHR+AMA
Sbjct: 339 RDAAELKVKESNRLATVAGELTKLGAAVEELPDGLIIKGGKPLTGAVVDSHGDHRIAMAM 398

Query: 411 SLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTF 442
++A A T I++ C +FP + D L +
Sbjct: 399 AVAGLAARGRTVIKEAQCIPVSFPGFADALKSL 431

>ref|ZP_07071831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia dentocariosa
M567]
gb|EFJ77557.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rothia dentocariosa
M567]

Length = 443

Score = 155 bits (393), Expect = 9e-36, Method: Compositional matrix adjust.
Identities = 139/447 (31%), Positives = 215/447 (48%), Gaps = 50/447 (11%)

```
Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+++PGSKSL+NR LLLAAL++ + + L+S D M+ AL LG E
Sbjct: 1 MRIPGSKSLTNRYLLLAALADSPSRLRAPLHSRDSALMISALEALGAQFER----- 51

Query: 79 VGCGGKF-----PVEDAKEE--VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ G +F P++ A ++ G AG MR + A G Y DG P
Sbjct: 52 IETGSEFGPDLVTPLDRAPSPSTAKIDCGLAGTVMRFVPALAALLPGE--YNFDGDPHA 109

Query: 130 RERPIGDLVVGLKQLGADVDCF--LGTDCPPVRVNGIG-----GLPGGKVKLSGSISSQY 182
R+RP+ L GL QLG ++ D P ++ G G P ++ + S SSQ+
Sbjct: 110 RKRPMALNGLHQLGVRIERSGDDSDVDTLPFTLHSPGLAASGTP-AEIFIDASASSQF 168

Query: 183 LSALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+SALL+ AP L G + + SIP++EMTL+ + GV+AE D + +
Sbjct: 169 VSALLLIAPRLPQGLTIRHGNVAPSIPIHIEMTLQTLRDLGVRAEAVA--DEYTWRFVFPD 226

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC-----GTTSLQGDVKFAEVL 292
S + VE D S+A FLA A +TG +VT+ GTT QG ++ +L
Sbjct: 227 TISGFDVTVEPDLNAGPFLAAMVTGNSVTIPDWPAPTADGSPGTT--QGGDEWRTILP 284

Query: 293 MMGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+G V ++ S+TVTGP E R L ++ N+ ++A T+A + D P+ +
Sbjct: 285 RLGGAVEFSNGSLTVTGP--EDITR--LSGVEFNLQTAGELAPTVAALVALLDSPSTLTG 340

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKL---NVTADITYDDHRMAM 408
+ R ET+R+ A+ E+ +LG EE D ++ P +L + + TY+DHR+A
Sbjct: 341 IGHRLGHETDRLAALVAEINRLGGLAEETADGIRVLRPVRRLPQDSPVTVQTYEDHRVAT 400

Query: 409 AFSLAACAEVPVTIRDPGCTRKTFFPDY 435
++ E V I + T KT P +
Sbjct: 401 FAAVIGLHEPGVRIENVQTTAKTLPQF 427
```

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>ref|YP_003164843.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia buccalis
DSM 1135]
gb|ACV39852.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia buccalis
C-1013-b]
Length = 431
```

Score = 155 bits (393), Expect = 9e-36, Method: Compositional matrix adjust.
Identities = 126/437 (28%), Positives = 221/437 (50%), Gaps = 32/437 (7%)

```
Query: 15 ISGTVKLPGSKSLSNRILLLAALSEG--TTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++GT+++P SKS S+R ++ AAL+E + +DNL S D+ + G ++ ++
Sbjct: 10 LNGTIEIPPSKSYSHRAVIAAALAESGKKSTIDNLKFSVDITTTTIDIMENWGAKIKRFES 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A ++G GK +D + VQ +G +R L + DG ++ +R
Sbjct: 70 ALE--IIGNDGKVVPKD--KYVQC--NESGSTIRFLIP--IGITDENELIFDGKGKLVDR 121

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + G G P+ VNG L G ++ G+ISSQ+++ LL A PL
Sbjct: 122 PLDSYYRIFDKQGILYKNENGK--LPLTVNG--KLKAGNYEIDGNISSQFITGLLYALPL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
GD ++ I L S Y+++TL +++ G++ +++ + F IKG Q YK P + VEG
Sbjct: 178 LDGDSKLTINKNLESGYIDLTLLEILKLAGIQIVNNN-YKSFIDIKGNQIYK-PFDYTVGE 235

Query: 253 DASSASYFLAGAAITGGTVTVEGC---GTTSLQGDVKFAEVLMMGAKVTWTETSVTVTG 309
D S ++++ I+ C SLQGD + E++ MGA + + V V
Sbjct: 236 DYSQVAFWIVAGIISANKDNEIKCLHVNKNSLQGDREIIEIVTRMGANLKIFDDYVLVK- 294

Query: 310 PPREPFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P + K +++++ PD+ L V+ ++G T I + R+KE++R+ +I+T
Sbjct: 295 PSK-----TKGTIIDISQCPDIGPILTVLGALSEGETRIINGERLRIKESDRITSIKT 347
```

Query: 370 ELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGC 427
EL KLGA+V E D II E ++ ++DHR+AM+ ++A+ E + + +
Sbjct: 348 ELNKLGANVVEEGDSLIIQGVGFTGGVTVNAWNDRHIAISLAIASTRCEKEIILEEAES 407

Query: 428 TRKTFPDYFDVLSTFVK 444
RK++P ++D FVK
Sbjct: 408 VRKSYPHFWD---DFVK 421

>ref|YP_001656551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microcystis
aeruginosa NIES-843]
dbj|BAG01359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microcystis
aeruginosa NIES-843]
Length = 446

Score = 155 bits (393), Expect = 9e-36, Method: Compositional matrix adjust.
Identities = 140/449 (31%), Positives = 216/449 (48%), Gaps = 25/449 (5%)

Query: 5 EEIVLQP--IKEISGTVKLPKSKLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRT 62
+++V+ P I + G + +PG KS+S+R L+L A++EG TV+ LL ED R
Sbjct: 13 QDLVIDPGKITGLRGKITIPGDKSISHRSLMLGAIAEGETVIHGLLLGEDPRSTASCFRA 72

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFNLGAGIAMRSLTAAVTAAGGNATYV 122
+G VE + V+V G +E+ E L GN+G +R L + A + +V
Sbjct: 73 MG--VEISQLNSEKVIKGRGLGNLEEPLE--ILDAGNSGTTIR-LMLGLLAGHQDRFFV 127

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ G +R RP+ +V LK++GA + P+ V+G P S S+Q
Sbjct: 128 VTGDASLRSRPMSRVVKPLKEMGAQIWGRKANSLAPLAVSGESLQP--IHYYSPVASAQV 185

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+A L G + I + +S + E R++ FG E + + G
Sbjct: 186 KSCLLLLAGLLTEG--KTTITEPALSRHSE---RMLRAFGANIEVDGETNSVTVTGYPTL 240

Query: 243 KSPKNAYVEGDASSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V GD SSA+++L AGA + + +E G + V +VL+ MGA +T
Sbjct: 241 TG-QTVIVPGDISAFAFWLVAGAIVPNSSELLIENVGINPRTTGV--LQVLQAMGADITL- 296

Query: 302 ETSVTVTGPPPREPFGRKH--LKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASW 356
E VTG P K L+A + +P D LAV A+FA G T I+D
Sbjct: 297 ENQRVVTGEPVADLRVKSSPLQATTIAGEIIPRLIDEIPILAAVAQGTIIKDAEEL 356

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC- 415
RVKE++R+ + T+L +LGA V E PD IT L T +D++ DHR+AM+ ++AA
Sbjct: 357 RVKESDRLTVMATQLDRLGAKVRELPGGLEITGGTGLFGTEVDSFTDHRIAMSLAIAALN 416

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ P TI ++PD+F L +
Sbjct: 417 SRQPTTIHRAEAAGISYPDFSTLQQICQ 445

>ref|YP_001227406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
RCC307]
sp|A5GT44.1|AROA_SYNR3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAK28053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
RCC307]
Length = 437

Score = 155 bits (393), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 220/439 (50%), Gaps = 21/439 (4%)

Query: 15 ISGTVKLPKSKLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++PG KS+S+R LL A++ GTT ++ LL +ED LR +G++V A ++
Sbjct: 12 LHGSVRVPGDKSISHRALLFGAIATGTTTIEGLLPADPLSTAACLAMGVTVSAIDSSG 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERP 133
V G G ++ +E Q+ GN+G MR + + G +VLDG +R RP
Sbjct: 72 VVRVEGVG---LDGLQEPAQVLDCGNSGTTMRLMLGLLAGRHGR-HFVLDGDGSLRRRP 126

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA++ G + P+ + G L GG ++ + S+Q SALL+A A
Sbjct: 127 MARVAQPLAQMGAEIGGREGGNKAPLAIAAG-QTLSGGTIR-TPVASAQVKSALLLAGLTA 184

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + I+ +S + E LR + H+ ++ G + ++ V GD
Sbjct: 185 KGSTTV--IEPALS RDHSERMLRAFGAELISEPHAAEGPTAIVRPGAELHG-QHVVPVPGD 241

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + GT +T+E G + +VLE MGA + V G P
Sbjct: 242 ISSAAFWLIAALVVPGETELTIENVGINPTR--TGILDVLEQMGAPLEV LNQR-DVAGEPV 298

Query: 313 EPFGRKH--LKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ LKA ++ +P D L+V AL A+G + +RD A RVKET+R+ +
Sbjct: 299 ADLRVRSPLKAFEIGGELIPRLVDEIPILSVAALCAEGTSVMRDAAELRVKETDRLAVM 358

Query: 368 RTELT KL GASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
+L +GA +EE D +I ++L +D+ DHR+AM+ ++AA A +I
Sbjct: 359 ARQLRAMGAEEETTDGMVIPGGQRLTGAQVDSETHRVAMSLAVAALIASGDTSIDQSE 418

Query: 427 CTRKTFPDYFDVLSTFVKN 445
++P ++D L+ ++
Sbjct: 419 AA AVSYPSFWDELARLQRS 437

>ref|YP_003683578.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Meiothermus silvanus
DSM 9946]
gb|ADH62070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Meiothermus silvanus
DSM 9946]
Length = 425

Score = 155 bits (392), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 135/440 (30%), Positives = 217/440 (49%), Gaps = 35/440 (7%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L P + + G++++PG KS+++R L+L AL++G + + + L + D G +R LG +
Sbjct: 5 LFPTRSLRGSRLVPGDKSVTHRGLMLGALAQGESWLYHPLKAGDTLSTAGVMRALGAEIH 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ A R VG K P + L GNAG +R ++ + AG VL G
Sbjct: 65 EEGAHFRIRGVGLALKEPGD-----ILDCGNAGTLIRLVSGLL--AGQEMFTVLTGDAS 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+G + L+Q+GA +D G P+ + G GGL G + +L + S+Q SA+L+
Sbjct: 117 LRRRPMGRVTAPLRQMGARIDGRDGGRLAPLAIRG-GGLKGIRYELPVA-SAQVKS AVLL 174

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G+ E+ P + T R+ +G+ E +R Q + + ++
Sbjct: 175 AGLFAEGETEVE-----PAPTRDHTERIFRHYGLPIEVQG--NRIRTHRAQPF AA-RDL 226

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL A IT + VT+EG G + VL+ MGA ++W T
Sbjct: 227 TVPGDFSSAAFLVAALITPDSEVTLEGVGLNPTR--TGLLTVLKEMGADLSWEVTE--- 281

Query: 308 TGPPREPFG-----RKHLKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G EP G LK + V+ + +P D L+ A +A+G T I + RVK
Sbjct: 282 -GQDGE PVGWIRARSSQLKGVAVDP SLIPLMVDEIPILSAAA AAEGETFIPGLEELRVK 340

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVP 419
E++R+ AI L LG E GPD+ I + ++ + DHR+AMAF++ +
Sbjct: 341 ESDRLEAIAKNLNLGVKTEVGPDWIRIF-GGSVQQGRVEPFHDHRIAMAFAVCGL-QTG 398

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
VT+ D +FP +++ L
Sbjct: 399 VTVHDAEWASISFSPFWEDL 418

>emb|CAO90621.1| aroA [Microcystis aeruginosa PCC 7806]
Length = 446

Score = 155 bits (392), Expect = 1e-35, Method: Compositional matrix adjust.

Identities = 140/449 (31%), Positives = 216/449 (48%), Gaps = 25/449 (5%)

Query: 5 EEIVLQP--IKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
+++V+ P I + G + +PG KS+S+R L+L A++EG TV+ LL ED R
Sbjct: 13 QDLVIDPGKITGLRGKITIPGDKSISHRSLMLGAIAEGETVIHGLLLGEDPRSTASCFRA 72

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+G VE + V+V G +E+ E L GN+G +R L + A + +V
Sbjct: 73 MG--VEISQLNSEKVIVKGRGLGNLEEPLE--ILDAGNSGTTIR-LMLGLLAGHQDRFFV 127

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQY 182
+ G +R RP+ +V LK++GA + P+ V+G P S S+Q
Sbjct: 128 VTGDASLRSRPMSRVVVKPLKEMGAQIWGRKANSLAPLAVSGEYLQP--IHYYSPVASAQV 185

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+A L G + I + +S + E R++ FG E + + G
Sbjct: 186 KSCLLLAGLLTEG--KTTITEPALSRDHSE---RMLRAFGANIEVDGETNSVTVTGYPTL 240

Query: 243 KSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V GD SSA+++L AGA + + +E G + V +VL+ MGA +T
Sbjct: 241 TG-QTVIVPGDISAFAFWLVAIAVPNSELLIENVGINPTRTGV--LQVLQAMGADITL- 296

Query: 302 ETSVTVTGPPREFFGRK--HLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASW 356
E VTG P K L+A + +P D LAV A+FA G T I+D
Sbjct: 297 ENQRVVTGEPVADLRVKSSQLQATTIAGEIIPRLIDEIPILAVAFAVFAQTIIKDAEEL 356

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAAC- 415
RVKE++R+ + T+L +LGA V E PD IT L T +D++ DHR+AM+ ++AA
Sbjct: 357 RVKESDRLTVMATQLDRLGAKVRELPGLEITGGTGLFGTEVDSFTDHRIAMSLAIAALN 416

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ P TI ++PD+F L +
Sbjct: 417 SRQPTTIHRAEAAGISYPDFSTLQKICQ 445

>ref|YP_003428040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pseudofirmus
OF4]
gb|ADC51148.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pseudofirmus
OF4]
Length = 429

Score = 155 bits (392), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 128/437 (29%), Positives = 221/437 (50%), Gaps = 27/437 (6%)

Query: 15 ISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+++PG KS+S+R ++ A+++G T V+ LN ED + + LG+++ D+ +
Sbjct: 13 LNGTIRVPGDKSISHRAVMFGAIAADGVTTVVEGFLNGEDCLSTIACFKKLGVNITQDE--E 70

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + G G VE + L +GN+G R + + ++ + D + +RP+
Sbjct: 71 RVKIEGKGWDGLVEPSN---ILDVGNSGTTTRLMLGILATRFHSMIGD--DSIAKRPM 125

Query: 135 GDLVVLGKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V L+++GA++D + P+ V G G G S S+Q SA+L+A +
Sbjct: 126 SRVVDPLREMGAEIDGRANGFTPLSVRG--GSTKGIDFTSKVASAQVKSAILLAGLQSA 183

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + + +S + E R++E +GVK + + +KGGQ K+ + V GD
Sbjct: 184 GTTSV--TEPALSRDHTE---RMLEAYGVKVKREGL--KVSVKGGQSLKA-SHIVVPGDI 235

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++FL AGA + +T+ G G + + +VL+ MGA +T + V V+G P
Sbjct: 236 SSAAFFLVAGAIVPNSQITLTGVGLNPTRSGI--IDVLQKMGASLTVSNEKV-VSGEPIA 292

Query: 314 PFG--RKHLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
LK I++ + +P D +AV+A A+G T I+D +VKET R+ +
Sbjct: 293 DLTITSSSLKGIIEGDLIPRLIDEIPVIAVLASQAEGKTVIKDAEELKVKETNRIDTVV 352

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGC 427
+EL +LGAS+E D II L +++Y DHR+ MA ++A E V I
Sbjct: 353 SELKRLGASIEATEDGMIEGSGSLKGATVNSYGDHRIGMAMAIAGLITEGQVDIERSEA 412

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + K
Sbjct: 413 IAVSYPSFFEHDRLTK 429

>ref|YP_003149664.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kytococcus
sedentarius DSM 20547]
gb|ACV06899.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Kytococcus
sedentarius DSM 20547]
Length = 476

Score = 155 bits (391), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 138/445 (31%), Positives = 205/445 (46%), Gaps = 46/445 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKS +NR L LAAL+ G + + + L++ D M GALR G V D +
Sbjct: 30 LDATVHVPGSKSWTNRWLALALASGPSTLHSPLDARDTRLMAGALRAFGHDVRIDAGST 89

Query: 75 RA---VVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
A V P E + G AG +R L + A G T+ D R+
Sbjct: 90 GAAWRVTPAHRWHAPAE-----PIDCGLAGTVLRFLVPLASLAHGPVTFDGD--ERLGH 141

Query: 132 RPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLP-----GGKV 172
RP+ L+ ++ LG V L D G G LP V
Sbjct: 142 RPLEPLLDVAVRSLGLTVSTGLHGHAGRTADRADSTATGAGVLPPLLMAGALHPSDPDDATV 201

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD--S 230
++ S SSQ++SALL+A + + + S P+++MT +++ GV AE D S
Sbjct: 202 EVDASASSQFVSALLLAGCTVHSGTLVRATGTVPSPRHIDMTCHALQQVGVVAEQRDETS 261

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
W +++G K P VE D SSA+ F A AA+ GGTVT+ G ++ Q ++
Sbjct: 262 W---WVEG--KRPDPFEVTVPEPDLSSAAVFAAAAAGGTVTLPGWPRSTTQAGDTIRDL 316

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAI 350
L MGA T+ + VTG L I+ +++ ++ +A A AD P+ +
Sbjct: 317 LTRMGHACELTDAGLRVTG-----GELHGIEADLSAAGELTPVVAATAALADSPSRL 368

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAF 410
+ R ET+R+ A+ TE+ LG V E PD IT P L+ + TY DHR+AMA
Sbjct: 369 TGIGHLRGHETDRLAALATEINALGGEVRELDPGLEIT-PRPLHRGSFATYHDHRLAMAG 427

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDY 435
+L + ++D T KT P +
Sbjct: 428 ALLGLRVPGIEVQDIDTTAKTVPGF 452

>ref|YP_001596458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
331]
sp|A9NC18.1|ARO_A_COXBR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX77767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA
331]
Length = 438

Score = 155 bits (391), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 138/436 (31%), Positives = 216/436 (49%), Gaps = 29/436 (6%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + +SG + +PG KS+S+R +LL A++EG T VD L D M+ AL+ +G S++
Sbjct: 7 PSQGLSGEICVPGDKSISHRAVLLVAIAEGQTQVDGFLMGADNLAMVSALQQMGASIQVI 66

Query: 71 KAAKRAVVVCGCG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 127
+ VV G G + P E L GN+G A+R L+ + AG VL G
Sbjct: 67 EDENILVVEGVGMTGLQAPPE-----ALDCGNSGTAIRLLSGLL--AGQPFNTVLTGDS 118

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
++ RP+ ++ L +GA +D + PP+++ G L G +L + S+Q S LL
Sbjct: 119 SLQRRMPKRIIDPLTLMGAKIDST--GNVPPLKIYGNPRLTGIHYQLPMA-SAQVKSCLL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G I P + T RL++ F + + GG K K+ +
Sbjct: 176 LAGLYARGKTCIT-----EPAPSRDHTERLLKHFTYTLQKDKQS--ICVSGGGKLA-ND 227

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTV 307
+ GD SSA++F+ A IT G+ + C + +L+MMGA + T +
Sbjct: 228 ISIPGDISSAAFFIVAATITPGS-AIRLCRVGVNPNTRLGVINLLKMMGADIEVTHYTEKN 286

Query: 308 TGPPREPFGRK-HLKAIDVNMNMK---PDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK ID+ +++ D L + A A G T +RD A RVKET+R
Sbjct: 287 EEPTADITVRHARLKGIDIPDQVLLTIDEFPVLLIAAAVAQGKTVLRDAAELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L KLG + E PD II L +++YDDHR+AMAF++A A+ PV I
Sbjct: 347 IAAMVDGLQKLGAIAESLPDGVIIQ-GGTLEGGEVNSYDDHRIAMAFVAGTLAKGPVRI 405

Query: 423 RDPGCTRKTFPDYFDV 438
R+ + +FP++ ++
Sbjct: 406 RNCDNVKTSFPNFVEL 421

>gb|ADI58632.1| AsuB1 [Streptomyces nodosus subsp. asukaensis]
Length = 983

Score = 155 bits (391), Expect = 1e-35, Method: Compositional matrix adjust.
Identities = 130/445 (29%), Positives = 226/445 (50%), Gaps = 34/445 (7%)

Query: 6 EIVLQPIKE-ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ L+P ++ + G + +P SK +R L+LA+L+EGT+ + + ++ V Y + LR LG
Sbjct: 2 HLTLPNRPQPLRGELTVPHSKYHVHRLILASLAEGTSRITGVSDARHVQYTIRLLRDLG 61

Query: 65 --LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
++VE D + VV G P D+ + G++G + + + A ++
Sbjct: 62 TRITVEGD-----SYVVRGGPYRPRDS-----VSAGSSGTTLYFMLGLASLA--DSPVT 109

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ G + RP+G L+ L++LG +D G CPPV V G GG+V + G++S Q+
Sbjct: 110 VTGQKYFQRRPVGPLLDALRELGVQLDSADG--CPPVHVR-PGRPSGGRVVVPGTSL-QW 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+S L++ AP A G IE+ ++ PY+E+T+ +M RFG++ SD W RF I+ GQ+
Sbjct: 166 VSGLVLLAPFATGRTVIEVRGQVNEQPYIELTVAMMRRFGLRVGVSDWRRFEIEPGQR- 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD-----VKFAEVLEMMGA 296
P + + D SA++ + AA+ V + G T L GD +F +V+ MG
Sbjct: 225 AVPADLTIPPDLSAAFGIVAAALHPSDVLRLGI--TRLGDGPDVDHPEARFLDVVGRMGV 282

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
+ E + G R L+A V+ ++PD+ LA +A FA G T +
Sbjct: 283 PMELDERA----GGLRIRHDGVRLRATTVDCREIPDMLPALATLATFAAGETVFEHIGHV 338

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC- 415
R+KE++R+ A+ +L +G + D ++ L + +Y+DHR+ M+ +LA
Sbjct: 339 RLKESDRVAAM-LQLNSMGDLRVAGDRLLVRGVSGLEGAGLSSYNDRVLSLALAGTR 397

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLS 440
A T+ P R ++P + D ++
Sbjct: 398 ARGAGTLTYPRAYRISYPAFLDDMT 422

>gb|EGC77431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Treponema denticola
F0402]
Length = 436

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 128/438 (29%), Positives = 222/438 (50%), Gaps = 30/438 (6%)

Query: 19 VKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL--LSVEADKAAKRA 76
+++P SKS S R L+LAA +EG++ + NLL S D + +LG +E +
Sbjct: 3 IEVPPSKSHSMRALVLAFAEGSSQIKNLLMSGDTKTAVSVFESLGVKFKIEQKNISSAD 62

Query: 77 VVV---GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 133
++V G K +E K+ +++ GN+G L + ++ + ++L G + +RP
Sbjct: 63 IIVFPPKEGLKKRIEKQKQ- IKIDAGNSGTLFYFLGSILSLMSSD--FILTGDSSILKRP 119

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNG----IGGLPGGKVKLSGSISSQYLSALLMA 189
L+ ++LG + G + P+RV G I GL K+ L G S Q +S LL+
Sbjct: 120 AKPLIEIYEELGLKYEFLDGFERAPIRVFGKDSSIKGLKEKKLCLEGDFS-QVISGLLLG 178

Query: 190 APLALGDVEIEI-IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A L D ++I + + +PY++MTL ++ G+K + SD + F I G QK +A
Sbjct: 179 A--GLLDFPLQINLKRAGELPYLKMTLHWLKTGKIFDVSDDFKTFKIIGSQKILGF-SA 235

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++ +A A IT T++++ +QGD + +VL+ M A + + E S T+
Sbjct: 236 GIPADSSAAPFALALITASTISIKNIDINDVQGDARIVKVKEMNADIRFEESQTLK 295

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LK + + +PD L+ +A FA G T +++++ R KE +R+ I
Sbjct: 296 IFPSS-----LKGTFDCSDIPDAVPALSAIACFAKGETILKNIEICRYKECDRLSVIS 349

Query: 369 TELTKLGASVEEGPD--YCIITPPEKLNVTATIDTYDDHRMAM-----AFSLAACAEPVPT 421
+EL KLGA + EG D + I + L+ ++D++ DHR+AM F + T
Sbjct: 350 SELKKLGADITEGRDVLHIIGNAGKNLSPASVDSHKDHRIAMMLTVIGFGIDDKDGTVFT 409

Query: 422 IRDPGCTRKTFPDYFDVL 439
+++ C ++P + + L
Sbjct: 410 LKNAECFDISYPSFLEDL 427

>ref|NP_126147.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrococcus abyssi
GE5]
sp|Q9V1H1.1|ARO_A_PYRAB RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAB49378.1| aroA 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrococcus
abyssi GE5]
Length = 410

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 139/433 (32%), Positives = 218/433 (50%), Gaps = 42/433 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E++++ + E+ G VK P SKS ++R L+ L++ + V N L SED L A+ G
Sbjct: 8 EMIIERVDEVRGKVKAPPSKSYTHRAYFLSLADSPSKVMNPLISEDTIASLDAISKFGA 67

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR-SLTAAVTAAGGNATYVLD 124
V +K + GK DA+E +G R SL A A G T V+
Sbjct: 68 QVNGNKIIPPQEL--TPGKI---DARE-----SGTTARISLAVASLARG---TSVIT 111

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G R+ ERP LV L+ L + + P+ V G G G VK+ S+SSQ+ +
Sbjct: 112 GKGRIVERPFKPLVDALRSLKVKISG---EKLPIAVEG-GNPVGEYVKVDCSLSSQFGT 166

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+ A +G + +E+++ +S PY+E+TL++ME FG++ E + F +K +
Sbjct: 167 AMLILAS-KIG-LTVEMLNP-VSRPYIEVTLKVMESFGIEFERNG----FKVKVHPGIRG 219

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K +V GD SSAS+FLA A+ G V V Q D + ++LE GA V
Sbjct: 220 SK-FHVPDGYSSASFFLAAGALY-GKVKVSNLVKDDPQADARIIDILEEFGADVVKGRKY 277

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V R +K I+V+ + PD+ LAV+A +A+G + I R+KE++R+
Sbjct: 278 VVVE-----RNEMKPINVDCSNFDFLPILAVLASAEGKSVITG-RQLRLKESDRV 328

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS-LAACAEPVTIR 423
A+ L K G V+E P+ I + T +++++DHR+ MA + L AE I+
Sbjct: 329 KAVAVNLRKAGIKVKELPNGLIEVGGKPRGFT-VESFNDHRIVMAMAILGLGAEKTIK 387

Query: 424 DPGCTRKTFPDYF 436
DP K++P +F
Sbjct: 388 DPHVVSXSYPSFF 400

>ref|ZP_03682045.1| hypothetical protein CATMIT_00676 [Catenibacterium mitsuokai DSM 15897]
gb|EEF94648.1| hypothetical protein CATMIT_00676 [Catenibacterium mitsuokai DSM 15897]
Length = 423

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 123/438 (28%), Positives = 213/438 (48%), Gaps = 35/438 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL- 64
+I + P K + GT+ +P SKSL++R ++ AAL+ G + + + SED+ + ++ LG
Sbjct: 3 KITITP-KTLQGTIAVPPSKSLAHRAIICAAAPGMSRISGIDYSEIEATIEGMKALGA 61

Query: 65 -LSVEADK-AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ E D ++ +G G V++ +G +R L +V
Sbjct: 62 IIKQEGDTLIIDGSITLGLG-----RVEIDAHESGSTLRFLMPLSLVNFVSRVHFV 111

Query: 123 LDGVPRMRERPIGDLVVGL--KQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISS 180
G ++ +RP+ D+ + KQ A +L D + V G L ++ G++SS
Sbjct: 112 --GKGKLGQRPL-DVYYDIFDKQKIA---YLRKDSERLDVILDGQLHSDIFEVPGNVSS 164

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q++S LL PL GD I+I L S Y+++TL ++E+FG++ + D + F I+G Q
Sbjct: 165 QFISGLLFTLPLQGDGLIKITTPLESKGYIDLTLDMLEKFGIEIINH-DYQAFQIRGNQ 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
YK P + VE D S A+++L A + G +T+ S QGD +++E MG ++
Sbjct: 224 NYK-PCDYNVEADFSQAAYFLV-ADLLGSDITLTNLNMHSSQGDRAILDIMEQMGGEIVE 281

Query: 301 TETSVTVTGPPPREPFGKHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
T + V +K ++ ++ PD+ ++V A+G + I + R+KE
Sbjct: 282 TSAGIKVVC-----DKIKPATIDASQCPDLPVVSACGLAEGTSHIINAGRLRIKE 333

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFS-LAACAEVP 419
+R+ A L G E D IT N + + +DHRM MA + L+ A P
Sbjct: 334 CDRLTASVELLKATGIDAVEEEDSMTITGSTSYNKA EVTSSNDHRMCMAEAILSTRANGP 393

Query: 420 VTIRDPGCTRKTFPDYFD 437
+TI D C +K++P +F+
Sbjct: 394 ITIDDKDCVKSYPGFFE 411

>ref|YP_003696703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcanobacterium haemolyticum DSM 20595]
gb|ADH92084.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcanobacterium haemolyticum DSM 20595]
Length = 461

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 128/451 (28%), Positives = 212/451 (47%), Gaps = 37/451 (8%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I G V++PGSKSL+ R L+LAA+ + L+SED M AL LG +E K
Sbjct: 17 EKIHNVRIPGSKSLTARWLVLAAGLNPVRLAGALDSEDTRAMGNALVALGAGIEWHKN 76

Query: 73 A-----KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ GG + + G AG MR + A G+ T
Sbjct: 77 WCHVTPIPRDTNGVITVRGGAY-----INAGQAGTVMRFILPLAAMAHGDVTVTC 126

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFL----GTDCP-PVRVNGIGGLPGGKVKLSGSI 178
R RPI L+ L QLG + C GT P+ ++G G L GG+V + +
Sbjct: 127 --ADNARHRPIAGLLSALTQLGVNYTCARDVAEGTGGGFPLTIHGRGPLRGGEVSVDAAG 184

Query: 179 SSQYLSALLMAAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
SSQ++SALL+A PL + + D L S P++ MT+ + + G+ A + + + +++
Sbjct: 185 SSQFVSALLLAGPLMERGITVRNCADTLPSTPHISMIDTLRKAGINA--AGTGETWHVP 242

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + K+ +E D S+A FLA A +TGG V +E S Q + + ++ GA
Sbjct: 243 HGSPNR--KHITIEPDLNAGPFLAALVTGGRVRIENWPKKSQQPGMAYLDIFRNAGAT 300

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWR 357
TW ET+ +T + G + + A +M + ++ T+A V F+DG + + ++ R
Sbjct: 301 FTW-ETNGPLTHLICQ--GHRTIWATHKMDGLGELVPTVAAVLAFSDGVSGLSNIGHLR 357

Query: 358 VKETERMVAIRTELTKLGASVEEGPD---YCIITPPEKLNVTDAIDTYDDHRMAMAFSLAA 414
ET+R+ A+ L+ +G E P + + T ID++ DHR+A ++
Sbjct: 358 GHETDRIAALTETLSAIGTQPEYDPHSETLWLRFDARYTTTIDIDSHADHRIATFGAILG 417

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
+ + + T KTFP + ++ V +
Sbjct: 418 LRIKGLRVANMEATAKTFPTFIELWERLVAD 448

>ref|ZP_06755918.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Scardovia inopinata
F0304]
gb|EFG27010.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Scardovia inopinata
F0304]
Length = 488

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 147/487 (30%), Positives = 227/487 (46%), Gaps = 71/487 (14%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ +V +PGSKSLSNR L+LAAL+ T + LL S D + M+ AL+ LG V AD+ +
Sbjct: 13 LDASVHPIPGSKSLSNRYLVLAALAGRPTTIHGLLRSDTNLMIQALKKLGAVLSAETS 72

Query: 74 KRAVVVCGCGKFPVEDA--KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V+ P E K ++ G AG MR + A A +++ V DG +
Sbjct: 73 TTVTVI-----PPESGIFKGRCRINCLAGTVMRFVPALALYA--DSSVVFDDQAYR 124

Query: 132 RPIGDLVVLGLQLGADVDCFLGTD--CP----PVRVNGIGGLPGGK----- 171
RP+ L+ GL QLGA V+ +LG + P P R N I + G+
Sbjct: 125 RPMKPLLDGLCQLGARVE-YLQEGHLPFMIIPDR-NFIAQISPGEESGFETESQLDRPQ 182

Query: 172 -VKLSGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTL-----RLMERF 221
V + S SSQ++S LL+AA V I L S+P+++MT+ RL+ R
Sbjct: 183 EVTIDSSASSQFISGLLLAASRYPRQVIIRHKGSHLPSLPHIQMTMDLKLACRLVMRQ 242

Query: 222 GVKAEHSDS-----WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGG 269
DS W F + + P+ +E D S+A+ FL A + GG
Sbjct: 243 QSADAQPDSSGSSQVRWSVVRWSVFPFRSKTGLQLPEEIRIEPDLNAAFLGAALLAGG 302

Query: 270 TVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SVTVTGPPREPFGGRKHLKAID 324
V++ + Q + L GA + T S T+T P + D
Sbjct: 303 RVSIPDWPEETTQPGGLLPQYLLDFGAHIDKTSQAADGRSYTLTA--SFPSASRPHGLGD 360

Query: 325 VNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDY 384
N++ ++A +LA +A+ AD PT+ + R ET R+ A+ ++ ++GA+ EE D
Sbjct: 361 YNLSAAGELAPSLAALAVVADKPTSFHGIGHLRGHETNRLAALVNQIHRVGANAEELEDG 420

Query: 385 CIITPPEK---LNVTAIDTYDDHRMAMAFSLAACAEVPV---TIRDPGCTRKTFPDYFDV 438
I PP+ L+ T ++TY DHRMA + AA +P+ TI + TRKT PD+ +
Sbjct: 421 ITIYPPQSLTDLHPTCMETYADHRMA---TFAAMLSIPIPLTISNIEATRKTLPDFPGM 477

Query: 439 LSTFVKN 445
++ ++
Sbjct: 478 WTSMIRQ 484

>ref|YP_003852222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacterium
thermosaccharolyticum DSM 571]
gb|ADL69138.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacterium
thermosaccharolyticum DSM 571]
Length = 423

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.

Identities = 126/436 (28%), Positives = 216/436 (49%), Gaps = 27/436 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVDNLLNSVDHYMLGALRTLGLSVEADKA 72
+ + G V +PG KS+S+R ++ +++EG T+V L S+D + +R LG+++
Sbjct: 9 RNVKGVVNVPGDKSISHRAIMFGSIAEGETIVKGFLRSDDCFSTINCMRKLGVNI---NI 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V V G + + D+ + L GN+G MR L+ + AG T VL G +R+R
Sbjct: 66 VKDEVYVKGNGMY-LHDSHD--ILDAGNSGTTMRLLSGIL--AGQKFTTVLTGDESLRKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L +GA++ + + P+ + G + G + S+Q S +++A+
Sbjct: 121 PMARIKPLNMMGAEISA-IDDNYAPLTIKG--NVLKGICYKTEVASAQVKSCIMLASLY 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D E I + L+S + E+ L FG E S++ + + V G
Sbjct: 178 A--DDETIIEEPLSRNHSELMLNY---FGGNFE---SYENKIVCHPVERLHGCKICVPG 229

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+YF+ A+I + ++ + + +V++ MG + + V P
Sbjct: 230 DISSAAYFIVAASILPQSEILIKNVNVNHTRTGI--IDVIKMGGNIEIKDERVLNNEPV 287

Query: 312 REPFGRKH-LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
E + LK I++ +P D +AV A +A+G T I+D +VKE+ R+ +
Sbjct: 288 AEIIVKSSCLKGIEIGGEIIPRLIDEIPIIAVAASYAEGETVIKDAEELVKVESNRIDTM 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
+EL K+GA +E D II E LN +D+Y+DHR+AM+ S+AA AE IR+
Sbjct: 348 VSELKKMGADIEATNDGMIIHGKETLNGALVDSYNDHRVAMSLSIAALKAEGITKIRNAE 407

Query: 427 CTRKTFPDYFDVLSTF 442
C +FPD++ VL+
Sbjct: 408 CVNISFPDFYSVLNL 423

>ref|ZP_03297599.1| hypothetical protein COLSTE_01506 [Collinsella stercoris DSM 13279]
gb|EEA90307.1| hypothetical protein COLSTE_01506 [Collinsella stercoris DSM 13279]
Length = 316

Score = 154 bits (390), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 107/318 (33%), Positives = 165/318 (51%), Gaps = 28/318 (8%)

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
ERPI L L G ++ G P+R +G + G+ +L G++SSQY+S LL+AA
Sbjct: 2 ERPIAPLSDELIAAGCTLE---GVGGFPLRASGR--MRAGRFELPGNVSSQYISGLLLAA 56

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG-----Q 240
PL GD EI + L S PYV++T+ ++ FGV + + GG Q
Sbjct: 57 PLLDGDTEIAVTGTLESRPYVDLTIDVLASFVTVDIEEG---ATPGGLPLTVFRVPRQ 112

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y++P VEGD S+A+++L A+ +VTG G TS+QGD + L + GAK
Sbjct: 113 GYRTPGTIAVEGDWSNAAFWLCAGALGRHSVTVRGVSPTSIIQGDRAISAALMLFGAKGQR 172

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ T+ P R L I+++ + +PD+ L+ VA A+G T A R+KE
Sbjct: 173 NARAATIR-PDR-----LHGIELDAHDIPDLVPVLSAVAACAEGTTRFTGCARLRIKE 224

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
++R+ EL LGA V D +I E+L+ +++++DHR+AM ++AA E P
Sbjct: 225 SDRLATTAELANLGCVRVDGGLLIEGRELSGGRVESHNDHRIAMMGAIAAVRCEGP 284

Query: 420 VTIRDPGCTRKTFPDYFD 437
V I K++P +FD
Sbjct: 285 VEIAGAEAVNKSYPAFFD 302

>ref|ZP_01131039.1| 3-phosphoshikimate 1-carboxyvinyltransferase [marine
actinobacterium PHSC20C1]
gb|EAR24327.1| 3-phosphoshikimate 1-carboxyvinyltransferase [marine
actinobacterium PHSC20C1]

Length = 468

Score = 154 bits (389), Expect = 2e-35, Method: Compositional matrix adjust.
Identities = 130/432 (30%), Positives = 214/432 (49%), Gaps = 12/432 (2%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+S TV LKSGKSL+NR L+LAAL++G + + + L+S D M+ ALR LG+ +E
Sbjct: 37 LSATVNLPGSKSLTNRELVLAAALADGPSRLHSPLHSRDSALMIQALRALGVEIEEIIATGN 96

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G + + + G AG MR L A G ++ DG RP+
Sbjct: 97 ---VFGPD LAVTPSELQGGSSIDCGLAGTVMRFLPPVAALALGPVSF--DGDEAALRRPM 151

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP-LA 193
+ L+ LG DV G P + G+G + GG++ + S SSQ++S LL+AA
Sbjct: 152 RTTIDSLRALGVDSDD-GRGTLPPFNLYGMGSVAGGEISIDASASSQFVSGLLLAARFD 210

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G D L S+P++EMT+ + GV E + + + G S + +E D
Sbjct: 211 HGLTLRHTGDTLPSPHIEMTIECLAARGVVVECPPEP-GVWVVPAGP--ISAIDVELEPD 267

Query: 254 ASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE 313
S+A+ FLA A + GGTVT+EG ++ Q ++L + GA + ++ ++T+ G
Sbjct: 268 LSNAAPFLAAAI VAGGTVTIEGWPESTTQVGADLEQLLPLFGATASRSDGALTIDGGAGI 327

Query: 314 PFGRKHLKAIDVNMNMPD VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G + +++++ ++A + +A A P+ I + R ET+R+ A+ E+
Sbjct: 328 IGGNSY-AGVELDLSTGGELAPAIVALAALASSPSTITGIGHLRGHETDRLAALCAEINA 386

Query: 374 LGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTTFP 433
LG +V E D I P E L+ +Y+DHRM+ A ++ A + + T KT P
Sbjct: 387 LGGAVTELDGDLHIEPRE-LHGGVWHSYEDHRMSTAGAIIGLAIAIGIEVEGIDATAKTLP 445

Query: 434 DYFDVLSTFVK 445
+ + +T V +
Sbjct: 446 QFPALWATLVGD 457

>ref|YP_001954667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum DJ010A]
ref|YP_004208584.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis 157F]
sp|B3DSQ0.1|AROABIFLD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD98169.1| 5-enolpyruvylshikimate-3-phosphate synthase [Bifidobacterium longum
DJ010A]
dbj|BAJ70806.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis 157F]
Length = 445

Score = 154 bits (389), Expect = 3e-35, Method: Compositional matrix adjust.
Identities = 138/443 (31%), Positives = 213/443 (48%), Gaps = 23/443 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTPVPGSKSLSNRYLILAAALGSKPVTILIGLLRSRDTLMMGALEALGVRCDDVDSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLQLGATVDYHGEVGRLPFTITPPATLPAAQAQVVSIDSSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +S + ++ S K
Sbjct: 189 ISSKLPGLHLAHTGKTPSLPHIRMTVADVTGAGGAVEADESARTWTVPRAMQLSSK- 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTV 307

VE D S+A+ FL A I GGTV V T+ Q LE MGA+V++ T+
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVHPWETTTQPGGLLPGYLEQMGAESFSP----TI 303
Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 GGVRYCEVTGDGTVRGLGTFDLTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETNRLE 363
Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVP-VTI 422
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P + +
Sbjct: 364 ALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPDIEV 422
Query: 423 RDPGCTRKTFPDYFDVLSTFVKN 445
+ TRKT PD+ + S ++
Sbjct: 423 INVATTRKTLPDFVGMWSGMLRQ 445

>ref|ZP_08117640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacterium
xylanolyticum LX-11]
gb|EGB24297.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacterium
xylanolyticum LX-11]
Length = 423

Score = 154 bits (389), Expect = 3e-35, Method: Compositional matrix adjust.
Identities = 127/445 (28%), Positives = 206/445 (46%), Gaps = 31/445 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+ + + G V +PG KS+S+R ++ +++ G TVV L SED + +R LG+
Sbjct: 2 EVEISKSHLKGVVNVPGDKSISHRAIMFGSIAVGDTVVKGFLKSEDCFSTINCMRKLGV 61
Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E V V G + E L GN+G MR L+ + AG + G
Sbjct: 62 EIEI---VNDDVYVKGNGMYLNEISLD---VLDAGNSGTTMRLLSGIL--AGQKFASTITG 113
Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVLKSGSISSQYLSA 185
+R+RP+ ++ L +GA + + P+ + G L G + +SS ++
Sbjct: 114 DESLRKRPKRIIQPLSMMGAKITAVY-DNYAPITIKG-NTLKG--INYTEVSSAQVKS 169
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLR--LMERFGVKAHSDSWDRFYIKGGQKYK 243
+M A L DV I PY+ ++ FG E S+D I +
Sbjct: 170 CIMLASLYAQDV-----TTIEEPYLSRNHSEMLNLYFGGNFE---SYDNKVICHPEVKL 220
Query: 244 SPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
V GD SSA+YF+ A+I + ++ + + + +VL MG V E
Sbjct: 221 HGCEVLVPGDISAAYFMVAASILPNSEILIKNVNINNTRTGI--IDVLNKMGGNVEIIE 278
Query: 303 TSVTVTGPPEPFGRK-HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRV 358
V P + + HLK ID+ +P D +AV A +ADG T I+D +V
Sbjct: 279 EKVVNNEPVADIVVKS SHLKGIDIGBEIIPRLIDEIPVIAVAAAYADGTTVIKDAEELKV 338
Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
KE+ R+ + ++L K+GA +E D II E L+ +D+Y+DHR+AM+ S+AA A+
Sbjct: 339 KESNRIDTMVSQLRKMGADIEATNDGMIHKGKTLHGATVDSYNDHRVAMSLSIAALKAD 398
Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
I++ C +FPD++ VL+
Sbjct: 399 GSTKIKNAECVNISFPDFYSVLNVL 423

>ref|YP_883328.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium avium
104]
Length = 435

Score = 154 bits (388), Expect = 3e-35, Method: Compositional matrix adjust.
Identities = 141/430 (32%), Positives = 210/430 (48%), Gaps = 32/430 (7%)

Query: 13 KEISGTVKLPKSKLSNRILLALLAALS---EGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ + TV +PGSKS +NR L+LAAL+ GT + L S D M+GALRTLGL V
Sbjct: 11 QPVHATVTVPGSKSQTNRALVLAALAAQGRGTPTLSGALRSRDTLDMIGALRTLGLRV- 69
Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D V G P ++ G AG +R + AA +A DG +

Sbjct: 70 -DGTGPELTVSGHIAPGP-----HARVDCGLAGTVLRFVPP--LAALADAVVEFDGDEQ 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
R RPI L+ L+ LG ++ GT P RV+G G L GG V + S SSQ++S LL+

Sbjct: 121 ARARPIAPLLDALRGLGVRIE---GTALP-FRVHGGGALAGGTVAIDASASSQFVSGLLL 176

Query: 189 -AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA G L S P++ MT+ ++ + GV + S +R+ ++ G + ++

Sbjct: 177 CAASFTEGLTVQHTGAALPSAPHIAMTVAMLRQAGVDVDDSVN-NRWQVRPGPV--AARH 233

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D ++A FLA A ++GGTV + G S+Q VL + A V+ T++S+ V

Sbjct: 234 WEVEPDLTNAVFPFLAAAVVSGGTVRITGWPADSVQPADNILSVLKLNAVVSQTDSSLEV 293

Query: 308 TGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMV 365
G DV++ + ++ ++A +A A + R +A R ET+R+

Sbjct: 294 R-----GSGSYDGFVDLRAVGELTPSVAALAALATPGSVSRLSGIAHLRGHETDRLA 346

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ E+ +LG E PD +IT L+ Y DHRMAMA ++ V + D

Sbjct: 347 ALSAEINRLGGDCTETPDGLVIT-ATPLHSGVWQAYADHRMAMAGAIVGLRVAGVRVDDI 405

Query: 426 GCTRKTFPDY 435
G T KT PD+

Sbjct: 406 GATGKTLPDF 415

>ref|NP_962268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium avium
subsp. paratuberculosis K-10]
sp|Q73UN2.1|ARO_A_MYCPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAS05884.1| AroA [Mycobacterium avium subsp. paratuberculosis K-10]
Length = 435

Score = 154 bits (388), Expect = 4e-35, Method: Compositional matrix adjust.
Identities = 141/430 (32%), Positives = 209/430 (48%), Gaps = 32/430 (7%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALS----EGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ + TV +PGSKS +NR L+LAAL+ GT + L S D M+GALRTLGL V

Sbjct: 11 QPVHATVTVPGSKSQTNRALVLAALAAQGRGTPTLSGALRSRDTLDMIGALRTLGLRV- 69

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D V G P ++ G AG +R + AA +A DG +

Sbjct: 70 -DGTGPELTVSGHIAPGP-----HARVDCGLAGTVLRFVPP--LAALADAVVEFDGDEQ 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
R RPI L+ L+ LG ++ GT P RV+G G L GG V + S SSQ++S LL+

Sbjct: 121 ARARPIAPLLDALRGLGVRIE---GTALP-FRVHGGGALAGGTVAIDASASSQFVSGLLL 176

Query: 189 -AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA G L S P++ MT+ ++ + GV + S +R+ ++ G + ++

Sbjct: 177 CAASFTEGLTVQHTGAALPSAPHIAMTVAMLRQAGVDVDDSVN-NRWQVRPGPV--AARH 233

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D ++A FLA A ++GGTV + G S+Q VL + A V+ T++S+ V

Sbjct: 234 WEVEPDLTNAVFPFLAAAVVSGGTVRITGWPADSVQPADNILSVLKLNAVVSQTDSSLEV 293

Query: 308 TGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMV 365
G DV++ + ++ ++A +A A + R +A R ET+R+

Sbjct: 294 R-----GSGSYDGFVDLRAVGELTPSVAALAALATPGSVSRLSGIAHLRGHETDRLA 346

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ E+ +LG E PD +IT L+ Y DHRMAMA ++ V + D

Sbjct: 347 ALSAEINRLGGDCTETPDGLVIT-ATPLRPGVWHAYADHRMAMAGAIVGLRVAGVRVDDI 405

Query: 426 GCTRKTFPDY 435
G T KT PD+

Sbjct: 406 GATSKTLPDF 415

>ref|YP_001624533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Renibacterium salmoninarum ATCC 33209]
gb|ABY23119.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Renibacterium salmoninarum ATCC 33209]
Length = 461

Score = 153 bits (387), Expect = 4e-35, Method: Compositional matrix adjust.
Identities = 135/454 (29%), Positives = 210/454 (46%), Gaps = 54/454 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K IS + +PGSKSL+NR L+LAAL++G + + L+S D M+ ALR LG ++
Sbjct: 21 KPISADLTVPGSKSLTNRYLVLAALADGPSRLRAPLHSDRSLLMVQALRQLGAEIKETP- 79

Query: 73 AKRAVVVGCGGKFP-----VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
G G P V + + G AG MR + G + D
Sbjct: 80 -----GQGAYGPDLLVTPIKVGQKIGQTAIDCGLAGTVMRFVPPPLAALVEGLIQF--D 130

Query: 125 GVPRMRERPIGDLVVGLKQLGADV-----DCFLGTDGCP---PVRVN 162
G R RP+G ++ L LG V D T P P ++
Sbjct: 131 GDEHARLRPMGPVLTSLSSLGVAVRPVKSVQSVQSVQEDHAAEDASQNTALPQSLPFVLD 190

Query: 163 GIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERF 221
G + GG + L S SSQ++SALL+AAP + +E + K + S+ ++ MT+RL+
Sbjct: 191 AAGSVEGGYISLDSSGSSQFVSALLLAAPQFKNGLHLEHLGKPVPSLDHIAMTVRLRLREA 250

Query: 222 GVKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 281
GV+ + DS +I ++ + VE D S+A FLA A ++ GTV + G +
Sbjct: 251 GVEVD--DSVPHWIVAAGPIRA-FDVIVEQDLSNAGPFLAAALVSRGTVRITGWPVHTS 307

Query: 282 QGDVKAFAEVLEMMGAKVWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVA 341
Q + E+L GA V ++ VT G H+ ++ + ++A T+A +
Sbjct: 308 QVGDSWREILTAFGADVLEGDTLIVT-----GGAHISGVE--LADTSELAPTVAALC 358

Query: 342 LFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITY 401
A+GP+ + +A R ET+R+ A+ E+ LG V E D II P+ L+ +Y
Sbjct: 359 ALAEGPSRLTGIAHLRGHETDRLAALAAEINALGGHVAETADGLIIE-PQPLHSGIFHSY 417

Query: 402 DDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
DHRMA A ++ A V + + T KT P++
Sbjct: 418 ADHRMATAGAIIGLAVPGVAVENIATTAKTMPEF 451

>ref|ZP_07834435.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp. HGF2]
gb|EFR36043.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp. HGF2]
Length = 420

Score = 153 bits (387), Expect = 5e-35, Method: Compositional matrix adjust.
Identities = 116/435 (26%), Positives = 206/435 (47%), Gaps = 42/435 (9%)

Query: 16 SGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL--LSVEADKAA 73
SG V +P SKS+++R ++ A+L+ GT+V+ N+ S+D+ + ++ LG + +EAD+
Sbjct: 11 SGHVIVPPSKSMAHRAIICASLANGTSVIKNVAYSQDIKTTIAGMQQLGADIRMEADQ-- 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V V F +++ ++F +G +R + T+ G R+ +RP
Sbjct: 69 ---VTVTGIKDFTIKNK---EVFCCESGSLTRFFIPIFSLCNQEITFT--GQGRLLQRP 119

Query: 134 ---IGDLV--VGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
DL GL D +C L G + L G +SSQ++S LL
Sbjct: 120 QKVYEDLFHAQGLT-FRQDASGITIREC-----LKS GDITLQGDVSSQFISGLLF 168

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNA 248
PL D I I+ S YV++TL++++ +G++A D +I G Q+Y + +
Sbjct: 169 TLPLLQEDSTIHILPPFESRSYVDLTQLMLKTYGIQASFEDDL-TIHIPGNQYTTAC-DY 226

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
+EGD S ++F AA +T+ G S QGD K +L+ G ++ + +
Sbjct: 227 TIEGDYSQLAFFAVLAA-CNHDLTITGVHDSRQGDKKILSILKDFGVRIEVEKNGYHIY 285

Query: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+ L +++ PD+ L V+A+++ G T I + R+KE++R+ A+
Sbjct: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368

Sbjct: 286 -----KSSLHGCRIDLADCPDLGPILTVLAMYSFGNTNIYNAGRLRIKESDRIEAME 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
EL K G + D IT + + +++DHR+ MA S+AA C+ I

Sbjct: 338 QELRKFVVDIHSTEDFITGNSSYTCASELSSHNDHRIVMALSAATCSNTSCIIDGAQ 397

Query: 427 CTRKTFPDYFDVLST 441
+K++P +F+ L +

Sbjct: 398 AIQKSYPTFFEDLQS 412

>ref|ZP_07270493.1| PlmJK [Streptomyces sp. SPB78]
gb|EFK98861.1| PlmJK [Streptomyces sp. SPB78]
Length = 1004

Score = 153 bits (387), Expect = 5e-35, Method: Compositional matrix adjust.
Identities = 122/437 (27%), Positives = 220/437 (50%), Gaps = 27/437 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++G V +P SK ++R L+LA+L+EG + V L ++ V Y + LR LG+ + +

Sbjct: 18 HQLTGEVLVPNSKYHAHRLILASLAEGVSRVHGLSDARHVQYTVQLLRGLGVKITTE-- 75

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G GG++ A + G++G + + A+ + + G R R

Sbjct: 76 GDTFVVHGLGGRYRPRRAA---VSAGSSGTTLYFMIG--LASLSDRDVAVTGQKYFRRR 129

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G L+ L+Q+G V+ DCPV V GG V+++G++S Q++S L++ AP

Sbjct: 130 PVGPLLTALRQMGVGVES--ADDCPPVHVTARRP-SGGHVRIAGTLS-QWISGLILLAPF 185

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE+ +L Y+E+T+ +M +FG+ S+ W RF ++ GQ + +

Sbjct: 186 ATGHTTIEVEGELNERSYLELTVAMMRQFGLAVTVSEDWRRFDVEPGQSAVA-TELTLPP 244

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQG-----DVKFAEVLEMMGAKVTWTETSVT 306
D SA++ +A AA+ V ++G T L+G + F ++ MG + E +

Sbjct: 245 DIGSAAFGIAAAALHPSDVLLKGM--TRLEGGPADHPEFHFLDIARAMGVPMELDEAAGG 302

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V P LK ++V+ +PD+ L+ + FA G + ++A R+KE++R A

Sbjct: 303 VRIRQETPM---LKGVEVDCRDVPMPLPILSTLGSFAYGESVFHNIAHTRLKESDRAAA 358

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ +L +G +E D + E L + +++DHR+ M+ ++A+ A T+ P

Sbjct: 359 M-LQLNAMGGDLELDGALRVRGVEGLVGAKLSSFNDRVLSLAVASSRARGHSTLTYP 417

Query: 426 GCTRKTFPDYFDVLSTF 442
R ++P + D ++T

Sbjct: 418 NAYRISYPTFLDAMNTL 434

>ref|ZP_07978743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actG]
ref|ZP_07984972.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptomyces sp.
SA3_actF]
Length = 996

Score = 153 bits (387), Expect = 5e-35, Method: Compositional matrix adjust.
Identities = 122/437 (27%), Positives = 220/437 (50%), Gaps = 27/437 (6%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++G V +P SK ++R L+LA+L+EG + V L ++ V Y + LR LG+ + +

Sbjct: 10 HQLTGEVLVPNSKYHAHRLILASLAEGVSRVHGLSDARHVQYTVQLLRGLGVKITTE-- 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G GG++ A + G++G + + A+ + + G R R

Sbjct: 68 GDTFVVHGLGGRYRPRRAA---VSAGSSGTTLYFMIG--LASLSDRDVAVTGQKYFRRR 121

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G L+ L+Q+G V+ DCPV V GG V+++G++S Q++S L++ AP

Sbjct: 122 PVGPLLTALRQMGVGVES--ADDCPPVHVTARRP-SGGHVRIAGTLS-QWISGLILLAPF 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE+ +L Y+E+T+ +M +FG+ S+ W RF ++ GQ + +
Sbjct: 178 ATGHTTIEVEGELNERSYLELTVAMMRQFGLAVTVSEDRRRFDVEPQSSAVA-TELTLP 236

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQG-----DVKFAEVLEMMGAKVTWTETSVT 306
D SA++ +A AA+ V ++G T L+G + F ++ MG + E +
Sbjct: 237 DIGSAAFGIAAAALHPSDVLKGM--TRLEGGPADHPEFHFLDIARAMGVPMELDEAAG 294

Query: 307 VTGPPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V P LK ++V+ +PD+ L+ + FA G + ++A R+KE++R A
Sbjct: 295 VRIRQETPM----LKGVEVDCRDVPMPLPILSTLGSFAYGESVFHNIAHTRLKESDRAAA 350

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ +L +G +E D + E L + +++DHR+ M+ ++A+ A T+ P
Sbjct: 351 M-LQLNAMGGDLGLDGLRVRGVEGLVGAKLSSFNDRVLSLAVASSRARGHSTLTYP 409

Query: 426 GCTRKTFPDYFDVLSTF 442
R ++P + D ++T
Sbjct: 410 NAYRISYPTFLDAMNTL 426

>ref|NP_603830.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
gb|AAL95129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
Length = 424

Score = 153 bits (386), Expect = 6e-35, Method: Compositional matrix adjust.
Identities = 108/433 (24%), Positives = 208/433 (48%), Gaps = 46/433 (10%)

Query: 17 GTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVLEADKAAKRA 76
G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A++ LG ++E
Sbjct: 16 GEVTPPPSKSVLHRYIIASSLAKGISKIENISYSDDIATIEAMKKLGANIEK---KDN 72

Query: 77 VVVGCGKGFVPEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F E + ++ +G +R L + G ++ +RP+
Sbjct: 73 LLIDGSKTFDKEYLNNDSIDCNESGSTLRFLFPLSIVKENKILF--KGKGKLFKRPLSP 130

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ C + N I G L G ++ G+ISSQ+++ LL + PL
Sbjct: 131 YFENFDKYQ-----IKSSINENKILLDGELKSGVYEIDGNISSQFITGLLFLSLPLL 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ +I I KL S Y+++TL + +FG+ + +S+ F I+G Q YKS N VE D
Sbjct: 183 NGNSKIIKKGLESSSYIDITLDCLNKFGINIIN-NSYKEFIIEGNQTYKSG-NYQVEAD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S ++FL +I G + + G SLQGD K +++ + WT+ +
Sbjct: 241 YSQVAFFLVANSI-GSNIKINGLNVNLSLQGDKK---IIDFISEIDNWTKNEKLI----- 290

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++ ++ PD+ L++ A + I ++A R+KE++R+ A EL+K
Sbjct: 291 -----LDGSETPDIIPILSLKACISKKEIEIVNIARLRIKESDRLSATVQELSK 339

Query: 374 LGASVEEGPDYCIITPPEKLN-----TAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
LG + E D +I + N ++ ++ DHR+AM ++A+ C E + + +
Sbjct: 340 LGFDLIEKEDSILINSRKNFNEISNNSPISLSSHSDHRIAMTVAIASCTCYEGEIIILDNLD 399

Query: 427 CTRKTFPDYFDVL 439
C +K++P++++V
Sbjct: 400 CVKKSYPNFWFVF 412

>ref|ZP_05218136.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium avium
subsp. avium ATCC 25291]
Length = 423

Score = 153 bits (386), Expect = 6e-35, Method: Compositional matrix adjust.
Identities = 141/428 (32%), Positives = 211/428 (49%), Gaps = 32/428 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALS----EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL+ GT + L S D M+GALRTLGL V+
Sbjct: 1 MHATVTVPGSKSQTNRALVLAALAAQGRGTPTLSGALRSRDTLDMIGALRTLGLRVDTG 60

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A + G P A+ + L AG +R + AA +A DG + R
Sbjct: 61 GPA----LTVSGHIAPGPHARVDCGL----AGTVLRFVPP--LAALADAVVEFDGDEQAR 110

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-A 189
RPI L+ L+ LG ++ GT P RV+G G L GG V + S SSQ++S LL+ A
Sbjct: 111 ARPIAPLLDALRGLGVRIE---GTALP-FRVHGSALAGGTVAIDASASSQFVSGLLLC 166

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G L S P++ MT+ ++ + GV + S +R+ ++ G + ++
Sbjct: 167 ASFTEGLTVQHTGAALPSAPHIAMTVAMLRQAGVDVDDSVN-NRWQVRPGPV--AARHWE 223

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
VE D ++A FLA A ++GGTV + G S+Q VL + A V+ T++S+ V
Sbjct: 224 VEPDLTNAVFPFLAAAVVSGGTVRITGWPADSVQPADNILSVLGLKLNNAVVSRTDSSLEVR- 282

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMVAI 367
G DV++ + ++ ++A +A A + R +A R ET+R+ A+
Sbjct: 283 -----GSGSYDGFVDLRAVGELTPSVAALAAALATPGSVSRLSGIAHLRGHETDRLAAL 336

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTIRDPGC 427
E+ +LG E PD +IT L+ Y DHRMAMA ++ V + D G
Sbjct: 337 SAEINRLGGDCETETPDGLVIT-ATPLHSGVWHAYADHRMAMAGAIVGLRVAGVRVDDIGA 395

Query: 428 TRKTFPDY 435
T KT PD+
Sbjct: 396 TSKTLPDF 403

>dbj|BAJ69373.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis JCM 1222]
Length = 445

Score = 153 bits (386), Expect = 6e-35, Method: Compositional matrix adjust.
Identities = 135/442 (30%), Positives = 208/442 (47%), Gaps = 21/442 (4%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+ AL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKSLSNRYLILAAALGSKPVTILIGLLRSRDTLMMNALEALGVRCVDVSA 75

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGK--VKLSGSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + V + S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEIGRLPFTITPPATLPAAQAHVSISSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + P
Sbjct: 189 ISSKLPGLHLHTHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPCAMQLPSK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE +GAKV++ T+
Sbjct: 248 VTVEPDLNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQIGAKVSFP----TI 303

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 DGVRYCEVTGDGIVRGLGTFDLTAAGEIAPSLAAILMFADKSTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTIR 423
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA ++ + +
Sbjct: 364 ALVNEIRRVGGAEEELPDGLRIEPVPAETLHGAVMETYADHRMATFAAMLGLRIPDIEVI 423

Query: 424 DPGCTRKTFPDYFDVLSTFVKN 445
+ TRKT PD+ + S ++
Sbjct: 424 NVATTRKTLPDFVGMWSGMLRQ 445

>emb|CBL01390.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Faecalibacterium
prausnitzii SL3/3]
Length = 424

Score = 153 bits (386), Expect = 6e-35, Method: Compositional matrix adjust.
Identities = 130/426 (30%), Positives = 210/426 (49%), Gaps = 30/426 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G + P SKS++R +L AAL+ G + + +L S+D+ L A L +V D A
Sbjct: 12 IGGVIAAPPSKMAHRAVLCAALAVGRSHITHLEFSKDISATLSAAQLCAAV--DTGAD 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A V G G P+ + + +G +R L + G T+ G R+ ERP
Sbjct: 70 NATVQGLHLPPLTAPVDCE-----SGSTLRFLIPIASLTGQPVTF--GRRLMERPQ 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L + P + G L G +L+G++SSQ++S LL A PL
Sbjct: 123 SVYETLYREQN-----LRFEQSPAGLTVEGALTPGDYRLAGNVSSQFISGLLFALPLLP 176

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD ++ +I + S Y++MT+ + FGV + D + GGQ+Y P + VEGD
Sbjct: 177 GDSQLHLIPPVESRSYIDMTRAVQAAGVHRSRWLDE-TTLLLPGGQYH-PCDYNVEGDY 234

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A++ A+ GG VT+ G +LQGD ++L GA T SVT
Sbjct: 235 SQAAPPAVLGAVCGG-VTITGLAPDTLQGDAAILDILRRCGAVFTRKGDSTV----- 285

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
F + L +D+++ PD+ L V+ L +G T IR+ R+KE++R+ A+ EL
Sbjct: 286 FAKAPLHGVDIDLADCPDLGPVLMVLGLLCEGTTVIRNAERLRLKESDRIAAMEAELRAC 345

Query: 375 GASVE-EGPDYCIITPPEKLNVT--IDTYDDHRMAMA-FSLAACAEVPVTIRDPGCTRK 430
G +E+G + E+L+ A + ++DHR+ M+ LAA A++P+T+ D +K
Sbjct: 346 GGVLESDGGTTTVHGCARLHAPAAPLHGHNDRVMSLAVLAAAALPLTVDDAEAIQK 405

Query: 431 TFPDYF 436
++P +F
Sbjct: 406 SWPGFF 411

>ref|YP_002323185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 15697]
gb|ACJ52807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 15697]
Length = 461

Score = 153 bits (386), Expect = 7e-35, Method: Compositional matrix adjust.
Identities = 135/442 (30%), Positives = 208/442 (47%), Gaps = 21/442 (4%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLSNR L+LAAL + LL S D M+ AL LG+ + D A
Sbjct: 32 QPLNATVTVPGSKSLSNRYLILAAALGSKPVTILIGLLRSRDTLMMNALEALGVRCDDVDSA 91

Query: 73 --AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 92 TDTTVTVTPPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 144

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGK--VKLSGSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + V + S SSQ++S LL+
Sbjct: 145 ARPMKPVLDGLEQLGATVDYHGEIGRLPFTITPPATLPAAQAHVSIDSSGSSQFISGLLL 204

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +D R + + P
Sbjct: 205 ISSKLPGLHLTHTGEKTPSLPHIRMTVADVTGAGGAVE-ADESARTWTVEPCAMQLPSK 263

Query: 248 AYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE +GAKV++ T+
Sbjct: 264 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPYLEQIGAKVSFP----TI 319

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 320 DGVRYCEVTGDGIVRGLGTFDLTAAGEIAPSLAAILMFADKSTDMVGIGHLRGHETNRLE 379

Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA ++ + +
Sbjct: 380 ALVNEIRRVGGAAEELPDGLRIEVPVPAETLHGAVMETYADHRMATFAAMLGLRIPDIEVI 439

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 445
+ TRKT PD+ + S ++
Sbjct: 440 NVATTRKTLPDFVGMWSGMLRQ 461

>ref|YP_948361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter
aureus TC1]
gb|ABM07311.1| 3-Phosphoshikimate-1-carboxyvinyltransferase (EPSP synthase)
[Arthrobacter aureus TC1]
Length = 456

Score = 152 bits (385), Expect = 7e-35, Method: Compositional matrix adjust.
Identities = 132/442 (29%), Positives = 213/442 (48%), Gaps = 36/442 (8%)

Query: 15 ISGTVKLPKSGKSLNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV +PGSKSL+NR L+LAAL++G + + L+S D M+ ALR LG +V
Sbjct: 30 VDATVTVPGSKSLTNRLVLALADGPSRLRAPLHSRDSALMIQALRQLGATVTE----- 84

Query: 75 RAVVVGCGGKF-----PVEDAKE--EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V G F P++ A E + G AG MR + AA N V DG
Sbjct: 85 ----VPGDGHFGPDLEITPMDPAASGAETAIDCGLAGTVMRFVPP--LAALRNGVTVFDG 138

Query: 126 VPRMRERPIGDLVVGLKQLGADV--DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
P R RP+G ++ L LG V D P V+G G + GG + + S SSQ++
Sbjct: 139 DPHARNRPMGTIIIEALIALGVPVAADGGRTPSALPFAVDGTGEVRGGHLVIDASASSQFV 198

Query: 184 SALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SALL+ + +E + K + S+ ++ MT+ ++ R + + + G+
Sbjct: 199 SALLLVGARFVEGLHLEHVGPVPSLDHITMTVEVL-RSVGVVVDDSVPNHWRVSPGRIR 257

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+ +E D S+A FLA A T GTV + + Q ++ +L +GA+VT+ +
Sbjct: 258 AF--DQRIEQDLSNAGPFLAALATRGTVRIPNWPAGTTQVGDQWRTILTALGAETVFD 315

Query: 303 TSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
++TVT G +K D ++ ++A T+A + A G + + +A R ET+
Sbjct: 316 GTLTVT-----GGAEIKGAD--FDESELAPTVAALCALATGTSRLTGIAHLRGHETD 366

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTI 422
R+ A+ E+ LG EE D +I P L+ + +Y DHRMA A ++ A V +
Sbjct: 367 RLAALVAEINGLGGDAEETADGLVIR-PATLHGGVVHSYADHRMATAGAILGLAVEGVQV 425

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
D T KT P++ + + ++
Sbjct: 426 EDIATTSKTMPEFPQMWAAMLQ 447

>ref|ZP_03980080.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
lipophiloflavum DSM 44291]
gb|EEI15840.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
lipophiloflavum DSM 44291]
Length = 428

Score = 152 bits (385), Expect = 8e-35, Method: Compositional matrix adjust.
Identities = 136/443 (30%), Positives = 210/443 (47%), Gaps = 46/443 (10%)

Query: 15 ISGTVKLPKSGKSLNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLS--VEADKA 72
I+ TV +PGSKSL+NR +L+AL++G + + L S D M AL ++G+ E D+
Sbjct: 18 ITHTVSVPGSKSLTNRAYVLSALAQQPSTIVGALRSRDTLMEALASMGVGFVTEGDE- 76

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G E + G AG MR L A A G + DG R R+R
Sbjct: 77 ----ISVTPGSLHGAE-----VDCGLAGTVMRFLPAVAFAAGEVRF--DGERARQR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI ++ L+ LG + P V+G GG V++ S SSQ++S LL+AA
Sbjct: 124 PIATILDALRDLGVQIQG----GSLPFSVHGASRRGGTVEIDASGSSQFVSGLLLA-- 177

Query: 193 ALGDVEIEIID---KLISIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKSPK 246
A D + I L S+P++EMTL ++ GV E + R I+G +
Sbjct: 178 ARFDEGVTITHTGGTLPSMPHIEMTLAMLADAGVAVESTGHTWRVAPQPIRG-----R 230

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE---- 302
VE D S+A+ F+A AA+TGG V V+ + Q ++E MG +
Sbjct: 231 TWVVEPDLSNATPFIAAAAVTGGCVAVKNWPAATTQPGDAIRTIVERMGCETVLEADAAG 290

Query: 303 -TSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
++ VTG R G I ++M+ + ++ T+A +A A P+ + +A R ET
Sbjct: 291 GHTLRVTGASRGTLG----GIRLMSDLGELTPTVAALAAVAKTPSELTGIAHLRGHET 345

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
+R+ A+ E+ +LG EE D I P +L+ +YDDHRMA A ++ V
Sbjct: 346 DRLKALTDEINRLGGDCCELADGLRIR-PARLHGGQWHSYDDHRMATAGAIIGLVTEGVE 404

Query: 422 IRDPGCTRKTTFPDYFDVLSTFVK 444
+ + T KT P + + + V+
Sbjct: 405 VENIATTAKTLPGFESMWADMVE 427

>ref|ZP_03990506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oribacterium sinus
F0268]
gb|EEJ52286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oribacterium sinus
F0268]
Length = 442

Score = 152 bits (385), Expect = 8e-35, Method: Compositional matrix adjust.
Identities = 139/442 (31%), Positives = 229/442 (51%), Gaps = 37/442 (8%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSDEVHYMLGALRTLGLSVEADKA 72
K I G++ +PG KS+S+R ++ +AL++G T V L ED + R +G+S+E ++
Sbjct: 10 KVIKGSITVPGDKSISHRAVMFSALAKGETVRGFLPGEDCLSTISVFRKMGSVIEQEED 69

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ R +G G A EEV L+ GN+G MR + + AG + + L G + +R
Sbjct: 70 SVRIQGLGLHGL---KAPEEV-LYCGNSGTTMRMLMAGIL--AGQSFSSCLTGDESLEKR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + + L+++GA + P+ ++G L G + S S+Q S++L+A
Sbjct: 123 PMKRVCLPLEKMGAKIKMQGEKGTAPLEISG-SPLKGIYYE-SPVASAQVKSSVLLAGLY 180

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS-PKNA 248
A G + +I+ +S + E RL+ GV+ + D ++GGQ+ K+ P
Sbjct: 181 AKG--KTSVIEPSLRDHTE---RLLGAMGVECTNTLEDGRVEISLEGGQELKALPGEY 235

Query: 249 YVEGDASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA+YF+A + G ++ ++ G + + VLE MGAK++ E TV
Sbjct: 236 LVPGDISSAAYFMASVFFLPGSSRLKNIPLNPSRCGI--LTVLEKMGAKISL-ENCSTV 292

Query: 308 TGPPPREPFGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G R ++ LKA+D+ + +P D LAV+A A+G T I D A +VKE+
Sbjct: 293 YGEERGDYILEYGPLKAVDIEGDLIPRLIDELPLLAVLATIAEGETRIYDAAELKVKNESN 352

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATID-----TYDDHRMAMAFS---LAA 414
R+ A L +LG S E D II P K +V +++ ++ DHR+AM+FS L
Sbjct: 353 RIKACVENLQRLGISAAETEDGMII--PGKGSVFSLEGKRIPSFLDHRIAMSFSVLGLLC 410

Query: 415 CAEVPVTIRDPGCTRKTTFPDYF 436
AE P+ I D C + ++P++F
Sbjct: 411 KAENPMQIEDSECIQISYPNFF 432

>ref|ZP_04859013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium varium
ATCC 27725]
gb|EES64675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium varium

ATCC 27725]
Length = 423

Score = 152 bits (385), Expect = 8e-35, Method: Compositional matrix adjust.
Identities = 117/426 (27%), Positives = 203/426 (47%), Gaps = 33/426 (7%)

Query: 16 SGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG + +P SKS+ +R ++ A+L+ G +V+ N+ S+D+ + +R LG +E +
Sbjct: 11 SQQIVIPPSKSMGHRRAICASLASGRSVIKNVAYSDDIKTTIEGMRKLGAEIEEN----- 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP-- 133
++ G + +E+ + +G +R + G T++ G R+ +RP
Sbjct: 66 GDILIIDGIKIDITRISDEI-INCNESGSTLRFFIPIFSLTGKKITFL--GKNRLLKRPQK 122

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + + ++L D ++ G L G + G+ISSQ++S LL PL
Sbjct: 123 IYEDIFKEQKLHYFHD-----ETKIEIEGRKLKAGTYVVDGNISSQFISGLLFTLPLL 174

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD +I+I S Y+E+TL ++ R+G++ +D F IKG QKYK P + +EGD
Sbjct: 175 EGDSEIKIKPPFESASYIELTLEMLRRYGIISKTDDEL-TFKIKGNQKYK-PCDYTIEGD 232

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S +F AI + G S QGD E+L G K+ E +
Sbjct: 233 FSQLGFFAVLGAIN-NNIECLGLNHGSNQDKAIIELRNAGIKIENIEGGYLIH----- 286

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ K+ ++++ PD+ L V+ ++ DG I + R KE++R+ A+ EL K
Sbjct: 287 ---KSTPKSCEIDLADCPDLGPILNVLGMYDGKFRINYAGRLRYKESDRIAAMEEELLK 343

Query: 374 LGASVEEGPDYCIITPPEKLNVTADIT--YDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
LG ++ D I+ +K+ I+ + DHR+ M+ ++AA PV I K
Sbjct: 344 LGVDIKTTTEDEFIS-GKKIYDGGIEAAGHKDHRIVMSLAVAATIMNKPVIIDGAEAVEK 402

Query: 431 TFPDYF 436
++PD+F
Sbjct: 403 SYPDF 408

>ref|YP_003700189.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
selenitireducens MLS10]
gb|ADH99623.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
selenitireducens MLS10]
Length = 431

Score = 152 bits (385), Expect = 8e-35, Method: Compositional matrix adjust.
Identities = 134/442 (30%), Positives = 207/442 (46%), Gaps = 25/442 (5%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+E +++ + ++GTV++PG KS+S+R +L A+L++G T + L ED + +R LG
Sbjct: 3 KETIVKAKQGLAGTVEIPGDKSISHRAVLFAVLADGVTTIKGFLEGEDCLSTIACMRKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + G G +D L GN+G +R L + AG + VL
Sbjct: 63 VVIEQNGTDVTVTGKGLQGLREPDDV-----LDTGNSGTTIRLLMGVL--AGLPFSSVLK 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + LK + A +D D P+ + G G G S S+Q S
Sbjct: 116 GDASIAKRPMARVTGPKMMNARIDGRQFGDLTPHIRG--GELRGITYYSPVASAQVKS 173

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+A A G + K + T R++ FGV+ E D D I GGQ
Sbjct: 174 AVLLAGLQAQGVTTVNEPHK-----SRDHTERMLRSFGVEVETDD--DSARIMGGQTL-D 225

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + V GD SSA++ L A I G V + G + + EVLEMMGA +T
Sbjct: 226 PAHIEVPGDISAAMFLTAALIVPGSKVKLFNTGLNPTRDGI--MEVLEMMGANITRENE 283

Query: 304 SVTVTGPPRE-PFGRKHLKAIDVNMNMPD---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ P + LK + + +P D +AV+A A G T I+D +VK
Sbjct: 284 RLAGDEFPVADLTVKTSSELKGVTTGGGLIPRLIDEIPAIAVLATQAHGTTVIKDAEELKVK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418
ET R+ + +L KLGA +E D +I P L D++ DHR+ MA +L +E
Sbjct: 344 ETNRIDTVVNQLKKLGADIEAKDDGMVIRGPISLTGGNADSFGRHIGMAMALCGLISEE 403

Query: 419 PVTIRDPGCTRKTFFPDYFDVLS 440
PVT+ ++P +FD L+
Sbjct: 404 PVTVSGTEAIAVSYPGFFDQLN 425

>ref|ZP_07315528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella atypica
ACS-134-V-Col7a]
gb|EFL58600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella atypica
ACS-134-V-Col7a]
Length = 422

Score = 152 bits (384), Expect = 9e-35, Method: Compositional matrix adjust.
Identities = 124/427 (29%), Positives = 205/427 (48%), Gaps = 31/427 (7%)

Query: 16 SGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 75
+GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V +
Sbjct: 10 TGTIASIPAKAHARALICAALANSPSTILLRSTSKDIDATMESLRGLGAHV----VYEN 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
VV G P + + +G +R L VTA+ N V D R+ +RP+
Sbjct: 66 KVVTVTPGPVPAKG-----NVVPHESGTTLR-LLLPVTASICNDVDV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + G L GG + G +SSQ+ S LL+AAP +G
Sbjct: 119 PMLSEMKAHGV-----FSQDKPPFTMTG--RLQGGNFSMVGDVSSQFFSGLLLAAP-QIG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHS----DSWDRFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FGV+ EH+ + + F + G + N +E
Sbjct: 172 LSTITATPTLQSSDYVTLTTEMTDRFGEVEHTLPDTNINEAFTVPFGASFIGRDNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S+A+ ++ A +TG +T+ G S+Q D + +V+ G V W ++TVTG
Sbjct: 232 GDWSNAAIWMVAAGMTGKPITITGMNKNSVQADRRIMQVMIDAGCDVVWDGMNITVTGRA 291

Query: 312 REPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P I ++ +MPD+ +A +A G ++ A R+KE++R++A+ +
Sbjct: 292 SKP-----IHADLEQMPDMLPVMAALACISGESSFIKARLRLKESDRLIIVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A ++ PVT++D K
Sbjct: 344 RDLGGTVREEGDDLYIINGILKGGQGDVCNDHRLVMAGTLMALISKNPVTLKDSEAITK 403

Query: 431 TFPDYFD 437
++PD+F+
Sbjct: 404 SYPDFFE 410

>ref|YP_730742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9311]
sp|Q0I9Y0.1|AROASYN3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI46412.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9311]
Length = 439

Score = 152 bits (384), Expect = 9e-35, Method: Compositional matrix adjust.
Identities = 138/446 (30%), Positives = 208/446 (46%), Gaps = 39/446 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V++PG KS+S+R LL A++EGTT ++ LL +ED LR++G ++ ++ +
Sbjct: 17 LRGRVRVPDGKSIHRALLFGAIAEGTTTIEGLLPAEDPISTAACLRSMTTISPIQSGE 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ G G D EE L GN+G MR + + G +VL G +R R
Sbjct: 77 IVTIEGVG-----LDGLEEPSEILDGNSGTMRLMLGLLAGREGR-HFVLTGDSSLRRR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+ + L LGA+V + P+ V G +L G++ S+Q SA+
Sbjct: 131 PMNRVGQPLSLLGANVRGRDHGNLAPLAVQG-----QRLRGAVVGTPVASAQVKSAL 182

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+AA A G + I+ S + E R++ FG E R ++ G K
Sbjct: 183 LLAALTAEGSTSV--IEPAHSRDHSE---RMLRAFGADLEVGEMGRHILVRPGATLKG- 236

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLMMGAKVTWTETS 304
++ V GD SSA++L AGA + G T+TVE G + EVLEMMGA +
Sbjct: 237 QHVVPDGISSAAFVLVAGALVPGATITVENVGLNPTR--TGILEVLEMMGASIEVLNRR 294

Query: 305 VVTGPPPREPFGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASVRVK 359
V G P H LKA MP D L+V A F DG + I A RVK
Sbjct: 295 -DVAGEPVGDLQVSHGPLKAFQFGEEIMPRLVDEVPLSVACFCDGESRISGAELRVK 353

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
ET+R+ + +L +GA ++E PD I L +D+ DHR+AM+ ++A AE
Sbjct: 354 ETDRLAVMARQLKAMGADIDEHPDGLTIRGGHSLKGAELDSETDHRVAMSLAVAGLMAEG 413

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
I ++P ++D L +
Sbjct: 414 DSRITRSEAAVSYPTFWDDLRLRR 439

>ref|ZP_03502269.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli Kim 5]
Length = 309

Score = 152 bits (384), Expect = 9e-35, Method: Compositional matrix adjust.
Identities = 113/331 (34%), Positives = 170/331 (51%), Gaps = 39/331 (11%)

Query: 120 TYVLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
T ++DG MR+RPIG LV ++ LG DV G CPPV V G G ++ + G +S
Sbjct: 2 TVIVDGDEHMRKRPVIGPLVEAMRTLGLDVSAETG--CPPVTVRGTRFEADRILIDGGLS 59

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSD--SWDRFYI 236
SQY+SALLM A V+IE++ + I ++ Y+++T M+ FG K E + +W R
Sbjct: 60 SQYVSALLMMAAGGDRPVDIELVGEDIGALGYIDLTTAAMQAFGAKVEKTSPTW-RVEP 118

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLMMGA 296
G Y++ + +E DAS+A+Y A ++ G + + Q D K E +
Sbjct: 119 TG---YRA-ADFVIEPDASAATYLWAAEVLSDGKIDLVGPNDRAFTQPAKAYETIA---- 170

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
R P HL A+ ++ +M D T+AV+A F + P +A+
Sbjct: 171 -----RFP----HLPV-IDGSQMQDAVPTIAVLAAFNETPVRVFGIANL 210

Query: 357 RVKETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFS 411
RVKE +R+ A+ T L + G +VEEG D + + P T IDT+ DHR+AM+F+
Sbjct: 211 RVKECDRIRALSTGLNNIREGLAVEEGDDLHVHSDPALAGQTLPAEIDTFADHRIAMSFA 270

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
LA +TI DP C KTFP Y+ L+
Sbjct: 271 LAGLKIDGITILDPCVGKTFPAYWRTLAAL 301

>ref|ZP_06244016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Victivallis vadensis
ATCC BAA-548]
gb|EFB00157.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Victivallis vadensis
ATCC BAA-548]
Length = 422

Score = 152 bits (384), Expect = 9e-35, Method: Compositional matrix adjust.
Identities = 125/402 (31%), Positives = 204/402 (50%), Gaps = 27/402 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++P + I G++ + GSKS + R + A +++G + + L S D L A + G
Sbjct: 2 KLLVKPSR-ICGSIATVGSKSHITIRGIAAALMADGVSTLYAPLESADTRSTLEAAKLFGA 60

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V + R + G GG+F D V L GN+G +R LT+ G + DG
Sbjct: 61 KVR--EFPDRWEITGTGGRFA--DPGRTVDL--GNSGTGLRMLTSLAALQGFRIGF--DG 112

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLS 184
+R R + L+ L++LGA V+ G CP +R G L GG + G+ +SQ+L+
Sbjct: 113 DASLRTRLMSGLLGALEKLGATVESSNGK-CPFSIR---GPLRGGATTVDGT-TSQFLT 166

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+LL A P GD +++ + L PY+++TL ++ FG++ SD + I GGQ +
Sbjct: 167 SLLFALPNVGGDSTVDL-EFLHEKPYIDITLSWLDSFGIRYRRSDDMLHWEIPGGQHIA 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + D S+A++ L AA+ G V + + QGD +LE MGA +
Sbjct: 226 FRRV-IPADFSTAAPFLVAAALAGDVEIRNLDFSDAQGDKHVFRLLLEEMGAVIERGGQL 284

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P GR L +++N PD +AV A ADG T + +V RVKET+R+
Sbjct: 285 RVL-----PGR--LAGCVLDLNPDPALPVMMAAALADGETRLENVPQARVKETDRI 336

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRM 406
+ ELT++GA +EE PD II +L+ + ++ DHR+
Sbjct: 337 AVMNAELTRMGADIEELPDGMIIRGG-RLHGAQVHSHADHRI 377

>ref|YP_004281417.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfurobacterium
thermolithotrophum DSM 11699]
gb|ADY73358.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfurobacterium
thermolithotrophum DSM 11699]
Length = 430

Score = 152 bits (384), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 133/448 (29%), Positives = 224/448 (50%), Gaps = 60/448 (13%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++++P KS+S+R ++L +L++GT VV N L SED L A LG+ +E D+ K
Sbjct: 10 LKGSIRVPSDKSISHRSIMLGSLNKGTVVVRNFLRSEDCLNTLKAFLELGEIE-DR--K 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATY-VLDGVPRMRER 132
+++ GK + KE + LGN+G ++R ++ ++ G Y VL G +R R
Sbjct: 67 DVIIIKGKGKHS---KEPFNIIDLNGSGTSIRLISGILS---GQPFYSVLTGDQYLRR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + + LK +GA++ G PP+ + G L G K S S+Q SA+L+A
Sbjct: 121 PMDRIAIPKMMGAEIFGREGGKYPPLTILGKRKLKGIDYK-SPKASAQVKSALLAG-- 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-----GQKYKSPKN 247
D + + + S + E R++ FGV E IKG G+ K+
Sbjct: 178 LFSDEPVSVTEPAKSRDHE---RMLRAFGVDVE-----IKGLTVCLGKNRNLEKD 225

Query: 248 AYVE--GDASSASYFLAGAAITGGT-----VTVEGCGT-----TSLQGDVKFAEVLEM 293
++ D SSA++FL GAAIT G+ V + T ++ +VK + +
Sbjct: 226 IEIDVPADISSAAFFLVGAATPGSEIVLKDVLNPRRTGILDVMKRMKANVKVENIKSV 285

Query: 294 MGAKVTWTETSVTVTGPPEPFRGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAI 350
G +V ++V+ P +LKA ++ ++P + + ++AL A +G T I
Sbjct: 286 SGEEVG---DISVSYSP-----NLKATEIKGEEIPRLIDEIPIIALLATQAEGETII 334

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF 410
+D RVKE++R+ + L +GA VEE PD II L + +Y DHR+AM F
Sbjct: 335 KDAQELRVKESDRIKSTVENLRAIGAEVEELPDGMIIRGKTSLRGGMVQSYGDHRIAMTF 394

Query: 411 SLAA-CAEVPVTIRDPGCTRKTFPDYFD 437
++A+ +E + I D C + ++P +F+
Sbjct: 395 TIASLISEEVIEIDVDVCIKTSYPRFFE 422

>ref|YP_003659482.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Segniliparus rotundus
DSM 44985]
gb|ADG98651.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Segniliparus rotundus
DSM 44985]

Length = 424

Score = 152 bits (383), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 134/429 (31%), Positives = 204/429 (47%), Gaps = 26/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ V +PGSKS++NR L+LAAL+ + + L S D ML ALR LG VE
Sbjct: 13 LDAVVVVPGSKSITNRLVLAALARTPSRIFGALRSRDTDLMLDALRQLGAGVEIGDDGT 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P+ +V L ++ AG MR L A G + DG + R RP+
Sbjct: 73 TVDVA----PAPLRGGSVDVGL----AGTVMRFLPPVAALAEGPVRF--DGDEQARARPL 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLA 193
G ++ L+ LG VD D P V G G + GG+V + S SSQ++S LL++ A
Sbjct: 123 GTILNALRDLGLVTVDG----DGLPFTVRGAGAVRGGEVAIDASASSQFVSGLLLSGARYD 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + L S P+++MT+ ++ GV+ E +R + S + +VE D
Sbjct: 179 EGLAVRHVGGLPSAPHIDMTVEMLAASGVRVEQP---ERHMWRIPPASFSGREWHVEPD 235

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A FLA AA+ GG V V ++ Q + +L MGA V W + +TV
Sbjct: 236 LSNAGPFLAAAAGGQVRVPSWPQSTTQAGDQIRHILASMGATVRWEDGWLTVN----- 290

Query: 314 PFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
G L ID+++ ++ ++ T+A +A A P+++R + R ET+R+ A+ +++
Sbjct: 291 --GSGELTGIDIDLGEIGELTPTVAALAAALASSPSSLRGITHLRGHETDRLAALSSQINA 348

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTRTFP 433
LG E D IT P+ L + DHRMA A ++ V + D CT KT P
Sbjct: 349 LGGHCVELDDGLSIT-PKALRGGPWKAFADHRMATAGAIIGLKIPGVRVDDVDCTSKTLP 407

Query: 434 DYFDVLSTF 442
+ D+ +
Sbjct: 408 GFADLWAQM 416

>ref|ZP_07373029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
subsp. curtisii ATCC 35241]
gb|EFL93206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
subsp. curtisii ATCC 35241]
Length = 463

Score = 152 bits (383), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 140/454 (30%), Positives = 217/454 (47%), Gaps = 50/454 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-----A 69
+ G V+LPGSKSLS R LLL+A+ + + +L + D M+ ALR+LG +
Sbjct: 15 VFGAVRLPGSKSLSARELLLSAIGDAEANLTGVLFARDTDLMVQALRSLGAVIAPWPPVV 74

Query: 70 DKAAKRAVVVGCGGKFPVEDAK-----EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
D+ + + P +DA + + G AG MR + A A G +V
Sbjct: 75 DQPVQIKPLPQLWTGAPAQDASGGPSGGAPITVDCGLAGTVMRFIPALAVAGRAVRFVA 134

Query: 124 DGVPRMRERPIGDLVVGLKQLGA-----DVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
D + RP+ L+ L QLGA D D F T PP G +V +
Sbjct: 135 DS--QANARPMRPLLDALVQLGARIEYESPDGDVFPYTIYPPAERLG-----AEVTVDA 186

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAH--SDSWDR 233
+ SSQ++SALL+AAPL I L S P++EMT++ + + G+ E SD
Sbjct: 187 TASSQFISALLAAPLLPDGCTIRSKTVALPSLPHIEMTMQCLSQHGITVEQGLSDDGKP 246

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
F+ + ++ ++E D S+A FLA I GG ++V ++Q + ++L +
Sbjct: 247 FWNVVSEPVFG-QDVFIEPDLSNAGPFLALVGIAGGRISVPAWPAKTMQAGAAWLQILPL 305

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDV 353
MG +V W +TV+ P L+ +D +++ + ++ T+A +A FA+G + +R +
Sbjct: 306 MGLRVEWNCGLTVSRP-----GPLQLDADLSAVGELVPTVAALAAFAEGTSHLRGL 358

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGP-DYCIIT----PPEKLNVTAD-----TY 401
R ET+R+ A+R ELT +G S E P D +IT P + ID +Y
Sbjct: 359 HHLRGHETDRLEALRAELTAIGISCEITPEDDLVITGKPVTPSWRDTPTIDAEPLLLHSY 418

Query: 402 DDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
DHR+A F PV I D G T KT PD+
Sbjct: 419 QDHRLA-TFGALLGLYPVQIDDIGATTKTLPDF 451

>gb|ACY25322.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
actinobacterium]
Length = 370

Score = 152 bits (383), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 118/344 (34%), Positives = 174/344 (50%), Gaps = 22/344 (6%)

Query: 101 AGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVR 160
AG R LTA G V+ G +R+RP+ DL L +G V G P+
Sbjct: 40 AGTTARFLTAVSALRAGEV--VITGEDSLRKRPMHDLHQALSDIGLHVSPNLGAGVLPFA 97

Query: 161 VNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMER 220
V G +++++ + SSQ+ +AL++ AP+ + I +++S Y++MT+ +
Sbjct: 98 VKR-GEQKSDRIRIAATTSQFTTALMLIAPMLSRGLAIVTEGEVVSQSYLDMTIGVQNS 156

Query: 221 FGV----KAEHSDSWDRF-YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
FGV + EH +D Y+ G Y+ +E DASSASY LA AAI G V V G
Sbjct: 157 FGVTPIERGEHIFRYDTGDYV--GAHYE-----IEPDASSASYPLAAAAIAAGRVVIG 208

Query: 276 CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAM 335
G +SLQGD KF +VL MG V V ++ P P L+ + ++M M D+
Sbjct: 209 LGRSSLQGDAKFVDVLVSMGCFVEVAGDDVLSRPQDRP-----LQGVITIDMRDMSDLVP 263

Query: 336 TLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 395
TLAVVA FA T I V R KE++R+ + EL LG V+E D + P K
Sbjct: 264 TLAVVAAFAQTATTINGVGFI RNKESDRIGDLAHELRLVGLVQVDELADGLTVH-PSKPRG 322

Query: 396 TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
++T+ DHR+AM+ +L V I DP K++P+Y+ +L
Sbjct: 323 GMVNTTHDHLRLAMSLALIGLVTPGVVINDPMVVTKSWPEYWTML 366

>ref|ZP_07909038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
subsp. holmesii ATCC 35242]
gb|EFU82749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
subsp. holmesii ATCC 35242]
Length = 463

Score = 152 bits (383), Expect = 1e-34, Method: Compositional matrix adjust.
Identities = 140/454 (30%), Positives = 217/454 (47%), Gaps = 50/454 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-----A 69
+ G V+LPGSKSLS R LLL+A+ + + +L + D M+ ALR+LG +
Sbjct: 15 VFGAVRLPGSKSLSARELLLSAIGDAEANLTGVLFARDTDLMVQALRSLGAVIAPWPPVV 74

Query: 70 DKAARAVVVGCGGKFPVEDAK-----EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
D+ + + P +DA + + G AG MR + A A G +V
Sbjct: 75 DQPVQIKPLPQLWTGAPAQDASGGPSGGAPITVDCGLAGTVMRFIPALAVAGRAVRVFA 134

Query: 124 DGVPRMRERPIGDLVVGLKQLGA-----DVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
D + RP+ L+ L QLGA D D F T PP G +V +
Sbjct: 135 DS--QANARPMRPLLDALVQLGARIEYESPDGDVFPYTIYPPAERLG-----AEVTVDA 186

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAH--SDSWDR 233
+ SSQ++SALL+AAPL I L S+P++EMT++ + + G+ E SD
Sbjct: 187 TASSQFISALLAAPLLPDGCTIRSKTVALPSLPHIEMTMQCLSQHGITVEQGLSDDGKP 246

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
F+ + ++ ++E D S+A FLA I GG ++V ++Q + ++L +
Sbjct: 247 FWNVVSEPVFG-QDVFIEPDLNAGPFLALVGIAGGRISVPAWPAKTMQAGAAWLQILPL 305

Query: 294 MGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353

MG +V W +TV+ P L+ +D +++ + ++ T+A +A FA+G + +R +
Sbjct: 306 MGLRVEWNCGLTVSRP-----GPLQPLDADLSAVGELVPTVAALAAFAEGTSHLRGL 358
Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGP-DYCIIT----PPEKLNVTAD-----TY 401
R ET+R+ A+R ELT +G S E P D +IT P + ID +Y
Sbjct: 359 HHLRGHETDRLEALRAELTAIGISCETIPEDDLVITGKPVTPSWRDTPTIDAEP LLRSY 418
Query: 402 DDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
DHR+A F PV I D G T KT PD+
Sbjct: 419 QDHRLA-TFGALLGLYPVQIDDIGATTKTLPDF 451

>ref|YP_001568242.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Petrotogeta mobilis
SJ95]
sp|A9BHP7.1|AROA_PETMO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX31919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Petrotogeta mobilis
SJ95]
Length = 432

Score = 151 bits (382), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 131/446 (29%), Positives = 217/446 (48%), Gaps = 33/446 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
+I + P + I+ + LPG KS+S+R L++ +L+EG T + N L+SED L L ++G
Sbjct: 2 KIEVTPTENINAEITLPGDKSISHRALIIGSLAEGETKIHNFSSD TLSTLNILNSIGA 61
Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
S++ + +V G G +E + L N+G MR + ++A N V+ G
Sbjct: 62 SIK-QISEDEVIVEGKGDNFIEPSN---VLNAKNSGTTMRLMMGVLSAQ--NFYSVITG 115
Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RERP+ ++ L ++G + P+ + G + K + S+Q SA
Sbjct: 116 DDSLRLRPMKRVIDPLSKMGGRRFFARKNGEFAPITILGTCDISPLVYKTPVA-SAQVKSA 174
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP 245
+L+AA A G E ++I+ S + E R+++ FG D+ I+G K
Sbjct: 175 ILLAALYAKG--ETQVIEPAKSRDHT---RMLKYFGADIAQKDTT--VVIRGLTKNLEG 227
Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ +V GD SSAS+F+ A IT T+ ++ G + + VL+MMGA +
Sbjct: 228 REFFVPGDLSSASFFIVAALITKNSTLLIKNVGINPRTGI--LSVLKMMGADIKIINEK 285
Query: 305 VTVTGPPEPFG-----RKHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASW 356
EP G LK +++ +P D LA+ A A G T I+D
Sbjct: 286 TL----NNEPVGDLLVSSSLKGVIEKGEMIPLIIDEIPILAIATQAKGKTTIKDAKEL 341
Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAA 414
R KET+R+ AI EL KLG + E D I +K+ N T ++Y+DHR+AM+ ++A
Sbjct: 342 RYKETDRIRAITRELKGLIDILEKEDGFDIIGNQKIRGNCTC-ESYNDRHRIAMSLAIA 400
Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVL 439
A+ P+ I+ C +FP++ ++
Sbjct: 401 LIADNPFIIDNFECVNISFPEFTEIF 426

>ref|YP_004146791.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoxanthomonas
suwonensis 11-1]
gb|ADV27560.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudoxanthomonas
suwonensis 11-1]
Length = 439

Score = 151 bits (382), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 143/440 (32%), Positives = 221/440 (50%), Gaps = 35/440 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP++ GT+++PG KS+S+R ++ AAL++GT+ +D L ED LG+ +E
Sbjct: 14 QPLR---GTLEIPGDKSVSHRAVMFAALADGTSTIDGFLEGEDTRSTAAIFERLGVRIET 70
Query: 70 DKAARAVVVCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

++R +V G G V+ + + L GNAG MR L + AG VL G
Sbjct: 71 PTPSRR-IVHVG-VDGLRAADGPLDCGNAGTGMRLLAGLL--AGQAFDSVLVG DAS 123

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + V L ++GA +D G D PP+R++G L G L S+Q SALL

Sbjct: 124 LSKRPMRRVTVPLAEMGARIDT--GADGTPPLRIHGGQALHGIDYTLF-VASAQVK SALL 180

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G+ I P + T R++ FGV E S R ++GGQ+ ++ +

Sbjct: 181 LAGLYAHGETSITEPH-----PTRDYTERMLAAGVDIEFSPG--RARLRGGQLRA-TD 232

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + ++ G + + A L +MGA +T E T

Sbjct: 233 IAVPADFSAAFFLVAASIVPGSELRLKAVGLNPRRTGLLHA--LRLMGADIT-EENPST 289

Query: 307 VTGPPREPFGGRKH--LKAIDVNMNKMVDVA---MTLAVVALFADGPTAIRDVASWRVKET 361
G P +H L+ + V +PD+ L V A A+GPT + RVKE+

Sbjct: 290 HGGEPVADLVVRHAPLRGVQVPEALVPMIDFEPALFVAAACAEGPTVVTGAGELRVKES 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ A+ L LG V+E D I P +L+ I++ DHR+AM+FS+A A+ V

Sbjct: 350 DRLAAMANGLRLTGLQVDETADGATIH-PGQLHGGIIESLHDHRIAMSFSVAGQRADGQV 408

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
I + +FP FD L+

Sbjct: 409 RINEIATVATSFPF-FDQLA 427

>ref|YP_001213903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
BAV1]
sp|A5FRZ3.1|AROA_DEHSB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ17025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
BAV1]
Length = 420

Score = 151 bits (382), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 132/426 (30%), Positives = 201/426 (47%), Gaps = 25/426 (5%)

Query: 17 GTVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS + R L+ AA + G + + + L ++D L LG+++ D ++

Sbjct: 12 GNIAPSSKSYTIRGLIAAAQANGQSHIISPLIADDTLATRQVLSGLGININTDTGSESW 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G K P + LF + +R +AV A ++L G MR RP+

Sbjct: 72 EITGNTFKAPSGN-----LFCRESAATLR-FMSAVCARLPFECHLLAGHSLMR-RPMLP 123

Query: 137 LVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L QLG +++ T +NG + KV L G+ISSQY+SAL++ AP

Sbjct: 124 LIQALHQLGIEIETRGNNTV----ING-QVITRSKVSPLPGNISSQYVSALMLMAPACTHG 178

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+EI + S+PY++MT + + FG+K S W I Q Y P VEGD SS

Sbjct: 179 LEIHLATPPASLPYLKMTKQTLGSFGKVVHSSIDWQEISIP-PQPYL-PARYRVEGDWSS 236

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
AS FLA AI V + T S Q D + L MGA++ + V V P

Sbjct: 237 ASSFLALGAI-AAPVFISNLDTSFQADRIMIKFLAEMGAIEESGQNVVKVNPKP----- 290

Query: 317 RKHLKAIDVNMNKMVDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L I+ ++ D+ LAV A A G + + V R+KE+ R+ A+ L+ +G

Sbjct: 291 ---LSGINADLTHSIDLLPALAVAAACAKGQSILSGVRQARIKESNRIRAVSQGLSAMGI 347

Query: 377 SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
++ E D II + ID++ DHR+AMAF + I D C KT+PD++

Sbjct: 348 NIIIEEDRLIIEGGQPKGAE-IDSFGDHRIAMAFGILGSVVGETHISDAECVTKTYPDFW 406

Query: 437 DVLSTF 442
L +

Sbjct: 407 KNLESL 412

>ref|ZP_03488339.1| hypothetical protein EUBIFOR_00910 [Eubacterium biforme DSM 3989]
gb|EEC90490.1| hypothetical protein EUBIFOR_00910 [Eubacterium biforme DSM 3989]
Length = 420

Score = 151 bits (381), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 118/431 (27%), Positives = 208/431 (48%), Gaps = 38/431 (8%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK+P SKS+++R L+ A+LS+GT++V N+ NS+D+ +G ++ LG +++
Sbjct: 9 KVVHGNV KIPASKSMAHRALICASLSDGTSIVSNVTNSKDIEATVGC MKALGANIKQIDET 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G ++ + +G +R L AA NA G R+ +RP
Sbjct: 69 TYEVT---GTNLFKQEGN--ITCNANESGSTLRFLIPL--AACTNAKVKFLGQGRLLRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ K+ + F +D + V+ G L + G ISSQ+++ + PL
Sbjct: 122 MDVYANEFKKQKQIE---FNQSD-KEIIVS--GNLQAKDYVVQGDISSQFITGFMFVLPLL 175

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D + I S YV +T++++ +FG++ + S + + IKG Q YK+ ++ VEGD
Sbjct: 176 NQDSTLTITKPYESKSYVNLTIQMLAKFGIEIETSS-NSYLIKGNQHYKA-QDVSVEGD 233

Query: 254 ASSASYFLAGAAITGGTVTVEGCGT---TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
S ++F A+ G C +S+QGD + + ++T T+T
Sbjct: 234 FSQLAFF----AVLGTLLNNALSCSNMMDSSIQGDKAILDCIP-----SFTSNKDTITFT 283

Query: 311 PREPFGKRHLKAIDVNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
++P + +++++ PD+ L V+A F +G T I + A R+KE++R++A+ TE
Sbjct: 284 KKQPAPQT-----IDL SNCPDLGPILCVLASFTNGETNIVNAARLRMKESDRILAMETE 337

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVT-AIDTY--DDHRMAMAFS-LAACA EVPVTIRDPG 426
L K G + D I E AI+ + +DHR+ MA + CAE I D
Sbjct: 338 LKKWGV DITSTFDSIQIHGKEHYQSNAKAEIFGHNDHRIVMAMTVFGLCAESECIIDDAQ 397

Query: 427 CTRKTFPDYFD 437
K++P +F+
Sbjct: 398 AITKSYPTFFE 408

>ref|ZP_07827894.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp. oral
taxon 158 str. F0412]
gb|EFR59580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp. oral
taxon 158 str. F0412]
Length = 422

Score = 151 bits (381), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 124/427 (29%), Positives = 204/427 (47%), Gaps = 31/427 (7%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V K
Sbjct: 10 TGTIASIPAKAHARALICAALANSPSTILLSRTSKDIDATMDSLRLGLAHV---VYKN 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G P + + +G +R L V A+ N V D R+ +RP+
Sbjct: 66 KIVTVTPGPAPAKG----NVVPHESGTTLR-LLLPAASICNDVDV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + +G L GG + G +SSQ+ S LL+AAP +G
Sbjct: 119 PMLSEMKAHVGT---FSQDKPPFTM--MGRLQGGNFSMVDVSSQFFSGLLLAAP-QIG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHS----DSWDRFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FG++ EH+ + + F + G + N +E
Sbjct: 172 LSTITSTPLQSSDYVTLTTETMRDFGIEVEHTLPDRNINEAFTVPFGASFIGRDNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S+A+ ++ A +TG +T+ G S+Q D + +V+ G V W +VTVTG
Sbjct: 232 GDWSNAAIWMVAAGMTGKPITITGMNKNVQADRRIMQVMIDAGCDVVDGMNVTVTGRA 291

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P I ++ +MPD+ +A +A G ++ A R+KE++R+VA+ +
Sbjct: 292 SKP-----IHADLEQMPDMLPVMAALACISGESSEFVKARLRLKESDRLVAVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A +E PVT++D K
Sbjct: 344 RDLGGTVREEGDDLYIIGSGILKGGQGDVCNDHRLVMAGTLMALISENPVTLQDSEAITK 403

Query: 431 TFPDYFD 437
++P +F+
Sbjct: 404 SYPHFFE 410

>ref|YP_003757868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalogenimonas
lykanthroporepellens BL-DC-9]
gb|ADJ25547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalogenimonas
lykanthroporepellens BL-DC-9]
Length = 421

Score = 151 bits (381), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 128/423 (30%), Positives = 204/423 (48%), Gaps = 28/423 (6%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V P SKS + R L AALS+G + + L+++D G L LG ++ K A +
Sbjct: 12 GVVNAPPSKSYTIRALFCAALSDGISIRRLPSADDTAATGVLSALGAVIDR-KGADWS 70

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
V GG+ + + + +R LT G + V D P + RP
Sbjct: 71 VT---GGQLTATRRRLDCR----QSAATLRLFLTPVCAMLSGVSRVFD--PALGRRPQTP 121

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSISSQYLSALLMAAPLALG 195
L L QLG + G + + + G GG +V L G ISSQ++S LL+AAPLA
Sbjct: 122 LRDILSQLGVSE-MSGNN---LNIYGRGGETTSTEVALPGDISSQFISGLLLAAPLARR 177

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I + + S Y+ MT+ + RFG+ E +F ++ Q Y+ P + VEGD S
Sbjct: 178 GLCIRLSSPVESREYIRMTIDCLARFGIDVETDADLRKFTVR-PQNYR-PADYTVEGDWS 235

Query: 256 SASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-SVTVTGPPREP 314
SASYFL A+ G +TV G S Q D L + A+ + S+TV+ P
Sbjct: 236 SASYFLGLGAL-AGRITVRGLSRDSFQADRMLNCLRSLNAETDVADDGSLTVSRSP--- 291

Query: 315 FGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
L ++ ++N+ D+ T+A + A G +A+ + R+KE++R+ A+ L ++
Sbjct: 292 -----LNGMEADLNESIDLLPTVACLCAAAGHSALSGIGRARLKESDRVAAVTENLLRM 346

Query: 375 GASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPD 434
G V + DY ++ + + ID+ DHR+AMAF++ A I C KT+P
Sbjct: 347 GIPVIQ-EDYLLMMMEGGQPHGAVIDSCGDHRIAMAFAMLASVCGDVTIEGAECVKGKTPG 405

Query: 435 YFD 437
+++
Sbjct: 406 FWE 408

>ref|ZP_04888260.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
gb|EDU09244.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
Length = 448

Score = 151 bits (381), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 121/447 (27%), Positives = 209/447 (46%), Gaps = 43/447 (9%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
++PIK + T+++P SK + R ++ A+L+ GT++V N L + M A R LG ++
Sbjct: 5 VEPIKSLGRTMRVPASKPETQRAIVAASLAHGTISVRNDLRCIETETMKAACRKLGI- 63

Query: 69 ADKAAKRAVVVGCGGKFPVE---DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
D+ A + + G GG+F + DAK +G+ R++ A + G +L
Sbjct: 64 -DETADQLTITGTGGRFSTDVHVIDAK-----GSGLVFRMTMMALSSMRG--IPTILT 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R R + L LGA+ +LG D +N L G L+G ISSQ+++
Sbjct: 113 GDATLRRRVMKPLFDALHALGANF-SYLGDDGKAPVINWKGALDGSHTLAGDISSQFVT 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL V+I + ++S Y++ TL M R G+ + S + + G+ Y++
Sbjct: 172 ALLMAAPLGQRSVDIRLTPPVLSQSYIDQTLFMRAGIDVQASPDYATYRASPGE-YQA 230

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ ++ D +S SY L A+ GT + G +LQG+ F +V+E +G ++ +T
Sbjct: 231 -FDTHINADFTLSYLLMACALFPGTYRIAGIQERTLQGEKLFVDVVEALGVRLRYTPGH 289

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V + +++ P++ TL ++LF G +R + R ++ R+
Sbjct: 290 VLEVDSSNAGLDGN----FEFDVSSGPNIIPTLVALSLFVKGKLTVRGGSVTRFHKSSRI 345

Query: 365 VAIRTELTKLGASVE--EGPD-----YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
++ E+ KLGA +E PD + + + DHR M+ +AA
Sbjct: 346 ESMVGVEVRKLGADIEIIRHPDGHTDGFVTRGRDRYAGGVTLSSNGDHRNFMSLFVAALRF 405

Query: 418 VPVTIRDPGCTRK-----TFPDYFD 437
D C+ +FPD+ D
Sbjct: 406 -----DNACSLDGYADVSCSFPDFID 426

>ref|YP_307544.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
CBDB1]
sp|Q3ZZI5.1|AROAEHSC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAI82628.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
CBDB1]
Length = 420

Score = 151 bits (381), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 132/426 (30%), Positives = 200/426 (46%), Gaps = 25/426 (5%)

Query: 17 GTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS + R L+ AA + G + + + L ++D L LG+ + D ++
Sbjct: 12 GNIAPVSSKSYTIRGLIAAAQANGQSHIISPLIADDTLATRQVLSELGIDISTDAGESW 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G K P + LF + +R +AV A ++L G MR RP+
Sbjct: 72 EITGNTFKAPSGN-----LFCRESAATLR-FMSAVCARLPFECHLLAGHSLMR-RPMLP 123

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L QLG +++ T +NG + KV L G+ISSQY+SAL++ AP
Sbjct: 124 LIQALHQLGIEIETRGNTTV----ING-QVITRSKVSPLGNISSQYVSALMLMAPACTHG 178

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+EI + S+PY++MT + + FG+K S W I Q Y P VEGD SS
Sbjct: 179 LEIHLATPPASLPYLKMTKQTLGSFGIKVHSSIDWQEISIP-PQPYL-PARYRVEGDWSS 236

Query: 257 ASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
AS FLA AI V + T S Q D + L MGA++ + V V P
Sbjct: 237 ASSFLALGAI-AAPVFISNLDTSFQADRIKIFLAEMGAIESGQNVKVNPKP----- 290

Query: 317 RKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L I+ ++ D+ LAV A A G + + V R+KE+ R+ A+ L+ +G
Sbjct: 291 ---LSGINADLTHSIDLLPALAVAAACAKGQSILSGVRQARIKESNRIRAVSQGLSAMGI 347

Query: 377 SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKTFPDYF 436
++ E D II + ID++ DHR+AMAF + I D C KT+PD++
Sbjct: 348 NIIEEDRLIIEGGQPKGAE-IDSFQDHRIAMAFGILGSVVGETHISDAECVTKTYPDFW 406

Query: 437 DVLSTF 442
L +
Sbjct: 407 KNLESL 412

>ref|YP_003880717.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia muelleri CARI]
gb|ADM90019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia muelleri CARI]
Length = 417

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 119/434 (27%), Positives = 213/434 (49%), Gaps = 52/434 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K+I+G + + GSKS SNR L+L AL + N+ NS+D + AL +
Sbjct: 11 KDIGYIHITGSKSESNRFLILKALFPNLI FLKNISNDDTLNLLNALSFS----- 60

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K+E+ + ++G AMR LTA + +L G R++ER
Sbjct: 61 -----NKKEINI--NHS GTAMRFLTAFFSIKEKKEV--LLTGSYRIQER 100

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI LV LK+LGA++ PP+R+ G L GG++ ++ ++SSQ++S++++ A
Sbjct: 101 PISILVETLKKLGANIVYEKEIGFPPLRIIG-KKLLGGEIYMNANLSSQFISSIMLIAS 159

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA---- 248
++I + K+ S Y++MT +++++ G+ SW+ I S K
Sbjct: 160 FENGLKIFLSKKITSHSYIKMTFKILKKIGLNI----SWNNNIYIKNIKFSKKKFKNKK 215

Query: 249 --YVEGDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMM-GAKVTWTETS 304
+E D SSASY+ + A++ + ++ SLQGD + ++ K + + +
Sbjct: 216 KILIESDWSSASYYSLVALSKKANLNLKFYKKKSLQGDKIITNIYKIFFNVKTIFKKN 275

Query: 305 VTVTGP-PREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ + +P K I++N+N PD+A T+AV ++ + + +VKET+R
Sbjct: 276 INLKNFLPKP-----KTININLNSTPDIAQTIAVCTGLKKKCIKGLKTLKVKETDR 329

Query: 364 MVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTI 422
+ A++ EL KLG + + ++ + I+TYDDHRMAM+FS P++I
Sbjct: 330 LNALKNELFKLGKIVLTKNSLKLNFKNKNKYINTYDDHRMAMSFSTLGLIL-YPISI 388

Query: 423 RDPGCTRKTTPDYF 436
K++P+++
Sbjct: 389 LHYNVINKSYPNFW 402

>ref|ZP_04903345.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei S13]
gb|EDS86357.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei S13]
Length = 469

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 121/455 (26%), Positives = 213/455 (46%), Gaps = 43/455 (9%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+ G+ + ++PIK + T+++P SK + R ++ A+L+ GT++V N L + M A
Sbjct: 18 IGGSMYLRVEPIKSLGRMTMRVPASKPETQRAIVAASLAHGTSIVRNDLRCIETETMKAAC 77

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVE----DAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
R LG ++ D+ A + + G GG+F + DAK +G+ R++ A + G
Sbjct: 78 RKLGIAT--DETADQLTITGTGGRFSTDVHVIDAK-----GSGLVFRMTMALSSMRG 127

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
+L G +R R + L L LGA+ +LG D +N L G L+G
Sbjct: 128 --IPTILTGDATLRRRVMKPLFDALHALGANF-SYLGDDGKAPVINWGKALDGSHTLAG 184

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
ISSQ+++ALLMAAPL V+I + ++S Y++ TL M R G+ + S + +
Sbjct: 185 DISSQFVTALLMAAPLQRSVDIRLTPPVLSQSYIDQTFEFMRAGIDVQASPDYTAYRA 244

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G+ Y++ + ++ D +S SY L A+ GT + G +LQG+ F +V+E +G
Sbjct: 245 SPGE-YQA-FDTHINADFTSLSYLLMACALFPGTYRIAGIQERTLQGEKLFVDVVEALGV 302

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASW 356
++ + V + +++ P++ TL ++LF G +R +
Sbjct: 303 RLRYAPGHVLEVDSSNAGLDGN---FEFDVSSGPNIPTLVALSLFVKGLTVRGGSVT 358

Query: 357 RVKETERMVAIRTELTKLGASVE--EGPD-----YCIITPPEKLNVTIDTYDDHRMAMA 409
R ++ R+ ++ E+ KLGA++E PD + + + DHR M+
Sbjct: 359 RFHKSSRIESMVGEVRKLGANIEIIRHPDGHDTGDFVTRGRDRYAGGVTLSSNGDHRNFMS 418

Query: 410 FSLAACAEVPVTIRDPGCTRK-----TFPDYFD 437
+AA D C+ +FPD+ D
Sbjct: 419 LFVAALRF-----DNACSLDGYADVSCSFPDFID 447

>ref|ZP_05979475.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Subdoligranulum
variabile DSM 15176]
gb|EFB76946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Subdoligranulum
variabile DSM 15176]
Length = 429

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 120/436 (27%), Positives = 202/436 (46%), Gaps = 27/436 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ +SG+ +P SKS ++R +L AAL++G + + N+ S+D+ LGA LG ++ +
Sbjct: 9 VSRLSGSATVPPSKSAHRAVLCAALADGVSHITNIEYSQDIRATLGAQAQAKIQEEP 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + G G V F +G +R + + + +G R+ +
Sbjct: 69 DS--LTITGRGNASGFVTVTRPV--FCNESGSTLRFMIPLFSLTAQKVRFTGNG--RLFD 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP + + G L + + G L G L G +SSQ++S LL A P
Sbjct: 123 RPQAVYQMLFDRQG-----LRFEQAHDGITIFGRLRPGGFTLPGDVSSQFISGLLFATP 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGGQKYKSPKNA 248
L + IE++ S YV++T+ M++FG+K + + I Q+Y + A
Sbjct: 177 LMESESTIEVLAPYESRSYVDLTIAAMQQFGIKVASRARKNGSVLYRIPAPQRYIASDFA 236

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
VEGD S A++ + GG ++V G S QGD E+L+ G K E
Sbjct: 237 -VEGDYSQAFLAVLGCVIGG-ISVTGLNPASQQGDKVILEILQRCGGKFKAVEGGYK-- 292

Query: 309 GPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
F R L+A +++ PD+ L + F G T I + R+KE++R+ A++
Sbjct: 293 -----FSRSLRLRATEIDLADCPDLGPVLFTLGCFCSGETVIHNAGRLRLKESDRIEAMQ 346

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAACAE-VPVTIRDPG 426
TEL K+GA +E D IT A + ++DHR+ MA ++AAC +P I
Sbjct: 347 TELKKMGARIEVDGDEVHITGVALHAPNAPLSGHNDHRIVMALAVAACGSGLPALISGAE 406

Query: 427 CTRKTFPDYFDVLSTF 442
K++P ++D L +
Sbjct: 407 AVNKSHPAFWDTLRSL 422

>ref|ZP_03935572.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
striatum ATCC 6940]
gb|EEI77935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
striatum ATCC 6940]
Length = 429

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 125/420 (29%), Positives = 203/420 (48%), Gaps = 35/420 (8%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR +LAAL++G +++ L S D M AL +G++ E V V
Sbjct: 27 VPGSKSITNRAYILAALADGPSILRYPLQSRDTRLMEAAALTNMGVAFEH---VGNDVHVT 83

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
G P+ A + L AG MR L AA N +DG P+ R+RP+ ++
Sbjct: 84 PG---PLHGASIDCGL----AGTVMRFLPP--VAALANGPVHVDGDPQARQRPMSITLNA 134

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLALGDVEI 199
L+ LG +V+ D P + + GG V + S SSQ++S LL++ A G
Sbjct: 135 LRDLGVEVEG----DSLPTITSLAVPEGGVTVVDASGSSQFVSGLLSGARFEKGITVK 190

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHEH-SDSWDRFYIKGGQKYKSP---KNAYVEGDAS 255
L S+P++EMT ++ GV+ E ++W + P ++ +E D S
Sbjct: 191 HEGGPLPSLPHIEMTCAMLREAGVQVEEGQNTW-----TVHPGPIAGRDWRIEPLDS 242

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPF 315
+A+ F+A AA+ GG +T+ + Q ++L MGA + T +VTV G
Sbjct: 243 NATPFMAAAAVAGGRITIPQWPEETQPGDAIRDILTAMGAHIEQTADAVTVIG-----A 297

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
+ +++NM+ + + T+A + AD P+ + +A R ET+R+ A+ LG
Sbjct: 298 SDGQIHGVELNMSNVGELTPTVAALCALADTPSRLTGIAHLRGHETDRLAALAAEINGLG 357

Query: 376 ASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDY 435
+V E D +I P L+ +Y DHRMA A ++ V + D T KT P +
Sbjct: 358 GNVTELDGGLLIE-PAPLHGKWHYSYADHRMATAGAIIGLRVPDVEVEDIETTSKTLPGF 416

>ref|YP_003916411.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter
arilaitensis Rel17]
emb|CBT75440.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrobacter
arilaitensis Rel17]
Length = 467

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 129/418 (30%), Positives = 197/418 (47%), Gaps = 17/418 (4%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
V +P SKSL+NR L+LAAL+ + + N L S D ML AL G+ +E +
Sbjct: 51 VSVPAKSLTNRYLILAAALASSPSTIHNTLISRDTEMLDALAFAFGIGIERTTQPDGSTT 110

Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
V P + A + + G AG MR + AG A+ DG R RP+ ++
Sbjct: 111 VAI---TPGKLATGPLSIDCGLAGTVMRFVPLAAVAG--ASVAFDGDEAARVRPMAVPL 165

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ LGA ++ T P ++ +V + S SSQ++SALL+ G ++
Sbjct: 166 DALETLGARIEYAGTTGMLPFTMDASALQERHEVLIDASGSSQFISALLLVGQALPGGLK 225

Query: 199 IEIIDKLISIP-YVEMTLRLMERFGVKAHEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ I+ P ++ MT++ + GV+ + + I GQ S VE D S+A
Sbjct: 226 LRAAAGHIASPDHIAMTVQTLRELGVAVGEDARSWSIAPGQ--LSGFTITVEPDLSNA 283

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
FLA A T GTV V ++ Q K+ ++L MGA+++ E V G
Sbjct: 284 GPFLAALATNGTVRVPFPWPASTTVGGKQWQILSRMGAEISHDEGVLTV-----RGT 337

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
++ ID ++A TLA + AD P+ + + R ET+R+ A+ TEL K+GA+
Sbjct: 338 GVIRGID--YADASELAPTLAALCTLADSPSKLTGIGHLRGHETDRLAALETAKVGAT 395

Query: 378 VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDY 435
V D I P L +D+Y+DHRMA A +L A V + + T KT PD+
Sbjct: 396 VTSTDDALEII-PGTLQAADLDSYEDHRMATAGALLGLAIEGVRVENIATTAKTMPDF 452

>ref|ZP_05634223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
ulcerans ATCC 49185]
ref|ZP_07928839.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
ulcerans ATCC 49185]
gb|EFS26865.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
ulcerans ATCC 49185]
Length = 423

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 113/426 (26%), Positives = 200/426 (46%), Gaps = 31/426 (7%)

Query: 16 SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG + +P SKS+ +R ++ A+++ G +++ N S+D+ + +R LG +E + +
Sbjct: 11 SQQIVIPPSKSMGHRRAICASMAPGRSIIKNTAYSDDIKTTIEGMRKLGAVIEENGST-- 68

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP-- 133
++ G + D + +G +R + G T++ G R+ +RP
Sbjct: 69 LIIDGIKDITKISDE----TINCNESGSTLRFFIPIFSLTGKKITFL--GKNRLLKRPQK 122

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + + ++L D ++ G L G ++ G+ISSQ++S LL PL
Sbjct: 123 IYEDIFKEQKLHYYHD-----ESKMEIEGKLKAGTYEIDGNISSQFISGLLFTLPLL 174

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD EI+I S Y+++TL +++RFG++ D F I+G QKY SP + +EGD
Sbjct: 175 EGDSEIKIRPPFESASYIDLTLLEMLKRFGIEIFQKDEL-TFKIRGNQKY-SPCDYTIIEGD 232

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S +F A+ + G S QGD E+L G + E +
Sbjct: 233 FSQLGFFAVLGAVNNDLKCL-GLNHDSKQGDKAVIEILRSSGVNIENIEGGYFIH----- 286

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ K ++++ PD+ L V+ ++ DG I + R KE++R+ A+ EL K
Sbjct: 287 ---KSTPKGCEIDLADCPDLGPILNVLMGYGDGDFRIYNAGRLRYKESDRIAAMEEELLK 343

Query: 374 LGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
LG S++ D I+ E + + + DHR+ M+ ++AA PV I K+
Sbjct: 344 LGVSIKTTTEDEFISGKEIYDGGIEVSGHKDHRIVMSMAVAATLMNKPVIIDGAEAVEKS 403

Query: 432 FPDYFD 437
+PD+F+
Sbjct: 404 YPDFFE 409

>ref|ZP_03055285.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pumilus ATCC 7061]
gb|EDW20847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pumilus ATCC 7061]
Length = 428

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 130/442 (29%), Positives = 221/442 (50%), Gaps = 36/442 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A+++GTTVV N L D + R +G VE ++
Sbjct: 9 MNGVIHIPGDKSISHRSVMFGAIADGTTVVKNFLPGADCLSTIDCFRKM--VEIEQKGT 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G G +++ KE + +GN+G +R + + ++T + D + +RP
Sbjct: 67 DVVIRGKG---LKEKLEPSDVLVDVNGSGTTIRLMMGILAGCEFHSTLIGD--ESIAKRP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + LKQLGA +D + P+ + G G L G + S S+Q SA+L+A A
Sbjct: 121 MQRVTGPLKQLGAKIDGRANGEYTPLSIRG-GHLKGVSYE-SPVASAQIKSAVLLAGLQA 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + K + T R++ FGK + + I+GGQ K+ + +V GD
Sbjct: 179 EGTTLTTEPHK-----SRDHTERMLSMFGVKLDEDEQS--VSIEGGQTLKAT-DIFVPGD 230

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++FL AG+ + ++ G + + +VL+ MGA + E V
Sbjct: 231 ISSAAFFLVAGSIVPNSRIVLKNVGLNKTRTGI--IDVLKQMGANLEINE----VDAKGG 284

Query: 313 EPFG-----RKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP+G LK I+++ ++++ D +A++A A+G T I+D A +VKET R+
Sbjct: 285 EPYGDLTISTSSLKGIEISGDMISRLIDEIPIIALLATQAEGTTIIKDAAELKVKETNRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVA-IDTYDDHRMAMAFSLAAC-AEVPVTI 422
+ +EL KLGA +E D I L A + +Y DHR+ M +AAC + V I
Sbjct: 345 DTVVSELKKLGAADIEATDDGMIHKGKTTLQGGATVSSYGDHRIGMMLGIAACITKQAVEI 404

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444

D R ++P++F+ + K
Sbjct: 405 EDTDAVRVSYNPFHEHIEYLTK 426

>ref|ZP_05845833.1| 3-phosphoshikimate 1-carboxyvinyltransferase (EPSP synthase)
[Corynebacterium jeikeium ATCC 43734]
gb|EEW17170.1| 3-phosphoshikimate 1-carboxyvinyltransferase (EPSP synthase)
[Corynebacterium jeikeium ATCC 43734]
Length = 429

Score = 150 bits (380), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 137/445 (30%), Positives = 218/445 (48%), Gaps = 42/445 (9%)

Query: 4 AEEIVLQPI--KEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
+E++ P+ + + TV +PGSKS++NR L+LAAL++ + + L S D M+ ALR
Sbjct: 2 SEQLWPAVPATEPVQATVAIPGSKSITNRALILAAALADAPSTITGGLVSRDELMMSALR 61

Query: 62 TLGLSV--EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
LG + + D+ GG ++ G AG MR + A G
Sbjct: 62 ALGTQILLKNDQMYVTPAEKLG-----EVDCGLAGTVMRFVPPIAALATG-- 108

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGP----PVRVNGIGGLPGGKVKLS 175
T DG R RP+ + L+ LGA V T+C P V G G + GG++ +
Sbjct: 109 TVAFDGDVEARRRPMSTTLDLRLALGATVKT--STECNPEGLPFFVEGSGEIQGGEITID 166

Query: 176 GSISQYLSALLMA-APLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRF 234
S SSQ++S LL+A A G I + L S P+VEMT++++ GV E S++R+
Sbjct: 167 ASQSSQFVSGLLLAGARFTEGVTVIHEGNSLPSQPHVEMTVQMLREAGVHVE--TSFNRW 224

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G + +VE D S+A+ F+A +TGGTV ++ T+ Q +F ++L M
Sbjct: 225 TVHPGPIRG--RQWHVEPDLSNATPFMAAGVLTGGTVRIQNWPAATTNPGDQFRQILLDM 282

Query: 295 GAK----VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAI 350
GA+ V + V+ TG + I +M+ + ++ T+A +A ADGP+ +
Sbjct: 283 GAFAELDVHGHDLVVSSTG-----RINGITWDMHDIGELTPTVAALALADGPSHL 333

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF 410
+A R ET+R+ A+ + LG +VE+ D II P L ++Y DHRMA A
Sbjct: 334 YGIAHLRGHETDRLQALADNINALGGNVEQTADGLIIH-PAALEGGRWESYADHRMATAG 392

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDY 435
++ + + D T KT P +
Sbjct: 393 AILGLRVEGIHVSDVDTTAKTLPGF 417

>ref|YP_001057853.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
pseudomallei 668]
gb|ABN83408.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 668]
Length = 448

Score = 150 bits (379), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 123/451 (27%), Positives = 209/451 (46%), Gaps = 51/451 (11%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++PIK + T+++P SK + R ++ A+L+ GT++V N L + M A R LG ++
Sbjct: 5 VEPIKSLGRTMRVPASKPETQRAIVAASLAHGTSIVRNDLRCIETETMKAACRKLGI- 63

Query: 69 ADKAAKRAVVVGCGGKFPVE---DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
D+ A + + G GG+F + DAK +G+ R++ A + G +L
Sbjct: 64 -DETADQLTITGTGGRFSTDVHVIDAK-----GSGLVFRTMMALSSMRG--IPTILT 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISQYLS 184
G +R R + L L LGA+ +LG D +N L G L+G ISSQ+++
Sbjct: 113 GDATLRRRVKMLPFDALHALGANF-SYLGDDGKAPVINWGKALDGSHTLAGDISSQFVT 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALLMAAPL V+I + ++S Y++ TL M R G+ + S + + G+ Y++
Sbjct: 172 ALLMAAPLQRSVDIRLTPPVLSQSYIDQTLFMRAGIDVQASPDYTAAYRASPGE-YQA 230

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ ++ D +S SY L A+ GT + G +LQG+ F +V+E +G ++ +
Sbjct: 231 -FDTHINADFTSLSYLLMACALFPPTYRIAGIQERTLQGEKLFVDVVEALGVRLRYAPGH 289

Query: 305 VTVTGPPPREPFRGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V + +++ P++ TL ++LF G +R + R ++ R+
Sbjct: 290 VLEVDSSNAGLDGN----FEFDVSSGPNIIPTLVALSLFVKGKLTVRGGSVTRFHKSSRI 345

Query: 365 VAIRTELTKLGASVE--EGPDYCIITPPEKLNVTATIDTY-----DDHRMAMAFSLA 413
++ E+ KLGA +E PD P+ D Y DHR M+ +A
Sbjct: 346 ESMVGEVRKLGADIEIIRHPD----GHPDGFVTRGRDRYAGGVTLSSNGDHRNFMSLFVA 401

Query: 414 ACAEVPVTIRDPGCTRK-----TFPDYFD 437
A D C+ +FPD+ D
Sbjct: 402 ALRF-----DNACSLDGYADVSCSFPDFID 426

>ref|YP_251417.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
jeikeium K411]
emb|CAI37799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
jeikeium K411]
Length = 429

Score = 150 bits (379), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 137/445 (30%), Positives = 218/445 (48%), Gaps = 42/445 (9%)

Query: 4 AEEIVLQPI--KEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
+E++ P+ + + TV +PGSKS++NR L+LAAL++ + + L S D M+ ALR
Sbjct: 2 SEQLWPAPVATEPVQATVAIPGSKSITNRALILALADAPSTITGGLVSRDELMMSALR 61

Query: 62 TLGLSV--EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
LG + + D+ GG ++ G AG MR + A G
Sbjct: 62 ALGTQILLKNDQIYVTPAEKLHGG-----EVDCGLAGTVMRFVPPIAALATG-- 108

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPFGKVKLS 175
T DG R RP+ + L+ LGA V T+C P V G G + GG++ +
Sbjct: 109 TVAFDGDVEARRRPMSTTLDSLRLALGATVKT--STECNPEGLPFFVEGSGEIQGGEITID 166

Query: 176 GSISSQYLSALLMA-APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
S SSQ++S LL+A A G I + L S P+VEMT++++ GV E S++R+
Sbjct: 167 ASQSSQFVSGLLLAGARFTEGVTVIHEGNSLPSQPHVEMTVQMLREAGVHVE--TSFNRW 224

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G + +VE D S+A+ F+A +TGGTV ++ T+ Q +F ++L M
Sbjct: 225 TVHPGPPIRG--RQWHVEPDLSNATPFMAAGVLTGGTVRIQNWPAATTNQPGDQFRQILLDM 282

Query: 295 GAK----VTWTETSVTVTGPPPREPFRGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAI 350
GA+ V + V+ TG + I +M+ + ++ T+A +A ADGP+ +
Sbjct: 283 GAEAELDVHGHDLVVSSTG-----RINGITWDMHDIGELTPTVAALALADGPSHL 333

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
+A R ET+R+ A+ + LG +VE+ D II P L ++Y DHRMA A
Sbjct: 334 YGIAHLRGHETDRLQALADNINALGGNVEQTADGLIIH-PAALEGGRWESYADHRMATAG 392

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDY 435
++ + + D T KT P +
Sbjct: 393 AILGLRVEGIHVSDVDTTAKTLPGF 417

>ref|ZP_07971108.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CB0205]
Length = 435

Score = 150 bits (379), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 213/439 (48%), Gaps = 25/439 (5%)

Query: 13 KEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V++PG KS+S+R LL A++EGTT ++ LL +ED LR +G+ V A KA
Sbjct: 11 RSLKGHVVRVPGDKSISHRALLFGAIAEGTTTRIEGLLPAEDPLSTAACLAMGVQVSAIKA 70

Query: 73 AKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

Sbjct: 71 K VV G G ++ +E E L GN+G MR + + G +V+ G +R
GKTVVVEVG---LDGFQEPESVLDGNSGTTMRLMLGLLAGRSGR-HFVVTGDDSLRR 125

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + L ++GA + G + P+ + G L G ++ + S+Q SA+L+AA

Sbjct: 126 RPMKRVGGPLSEMGATIQGRAGGNLAPLAIEGR-QLKGATIR-TPVASAQVKSAILLAAL 183

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A D +I+ + S + E R++ FG + + G K ++ V

Sbjct: 184 TA--DGPTTVIEPVQSRDHSE---RMLRAFGADLSVGGPGQTEVTVVPGSSSLKG-QDVVV 237

Query: 251 EGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++L AIT G +TVE G + +VLE MGA++ V G

Sbjct: 238 PGDISSAAFVWLAGAITPGADLTVENVGLNPSR--TGILDVLEQMGARIEVLNAR-DVAG 294

Query: 310 PPREFPGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P H LK + + +P D LAV A A+GP+ + RVKET+R+

Sbjct: 295 EPVGDRLRVVHGPLKGSIGADLIPRLVDEIPVLAACAACGSPSRVTGAEEELRVKETDRL 354

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
+ +L +GA +EE PD I L+ +D+ DHR+AM+ +AA A TI

Sbjct: 355 AVMARQLGAMGAQIEEFPDGMTIQGGVTLHGAEVDSETDHRVAMSLAVAAQIASGMTTIA 414

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
P ++P ++D L

Sbjct: 415 RPEAAAVSYPGFWDDLRL 433

>ref|ZP_06011838.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia
goodfellowii F0264]
gb|EEY35024.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptotrichia
goodfellowii F0264]
Length = 418

Score = 150 bits (379), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 122/430 (28%), Positives = 217/430 (50%), Gaps = 32/430 (7%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEG-TTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++GT+++P SKS S+R ++ AAL+ G + +DNL S D+ + G V +

Sbjct: 10 LNGTIEIPPSKSYSHRAVIAAALASGEKSKIDNLKFSVDITTTDIMENWGAKV--IRGE 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT-AAVTAAGGNATYVLDGVPRMRER 132
+VG GK D + +G +R L +T+ + DG ++ +R

Sbjct: 68 NFLEIVGNDGKVVPRDKYTQCN---ESGSTIRFLIPIGITSEN---ELIFDGKGKLVDR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ F T+ + + G L G ++ G+ISSQ+++ LL A PL

Sbjct: 121 PLDTYY---KIFDKQKIFYKTEKGKLPLEIKGKLQSGIYEIDGNISSQFITGLLYALPL 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G+ +I I L S Y+++TL +++ G++ ++ + F I+G QKYKS + VEG

Sbjct: 177 LEGNSKIVINKSLESKGYIDLTLLEILKIAGIEI-INNGYKSFDIRGNQKYKSF-DYTVEG 234

Query: 253 DASSASYFLAGAAITGGTVTVEGC---GTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D S ++++ I+ C SLQGD + E+++ MGA + + V V

Sbjct: 235 DYSQVAFWIVAGIISNRDNKIKCLHVNKNSLQGDREIIEIVQRMGANLEIYDDYVIVK- 293

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P + K +++++ PD+A L V+ ++G T I + R+KE++R+ +I+T

Sbjct: 294 PSK-----TKGTVIDVSQCPDIAPILTVLGALSEGETQIINGERLRIKESDRITSIKT 346

Query: 370 ELTKLGASVEEGPDYCIITPPE--KLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
EL KLGA VEE D +I + K VT + ++DHR+AM+ ++A+ E + I +

Sbjct: 347 ELNKLGAKEEKGDLDVIQVDGFGKGGVT-VSAWNHRIAMSLAIASTRCEKEIVIEEAE 405

Query: 427 CTRKTFFPDYF 436
+K++P +

Sbjct: 406 SVKKSYPHFL 415

>ref|ZP_07708388.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. m3-13]

Length = 430

Score = 150 bits (379), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 127/440 (28%), Positives = 223/440 (50%), Gaps = 35/440 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ +++G T V+N L +D + LG+ +E +
Sbjct: 11 LKGTIQIPGDKSISHRSVMFGSMAGKTTVENFLPGDDCLSTISCFKGLGVKIEQN--GS 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G G K E ++ L +GN+G R + ++ G VL G + +RP+
Sbjct: 69 NVTVYGNGLKGLRESSE---ILDVGNSGTTARLMMGILS--GLPIHSLVLIGDESIKRP 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ V L+ +GA + + P+ + G GGL G +S S+Q SA+L+A A
Sbjct: 124 KRVTVPRLRDMGAIQGNQDGNFTPIISIQG-GGLRGLDY-VSPVASAQVKSAILLAGLQAE 181

Query: 195 GDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G + S P+ + T R++ FGV+ + + + GGQK S + V G
Sbjct: 182 GVTSV-----SEPFKSRDHTERMLRAFGEVKEEEGG-KVSLVGGQKLVSDLHIVVPG 233

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL AGA + G +T+E G + + EVL+ MGA++++ +V GP
Sbjct: 234 DISSAAFFLVAGAIVPGSRITLERVGLNPTRTGI--LEVLMKMGASLSYS--NVIEDGP- 288

Query: 312 REPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
EP+ LK +++ + +P + + ++AL A +G T I+D +VKET R
Sbjct: 289 -EPYADITVESDLKGVEIGGDIIPRLIDEVPIIALMATQAEGTTVIKDAEELKVKETNR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ + EL KLGA +E D II +L+ +D+Y DHR+ M ++A+ AE +
Sbjct: 348 IDTVVNELKKLGADIEATEDGMIKGIKIRLHGCTLDYSYGDHRIGMMGAVASLIAEGETVL 407

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
++ ++P +F+ + +
Sbjct: 408 QNDKAINVSYPSPFFEHMESL 427

>ref|YP_001559640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
phytofermentans ISDg]
gb|ABX42901.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
phytofermentans ISDg]
Length = 436

Score = 150 bits (379), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 126/445 (28%), Positives = 221/445 (49%), Gaps = 32/445 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+K+I+GT+ +PG KS+S+R ++ A++EGTT V N L D + R LG+++E
Sbjct: 3 FHKVKQINGTLTVPGDKSISHRAVMFGAIAEGTTEVYNFLKGADCLSTIQCFRQLGINIE 62

Query: 69 ADKAAKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
D + + G G G P L +GN+G +R ++ ++ + + G
Sbjct: 63 EDTKQQVIRIHGKGLHGLTP-----PSTILDVGNSGTTLRLISGILSGQPFESN--ITGD 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKL-----SGSISS 180
+++RP+ ++ L + AD+ LG C P+ +NG G K L S S+
Sbjct: 116 SSIQKRPMNRVITPLSLMNADIKSVLGNCGAPLCING-SYQNGAKSALKSIHNSPIASA 174

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q S++L+A A G E + + +S + E+ +++++FG +D I+
Sbjct: 175 QVKSSILLAGLYAEG--ETSVTEPYVSRNHTL---MLQKFGANLSVNDKT--VTIQPEP 227

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + K +V GD SSA+YFLA A I + + G + + +VL MGA +T
Sbjct: 228 RLMAQK-VHVPGLDISSAAYFLAAACILPNSELVINNVGVNPNTRDGI--IDVLLAMGADIT 284

Query: 300 WTETSVT---VTGPPREPFGKHLKAIDVNM-NKMPDVAMTLAVVALFADGPTAIRDVAS 355
+ R + H I+ ++ ++ D +AVVA FA+G T I+D A
Sbjct: 285 KEDLNQEGEAVCNLRVRSSKLHGTVEGSIIPRLIDEIPVIAVVACFAEGDTIIKDAAE 344

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC 415
+VKE+ R+ + +L +GA++ D II +KL+ T I++ +DHR+AM+F++A+
Sbjct: 345 LKVKESNRIDVMVQQLKHMGANLTATEDGMIHGGQKLSGTVIESKEDHRIAMSFAIASL 404

Query: 416 -AEVPVTIRDPGCTRKTFFPDYFDVL 439
AE TI+ C ++P+++ L
Sbjct: 405 MAEGETTIQGAECVNISYPEFYQDL 429

>ref|YP_003886854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothecae sp. PCC
7822]
gb|ADN13579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothecae sp. PCC
7822]
Length = 448

Score = 150 bits (378), Expect = 4e-34, Method: Compositional matrix adjust.
Identities = 130/450 (28%), Positives = 219/450 (48%), Gaps = 26/450 (5%)

Query: 5 EEIVLQPIKE---ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
+E+++ P + G + +PG KS+S+R L+L AL+ G TV+ LL ED R
Sbjct: 15 QELIITPSSGLSLGKITVPGDKSISHRALMLGALAAGETVIKGLLLGEDPRSTASCFR 74

Query: 62 TLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG + ++ A L++ D + + + +S E A L GN+G +R L + A+ +
Sbjct: 75 ALGAEI-SELNTEKIVVSGIGLGNLTPEADV---LDAGNSGTTLR-LMLGLLASHPGRFF 129

Query: 122 VLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
+ G +R RP+ +V L+++GA + P+ V+G P + I+S
Sbjct: 130 TVTGDSSLRSRPMSRVVKPLQEMGAQIWGRKNNSLAPLAVSGQQLKP---IHYHSPIASA 186

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+ + ++ A L++ D + + + +S + E R+++ FG E + G +
Sbjct: 187 QVKSCILLAGLSI-DGKTTVTPEALSRDHSE---RMLKAFGADLEIDPQTHSVSVIGPTR 242

Query: 242 YKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLGQDVKFAEVLEMMGAKVTW 300
S + V GD SSA+++L AG+ + G + +E G + + +VLEMMGA +T
Sbjct: 243 L-SGQTVIVPGDISAFAFWLVAGSIVPGSELIIENVGINPTRTGI--LDVLEMMGADLTL 299

Query: 301 TETSVTVTGPPREPFGGRKH--LKAIIDVNMNMP---DVAMTLAVVALFADGPTAIRDVAS 355
VTG P ++ L+A ++ + +P D LAV A+FA G T IRD
Sbjct: 300 LNQR-EVTGEPVADIQVQYSQLQACTISGDLIPRLIDEIPI LAVA AVFAQGTTVIRDAQE 358

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC 415
RVKE++R+ + +EL ++GA + E PD IT L +D+Y DHR+AM+ ++AA
Sbjct: 359 LRVKESDRLAVMASELNRMGAKITELPDGLEITGGGSLVGAQVDSYTDHRIAMSLAIAAL 418

Query: 416 -AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
A TI ++P++F L +
Sbjct: 419 NASYSTTIHRAQAASISYPEFFSTLQQVCQ 448

>ref|YP_001014495.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. NATL1A]
Length = 444

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 136/444 (30%), Positives = 216/444 (48%), Gaps = 26/444 (5%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQ E+ G VK+PG KS+S+R LL A+++G T+++ LL +ED LR++G+ +
Sbjct: 13 LQKGGELYGKVKVPGDKSISHRALLFGAIAKGTLLIEGLLPAEDPLSTAECRLSMGVKIS 72

Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
K + G G + +E Q L GN+G MR L + A + ++L G
Sbjct: 73 PIKKGDIIEIEGVG-----LNGLQEPQDILNCGNSGTTMR-LIMGLLAGQKDHFFILTGD 126

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R RP+ + LK +GA V G D P+ + IG G V + S+Q SA+
Sbjct: 127 KSLRNRPMKRVGQPLKMMGAKVFGRCGGDLAPLSI--IGNKLRGAVIGTPVASAQIKSAI 184

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

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      L+AA A G + I+ S + E R+++ FG E R K +
Sbjct: 185 LLAALNAEGSTTV--IEPARSRDHSE---RMLKAFGANLEVGGEMGRHITVSPGKDLKGQ 239

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      + V GD SSA+++L AG+ I G + VE G + + +VLE M A +
Sbjct: 240 SIIIVPGDISAFLVAGSIIIPGSELVVENVLNPTRTGI--LDVLEAMEANINVINKR- 296

Query: 306 TVTGPPR---EPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
      V G P E F +++LK ++ MP D L+V A F +G + I+ + RVK
Sbjct: 297 DVAGEPVGDIIEVIFYKENLKPFIKIDDEIMPLVDEIPILSVGACFCNGISQIKGASELRVK 356

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEV 418
      ET+R+ + +L ++GASV+E D I + L +D+ DDHR+AM+ ++A+ A
Sbjct: 357 ETDR LAVMARQLKRMGASVDEHQDGLTIYGGKSLEGCELDSEDDHRIAMSLAIASIMANS 416

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
      T+R ++PD++ L
Sbjct: 417 NSTLRRSEAAASYPDFWSDLKRL 440

```

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>ref|ZP_07468515.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
      accolens ATCC 49726]
gb|EFM44159.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
      accolens ATCC 49726]
      Length = 433

```

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 131/435 (30%), Positives = 206/435 (47%), Gaps = 35/435 (8%)

```

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      ++G ++PGSKS++NR +LAAL++ +++ L S D M AL +G+ +
Sbjct: 21 VTGEHQVPGKSITNRAFILAALADSPSILHAPLVSRDTQLMEDALSAMGVRFTH----- 76

Query: 75 RAVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      G V+ K + G AG MR + A G +DG + RP
Sbjct: 77 -----GADIHVQPGKLHGATVDCGLAGTVMRFVPPVAALADGPVR--VDGDKQAYNRP 127

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APL 192
      + + L+ LG DV D P V+ G GGVK + S SSQ++S LL++ A
Sbjct: 128 MSTTLDALRSLGVDVKG---DSLPTVSANGVPEGGKVTIDASGSSQFVSGLLLSGARF 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG---GQKYKSPKNAY 249
      + G +L S+P+VEMT+ ++ + GV+ + SD G G+++ +
Sbjct: 184 SQGIQLTHEGGQLPSMPHVEMTVGMLRQAGVRVD-SDGTTWTVHPGPIAGREW-----F 236

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
      +E D S+A+ FLA AA+TGG +T++ + Q +L MG VT SVT G
Sbjct: 237 IEPDLNATPFLAAA AVTGRLTIKNWPANTTQPGDAIRHILLDMGVMVTQEHSNVTAE 296

Query: 310 PPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
      P GR L+ I+ NM + ++ T+A + A+ P+ + +A R ET+R+ A+
Sbjct: 297 ---NPAGR--LQGIERNMGDIGELTPTVAALCALAETPSRLTGIAHLRGHETDRLQALAA 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
      + LG V E D +I P E L+ Y DHRMA A ++ + I D T
Sbjct: 352 NINALGGRVTELDGLVIEPAE-LHGGDWPCYADHRMATAGAI VGLKVPGIQIEDISTTS 410

Query: 430 KTFPDYFDVLSTFVK 444
      KT P + + T +
Sbjct: 411 KTLPGFARMWETMLH 425

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>ref|YP_001487221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pumilus
      SAFR-032]
sp|A8FEJ4.1|AROABACP2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV62661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus pumilus
      SAFR-032]
      Length = 428

```

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 129/442 (29%), Positives = 220/442 (49%), Gaps = 36/442 (8%)

```
Query: 15  ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      ++G + +PG KS+S+R ++ A++ GTTVV N L D + R +G+ +E +
Sbjct: 9  MNGVIHPIPGDKSISHRSVMFGAIAANGTTVVKNFLPGADCLSTIDCFRKMGV DIE--QKGT 66

Query: 75  RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      V+ G G +++ KE + +GN+G +R + + ++T + D + +RP
Sbjct: 67  DVVIHGKG----LKEKLEPSDVLGVNSGTTIRLMMGILAGCEFHSTLIGD--ESIAKRP 120

Query: 134  IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      + + LKQLGA +D + P+ + G G L G + S S+Q SA+L+A A
Sbjct: 121  MQRVTGPLKQLGAKIDGRANGEYTPLSIRG-GHLKGISYE-SPVASAQIKSAVLLAGLQA 178

Query: 194  LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      G + K + T R++ FGVK + + I+GGQ K+ + +V GD
Sbjct: 179  EGTTTTLEPHK-----SRDHTERMLSMFGVKLDEDEQ--SVSIEGGQTLKAT-DIFVPGD 230

Query: 254  ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      SSA++FL AG+ + + ++ G + + +VL+ MGA + E V
Sbjct: 231  ISSAAFFLVAGSIVPNSRIVLKNVGLNKTRTGI--IDVLKQMGANLEINE----VDAKGG 284

Query: 313  EPGF-----RKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      EP+G LK I+++ ++++ D +A++A A+G T I+D A +VKET R+
Sbjct: 285  EPYGDLTISTSSLKGIEISGDVISRLIDEIPIIALLATQAEGTTI IKDAAELKVKETNRI 344

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAAC-AEVPVTI 422
      + +EL KLGA +E D I L A + +Y DHR+ M +AAC + V I
Sbjct: 345  DTVVSELKKLGDADIEATEDGMKIHGKTPLQGGAVVSSYGDHRIGMMLGIAACITKQAVEI 404

Query: 423  RDPGCTRKTFPDYFDVLSTFVK 444
      D R ++P++F+ + K
Sbjct: 405  EDTDAVRVSYPNFFEHLEYLTK 426
```

>sp|Q8U0A0.2|AROA_PYRFU RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
Length = 406

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 217/441 (49%), Gaps = 47/441 (10%)

```
Query: 11  PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P KEI G V P SKS ++R L+ L++ ++V+ L S+D + A+R G + +
Sbjct: 6  PPKEIQGEVIAPPSKSYTHRGYFLSLLADEKSIVERPLISDDTLATIDAIRAFGADLIEE 65

Query: 71  KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      VV +P E+ + +F ++G R + + ++ V+DG ++R
Sbjct: 66  -----VV-----YPPEELRPNY-IFARDSGTTAR--ISIIVSSLAKGVSVIDGREQLR 110

Query: 131  ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA-LLMA 189
      RP+ D V L+ +G + +G P V+V G G + +V + SSQ+ + L++A
Sbjct: 111  RRPMDGVSSLRMIGVEA---IGKRLP-VKVFGRGRISAKEVSIVAEEKSSQFATGFLILA 166

Query: 190  APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYI-----KGGQKYKS 244
      A + L ++EI+ K +S PY+EMTL+ ME FGVK + + +R I G K+K
Sbjct: 167  AKIGL---KVEIV-KPVSKPYIEMTLKTMEEFGVKYDKAQENERLVIFVDPGVKGTGKFKV 222

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P GD SSA+ FL A+ G + V +Q D + +L GAKV +
Sbjct: 223  P-----GDYSSAANFLVAGALY-GKIRVRNLMRDDVQADKEILNILREYGAKVKVDEY 275

Query: 305  VTVTGPPREPFRGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
      V V R P ++V+ + PD+ LAV+A +A+G + IR R+KE++R+
Sbjct: 276  VEVESNERNP-----LNVDCSNFPDLFPLLAVALAAYAEKSVIRG-RQLRIKESDRI 326

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFS-LAACAEVPVTIR 423
      A+ L++ G V E D I + T++DHR+ MA + LA A+ I
```

Sbjct: 327 HAMAVNLSRAGIRVRELS DGLEIWGGQPKGFRG-KTFNDHRITMALAILALGAKGESIIP 385

Query: 424 DPGCTRKTFFDYFDVLSTFVK 444

+ K++P++F+ L +K

Sbjct: 386 ETKSIKSYPNFFEDLMRVIK 406

>gb|ABK65737.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium avium
104]

Length = 419

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 139/424 (32%), Positives = 206/424 (48%), Gaps = 32/424 (7%)

Query: 19 VKLPGSKSLSNRILLALLAAL---SEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74

+ +PGSKS +NR L+LAAL GT + L S D M+GALRTLGL V D

Sbjct: 1 MTVPGSKSQTNRALVLAALAAQGRGTPTLSGALRSRDTLDMIGALRTLGLRV--DGTGP 58

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

V G P ++ G AG +R + AA +A DG + R RPI

Sbjct: 59 ELTVSGHIAPGP-----HARVDCGLAGTVLRFVPP--LAALADAVVEFDGDEQARARPI 110

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-AAPLA 193

L+ L+ LG ++ GT P RV+G G L GG V + S SSQ++S LL+ AA

Sbjct: 111 APLLDALRGLGVRIE--GTALP-FRVHGGGALAGGTVAIDASASSQFVSGLLLCASFT 166

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253

G L S P++ MT+ ++ + GV + S +R+ ++ G + ++ VE D

Sbjct: 167 EGLTVQHTGAALPSAPHIAMTVAMLRQAGVDVDDSVN-NRWQVRPGPV--AARHWEVEPD 223

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313

++A FLA A ++GGTV + G S+Q VL + A V+ T++S+ V

Sbjct: 224 LTNAVPLFAAAVVGSGTVRITGWPADSVQPADNLSVLKLNNAVVSQTDSSLEVR----- 278

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMVAIRTEL 371

G DV++ + ++ ++A A + R +A R ET+R+ A+ E+

Sbjct: 279 --GSGSYDGFVDLRAVGELTPSVAALALATPGSVSRLSGIAHLRGHETDRLAALSAEI 336

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 431

+LG E PD +IT L+ Y DHRMAMA ++ V + D G T KT

Sbjct: 337 NRLGGDCTETPDGLVIT-ATPLHSGVWQAYADHRMAMAGAIVGLRVAGVRVDDIGATGKT 395

Query: 432 FPDY 435

PD+

Sbjct: 396 LPDF 399

>ref|YP_001803197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. ATCC
51142]

sp|B1WZH9.1|ARO_A_CYAA5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS

gb|ACB51131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. ATCC
51142]

Length = 451

Score = 150 bits (378), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 127/434 (29%), Positives = 211/434 (48%), Gaps = 27/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74

+ GT+++PG KS+S+R L+L A++EG T++ LL ED R +G + + K

Sbjct: 28 LQGTLLQIPGDKSISHRALMLGAIAEGETIIAGLLLGEDPRSTAECFRAMGAQISPLNSEK 87

Query: 75 RAVVVGCG-GKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132

+ G G GK +E + L GN+G MR L + A+ + + + G +R R

Sbjct: 88 -VTIQIGLGLK-----QEPLDVNLNAGNSGTTMR-LMLGLLASHPDRLFCVTGDASLRSR 140

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192

P+ ++ L+ +GA++ P+ V G P + I+S + + ++ A L

Sbjct: 141 PMSRVIQPLQDMGANIWGRKNNTLAPLAVQGKSLKP---IHYHSPIASAQVKSCILLAGL 197

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ D + + + S + E R+++ FG + + I G K + V G
Sbjct: 198 -MTDGKTTVTEPALSRDHSE---RMLQAFGATLDIDSQTSVNTINGHPKLIG-QTVIVPG 252

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SS++++L A+I G+ + +E G + + E LEMMGA +T E +TG P
Sbjct: 253 DISSSAFWLVAASIVPGSELLIENVGINPRTGTI--LEALEMMGADITL-ENKRILTGP 309

Query: 312 REPFGRK--HLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
K LK + N +P D LAV +FA G T I+D A RVKE++R+
Sbjct: 310 VADLRVKSCQLKGCTIGGNIIPRLIDEVPILAVAGIFATGKTIKDAELRVKESDRLAV 369

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ +ELTK+GA + E PD IT L +D+Y DHR+AM+ ++AA A+ I
Sbjct: 370 MASELTKMGAKITELPDGLEITGGTPLKAAEVDSYTDHRIAMSLAIAALNAKGTIINRA 429

Query: 426 GCTRKTFFPDYFDVL 439
++P + + L
Sbjct: 430 EAAAISYPKFVETL 443

>ref|ZP_02235407.1| hypothetical protein DORFOR_02293 [Dorea formicigenerans ATCC 27755]
gb|EDR45692.1| hypothetical protein DORFOR_02293 [Dorea formicigenerans ATCC 27755]
Length = 432

Score = 150 bits (378), Expect = 6e-34, Method: Compositional matrix adjust.
Identities = 127/439 (28%), Positives = 216/439 (49%), Gaps = 22/439 (5%)

Query: 8 VLQPIKEISGTVKLPKSKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ P K + G + +PG KS+S+R ++L AL+ GTT + N L D +G +++G+ +
Sbjct: 5 IICPCKGLHGEIMIPGDKSISHRSIMLGALALGTTEITNFLEGADCLSTIGCFQSMGIQI 64

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D+ ++ +V G G A +++ L +GN+G R ++ ++A + T V+ G
Sbjct: 65 --DRTPEKIIIVHGKGMHGLA--APKDI-LNVGNSGTTTRLMSGILSAQ--DFTSVMSGDA 117

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+G ++ L Q+GA + G C P+++ G G S S+Q SA+L
Sbjct: 118 SLNSRPMGRVITPLTQMGAHITSVNGDLCAPLKIEP--GTLHGIDYTSPPVSAQVKSAIL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A D + + + S + E+ L+ + D ++K Q+ S ++
Sbjct: 176 LAGLYA--DGKTSVTEPALSRNHTELMLKSFADITSTVNPDTATAHVKPCQELYS-QS 232

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA+YF+A +T + V+ G + F EV MGA +T S+
Sbjct: 233 ICVPGDISSAAYFIAAGLLTLDSELLVKNVGINKTRA--GFLEVCRNMGADITLVNESLE 290

Query: 307 VTGPPREPF----GRKHLKAID-VNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
G PR + H I+ + + D +AV+A A G T I+D A +VKET
Sbjct: 291 -GGEPRADILVRTSKLHGTTIEGALIPTLIDEIPMIAVMAACAKGTTIHKDAELVKET 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPV 420
R+ L +GA + D II L+ I++Y DHR+AMAF++AA A+
Sbjct: 350 NRIDTTEALRSMGADITPTDDGMIQGGRTLHGAKINSYLDHRIAMAFATAALSADGDT 409

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
I D C ++P++F++L
Sbjct: 410 IIHDSQCVDVSYPEFFEIL 428

>ref|NP_939080.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium diphtheriae NCTC 13129]
emb|CAE49223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium diphtheriae]
Length = 431

Score = 150 bits (378), Expect = 6e-34, Method: Compositional matrix adjust.
Identities = 139/439 (31%), Positives = 211/439 (48%), Gaps = 23/439 (5%)

Query: 11 PIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EAD 70
P + TV++PGSKS++NR L+A++ ++ L S D M+ AL LG SV D
Sbjct: 10 PTNAVHATVRVPGSKSMTNRALILSAIAHRPAQINGALRSRDTDLIRALTA LGASVRFD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A + + G AG MR + A G+ + DG + R
Sbjct: 70 DPNHGAASSTSL---YVTPAPFHSATIDCGLAGTVMRFVPIAALAHGSVFF--DGDVQAR 124

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA- 189
RP+G+++ L+ LG V GT P V G GG V + S SSQ++S LL+A
Sbjct: 125 TRPMGEILDALRTLGVTV---TGTQL-PFHVEASGQPAGGVVDIDASGSSQFVSGLLLAG 180

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G I KL S+P++EMT+ ++ GV+ + S + + ++ N
Sbjct: 181 ARYRTGLTVRHIGGKLPSPHIEMTVDMRLLAGVQVDDSV-NEWRVPSDVEARTWN-- 237

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDKVFAEVLEMMGAKVTW----TETSV 305
+E D S+A+ FLA AA+TGGTVT+ + Q ++L MG V + +
Sbjct: 238 IEPDLNAAAPFLAAAVTGGTVTIPDWPQRTTQAGNVIRIDILSRMGCTVEMISRGSFDDL 297

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
VTGP R LK I ++M+ + ++ T+A +A A P+ + +A R ET+R+
Sbjct: 298 RVTGP-----ARGQLKGISLDMSDIGELTPTVAALALATTPSKLVGIAHLRGHETDRLA 352

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ E+T LG S E D IT P L+ +Y DHRMA A ++ V + D
Sbjct: 353 ALTQETITGLGGSCTEADGLHIT-PSTLHGGTWHSYADHRMATAGAIIGLVVGGVQVDDI 411

Query: 426 GCTRKTFPDYFDVLSTFVK 444
T KT P + D+ T V+
Sbjct: 412 DTTSKTLPGFADMWHTMVR 430

>ref|ZP_03226651.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus coahuilensis
m4-4]
Length = 430

Score = 149 bits (377), Expect = 6e-34, Method: Compositional matrix adjust.
Identities = 131/442 (29%), Positives = 221/442 (50%), Gaps = 36/442 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAK 74
+SGT+++PG KS+S+R ++ AL++GTT V N L ED + + LG+ + D+
Sbjct: 13 LSGTIEVPGDKSISHRSIMFGALADGTTTVQNFLMGEDCLSTMECFKKLGV DITIDED-- 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+V GK ++ KE +++ +GN+G R + + +G V+ G + RP
Sbjct: 71 ---LVTINGK-GIQLKEPIEVLVDGNSGTTARLMLGIL--SGLPFYTVIQDQSIGRRP 124

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+++GA + + P+ + G L G KL + S+Q SA+L+A A
Sbjct: 125 MKRVVAPLREMGAIHGRNNGEYTPLSIIG-NPLSGITYKLPVA-SA QVKSAILLAGLHA 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G E +I+ S + E +++E FG K HS+ + G Q + + ++ YV GD
Sbjct: 183 EG--ETVVIEPEKSRNHTE---KMIEYFGGKI-HSEQQ-VIRLNGNQTF-TGRDVYVPGD 234

Query: 254 ASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDKVFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++FL AAI G VT+E G + + EVLE MGA + V +
Sbjct: 235 ISSAAFFLVAAAIVPGSKVTIENVGLNPTRTGI--IEVLEKMGANIV-----VELNDSTF 287

Query: 313 EPFGR-----KHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERM 364
EP G L+ I++ + +P + + ++AL A G T I+D + +VKET R+
Sbjct: 288 EPIGTVTVEYSELQIEIGDLPKLIDEIPIIALLATQCKGETI IKDASELKVKETNRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
A+ L KLGAS+E D +I L + + DHR+ M +A+ P+T+
Sbjct: 348 DAVVDSLKKLGASIEGTDGMMIKGSSNLGAEVSSLGDHRIGMMLGVASYLTNSPITLH 407

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
+ ++P +F+ L ++N

Sbjct: 408 NDEAVASISYPTFFFEHLQKLIEN 429

>ref|YP_001737477.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Korarchaeum cryptofilum OPF8]
sp|B1L5R5.1|AROA_KORCO RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACB07794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Korarchaeum cryptofilum OPF8]
Length = 423

Score = 149 bits (377), Expect = 6e-34, Method: Compositional matrix adjust.
Identities = 116/396 (29%), Positives = 196/396 (49%), Gaps = 24/396 (6%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G+V+ P SKS S+R L ++ L E + ++N+ + DV + A+++ G + +D
Sbjct: 8 QAQGSVRAPPSKSYSHRALAVSLLEAPSKNIENISRARDVIATINAKSFGAKL-SDNLT 66
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVDGVPVPRMRER 133
+ + + P + + + G +G +R T G T VL G +R RP
Sbjct: 67 EIKI-----EPPQRPSPDDVIDCGSGTTIRFFAPISTLTGEGYT-VLTGNDLRLRRP 119
Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G ++ + +LG PP+ V G GGL GG+V++ GSISSQ+ S L++A+
Sbjct: 120 MGPIIDAINKLGWAISSRMNGLPPLIVRG-GGLKGGEVEIDGSISSQFFSGLMIATR 178
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI-KGGQKYKSPKNAYVEG 252
++I+ I +L+S PY+EMT ++ R G E ++ + G ++K P G
Sbjct: 179 ERGLKIKPIGELVSRPYLEMTKEVLRSSGSHVELNEEIKVEPVPPKGLEFKIP-----G 232
Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D A++ + A++TGG V VE +T Q D +VL G +V + V V G P+
Sbjct: 233 DYGLAAPHMLTASVTGGKVIVEDLDSTVPQADYAAIDVLSFGVEVQEVGSRVIVEGRPK 292
Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ +N+ PD+ V+A F + IR VA RVKE++R+ + +EL
Sbjct: 293 -----RGSKLNLDSPDIFPIACVLASFVSEISEIRGVAHARVKESDRVANMASELK 344
Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAM 408
K+G V+E D +I +D++ DHR+ M
Sbjct: 345 KVGVEVKELYDGLVIRGGSPKGGVKLDSHGHRIFM 380

>ref|ZP_00741040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar israelensis ATCC 35646]
gb|EA054687.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar israelensis ATCC 35646]
Length = 432

Score = 149 bits (377), Expect = 6e-34, Method: Compositional matrix adjust.
Identities = 132/460 (28%), Positives = 220/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L+ D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLSGADCLSTISC 60
Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGILA----N 110
Query: 119 ATYV--LDGVPVPRMRERIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFFSCVQGDSEIAKRPKRVNTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164
Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 165 YISPSAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215
Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289

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      + GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 216 GKT VKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLILQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVMATLAVVALFA---D 345
      VLE MGA T + + P LK I++ + +P + + V+AL A +
Sbjct: 273 VLEKMGATFTTIEPINEGASEPAANITITETSSLKGIEIGDIIPLRIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHR 405
      G T IRD +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIRDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
      + M ++A C AE + I D ++P +FD L K
Sbjct: 393 IGMMLAIAGCLAEGKIIIEDAEAVGVSYPYTFDELQKLAK 432

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>ref|ZP_06759571.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp.
      3_1_44]
gb|EFG23138.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella sp.
      3_1_44]
Length = 422

```

Score = 149 bits (377), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 122/427 (28%), Positives = 201/427 (47%), Gaps = 31/427 (7%)

```

Query: 16 SGT VKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
      +GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V +
Sbjct: 10 TGTIASIPAKAHRAHALICAALANSPSTILLSRTSKDIDATMDSLRLGLGAQV----VYEN 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERPIG 135
      VV G P + + +G +R L V A+ N V D R+ +RP+
Sbjct: 66 KVVTVTPGPVPVTKG-----NVVPHESGTTLR-LLLPAASICNEVDV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
      ++ +K G D PP + G L GG+ + G +SSQ+ S LL+AAP G
Sbjct: 119 PMLGEMKAHGV T----FSQDKPPFTMTG--RLQGGEFGMVGDVSSQFFSGLLLAAP-QCG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVKAEHSDSWD---RFYIKGGQKYKSPKNAYVE 251
      I L S YV +T M FGV +H+ + D F + +K N +E
Sbjct: 172 GATITSTTPLQSSDYVTLTTT TMANFGVTVDHTPASDTVQESFAVAANTTFKGQS NYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
      GD S+ + ++ A +TG +T+ G S+Q D + +++ G V W +VTV G
Sbjct: 232 GDWSNTAIWMVAAGMTGKPITITGMNKNVQADRRIMQIMIDTGC DVVWDGMNVTVMG-- 289

Query: 312 REPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
      + +K I ++ +MPD+ +A +A G ++ A R+KE++R+ A+ +
Sbjct: 290 -----RAVKPIHADLEQMPDMLPVMAALACSIHGESSFVKGARLRLKESDRLEAVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
      LG +V E D I L D +DHR+ MA +L A +E PVT++D K
Sbjct: 344 RDLGGTVREDGDDLYIIGSGILKGGQGDVCNDHRLVMAGTLMALISENPVTLKDSEAITK 403

Query: 431 TFPDYFD 437
      ++PD+F+
Sbjct: 404 SYPDFFE 410

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>ref|ZP_03708034.1| hypothetical protein CLOSTMETH_02792 [Clostridium methylpentosum
      DSM 5476]
gb|EEG29611.1| hypothetical protein CLOSTMETH_02792 [Clostridium methylpentosum
      DSM 5476]
Length = 423

```

Score = 149 bits (377), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 126/424 (29%), Positives = 208/424 (49%), Gaps = 26/424 (6%)

```

Query: 14 EISGT VKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      +SG + +P SKSLS+R +L AAL+ GT+ ++N++ S+D+ L A++ LG E
Sbjct: 9 RLSSGITVPPSKSLSHRAILCAALAAAGTSRIENVIFSKDILATLDAVKALG--GEYRIQG 66

```

Query: 74 KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VV G ++ ++ +G +R L +A G ATY +G ++ RP
Sbjct: 67 NSVVVTG-----IQSPAAAEIDCCESGSLRFLIPIASALGVRATYRGEG--KLPSRP 118

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ + + G D + P G L G + G ISSQ+++ LL A PL
Sbjct: 119 LTPYLIEMTRNGVTFDY--QNTMPFTTEG--QLKNGTYTIDGDISSQFVTGLLFALPLL 173

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G I I +L S PY EMT+ ++ R G++ + D + I GGQ+Y+ P + VEGD
Sbjct: 174 EGSSVIRINGRLESKPYAEMTIAMLRARCGIQV--NSLADGYEIPGGQQYQ-PLDYRVEGD 230

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S A+++ AA GG + + G S QGD + +++ GA V W V +
Sbjct: 231 YSQAIFYAVAAACGGGDLGLLQPDSPQGDREILAIVQECGAVVRWEADGVLICAA--- 287

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
K L+ V+ +PD+ L V+A +G + I ++KE++R+ AI + L
Sbjct: 288 ----KTLRPFTVDAADIPDLVPIGLVASCCEGRSVITGAKRLKIKESDRLAIAISSALNA 343

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTF 432
LG + D I D+ +DHR+AM+ ++AA A+ PV + K++
Sbjct: 344 LGGQLTFPEDRLEIEGTGGFRAGTADSCNDHRIAMSVAVAALLADGPVELSCAQSVNKS 403

Query: 433 PDYF 436
PD++
Sbjct: 404 PDFY 407

>ref|ZP_08146095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
casseliflavus ATCC 12755]
gb|EGC68886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
casseliflavus ATCC 12755]
Length = 429

Score = 149 bits (377), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 214/446 (47%), Gaps = 34/446 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L+ + GT+ +P KS+S+R ++ AL+EGTT+V N L ED + L A ++LG+ +
Sbjct: 3 LKKATHLKGTIAVPADKSISHSRSMFGALAEAGTTIVRNLRGEDCYSTLHAFQSLGVPIH 62

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D + G G P +D + +GN+G +R + + AG T L G
Sbjct: 63 DDGQSITIEGQGFNGLKPAQDP-----IDIGNSGTTIRLMMGIL--AGQPFTTTTLFGDNS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ ++ L+++GA+V T+ PP+ VNG L ++ + S+Q SAL+
Sbjct: 116 LNKRPMPNRVMLPLREMGANVRGHEQTEFPPIVNGTASLQPINYQMPVA-SAQVKSALIF 174

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G I I+K S + E +R +FG + + G Q + +
Sbjct: 175 AALQAQGTSTI--IEKEASRNHTEEMIR---QFG--GVITTQKKTITVTGPQTLQG-QEV 226

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET---- 303
V GD SSA++FL AGA + + ++ G + + +VLE MGA + ++
Sbjct: 227 IVPGDISSAAFFLTAGAIMPESEIVLKNVGINPRTGI--LDVLEEMGASIAFSNQDDQN 284

Query: 304 -SVTVTGPPREPFGGRHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
S +T L+A+ + + +P + L ++AL A G T I+D +VK
Sbjct: 285 QSADLT-----VRSSTLQAVTIAGDIIPRLIDELPIIALLATQAHGKTVIKDAEELKVK 338

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418
ET R+ A ELTKLGA + D II P L+ + + DHR+ M +AA +
Sbjct: 339 ETNRIDATAEELTKLGADITPTEDGLIINGPTPLHGGRVSSRGDHRIGMMLQIAALLTDE 398

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
V + ++PD+F ++ K
Sbjct: 399 EVELEKAEAVAVSYPDFQDVARLAK 424

>ref|ZP_07318142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella atypica
ACS-049-V-Sch6]
gb|EFL55926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella atypica
ACS-049-V-Sch6]
Length = 422

Score = 149 bits (377), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 123/427 (28%), Positives = 203/427 (47%), Gaps = 31/427 (7%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
+GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V +
Sbjct: 10 TGTIASIPAKAHARALICAALANSPSTILLSRTSKDIDATMESLRGLGAHV----VYEN 65

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
VV G P + + +G +R L V A+ N V D R+ +RP+
Sbjct: 66 KVVTVTPGPVPAKG-----NVVPHESGTTLR-LLLPVAASICNDVDV-DAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + G L GG + G +SSQ+ S LL+AAP +G
Sbjct: 119 PMLSEMKAHGVT---FSQDKPPFTMTG--RLQGGNFSMVGDVSSQFFSGLLLAAP-QIG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHS----DSWDRFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FGV+ EH+ + + F + G + N +E
Sbjct: 172 LSTITATTPQLQSSDYVTLTTETMRDFGVEVEHTLPDNTINEAFTVPFGASFIGRDNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S+A+ ++ A +TG +T+ G S+Q D + +V+ G V W ++TVTG
Sbjct: 232 GDWSNAAIWMVAAGMTGKPITITGMNKNSVQADRRIMQVMIDAGCDVVDGMNITVTGRA 291

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+P I ++ +MPD+ +A +A G ++ A R+KE++R++A+ +
Sbjct: 292 SKP-----IHADLEQMPDMLPVMAALACSISSGESSFIKGARLRLKESDRLIAVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A +E VT++D K
Sbjct: 344 RDLGGTVREEGDDLYIIGSGILKGGQGDVNDHRLVMAGTLMALISENSVTCLKDSEAITK 403

Query: 431 TFPDYFD 437
++PD+F+
Sbjct: 404 SYPDFFE 410

>ref|ZP_05441142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D11]
Length = 421

Score = 149 bits (376), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 108/433 (24%), Positives = 208/433 (48%), Gaps = 46/433 (10%)

Query: 17 GTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V P SKS+ +R ++ ++L+ G + ++N+ S+D+ + A+ LG +E
Sbjct: 13 GEVTPPPSKSILHRYIIASSLANGVSKNIENISYSDDIIATIEAMEKLGAKIEK---KDN 69

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F + ++ +G +R L + G ++ +RP
Sbjct: 70 LLIDGSKTFDKYLNNAEIDCNESGSTLRFLFPLSIVKKNKILF--KGKGLFKRP--- 124

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193
L + D + + N I G L G+ ++ G+ISSQ+++ LL + PL
Sbjct: 125 ----LSLYFENFDKY-QIKYSYINENEILLDGELKSGEYEIDGNISSQFITGLLFSPLPL 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD +I + KL S Y+++TL + +FG+K + +S+ F I+G Q YKS +N VE D
Sbjct: 180 NGDSKIIVKKGKLESSYIDITLNLNCFGIKIIN-NSYREFIIEGNQTYKS-RNYQVEAD 237

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S ++FL +I G + + G +SLQGD K +++ + W + V
Sbjct: 238 YSQVAFFLVANSI-GSNIKINGLNVSSLQGDKK---IIDFISQIDWNKKEKLV----- 287

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++ ++ PD+ L++ A + I ++A R+KE++R+ A EL+K

Sbjct: 288 -----LDGSETPDIIPIILSLKACISKKEIEIINIARLRIKESDRLKATVQELSK 336
Query: 374 LGASVEEGPDYCIITPPEKLVN-----TAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
LG + E D +I + N ++ ++ DHR+AM ++A+ C + + + +
Sbjct: 337 LGFDLIEKEDSILINSRKNFNKIFNNSPISLSSHSDHRIAMMIAIASTCYDGEIVLDNSD 396
Query: 427 CTRKTFPDYFDVL 439
C +K++P++++V
Sbjct: 397 CVKKSYPNFWVEVF 409

>gb|ACF09788.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured marine
crenarchaeote KM3-153-F8]
Length = 429

Score = 149 bits (376), Expect = 7e-34, Method: Compositional matrix adjust.
Identities = 126/446 (28%), Positives = 218/446 (48%), Gaps = 33/446 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + ++P K +SG +K P SKS ++R L L LS T++ N L S D H L + G
Sbjct: 2 DSVKVKPSK-LSGVIKPPTSKSYTHRALCLGLLSNSPTLIVNPLSRDTHATLDSCIKFG 60
Query: 65 LSVEADKAAKRAV---VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ ++ V+ G+ VE N+G +R LT+ ++A +
Sbjct: 61 AEINHLDSSELTTPPSVLSNPGEINVE-----NSGTTLRFLTIS-ISALIPEGST 108
Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISSQ 181
L G +++RP+ L+ L LG PP+ V G GG+ GG ++ GSISSQ
Sbjct: 109 KLMGDSISQKRPQPLIDSLNDLGVSCRSLDNDGTPPILVEG-GGIHGGHTEMFGSISSQ 167
Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++S+LL++ A + I++I+ ++S PY++ T+ ++ +FG + +++ F I+ K
Sbjct: 168 FISSLLISCSNADNETTIKLEPIVSEPYIDSTIFMISKFGGLVQRNNNV--FKIEP-SK 224
Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGA--KVT 299
Y S N + D S+A++ AGA ++ G VTV G Q D +L MGA K+
Sbjct: 225 Y-SCNNINIPSDFSAAAFLLFAGALLSNGEVTVMNGNDMPQADRNLNLSQMGAFAVKID 283
Query: 300 WTE---TSVTVTGPPREPFGKHLKKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
+E +S T++ L N++ PD+ ++V++L + I +
Sbjct: 284 SSEPNNSSTFISS-----DGSLLNGGTFNLSSCPDLLPVVSVLSLISSESVKITGIEHT 336
Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAACA 416
+ KE+ R+ + EL K GA+V E D II P + ++++DDHR+ MAFSL
Sbjct: 337 KYKESNRKLVALELRKTGANVVEDSLIIDAPNTIKSCKLNSHDDHRLFAFSLIGLN 396
Query: 417 EVPTVIRDPGCTRKTFPDYFDVLSTF 442
+ + ++PD+ + L +
Sbjct: 397 SAEIEVVGLKSIDVSYPDFIEDLRSL 422

>ref|YP_002881285.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beutenbergia cavernae
DSM 12333]
gb|ACQ79523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beutenbergia cavernae
DSM 12333]
Length = 434

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 141/426 (33%), Positives = 207/426 (48%), Gaps = 22/426 (5%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P I V +PGSKSL+NR L+LAAL++ T + L+S D M+ ALRTL 64
Sbjct: 15 PSAPIDALVDVPGSKSLTNRLVLAALADAPTTHAPLHRSRDSALMIAALRTLGTGIVEL 74
Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AV G PV + G AG MR + V AA +A DG P R
Sbjct: 75 PGDDLAVTPG-----PVTGGG---HVDGGLAGTVMRFV--PVVAALADAPVSFDGDPYAR 124
Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+G ++ L+ LG VD P V G + GG++ + S SSQ++SALL++A
Sbjct: 125 NRPMPGLVLDALRSLGVGVDDAATPGFLPFTVLPSGAVRGGLTVDASGSSQFVSALLLSA 184

Query: 191 PLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
P +++ + L S+P+++MT+ L+ GV + + G + P +
Sbjct: 185 PRFTDGLDLRHVGATLPSVPHIDMTVALLRAAGVGVDVPEPGHWVTPGPIR---PGDVV 241

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
VE D S+A FLA A GG+V + + Q +LE MG V + VTG
Sbjct: 242 VEPDLNAGPFLAAALAAGGSVRIPRWPARTTQPGDLLPGLLERMGTVRRDGDVLTQVTG 301

Query: 310 PPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ ID +++ ++ T+A +A A PT IR VA R ET+R+ A+
Sbjct: 302 -----TGVTGIDADLSPAGELTPTIAALAALATPTTIRGVAHLRGHETDRLAALVA 354

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E+T+LG EE PD +I P L+ + +YDDHRMA ++ A + + D T
Sbjct: 355 EITRLGGDAEETPDGLVIR-PADLHGGRVRSYDDHRMATFGAVLGLAVPGIEVDDVATTA 413

Query: 430 KTFPDY 435
KT PD+
Sbjct: 414 KTLPDF 419

>gb|ACF09630.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured marine
crenarchaeote AD1000-325-A12]
Length = 426

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 121/429 (28%), Positives = 212/429 (49%), Gaps = 29/429 (6%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL---LSVEAD 70
++ GT++ P SKS ++R L L+ LS+ T + N L S D L + G L +++
Sbjct: 10 KLKGTIRPPSSKSYTHRALCLSLSDSPTSIVNPLFSRDTGATLTSCINFGAQLDLKST 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V+ G+ VE N+G +R LT+ ++A +L+G ++
Sbjct: 70 IDVTPPSVLNPNLVE-----NSGTTLRFLTS-ISALVPRGEVILNGDDSIQ 117

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ L+ L LG PP+ V G GG+ GG ++SGS+SSQ++S+LL++
Sbjct: 118 KRPMTPLINSLNDLGVSCHSLDNDGTPPIVVEG-GGIKGGNTEISGSVSSQFISSLLISC 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A + I++++ ++S PY++ TL ++ +FG +++ F I+ KY S K +
Sbjct: 177 SRAETETSIKLEPIVSGPYIDSTLFMINKFGLVTRTNM--FKIEP-SKY-SCKKINI 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVT 308
D S+A++ AGA ++ G VTV G Q D ++ MGA V +S TV+
Sbjct: 233 PSDFSAAAFLLFAGALLSNGEVTVIDGQDLPPADRNLNIIISQMGALVETNSNNSSFTVS 292

Query: 309 GPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
L +++ PD+ ++V++L + I + + KE+ R+ +
Sbjct: 293 S-----EGTLNGGTFDLSSCPDLLPVVSVLSLISSNSVKITGIGHTKYKESNRLKLVA 345

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
+EL+K GA+V E D II P + +++YDDHR+ MAFSL V +
Sbjct: 346 SELSKTGANVVESEDSLIIDAPTAIKSCKLNSYDDHRLFMFASLIGLNSSEEVEVSGLKSI 405

Query: 429 RKTFFPDYFD 437
++P++ +
Sbjct: 406 DVSYPNFIE 414

>ref|YP_003024563.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
SC84]
ref|YP_003026464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
P1/7]
ref|YP_003028987.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
BM407]
emb|CAZ51311.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
SC84]
emb|CAZ56122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis

BM407]
emb|CAR45232.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
P1/7]
gb|ADE31051.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
GZ1]
gb|ADV69658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
JS14]
Length = 426

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 125/446 (28%), Positives = 226/446 (50%), Gaps = 37/446 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEA 69
+ +++++ GT+++PG KS+S+R ++ +L++G T N+L EDV + R LG+ +E
Sbjct: 5 RSVEKLGKTIRVPGDKSISHRSIIFGSLAKGVTRFHNILRGEDVLSTMQVFRDLGVKIED 64

Query: 70 DKAARKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G + P D L +GN+G ++R ++ + AG + + G
Sbjct: 65 NGDIVEVHGVGFDGLQAPKND-----LDMGNSGTSIRLISGVL--AGQDFEATMFGDDS 116

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + + L Q+G ++ D PP+ + G L + +L + S+Q SAL+
Sbjct: 117 LSKRPMDRVITIPLSQMGVEISGQTERDLPPLTIKGNKLNKPIRYQLPVA-SAQVKSALIF 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G E I++K ++ + E ++ +FG + E + R I+GGQ++ + +
Sbjct: 176 AALQAEQ--ESVIVEKELTRNHT---DMIVQFGGQLEVNGKEIR--IQGGQEFIA-QEI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V GD SSA+++L AG I G + +E G + + +V++ MG K+T +
Sbjct: 228 TVPGDISAALFVAGLIIPGSKIVLENGVNETRTGI--LDVIKAMGGKMTLSNIDELA 285

Query: 303 TSVTVTGPPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
S T+T E LKA ++ +P + L ++ L A G T IRD +VK
Sbjct: 286 KSATITVETSE-----LKATEIAGELIPRLIDELPIITLLATQAHGTTIIRDAEELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAE 417
ET+R+ + L +GA++E D II P L+ I+T+ DHR+ M +++AA +
Sbjct: 340 ETDRIQVVADALNSMGATIEPTEDGMIHGPALHGAEINTFGDHRIGMMTAIAALLAKD 399

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +F+ L++ +
Sbjct: 400 GEVVLERAEAINTSYPAFFEHLNSLM 425

>ref|ZP_06524660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D11]
gb|EFD80849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D11]
Length = 424

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 108/433 (24%), Positives = 207/433 (47%), Gaps = 46/433 (10%)

Query: 17 GTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G V P SKS+ +R ++ ++L+ G + ++N+ S+D+ + A+ LG +E
Sbjct: 16 GEVTPPPSKSILHRYIIASSLANGVSKIENISYSDDIIATIEAMEKLGAKIEK---KDN 72

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 136
+++ F + ++ +G +R L + G ++ +RP
Sbjct: 73 LLIDGSKTFDKKYLNNNAEIDCNESGSTLRFLFPLSIVKKNKILF--KGKGLFKRP--- 127

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193
L + D + + N I G L G+ ++ G+ISSQ+++ LL + PL
Sbjct: 128 ----LSLYFENFDKY-QIKYSYINENEILLDGELKSGEYEIDGNISSQFITGLLFSPL 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
GD +I + KL S Y+++TL + +FG+K ++S+ F I+G Q YKS +N VE D
Sbjct: 183 NGDSKIIVKGKLESSSYIDITLNLNKFGIKI-INNSYREFIIEGNQTYKS-RNYQVEAD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313

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      S ++FL  +I G  + + G  +SLQGD K  + + +      W +      V
Sbjct: 241 YSQVAFFLVANSI-GSNIKINGLNVSSLQGDKKIIDFISQID---NWNKKEKLV----- 290

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      ++ ++ PD+  L++ A  +      I ++A  R+KE++R+ A  EL+K
Sbjct: 291 -----LDGSETPDIIPILSLKACISKKEIEIINIARLRIKESDRLKATVQELSK 339

Query: 374 LGASVEEGPDYCIITPPEKLV-----TAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
      LG + E D +I  + N      ++ ++ DHR+AM  ++A+ C +  + + +
Sbjct: 340 LGFDLIEKEDSILINSRKNFNKIFNNSPISLSSHSDHRIAMMIAIASTCYDGEIVLDNSD 399

Query: 427 CTRKTFPDYFDVL 439
      C +K++P++++V
Sbjct: 400 CVKKSYPNFWFVF 412

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>ref|ZP_08149589.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
      bacterium 4_1_37FAA]
gb|EGC75680.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
      bacterium 4_1_37FAA]
Length = 431

```

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 210/440 (47%), Gaps = 27/440 (6%)

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Query: 9  LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L+P ++ GTV +PG KS+S+R ++ AL+ G T + L D + +G+S+E
Sbjct: 3  LKPTTKLRGTVTIPGDKSISHRAVMFGALANGLTEIHGFLQGADCLATIDCFAQMGISIE 62

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
      ++ V GK + L N+G R ++ + AG L G
Sbjct: 63 NNQD-----TVLVHGKGLRGLRRPSSALDTKNSGTTTRLISGIL--AGQPFETTLSGDAS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS-QYLSALL 187
      + RP+G ++ L +GAD+ G C P+R+ L G + S +I+S Q SA+L
Sbjct: 116 LNTRPMGRIITPLSMMGADITSLSGNGCAPLRIRP-ADLHG--ISYSSNIAAQVKSAIL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSP 245
      +A A D E + + +S + E RL+ FG + + +D+ I+ +
Sbjct: 173 LAGLYA--DSETSVTEPELSRDHTE---RLRAFGAELTSTKTDAGAVSMIQCNEFGQ 227

Query: 246 KNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      K +V GD SSA+YF+A G + + ++ G + + V E MGA +T+ +
Sbjct: 228 K-IFVPGDISAAYFIAAGLLVPHSEIVIKNVGINPTRAGI--LSVCEAMGADITYLSKT 284

Query: 305 VTVTGPPEPFGR-KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      P + R L + +++P D +AV+A A+G T IRD A +VKE
Sbjct: 285 NDGGEPTADLLVRTSELHGTVEGSGQPTLIDEIPMIAVLAACAEGTTIIRDAAEKVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLVNTAIDTYDDHRMAMAFSLAA-CAEVP 419
      T R+ + L K+GA + D II L+ ID+Y DHR+AMAFS+AA A+
Sbjct: 345 TNRIDTVTENLKKMGADITPTDDGMIIRGKTPLHGAVIDSYFDHRIAMAFSIAALVADGT 404

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
      TI++ C ++PD++ L
Sbjct: 405 TTIQNSSCVDVSYPDFYRTL 424

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>ref|NP_579428.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrococcus furiosus
      DSM 3638]
gb|AAL81823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrococcus furiosus
      DSM 3638]
Length = 440

```

Score = 149 bits (376), Expect = 8e-34, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 217/441 (49%), Gaps = 47/441 (10%)

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Query: 11 PIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P KEI G V P SKS ++R L+ L++ ++V+ L S+D + A+R G + +
Sbjct: 40 PPKEIQGEVIAPPSKSYTHRGYFLSLLADEKSIVERPLISDDTLATIDAIRAFGADLIEE 99

```


Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V +P E+ + +F ++G R + + ++ V+DG ++R
Sbjct: 100 -----VV-----YPPEELRPNY-IFARDSGTTAR--ISIIVSSLAKGVSVIDGREQLR 144

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA-LLMA 189
RP+ D V L+ +G + +G P V+V G G + +V + SSQ+ + L++A
Sbjct: 145 RRPMDGVSSSLRMIGVEA---IGKRLP-VKVFGRGRISAKEVSIVAEEKSSQFATGFLILA 200

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI-----KGGQKYKS 244
A + L ++EI+ K +S PY+EMTL+ ME FGVK + + +R I G K+K
Sbjct: 201 AKIGL---KVEIV-KPVSKPYIEMTLKTMEEFGVKYDKAQENERLVFVDPGVKGTGKFKV 256

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P GD SSA+ FL A+ G + V +Q D + +L GAKV +
Sbjct: 257 P-----GDYSSAANFLVAGALY-GKIRVRNLMRDDVQADKEILNILREYGAKVKVKEY 309

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
V V R P ++V+ + PD+ LAV+A +A+G + IR R+KE++R+
Sbjct: 310 VEVESNERNP-----LNVDCSNFPDLFPLLAVALAAYAEKSVIRG-RQLRIKESDRI 360

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEVPVTIR 423
A+ L++ G V E D I + T++DHR+ MA + LA A+ I
Sbjct: 361 HAMAVNLSRAGIRVRELSDDGLEIWGGQPKGFRG-KTFNDHRITMALAILALGAKGESIIP 419

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
+ K++P++F+ L +K
Sbjct: 420 ETKSIKSYPNFFEDLMRVIK 440

>ref|YP_003973698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus atrophaeus
1942]
gb|ADP32767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus atrophaeus
1942]
Length = 428

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 129/444 (29%), Positives = 219/444 (49%), Gaps = 34/444 (7%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ ++ ++G + +PG KS+S+R ++ AL+ G T V N L D + + +G+ +E
Sbjct: 4 EKVQSLNGEIIHPGDKSISHRSVMFGALANGKTTVKNFLPGADCLSTIECFKKMGVHIE- 62

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ V GK + E L +GN+G +R + + AG + G +
Sbjct: 63 ----RSGSDVTIHGKGISALQEPESLLDVGNSGTTIRLMLGIL--AGRPFYSAVAGDESI 116

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + LK++GA +D G + P+ VNG G L G +S S+Q SA+L+A
Sbjct: 117 AKRPMKRVTDPLKKMGAHIDGRAGGEFTPLSVNG-GDLTGINY-VSPVASAQIKSAVLLA 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G + K + T R++ FG+ E S+ IKGGQ + ++ +
Sbjct: 175 GLQAEGTTTVEPHK-----SRDHTEMLSAFGI--ELSEDNTSVSIKGGQSL-TAQDIF 226

Query: 250 VEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FLA GA I + ++ G + + +VL+ MGAK+ TE+S
Sbjct: 227 VPGDISSAAFFLAAGAIIPNSRIVLKNVGLNPRTGTI--IDVLQKMGAKLHITESS---- 280

Query: 309 GPPREPFG-----RKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
G EP+G L A+++ + +P + + ++AL A +G T I+D A +VKE
Sbjct: 281 GDSAEPYGDLTITETSELNALEIGGDIIPRLIDEIPIIALLATQAEGTTIIKDAAELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ITYDDHRMAMAFSLAAC-AEV 418
T R+ + +EL KLGA++E D I + L A + ++ DHR+ M +A+C +
Sbjct: 341 TNRIDTVVSELKRLGANIEATDDGMKIYKQTLKGGATVSSHGDHRIKMMLGIASCLTQE 400

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTF 442
+ I ++P +FD L+
Sbjct: 401 SIEILQTEAIHVSYPPTFFDHLNKL 424

>ref|ZP_02072284.1| hypothetical protein BACUNI_03730 [Bacteroides uniformis ATCC 8492]
gb|EDO52933.1| hypothetical protein BACUNI_03730 [Bacteroides uniformis ATCC 8492]
Length = 345

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 114/345 (33%), Positives = 170/345 (49%), Gaps = 46/345 (13%)

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
M++RPI LV L++LGA ++ PP+R+ G L G ++ L+G++SSQY+SALLM
Sbjct: 1 MQRPIRILVDALRELGARIEYVGNFPPPLRITGTE-LTGSEISLAGNVSSQYISALLM 59

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNA 248
+ + + +IS PY+ +TL+LM FG +A+ S D + G +P
Sbjct: 60 IGTVLPKGLRLHLTGDIISRPYINLTQLMRDFGAQADWV-SEDCITVSPGGYTDTPTFT- 117

Query: 249 YVEGDASSASYFLAGAAITG-----GTVTVE--GCGTTSL 281
VE D S+ASY+ AI G T +E G S
Sbjct: 118 -VESDWSAASYWYQMMMAIEGIKNEIKGGDRSSAKESEDSTKEEAHTAEIELLGLFAHSY 176

Query: 282 QGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKA--IDVNMNMPDVAMTLAV 339
QGD + AEV +G +T+ V +T RK A +D +M +PD+A T V
Sbjct: 177 QGDSRGAEVFTRLGVHTEYTRDGVKLT-----RKGTPATRLDEDMVDIPDLAQTFVV 228

Query: 340 VALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAA-- 397
D P + S ++KET+R+ A+ TEL KLG V D ++ E+ A
Sbjct: 229 TCCLMDIPFRFTGLQSLKIKETDRITALITELRKLGYYVRSEQDSILLWDGERCPADADP 288

Query: 398 -IDTYDDHRMAMAFSLAACAEVP-VTIRDPGCTRKTFPDYFDVLS 440
I TY+DHRMAMAF+ AC +P + I +P K++P Y++ L
Sbjct: 289 VIATYEDHRMAMAF+PACLVLPQIRINEPQVVTKSYPAYWEDLQ 332

>ref|YP_007881.1| putative 3-phosphoshikimate
1-carboxyvinyltransferase(5-enolpyruvylshikimate-3-
phosphat e synthase, EPSP synthase) [Candidatus
Protochlamydia amoebophila UWE25]
emb|CAF23606.1| putative 3-phosphoshikimate
1-carboxyvinyltransferase(5-enolpyruvylshikimate-3-
phosphate synthase, EPSP synthase) [Candidatus
Protochlamydia amoebophila UWE25]
Length = 939

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 128/426 (30%), Positives = 209/426 (49%), Gaps = 20/426 (4%)

Query: 15 ISGTVLKPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + LP SKS S R +LL A+++G + V NLL+S DV + L + L + ++
Sbjct: 525 LAGEISLPPSKSHSIRAILLGAMTQGISRVKNLLDSPDVEH--AKLAAIALGAKIEQVQD 582

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G+ +V GN+G +R A A T + RP
Sbjct: 583 EYLISGVAGQPKTPSGIIDV---GNSGQVLR-FAGAFALNHGYTVITGDHSICSNRPA 637

Query: 135 GDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ GL+ LGA P+ + G + G +L G SQ +SALLMA+
Sbjct: 638 QPLLDGLRCLGAFKSTRENGYAPLIIG--PIYEGTAELEGQ-DSQPVSAALLMASAFIH 694

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G EI + P++++TL + R GV + + +++ F I+G Q+ + + GD
Sbjct: 695 GTTEI-FVKYPGEKPWDLTLLHNLRLGV-SYINQNYEYFKIEGIQQ-RPHFEVNIPGDL 751

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+A++ +A A +T +T+ + +QGD + VL+ MGA + + S T+T P
Sbjct: 752 SAAAFVAAAILTQSKITLYNVDMSDVQGDQVIHVLQEMGADIQIDQASHTLTVLPGAL 811

Query: 315 FGRKHLKAIDVNMNMPDVAMTLAVLADGPTAIRDVASWRVKETERMVAIRTELTKL 374
LK +++N D LAV+A FA G T + + A R KE+ R+ I EL K+
Sbjct: 812 -----LKGTTIDVNPFDIVPILAVLACFAKGETHLINAAIARQKESNRLSCITIELKKM 866

Query: 375 GASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT-IRDPGCTRKTFP 433
GA + E D +I L +++YDDHR+AMA +A A +T ++ C +K+FP

Sbjct: 867 GAQIMETDDGLLIR-NSNLRGAIVESYDDHRLAMALIVAGLASEGITEVKGIDCIKKSFP 925

Query: 434 DYFDVL 439

++ L

Sbjct: 926 NFIQDL 931

>ref|YP_003462227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
GT]

gb|ADC73771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
GT]

Length = 420

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 132/426 (30%), Positives = 201/426 (47%), Gaps = 25/426 (5%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76

G + +P SKS + R L+ AA + G + + + L ++D L LG+ + D ++

Sbjct: 12 GNIAVPSSKSYTIRGLIAAAQANGQSHIISPLIADDTLATRQVLSGLGIDISTDAGSENV 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136

+ G K P + LF + +R ++A V A ++L G MR RP+

Sbjct: 72 EITGNTFKAPSGN-----LFCRESAATLRFMSA-VCARLPFECHLLAGHSMLR-RPMLP 123

Query: 137 LVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196

L+ L QLQ +++ T +NG + KV L G+ISSQY+SAL++ AP

Sbjct: 124 LIQALHQLGIEIETRGNTTV----ING-QFITRSKVSPLPGNISSQYVSALMLMAPACTHG 178

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256

+EI + S+PY++MT + + FG+K S W I Q Y P VEGD SS

Sbjct: 179 LEIHLATPPASLPYLKMTKQTLGSFGIKVHSSIDWQEISIP-PQPYL-PARYRVEGDWSS 236

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFG 316

AS FLA AI V + T S Q D + L MGA++ + V V

Sbjct: 237 ASSFLALGAI-AAPVFISNLDTSFQADRIMIKFLAEMGAIESGQNVVKVN----- 287

Query: 317 RKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376

K L I+ ++ D+ LAV A A G + + V R+KE+ R+ A+ L+ +G

Sbjct: 288 PKLLSGINADLTHSIDLLPALAVAAACAKGQSILSGVRQARIKESNRIRAVSQGLSAMGI 347

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTTIRDPGCTRKTFFPDYF 436

++ E D II + ID++ DHR+AMAF + I D C KT+PD++

Sbjct: 348 NIIIEYDRLIIEGGQPKGAE-IDSFGDHRIAMAFGILGSVVGETHISDAECVTKTYPDFW 406

Query: 437 DVLSTF 442

L +

Sbjct: 407 RNLESL 412

>ref|ZP_04575009.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
7_1]

gb|EEO41969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
7_1]

Length = 424

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 109/433 (25%), Positives = 203/433 (46%), Gaps = 46/433 (10%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76

G V P SKS+ +R ++ ++L+ G + ++N+ S+D+ + A++ LG +E

Sbjct: 16 GEVTPPPSKSLHRYIIASSLANGVSKIENISYSDDIIATIEAMKKGAKIEK---KDNV 72

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136

+++ F E + ++ +G +R L + G ++ +RP+

Sbjct: 73 LLIDGSKTFADYELNNDNEIECNESGSTLRFLFPLSIVKKNKILF--KGKGKLFKRPLSP 130

Query: 137 LVVGLKQLGADVDCFLGTDCCPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193

+ + + N I G L G ++ G+ISSQ+++ LL + PL

Sbjct: 131 YFENFDKYQINY-----SYINENEILLDGELKSGVYEIDGNISSQFITGLLFSPLPL 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253

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      D +I + KL S Y+++TL + +FGV ++S+ F IKG Q YKS N VE D
Sbjct: 183 NEDSKIIVKKGKLESSSYIDITLNLNKFVNI-INNSYKEFIKGNQYKSG-NYQVEAD 240

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
      S ++FL +I G + + G SLQGD K + + + W +
Sbjct: 241 YSQVAFILVANSI-GSNIKINGLNVNSLQGDKKIIDFISQID---NWNKK----- 286

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      K + ++ ++ PD+ L++ A + I ++A R+KE++R+ A ELTK
Sbjct: 287 -----KKLILDGSETPDIIPILSLKACISKKEIEIVNIARLRIKESDRLKATVQELTK 339

Query: 374 LGASVEEGPDYCIITPPEKLN-----VTAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
      LG + E D +I E N + ++ DHR+AM ++A+ C + + + +
Sbjct: 340 LGFDLIERKDSILINSRENFNKIINNSSVYLSSHLDHRIAMMIAIASTCYDGEIVLDNSD 399

Query: 427 CTRKTFPDYFDVL 439
      C +K++P++++V
Sbjct: 400 CVKKSYPNFWFVF 412

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>ref|ZP_03799108.1| hypothetical protein COPCOM_01365 [Coprococcus comes ATCC 27758]
gb|EEG90128.1| hypothetical protein COPCOM_01365 [Coprococcus comes ATCC 27758]
Length = 451

Score = 149 bits (376), Expect = 9e-34, Method: Compositional matrix adjust.
Identities = 133/458 (29%), Positives = 220/458 (48%), Gaps = 33/458 (7%)

```

Query: 1  MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      M G + +QP+K++ G V +PG KS+S+R ++ AL++GTT + + L+ D +G
Sbjct: 9  MRGYIIMQIQPVKQLRGEVSVPGDKSISHRSIMFGALAKGTTEITHFLHGADCLSTIGCF 68

Query: 61  RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
      R +G+++E R +V G G E + L +GN+G R ++ ++ G
Sbjct: 69  RAMGINIE--DTPDRILVHGKGLHGLSEPSS---FLDVGNSGTTTTLISGILS--GQPFA 121

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-- 178
      L G + RP+ ++ L +GAD+ G C P+ +N + LP G+ +I
Sbjct: 122 TTLSGDASLNSRPMKRIMEPLGMMGADILSQNGNGCAPLLINSL--LPAGQNPSLHAIHY 179

Query: 179 -----SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE---HSDS 230
      S+Q S++L+A A D + + ++S + E+ ++ FG + HSD
Sbjct: 180 HSKVASAQVKSSVLLAGLYA--DGLTLVTEPVLRSRNHTEL---MLNGFGANVQTEIHS DG 234

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAE 289
      I ++ K V GD SSA+YF+A A + G+ + ++ GT + + E
Sbjct: 235 SATASILPCEELYGQK-ILVPGDISAAYFIAAALLVPGSELLIKNVGTNPTRAGI--LE 291

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFRGRKH-LKAIDVNMNKMMP---DVAMTLAVVALFAD 345
      + MGA +T+ + P + R L V +P D +AV+A FA+
Sbjct: 292 ICRAMGADITYLNENCDSGEPTADLLVRTSALHGTTEGAIIPTLIDEIPMIAVMAAF AE 351

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHR 405
      G T IRD A +VKET+R+ L +G V D II ++ I++Y DHR
Sbjct: 352 GTTIIRDAAELKVKETDRIKTTTEGLLAMGVDPVTPDDGMIIRGGNPVHGGQINSYLDHR 411

Query: 406 MAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
      +AMAFS+AA AE I+D C ++P +F L +
Sbjct: 412 IAMAFSIAALAAEGNTEIQDGCVDVSYPSPFTELHSL 449

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>ref|ZP_05863876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus fermentum 28-3-CHN]
gb|EEX25604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus fermentum 28-3-CHN]
Length = 432

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 137/437 (31%), Positives = 217/437 (49%), Gaps = 37/437 (8%)

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Query: 13  KEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      + ++G + +PG KS+S+R L++ ALSEGTTV+D+ L ED L AL+ LG VE ++

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Sbjct: 11 RGLNGELAVPGDKSISHRALMIGALSEGTTVIDHFLAGEDCLSTLRALQDLG--VEIERK 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V+G G VE A L + N+G + R L + AG T L G + R

Sbjct: 69 GEHVEVIGRGIAGLVEPAAP---LQMNNSGTSTRLLMGIL--AGQPFTSQLVGDASLSRR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L +LGA + P V L G +VKL + S+Q SA+++AA

Sbjct: 124 PMKRVQGFLARLGAQIGLSEAGTLPATVVG--HPLQGARVKLEVA-SAQVKSAVILAALQ 180

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G + +P + T RL++ FG + + + G + + V G

Sbjct: 181 AQGSTTVS-----EPLPTRDHTERLLKAFGANLTVDRAANSITVTPGARLVG-QEVLVPG 234

Query: 253 DASSASYFL-AGAAITGGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++FL AGA I +TV+ C + G ++ VL+ MGA+++ ET+

Sbjct: 235 DPSSAAFFLVAGAVIANSHLTVKDVCLNPTRTGLIR---VLKMGARLSIKETASG---- 287

Query: 311 PREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
EP G L+A+ V +PD+ L +VAL ADG + I RVKET+

Sbjct: 288 -GEPLGDVTIQTSQLRAVTVTAKDVPDLIDELPLVALLAACADGVSKISGAGELRVKETD 346

Query: 363 RMVAIRTELTKLGASVEEGPD-YCIITPPE-KLNVTAIDTYDDHRMAMAFSLAAC-AEVP 419
R+ + +LG VEEGPD + I+ P ++ +++++ DHR+ M ++AA + P

Sbjct: 347 RIQTVAELFLQLGVDVEEGPDGWRIVGRPNWQVQKPNLNSHGDHRLGMLAAVAALRSTTP 406

Query: 420 VTIRDPGCTRKTFPDYF 436
+ + DP ++P +F

Sbjct: 407 LFLIDPDAVAVSYPSFF 423

>ref|ZP_05649018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
gallinarum EG2]
gb|EEV32351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
gallinarum EG2]
Length = 429

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 133/438 (30%), Positives = 209/438 (47%), Gaps = 36/438 (8%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ GT+ +P KS+S+R ++ AL+EGTT V N L ED L A + LG+ ++ D

Sbjct: 8 NHLRGTLTVPSPDKSISHRSIMFGALAEGTTTVRNFLRGEDCLSTLHAFQELGVPIQDDGE 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G GG ++ A + + GN+G +R + + AG T L G + +R

Sbjct: 68 TITITGQGGFG---LKAADRSIDV--GNSGTTIRLMMGIL--AGQPFTTTLGDDSLNQR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAP 191
P+ +++ L Q+GA ++ ++ PP+ + G L + S ++S Q SALL AA

Sbjct: 121 PMNRVMLPLNQMGARLNGSNESEFPPIITIQGTRDL--SPIDYSMPVASAQVKSALLFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G I ++K S + E +R +FG E + I G Q + + V

Sbjct: 179 QAQGSRI--VEKEPSRNHTEEMIR---QFG--GEITVKGKEIQITGPQSFVG-QEVIVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-----ETSV 305
GD SSA++FL AGA + +T+E G + + +VLE MGA+++ T S

Sbjct: 231 GDISAFAFLTAGAVLPNSEITLENVGINPTRTGI--LDVLEQMGAQISLTAIDQNNQSA 288

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETE 362
T+T LK I++ +P + L ++AL A G T IRD +VKET

Sbjct: 289 TIT-----IRSALKGIEIQGAIIPRLIDELPIIALLATQAVGQTVIRDAEELKVKETN 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVT 421
R+ A ELTKLGA + D II P L+ + + DHR+ M ++AA + V

Sbjct: 343 RIDATAEELTKLGADITPTEDGLIINGPTPLHGGNVSSRGDHRIGMMLQVAALLTQEDVE 402

Query: 422 IRDPGCTRKTFPDYFDVL 439
+ ++P +F+ L

Sbjct: 403 LEQAEAVAVSYPHFFEDL 420

>dbj|BAI85758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. natto BEST195]
Length = 439

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 130/453 (28%), Positives = 225/453 (49%), Gaps = 36/453 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ + ++ + G + +PG KS+S+R ++ AL+ GTT V N L D + R +G
Sbjct: 10 EKMKEKQVQALHGEIHIPGDKSISHRSVMFGALAAAGTTTVKNFLPGADCLSTIDCFRKM 69

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E ++ V+ G G ++ KE E L +GN+G +R + + AG +
Sbjct: 70 VHIE--QSGSDVVIHGKG----IDALKEPESLLDVGNSGTTIRLMLGIL--AGRPFYSAV 121

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + +RP+ + LK++GA +D G + P+ V+G L G +S S+Q
Sbjct: 122 AGDESIAGKRPMPKRVTEPLKMGAKIDGRAGGEFTPLSVSG-ASLKGIDY-VSPVASAQIK 179

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+L+A A G + K + T R++ FGK S+ I GGK
Sbjct: 180 SAVLLAGLQAEGTTTTEPHK-----SRDHTEMLSAFGVKL--SEDQTSVSIAGGQKL- 231

Query: 244 SPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKAFAEVLEMMGAKVTWTE 302
+ + +V GD SSA++FL AGA + + ++ G + + +VL+ MGAK+
Sbjct: 232 TAADIFVPGDISAFAFLAAGAMVPNSRIVLKNVGNPRTGTI--IDVLQNMGAKEIKP 289

Query: 303 TSVTVTGPPPEPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVA 354
++ + EP+G LKA+++ + +P + + ++AL A+G T I+D A
Sbjct: 290 SADSGA----EPYGDIIETSSSLKAVEIGGDIIPRLIDEIPIIALLATQAEGTTVIKDAA 345

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLA 413
+VKET R+ + +EL KLGA +E D + + L A+ ++ DHR+ M +A
Sbjct: 346 ELKVKETNRIDTVVSELRLKGAIEIPTADGMKVYKQTLKGGAAVSSHGDHRIGMMLGIA 405

Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
+C E P+ I ++P +F+ L+ K
Sbjct: 406 SCITEEPIEIEHTDAIHVSYPPTFFHEHLNKLSSK 438

>ref|YP_291244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. NATL2A]
sp|Q46LT7.1|ARO_A_PROMT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAZ57541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. NATL2A]
Length = 444

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 135/444 (30%), Positives = 216/444 (48%), Gaps = 26/444 (5%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQ E+ G VK+PG KS+S+R LL A+++G T+++ LL +ED LR++G+ +
Sbjct: 13 LQKGGEELCGKVKVPKDKSISHRALLFGAIAKGTLEGLLPAEDPLSTAECRLSMGVKIS 72

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
K + G G + +E Q L GN+G MR L + A + ++L G
Sbjct: 73 PIKKGDIIEIEGVG-----LNGLQEPQDILNCGNSGTTMR-LIMGLLAGQKDHFFILTGD 126

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R RP+ + LK +GA V G + P+ + IG G V + S+Q SA+
Sbjct: 127 KSLRNRPMPKRVQPLKMMGAKVFGRCGNLAPLSI--IGNKLRGAVIGTPVASAQIKSAI 184

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+AA A G + I+ S + E R+++ FG E R K +
Sbjct: 185 LLAALNAEGSTTV--IEPARSRDHSE---RMLKAFGANLEVGGEMGRHITVSPGKDLKGQ 239

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKAFAEVLEMMGAKVTWTETSV 305

```

      + V GD SSA+++L AG+ I G + VE G + + +VLE M A +
Sbjct: 240 SIIVPGDISAFAWLIAGSIIPGSELVVENVLNPTRTGI--LDVLEEMEANINVINKR- 296

Query: 306 TVTGPPR---EPFGRKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
      V G P   E F +++LK  ++  MP   D   L+V A F +G + I+ + RVK
Sbjct: 297 DVAGEPVGDIIEVIFYKENLKPFIKIDGIMPRLVDEIPILSVGACFCNGISQIKGASELRVK 356

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEV 418
      ET+R+ + +L ++GASV+E D I + L +D+ DDHR+AM+ ++A+ A
Sbjct: 357 ETDRLAVMARQLKRMGASVDEHQDGLTIYGGKSLEGCELDSEDDHRIAMSLAIASIMANS 416

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
      T+R      ++PD++ L
Sbjct: 417 NSTLRRSEAAAISYPDFWSDLKRL 440

```

```

>gb|EFS75355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
      acnes HL037PA2]
gb|EFT16678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
      acnes HL037PA3]
Length = 429

```

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 137/439 (31%), Positives = 222/439 (50%), Gaps = 31/439 (7%)

```

Query: 13 KEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      ++G V +PGSKS +NR L+LAAL +G +++D +L S D M L+ LG +++
Sbjct: 15 HRLAGRVVVPKSKSQTNRALVLAALGDGPSILDGVLTSRDSLLMSAGLQRLGADIQSVGP 74

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
      + VV      A+ + G AG MR L G+ +V D P R R
Sbjct: 75 SSVRVVPR-----ARPAGPIECGLAGTVMRFLPVVAALVPGSTQFVGD-EPASR-R 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      PIG ++ GL+QLG +VD +D P + L G +V + + SSQ++SALL+A
Sbjct: 125 PIGPVLNGLRQLGVEVD----SDQLPFSLRAPDRLGGPEVTIDSAASSQFISALLLAGAR 180

Query: 193 ALGDVEIEIIDLKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-- 249
      +++ + S P++ MT ++ GV SD + ++ G P +A+
Sbjct: 181 FPRGIDLHRDGVSPSAPHIAMTCAMLADRGVTVV-SDEPCHWVVRPG-----PIHAFDD 234

Query: 250 -VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLSQGDVKFAEVLEMMGAKVWTETSVTVT 308
      +E D ++A+ FLA A + GG+VTV S+Q +F + + MGA+++ T+ S+T+T
Sbjct: 235 AIEPDLTNAAVFLAAALVVGGSVTVPAWPAWPAWPAWPAWPAWPAWPAWPAWPAWPAW 294

Query: 309 GPPREPFGKHLKAIDVNMNMPDPVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      G + L+ IDV++++ ++ +AVVA A G + IR VA R ET+R+ A+
Sbjct: 295 AQ-----GWQELRPIDVDLHEASELTPVAVVASVAFGRSRIRGVVAHIRGHETDRLAALA 349

Query: 369 TELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
      EL LG +++ D IT +K + Y DHRMA A +L + + D
Sbjct: 350 HELANLGVIEIQTDDGLDITGQGADKPHGAKFRCYADHRMAHAGALLGLVIDGIELDDIA 409

Query: 427 CTRKTFPDYFDVLSTFVKN 445
      CT KT P + + + V+
Sbjct: 410 CTSKTMPPQFPQMWADLVQE 428

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>ref|ZP_06259151.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella parvula
      ATCC 17745]
gb|EFB86103.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella parvula
      ATCC 17745]
Length = 422

```

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 118/427 (27%), Positives = 198/427 (46%), Gaps = 31/427 (7%)

```

Query: 16 SGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
      +GT+ +K+ ++R L+ AAL+ + + S+D+ + +LR LG V +
Sbjct: 10 TGTIASIPAKAHARALICAALANSPSTILLSRTSKDIDATMDSLRGLGAHV---VYEN 65

```

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
VV G P + + +G +R L + +D R+ +RP+
Sbjct: 66 KVVTVIPGPVPVTKG-----NVVPHESGTTLRLLLPVAVSICNEV--AVDAKGRLPDRPLE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
++ +K G D PP + G L GG+ + G +SSQ+ S LL+AAP G
Sbjct: 119 PMLGQMKAHGVT---FSQDKPPFTMTG--RLQGGEFGMVGDVSSQFFSGLLLAAP-QCG 171

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKSPKNAYVE 251
I L S YV +T M FGV +H+ + D F + +K N +E
Sbjct: 172 GATITSTPLQSSDYVLTITTTMANFGVTVVDHTPASDTVQESFAVAANTTFKGQSNYQIE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S+ + ++ A +TG +T+ G S+Q D + +++ G V W +VTV G
Sbjct: 232 GDWSNTAIWMVAAGMTGKPITITGMNKNSVQADRRIMQIMIDTGCDVVDGMMNVTVMG-- 289

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ +K I ++ +MPD+ +A +A G ++ A R+KE++R+ A+ +
Sbjct: 290 -----RAVKPIHADLEQMPDMLPVMALACSIHGESSFVKGARLRKESDRLEAVANLV 343

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
LG +V E D I L D +DHR+ MA +L A +E PVT++D K
Sbjct: 344 RDLGGTVREDGDDLYIIGSGILKGGQGDVNDHRLVMAGTLMALISENPVTLKDSEAITK 403

Query: 431 TFPDYFD 437
++PD+F+
Sbjct: 404 SYPDFFE 410

>ref|ZP_00519130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Crocospaera watsonii
WH 8501]
gb|EAM47785.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Crocospaera watsonii
WH 8501]
Length = 449

Score = 149 bits (375), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 127/436 (29%), Positives = 214/436 (49%), Gaps = 25/436 (5%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R L+L A++EG T+++ LL ED R +G + K
Sbjct: 28 LQGTQLQIPGDKSISHRALMLGAIAEGETIIEGILLGEDPRSTADCFRAMGAKISPLNNEK 87

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V V G +++ E ++ GN+G MR L + A+ + + + G +R RP+
Sbjct: 88 --VTVQGIGLGLHQPSEVLEA--GNSGTTMR-LMLGLLASHPDLRFVCTGDASLRSRPM 142

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLA 193
++ L+ +GA + P+ + G P + I+S Q S +L+A +
Sbjct: 143 SRVIKPLQTMGAKIWGRNNNSLAPLAIQGQTLKP---IHYHSPIASAQVKSICILLAGLMT 199

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + + + +S + E R+++ FG + + + I G + K V GD
Sbjct: 200 EG--KTTVTPEPALS RDHSE---RMLQAFGATLDIDATNSVTITGHPELTGQK-VIVPGD 253

Query: 254 ASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A+I G + +E G + + E LEMMGA ++ E +TG P
Sbjct: 254 ISSAAFVLAASIVEGAELLIENVGINPRTGI--LEALEMMGANISL-ENERVITGEPV 310

Query: 313 EPFGRK--HLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
K LKA + +P D LAV ALFA G T I+D A RVKE++R+ I
Sbjct: 311 ADLRVKATQLKACTIQGEIIPRLIDEVPILAVAALFAQGTTI IKDAAELRVKESDR LAVI 370

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
++L K+GA++ E PD IT ++LN +D+ DHR+AM+ ++AA A+ I
Sbjct: 371 ASQLGKMGANITELPDGLEITGGKELNGAEVDSGCDHRIAMSLAIAALRAKGTIINGAE 430

Query: 427 CTRKTFPDYFDVLSTF 442
++P++ + L
Sbjct: 431 AAAISYPEFVESLQAI 446

>ref|ZP_02090016.1| hypothetical protein FAEPRAM212_00252 [Faecalibacterium prausnitzii
M21/2]
gb|EDP22943.1| hypothetical protein FAEPRAM212_00252 [Faecalibacterium prausnitzii
M21/2]
Length = 424

Score = 148 bits (374), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 131/429 (30%), Positives = 210/429 (48%), Gaps = 36/429 (8%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G + P SKS+++R +L AAL+ G + + +L S+D+ L A L +V A
Sbjct: 12 IGGVIAAPPSKSMRAVLCAALAVGRSHITHLEFSKDISATLSAAQLCAAV--GTGAD 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A V G G P+ V + +G +R L + G T+ G R+ ERP
Sbjct: 70 DATVQGLGHFLPLT-----VPVDCESGSLRFLIPIASLTGQPVTFT--GRGRLMERPQ 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAP 191
++ + L +G+ G L G +L+G++SSQ++S LL A P
Sbjct: 123 CVYETLYREQNLRFEQSL-----SGLTVEGALTGPDYRLAGNVSSQFISGLLFALP 173

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L GD +I + S Y++MT + FGV + D+ + GGQ+Y P + VE
Sbjct: 174 LLPGDSTLHLIPPVESRSYIDMTRAVQAAGVHRSWLDA-TTLLLPGGQQYH-PCDYNVE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD S A++ A+ GG VT+ G +LQGD ++L GA T T SVT
Sbjct: 232 GDYSQAAPPAVLGAVCGG-VTITGLAPDTLQGDAAILDILRRCGAVFTRTGDSVT----- 285

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
F + L +D+++ PD+ L V+ L +G T IR+ R+KE++R+ A+ EL
Sbjct: 286 ---FAKAPLHGVIDIDLADCPDLGPVLMVLGGLLCEGTTVIRNAQRLRLKESDRIAAMEAEL 342

Query: 372 TKLGASVE-EGPDYCIITPPEKLNVT--IDTYDDHRMAMA-FSLAACAEVPTVIRDPGC 427
G +E +G + E+L+ A + ++DHR+ M+ LAA A +P+T+ D
Sbjct: 343 RACGGVLESDGGTITVHGAERLHAPAAPLHGHNDRVVMASLAVLAAAAALPLTVDDAEA 402

Query: 428 TRKTFPDYF 436
+K++P +F
Sbjct: 403 IQKSWPGFF 411

>ref|YP_003312568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella parvula
DSM 2008]
gb|ACZ25288.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Veillonella parvula
DSM 2008]
Length = 422

Score = 148 bits (374), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 125/427 (29%), Positives = 208/427 (48%), Gaps = 35/427 (8%)

Query: 17 GTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLN--SEDVHYMLGALRTLGLSVEADKAAK 74
GT+ +K+ ++R L+ AAL+ + + LLN S+D+ + +LR LG V +
Sbjct: 11 GTIASIPAKAHARALICAALASSPSTI--LLNRTSKDIDATMDSLRLGLGAHVYEN--- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V V A ++ + +G +R L V A+ N V D R+ +RP+
Sbjct: 66 KVVTV-----TPSPAPQKGNVVPHESGTTLR-LLLPVAASICNEVAV-DAKGRLPDRPL 117

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ +K G D PP + G+ L GG+ + G +SSQ+ S LL+AAP
Sbjct: 118 EPMLGEMKAHGVV---FSQDKPPFTMTGL--LQGGQFSMVGDVSSQFFSGLLLAAPQCG 171

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAH---SDS-WDRFYIKGGQKYKSPKNAYV 250
G + I L S YV +T M FGV +H SD+ + F + +K + +
Sbjct: 172 GAI-ITSTTPLQSSDYVLTITTTMVDVGVTVDHIPASDTVQESFTVAANATFKGQNDYQI 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 310
EGD S+ + ++ AA+TG +T+ G S+Q D + +V+ G V W +VT+TG
Sbjct: 231 EGDWSNTAIWMVAAAMTGKPIITITGMNKNVQADRRIMQVMIDAGCDVVWNGMNVITG- 289

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ +K I ++ +MPD+ +A +A G ++ + A R+KE++R+ A+
Sbjct: 290 -----RAVKPIHADLEQMPDMLPVMAALACSIQKSSSFVNGARLRLKESDRLEAVANL 342

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTR 429
+ LG +V E D I L D +DHR+ MA +L A +E PV ++D
Sbjct: 343 VRDLGGTVREDGDDLYIIGSGILKGGQDCVNDHRLVMAGTLMALISENPVILQDSEAIT 402

Query: 430 KTFPDYF 436
K++PD+F
Sbjct: 403 KSYPDFF 409

>ref|ZP_00206361.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase
[Bifidobacterium longum DJ010A]
Length = 433

Score = 148 bits (374), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 136/431 (31%), Positives = 207/431 (48%), Gaps = 23/431 (5%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++ TV +PGSKSLNR L+LAAL + LL S D M+GAL LG+ + D A
Sbjct: 16 QPLNATVTVPGSKSLNRYLILAAALGSKPVTILIGLLRSRDTLMMGALEALGVRCDVDSA 75

Query: 73 --AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G+F V +F G AG MR + A G + DG +
Sbjct: 76 TDTTVTVTPVSGRF-----HGNVNVFCGLAGTVMRFVPGALFADGPVNF--DGDEQAY 128

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GL+QLGA VD P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMKPVLDGLEQLGATVDYHGEVGRPLPFTITPPATLPAAQVQVSISSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ G + + +K S+P++ MT+ + G E +S + ++ S K
Sbjct: 189 ISSKLPGLHLAHTGEKTPSLPHIRMTVADVTGAGGAVEADESARTWTVEPRAMQLSSK- 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE MGA+V++ T+
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQMGAEVSFPP----TI 303

Query: 308 TGPPR-EPFGRKHLKAIDV-NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A +LA + +FAD T + + R ET R+
Sbjct: 304 GGVRYCEVTGDGTVRGLGTFDLTAAGEIAPSLAAILVFADKSTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP-VTI 422
A+ E+ ++G + EE PD I P E L+ ++TY DHRMA F+ +P + +
Sbjct: 364 ALVNEIRRVGGAEEELPDGLRIEVPVPAETLHGAVMETYADHRMA-TFAAMLGLRIPDIEV 422

Query: 423 RDPGCTRKTFF 433
+ TRKT P
Sbjct: 423 INVATTRKTLP 433

>ref|ZP_08041384.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equinus
ATCC 9812]
gb|EFW88961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equinus
ATCC 9812]
Length = 434

Score = 148 bits (374), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 127/449 (28%), Positives = 230/449 (51%), Gaps = 37/449 (8%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+L + ++ GT+++PG KS+S+R ++ +L+EGTT + ++L EDV + R LG+ +
Sbjct: 10 LLTNVSQQLQGTLRVPGDKSISHSIMFGSLAEGTTTIRDILRGEDVLSTMQVFRDLGVDI 69

Query: 68 EADKAAKRAVVVCGGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D VG G K P + +L +GN+G ++R ++ + AG + T + G
Sbjct: 70 QDDGELVTITGVGFDGLKAP-----KNKLNMGNSGTSIRLISGVL--AGQDFTVEMFGD 121

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

```

      + +RP+ + + L+Q+G +V      D PP+ ++G L      +L + S+Q SAL
Sbjct: 122 DLSLSKRPMDRVTIPLRQMGVEVSGQTERDLPLTMHGSKALKPIHYQLPVA-SAQVKSAL 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      + AA A D E II+K + + E      ++ +FG K + + R IKGGQ++ + +
Sbjct: 181 IFAALQA--DGESVIEKEKTRNTE---DMIVQFGGKIDVNGKEIR--IKGGQEF-TGQ 232

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303
      + V GD SSA+++L AG + V ++ G + + +V++ MG K+T ++
Sbjct: 233 DVVVPGLDISSAFLVAGLIVPNAKVILKNVGINETRTGI--LDVIKAMGGKMTISDVDD 290

Query: 304 ---SVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWR 357
      S T+T E L+ ++ +P + L ++AL A +G TAIRD +
Sbjct: 291 IAKSATITVETSE-----LRGTEIGGEIIPRLIDELPIIALLATQANGTTAIRDAEELK 344

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--C 415
      VKET+R+ + L +GA++ D II L+ I+T+ DHR+ M ++AA
Sbjct: 345 VKETDRIQVADALNAMGANITPTDDGMIKGTPLHGAKINTFGDHRIGMMAAIAALLV 404

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
      ++ V + ++P +F+ L +
Sbjct: 405 SDGDVELERAEAINTSYPSFFNDLEVLRS 433

```

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>ref|ZP_01895125.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter algicola
      DG893]
gb|EDM46783.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter algicola
      DG893]
      Length = 751

```

Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 133/435 (30%), Positives = 212/435 (48%), Gaps = 28/435 (6%)

```

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      LQP ISG +++PG KS+S+R ++L AL++G T V L ED L A R +G+++E
Sbjct: 320 LQPGGRISGEIRVPGDKSISHRSIMLGALADGITEVKGFLGEGEDSLATLQAFRDMGVITIE 379

Query: 69 A-DKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
      D R VG G + P L+LGN+G AMR + + A ++ L G
Sbjct: 380 GPDAGFVRIHGVGINGLQAP-----RGPLYLGNSGTAMRLFSGLLAAQPFDE--LTGD 431

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
      + +RP+G + L+ +GA +D G PP+++ G L G ++ + S+Q S L
Sbjct: 432 ELSLSKRPMDRVDPLRAMGAVIDTAEGGR-PPLKIRGGHALTGIHYEMPVA-SAQVKSCL 489

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      L+A A G + P + T R++E FG H D+ GG+ +
Sbjct: 490 LLAGLYAEG-----VTSVTETAPTRDHTERMLEGFGYHV-HRDTATASVTGGGRLTATAI 543

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      + V D SS+++FL A+I + +T+ G + V +L MMGA + E V
Sbjct: 544 D--VPADISSAFFLVAASIAPDSDLTIRHVGMPNTR--VGVINILRMMGANIEVLEERV 599

Query: 306 TVTGGPPPREPFGRK-HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
      P + R LK ID+ +++P D L + A+ A+G T +R RVKE+
Sbjct: 600 IGGEFVADLVRVSAELKGIDIPEDQVPLAIDFPPVLFIAAVCAEGRTVLRGAEELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
      +R+ + LT LG PD II + + ++++ DHR+AMAFS+A+ AE +
Sbjct: 660 DRIQVMADGLTALGVETTVTPDGIIIDGGQTMAGTVNSHGDHRIAMAFSVASLRAEGDI 719

Query: 421 TIRDPGCTRKTFPDY 435
      + D +FP +
Sbjct: 720 EVTDCANVSTSFPGF 734

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>ref|ZP_03944986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
      fermentum ATCC 14931]
gb|EEI22013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
      fermentum ATCC 14931]
      Length = 432

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Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 137/437 (31%), Positives = 218/437 (49%), Gaps = 37/437 (8%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++G + +PG KS+S+R L++ ALSEGTTV+D+ L ED L AL+ LG VE ++
Sbjct: 11 RGLNGELAVPGDKSISHRALMIGALSEGTTVIDHFLAGEDCLSTLRALQDLG--VEIERK 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 132
+ V+G G VE A L + N+G + R L + AG + T L G + R
Sbjct: 69 GEHVEVIGRGIAGLVEPAAP---LQMNSGTSTRLLMGIL--AGQSFTSQLVGDASLSRR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L +LGA + P V L G +VKL + S+Q SA+++AA
Sbjct: 124 PMKRVQGPLARLGAQIGLSEAGTLPATVVG--HPLQGARVKLEVA-SAQVKSAVILAALQ 180

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G + +P + T RL++ FG + + + G + + V G
Sbjct: 181 AQGSTTVS-----EPLPTRDHTERLLKAFGANLTVDRANSITVTPGARLVG-QEVLVPG 234

Query: 253 DASSASYFL-AGAAITGGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++FL AGA I +TV+ C + G ++ VL+ MGA+++ ET+
Sbjct: 235 DPSSAAFFLVAGAVIANSHLTVKDVCLNPTRTGLIR---VLKKMGARLSIKETASG---- 287

Query: 311 PREPFG----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
EP G L+A+ V +PD+ L +VAL ADG + I RVKET+
Sbjct: 288 -GEPLGDVTIQTSQLRAVTVTAKDVPDLIDELPLVALLAACADGVSEISGAGELRVKETD 346

Query: 363 RMVAIRTELTKLGASVEEGPD-YCIITPPE-KLNVTAIDTYDDHRMAMAFSLAAC-AEVP 419
R+ + L +LG VEE PD + I+ P ++ + + + DHR+ M ++AA + P
Sbjct: 347 RIQTVAELLLQLGVDVEERPDGWRIVGRPNWQVQKPNLNSHGDHRLGMLAAVAALRSTTP 406

Query: 420 VTIRDPGCTRKTFPDYF 436
+ + DP ++P +F
Sbjct: 407 LFLIDPDAVAVSYPSFF 423

>ref|NP_390141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. subtilis str. 168]
ref|ZP_03592023.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. subtilis str. 168]
ref|ZP_03596303.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. subtilis str. NCIB 3610]
ref|ZP_03600714.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. subtilis str. JH642]
ref|ZP_03604990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. subtilis str. SMY]
sp|P20691.1|ARO_A_BACSU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAA20869.1| AroE [Bacillus subtilis]
emb|CAB14176.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) [Bacillus
subtilis subsp. subtilis str. 168]
Length = 428

Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 222/446 (49%), Gaps = 36/446 (8%)

Query: 12 IKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++ + G + +PG KS+S+R ++ AL+ GTT V N L D + R +G+ +E +
Sbjct: 6 VQTLHGEIHPGDKSISHRVSMFGALAAAGTTTVKNFLPGADCLSTIDCFRKMGVHIE--Q 63

Query: 72 AAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
++ V+ G G ++ KE E L +GN+G +R + + AG + G +
Sbjct: 64 SSSDVVIHGKG---IDALKEPESLLDVGNSGTTIRLMLGIL--AGRPFYSAVAGDESIA 117

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + LK++GA +D G + P+ V+G L G +S S+Q SA+L+A
Sbjct: 118 KRPMKRVTEPLKKMGAKIDGRAGGEFTPLSVSG-ASLKGIDY-VSPVASAQIKSAVLLAG 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + K + T R++ FGVK S+ I GGQK + + +V
Sbjct: 176 LQAEGTTTVTEPHK-----SRDHTERMLSAFGVKL--SEDQTSVSIAGGQKL-TAADIFV 227

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + + ++ G + + +VL+ MGAK+ ++ +
Sbjct: 228 PGDISSAAFFLAAGAMVPNSRIVLKNVGLNPTRTGI--IDVLQNMGAKLEIKPSADSGA- 284

Query: 310 PPREPG-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP+G LKA+++ + +P + + ++AL A+G T I+D A +VKET
Sbjct: 285 ---EPYGDIIETSSLKAIVEIGGDIIPRLIDEIPIIALLATQAEGTTVIKDAELKVKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLN-VTAIDTYDDHRMAMAFSLAAC-AEVP 419
R+ + +EL KLGA +E D + + L A+ ++ DHR+ M +A+C E P
Sbjct: 342 NRIDTVVSELRLKGAIEPTADGMKVYGKQTLKGGAAVSSHGDHRIGMMLGIASCITEEP 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 445
+ I ++P +F+ L+ K
Sbjct: 402 IEIHTDAIHVSYPFFEHNLKLSK 427

>ref|YP_909548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
adolescentis ATCC 15703]
dbj|BAF39466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
adolescentis ATCC 15703]
Length = 450

Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 137/448 (30%), Positives = 208/448 (46%), Gaps = 32/448 (7%)

Query: 13 KEISGTVKLPKSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++ TV +PGSKSLNR L+LAAL + LL S D M+ ALR LG+ E D
Sbjct: 19 KPLNATVVVPGSKSLNRYLILAAALGSEPVRVLVGLLRSDTELMMEALRALGVRCEVDVE 78

Query: 73 AKRAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V G F +++ G AG MR + A G + DG +
Sbjct: 79 TDTTVTVTPPADGHF-----HGNakiYcGLAGTVMRFVPLAMFADGPVDF--DGDEQAY 131

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
RP+ ++ GL+QLGA ++ + G T PP + + P V + S SSQ++
Sbjct: 132 ARPMKPVLDGLRQLGATIE-YHGEGRLPFTITPPAFDSAVRETP-NVVSIDSSGSSQFI 189

Query: 184 SALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+ G +E+ K S+P++ MT+ ++ GV A + + + G
Sbjct: 190 SGLLLIGSRVPGGLELHHTGKKTPSLPHIRMTVADLKSAGVDAIADEDVHVGVAPG-TV 248

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ P VE D S+A+ FL A I GGTV V T+ Q LE MGA+V++ E
Sbjct: 249 QLPGQVTVPEPDLNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLERMGAQVSFPE 308

Query: 303 TS----VTVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ VTG G D ++ ++A +LA + FAD PT + + R
Sbjct: 309 KNGIRYCEVTG-----GHAINGLDGFDLTAAGEIAPSLAAILAFADKPTNMIGIHLRG 362

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPEK--LNVTAIDTYDDHRMAMAFSLAACA 416
ET R+ A+ E+T++G E PD ITP L ++TY DHRMA ++
Sbjct: 363 HETNRLEALVNEITRIGGEARELPDGLKITPVSAGCLRPVAMETYADHRMATFAAMLGLR 422

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ + + T KT P++ ++ + +
Sbjct: 423 IKGIQVENIAATAKTLPNFVNMWMDMLS 450

>ref|YP_002446433.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
G9842]
ref|ZP_04065668.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis IBL 4222]
sp|B7ILG9.1|AROABACC2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACK93840.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus

G9842]
gb|EEN02666.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis IBL 4222]
Length = 429

Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 131/456 (28%), Positives = 219/456 (48%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ +++EG T + L+ D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLSGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VEITQNGDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGILA---NTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K +S
Sbjct: 112 SCVQGDSEIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYISP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLILQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTIEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
IRD +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IRDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRTKTFPDYFDVLSTFVK 444
++A C AE + I D ++P +FD L K
Sbjct: 394 LAIAGCLAEGKIIIEDAEAVGVSYPPTFFDELQKLAK 429

>ref|ZP_06384771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrospira platensis
str. Paraca]
dbj|BAI92503.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arthrospira platensis
NIES-39]
Length = 450

Score = 148 bits (373), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 131/442 (29%), Positives = 219/442 (49%), Gaps = 31/442 (7%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R L+L AL+EG T ++ LL D LG + ++ ++
Sbjct: 28 LQGSALTIPGDKSISHRALMLGALAEGVTTIEGLLLGADPRSTAECFSGLGAEI-SELNSQ 86

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ V GCG + + +E ++ GN+G MR L + A+ + + + G + +RP
Sbjct: 87 QIKVKGCG---IGNLQEPDRVLDAGNSGT'TMR-LMLGILASHPDRLFTITGDSSSLVKRP 141

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
+ ++ L Q+G + P+ V G P + I+S Q S +L+A +
Sbjct: 142 MDRVIRPLTQMGAATIWGRRSGSLAPLAVRGQQLQP---IHYHSPIASAQVKSCILLAGLM 198

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G + + +S + E R+++ FG + + + + G K + + V G
Sbjct: 199 VEGATTV--TEPALSRDHTE---RMLKAFGAQLTVNPDNTNSVTVFGPAKLQG-QTVIVPG 252

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L A+I G+ +T+E G + + E + MMGA + ++ V G P
Sbjct: 253 DISSAAFVLVAASIVPGSDITIENLVGNPRTGTI--LEAMAMMGADIE-SQGERLVAGEP 309

Query: 312 ----REFPGRKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364

R F R LKA ++ + +P D LAV A FA+G T IRD A RVKE++R+
Sbjct: 310 VADLRVRF--LKACEIKGDLIPRLIDEIPILAVAAFAEGTTTIRDAELRVKESDRI 367
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
+ TELTK+GA + E PD IT L +D+ DHRMAM+ ++AA A+ TI
Sbjct: 368 TVMATELTKMGAKISELPDGLITGGFPLRGAEVDSDDTDRMAMSLAIAALNAKGSTTIH 427
Query: 424 DPGCTRKTFPDYFDVLSTFVKN 445
++PD+ + L + N
Sbjct: 428 RAEAAAIISYPDFVESLQQLIIN 449

>ref|ZP_01728795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp.
CCY0110]
gb|EAZ91810.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp.
CCY0110]
Length = 450

Score = 147 bits (372), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 134/437 (30%), Positives = 210/437 (48%), Gaps = 31/437 (7%)

Query: 15 ISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R L+L A++EG T+++ LL ED R +G + + K
Sbjct: 28 LQGTQLQIPGDKSISHRALMLGAIAEGETIIEGLLLGEDPRSTAECFRAMGAKISPLNSDK 87
Query: 75 RAVVVGCG-GKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V G G GK EE Q L GN+G MR L + A+ + + + G +R
Sbjct: 88 -VTVQIGLGLK-----EEPQDVLNAGNSGTMR-LMLGLLASHPDLFCVTGDASLRS 139
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAA 190
RP+ ++ L+++ A + P+ V G P + I+S Q S +L+A
Sbjct: 140 RPMSRVIKPLQEMSAQIWGRKNNTLAPLSVKGQTLKP---IHYHSPIASAQVKSCILLAG 196
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+ G + + + +S + E RL++ FG E I G K K V
Sbjct: 197 LMTEG--KTTVFEPALSRDHSE---RLQAFGATLEIDSKTHSVTIIGHPKLTGQK-VIV 250
Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++L A+I G+ + +E G + + E LEMM A +T E VTG
Sbjct: 251 PGDISSAAFVLAASIVPGSELLIENVGINPRTGI--LEALEMDADITL-ENKRIVTG 307
Query: 310 PPREFPGRK--HLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P K LK + + +P D LAV A+FA G T I+D A RVKE++R+
Sbjct: 308 EPVADLRVKSCQLKGCTIAGDILPRLIDEVPILAVAAIFATGKTVIKDAELRVKESDRL 367
Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
+ +ELTK+GA++ E D I LN +D+Y DHR+AM+ ++AA A+ I
Sbjct: 368 AVMASELTKMGANITELSDGLEIIGGTPLNAADVDSYTDHRIAMSLAIAALNAKGKTIIN 427
Query: 424 DPGCTRKTFPDYFDVLS 440
++P++ L
Sbjct: 428 RAEAAAIISYPEFVGTLQ 444

>gb|EGC23518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK353]
Length = 427

Score = 147 bits (372), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 123/443 (27%), Positives = 223/443 (50%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + G +++PG KS+S+R ++ +L++G T+V ++L EDV + R LG+ +E D
Sbjct: 7 VKGLKGRIRVPGDKSISHRSIIFGSLAKGVTIVRDILRGEDVLSTMQVFRDLGVQIEDDG 66
Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ VG G ++ +L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 NLVKIHGVGFEGQLAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAMFGDDSLSK 119
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ + D PP+++ G L +LS + S+Q SAL+ AA

Sbjct: 120 RPMDRVTIPLRQMGVEISGWTERRDLPLPLKMGSRQLPIHYQLSVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K I+ + E ++ +FG + E R I+GGQ++ + + V

Sbjct: 179 QAQG--ESVIEKEITRNHTE---DMAQFGGQIEVEGKEIR--IQGGQEF-TAQEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + +V+E MG ++T ++ S

Sbjct: 231 GDISSAAFVLVAGLIVPDSKIVLENGINETRTGI--LDVIEAMGGRMTLSVDVDPVAKSA 288

Query: 306 TVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+

Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIIALLATQAQGRTVIRDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA++ D II LN ++T+ DHR+ M ++AA V

Sbjct: 343 RIQVVADALNSMGAAITPTEDGMIIEGKTPNLGAQVNTFGDHRIGMMTAIAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ + ++P +F L +

Sbjct: 403 ELERSEAIKTSYPRFFSDLEDLM 425

>ref|ZP_06875459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. spizizenii ATCC 6633]
ref|YP_003866566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. spizizenii str. W23]
gb|EFG90745.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
subsp. spizizenii ATCC 6633]
gb|ADM38257.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvoylshikimate-3-phosphate synthase) [Bacillus
subtilis subsp. spizizenii str. W23]
Length = 428

Score = 147 bits (372), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 127/445 (28%), Positives = 221/445 (49%), Gaps = 36/445 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEA 69
+ ++ ++G + +PG KS+S+R ++ AL++GTT V N L D + R +G+ +E

Sbjct: 4 EKVQALNGEIHIPGDKSISHRSVMFGALAKGTTTVKNFLPGADCLSTIDCFRKMVGQIEQ 63

Query: 70 DKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V+ G G ++ E E L +GN+G +R + + AG + G

Sbjct: 64 N--GSNVVIHGNG----IDSLSEPESSLDVGNSGTTIRLMLGIL--AGRPFYSAVAGDES 115

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + LK++GA +D G + P+ V+G L G +S S+Q SA+L+

Sbjct: 116 IAKRPMKRVTEPLKEMGAKIDGRAGGEFTPLSVSG-ASLKGIDY-VSPVASAQIKSAVLL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G + K + T R++ FGVK S+ I GGQK + +

Sbjct: 174 AGLQAEGTTTTEPHK-----SRDHTERMLSAFGVKL--SEDQTSVSITGGQKL-TAADI 225

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+V GD SSA++F+L AGA + + ++ G + + +VL+ MGAK+ ++ +

Sbjct: 226 FVPGDISSAAFFLIAGAMVPNSKIVLKNVGLNPTRTGI--IDVLQNMGAKLEIKPSADSS 283

Query: 308 TGPPPEPFG----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
EP+G LKA+++ + +P + + ++AL A+G T I+D A +VK

Sbjct: 284 A----EPYGDLVIEETSSLKAVEIGGDIIPRLIDEIPIIALLATQAEGTTVIKDAELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ATIDYDDHRMAMAFSLAAC-AE 417
ET R+ + +EL KLGA +E D + + L A + ++ DHR+ M +A+C E

Sbjct: 340 ETNRIDTVVSELRLKLGAEIEPTADGMKVYKQTLRGGATVSSHGDHRIGMMLGIASCITE 399

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
P+ I ++P +F+ L+

Sbjct: 400 EPIEIEQTDIAHVSYPTFFFEHLNKL 424

>ref|ZP_03624240.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis

89/1591]
gb|EEF65574.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis
89/1591]
Length = 426

Score = 147 bits (372), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 124/446 (27%), Positives = 226/446 (50%), Gaps = 37/446 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ +++++ GT+++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E
Sbjct: 5 RSVEKLKGTIRVPGDKSISHRSIIFGSLAKGVTRVHDILRGEDVLSTMQVFRDLGVKIED 64

Query: 70 DKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G + P D L +GN+G ++R ++ + AG + + G
Sbjct: 65 NGDIVEVHGVGFDGLQAPKND-----LDMGNSGTSIRLISGVL--AGQDFEATMFGDDS 116

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + + L Q+G ++ D PP+ + G L + +L + S+Q SAL+
Sbjct: 117 LSKRPMDRVITPLSQMGVEISGQTERDLPPLTIKGNKLNKPIRYQLPVA-SAQVKSALIF 175

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G E I++K ++ + E ++ +FG + E + R I+GGQ++ + +
Sbjct: 176 AALQAEG--ESVIVEKELTRNHE---DMIVQFGGQLEVNGKEIR--IQGGQEFIA-QEI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V GD SSA+++L AG + G + +E G + + +V++ MG K+T +
Sbjct: 228 TVPGDISAFAFWLAVGLIVPGSKIVLENVGINETRTGI--LDVIKAMGGKMTLSNIDELA 285

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
S T T E LKA ++ +P + L ++ L A G T IRD +VK
Sbjct: 286 KSATFTVETSE-----LKATEITGELIPRLIDELPIITLLATQAHGTTIIRDAEELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAE 417
ET+R+ + L +GA++E D II P L+ I+T+ DHR+ M +AA +
Sbjct: 340 ETDRIQVVADALNSMGATIEPTEDGMIHGPALHGAEINTFGDHRIGMMAIAALLAKD 399

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +F+ L++ +
Sbjct: 400 GEVVLERAEAINTSYPAFFEHLNSLM 425

>ref|ZP_06871415.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 23726]
gb|EFG94832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 23726]
Length = 423

Score = 147 bits (372), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 103/429 (24%), Positives = 210/429 (48%), Gaps = 39/429 (9%)

Query: 17 GTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAakra 76
G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A++ LG ++E
Sbjct: 16 GEVTPPPSKSVLHRYIIASSLAKGISKIENISYSDDIIATIEAMKKLGANIEK---KDNy 72

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F E + ++ +G +R L + G ++ +RP+
Sbjct: 73 LLIDGSKTFDKEYLNNDSEIDCNESGSTRFLFLPLSIVKENKILF--KGKGKLFKRPLSP 130

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ + + ++G+ L G+ ++ G+ISSQ+++ LL + PL G+
Sbjct: 131 YFENFDKYQIK---YSYINENEILLDGV--LKNGEYEDGNISSQFITGLLFSPLPLNGN 185

Query: 197 VEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+I I KL S Y+++TL + +FG+ ++S+ F I+G Q YKS N VE D S
Sbjct: 186 SKIVIKGKLESSYIDITLDCLNKFGINI-INNSYKEFIEGNQTYKSG-NYQVEADYSQ 243

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
++FL +I G + + G SLQGD K +++ + WT+ +
Sbjct: 244 VAFFLVANSI-GSNIKINGLVNSLQGDKK---IIDFISEIDNWTNKELI----- 290

Query: 317 RKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376

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          ++ ++ PD+   L++ A   +       I ++A R+KE++R+ A   EL+KL
Sbjct: 291 -----LDGSETPDIIPILSLKACISKKEIEIVNIARLRIKESDRLSATVQELSKLDF 342

Query: 377 SVEEGPDYCIITPPEKL-----NVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
          + E D +I   +           + ++ ++ DHR+AM ++A+ C E + + + C +K
Sbjct: 343 DLIEKEDSILINSRKNFIYNSKEIVSLSSHSDHRIAMTVAIASTCYEGEIIILDNLDCVKK 402

Query: 431 TFPDYFDVL 439
          ++P++++V
Sbjct: 403 SYPNFWEVF 411

```

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>ref|ZP_01773103.1| Hypothetical protein COLAER_02133 [Collinsella aerofaciens ATCC
25986]
gb|EBA38682.1| Hypothetical protein COLAER_02133 [Collinsella aerofaciens ATCC
25986]
Length = 439

```

Score = 147 bits (372), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 134/452 (29%), Positives = 213/452 (47%), Gaps = 50/452 (11%)

```

Query: 6   EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
          I P+K GTV SKS+++R+++ AAL+ G T V D+ + L LG
Sbjct: 4   RITPSPK---GTVPAIASKSMAHRLIICAALANGETHVTCNTTCADIEATVHCLTALGA 60

Query: 66  SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
          +E + + +F+ A L G +G +R + A G AT+V G
Sbjct: 61  RIETVEDGFQVHPTMKSIIEFGLLKALAGGTLDCGESGSTLRFMLPVACALGAEATFV--G 118

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLP---GGKVK-----LSGS 177
          R+ RP+ L + G D+ G+GG P G+++ L G+
Sbjct: 119 RGRLGARPLSPLSDEIIAAGCDL-----QGLGGFPLKTSGRMRPGTFILPGN 165

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
          +SSQY+S LL+AAPL +++ + S PY+ +T++ M+ FGV+ + +R K
Sbjct: 166 VSSQYISGLLLAAPLLAQPSVCVQVTGLIESRPYINLTIQAMKAFGVEV---NVERIPAK 221

Query: 238 GGQ-----KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
          GQ Y++P + VEGD S+A+++L AI +TVEG +S QGD
Sbjct: 222 DQQPEVTNFRVNSGSRTPGSAVEGDWSNAAFWLCAGAIGSDPITVEGVSLSSAQGDRN 281

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVALFADG 346
          L GA++ + + TV L +++ + +PD+ ++ VA A G
Sbjct: 282 VLAALSRFGARIVRSTNAATVQS-----DKLAGFEMSAHDIPDLVPVISAVASLAQG 333

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRM 406
          T IRD A R+KE++R+ ELT LGA V D II + +D+++DHR+
Sbjct: 334 RTFIRD CARLRIKESDRLATTTRELTALGAQVRIAGDDLIIKGVDAFTGGEVD SHNDHRI 393

Query: 407 AMAFSLAACAEV-PVTIRDPGCTRKTFPDYFD 437
          AM ++AA V I K++PD+FD
Sbjct: 394 AMMAAIAASRATGDIVIHGAEAVNKSYPDFD 425

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>ref|ZP_06595904.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium breve
DSM 20213]
gb|EFE89309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium breve
DSM 20213]
Length = 444

```

Score = 147 bits (371), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 135/432 (31%), Positives = 205/432 (47%), Gaps = 21/432 (4%)

```

Query: 13  KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
          + ++ TV +PGSKSLSNR L+LAAL + LL S D M+GAL LG+ + D
Sbjct: 16  RPLNATVTVPGSKSLSNRYLILAALGNEPVTLVGLLRSRDTLMMGALEALGVRCDVDTT 75

Query: 73  AKRAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
          V V G+F V +F G AG MR + A G + DG +
Sbjct: 76  TDTTVTVTPSSGRF-----NGNVDFVFCGLAGTVMRFVPLGLALFADGPVHF--DGDEQAY 128

```

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS--GSISSQYLSALLM 188
RP+ ++ GLKQLGA ++ P + LP + ++S S SSQ++S LL+
Sbjct: 129 ARPMRPVLDGLKQLGAKIEYHGEVGRLPFTITPPTLPAAQARVSISSGSSQFISGLLL 188

Query: 189 AAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKN 247
G + + +K S+P++ MT+ + G E +D R + + +
Sbjct: 189 IGSKLPGGLRLTHTGEKTPSLPHIRMTVVDTGAGGAIE-ADESARTWTVEPRAIQLLDK 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ FL A I GGTV V T+ Q LE MGAKV++ T+
Sbjct: 248 VTVEPDLSNAAPFLGAALIAGGTVRVPHWPETTTQPGGLLPGYLEQMGAQVSFP----TI 303

Query: 308 TGPPR-EPFGRKHLKAI-DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
G E G ++ + ++ ++A+LA + +FAD PT + + R ET R+
Sbjct: 304 DGVRYCEVTGDTVGRGLGSFDLTAAGEIAPSLAAILVFADKPTDMVGIGHLRGHETNRLE 363

Query: 366 AIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
A+ E+ ++G EE PD I P E L+ ++TY DHRMA ++ + +
Sbjct: 364 ALVNEIRRIGGVAEELPDGLRIEVPVSETLHEANMETYADHRMATFATMLGLRIPDIQVI 423

Query: 424 DPGCTRKTFPDY 435
+ TRKT PD+
Sbjct: 424 NVATTRKTLPDF 435

>ref|YP_475693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
JA-3-3Ab]
sp|Q2JSF1.1|AROASYNJA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABD00430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
JA-3-3Ab]
Length = 444

Score = 147 bits (371), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 133/453 (29%), Positives = 218/453 (48%), Gaps = 33/453 (7%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ + L P + + G V +PG KS+S+R L+L +L+EG TV+ L ED R L
Sbjct: 8 ADILTLPARGLRGQVSIPGDKSISHRALMLGSLAEGETVIHGLSLGEDPRSTAACFRAL 67

Query: 64 GLSV-EADKAAKRAVVVGCGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATY 121
G + E + R VG ++ +E ++ GN+G +R L + A +
Sbjct: 68 GADIPELNSECVRIGVG-----LDRLQEPAEVLDAGNSGTTLR-LMLGILAGQAGRFF 120

Query: 122 VLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ G +R RP+G +V L+Q+GA++ G + P+ V G G L G + ++S
Sbjct: 121 AVTGDRLSRSRPMGRVVEPLRQMGANIWGRAGGNLAPLAVQG-GSLKG--IHYHSPVASA 177

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+ + L+ A L ++ + +S + E R++ FG + + + GG +
Sbjct: 178 QVKSCLLAGLLAEGT-TQVTEPALSRDHSE---RMLRAFGAEISVDVAAKTVAVVGGS 233

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ V GD SSA+++L A+I + + ++ G + V +VL+ MGA +
Sbjct: 234 LVG-QTVQVPGDISSAAFVLAASIVPESELLQDVGLNPTRTG--LQVLQEMGADIQ- 289

Query: 301 TETSVTVTGPPREPFG-----RKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRD 352
E V G EP G L+ + + +P D LAV A FA+G T IRD
Sbjct: 290 VEKRREVAG---EPLGDLRVR SARLRGCSIAGDLIPTLIDEIPVLAVAAFAEGTTVIRD 346

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSL 412
A RVKE++R+ AI EL+++GA V E PD I L +D++ DHR+AM+ +
Sbjct: 347 AAELRVKESDRLAIAQELSRMGAQVTEYPDGLEIKGGIPLQGAEVDSHADHRIAMSLMV 406

Query: 413 AA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
AA A+ T+R C R ++PD+ L +
Sbjct: 407 AALAAQGSTTLRGADCARISYPDFIPTLQRLIN 439

>ref|YP_001117356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia

vietsnamiensis G4]
gb|ABO57891.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
vietsnamiensis G4]
Length = 460

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 124/442 (28%), Positives = 220/442 (49%), Gaps = 34/442 (7%)

Query: 9 LQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++PI + G P SK + R +L A L++GT++V N L + M A R LG +
Sbjct: 10 VEPIHSLKGYAVTPSSKPEQTQRAILAAATLADGTSIVHNDLRVETSAMKQACRALGARI- 68

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D+ A + G G + + V +G +G+ R+ TA + A ++ ++ G
Sbjct: 69 -DEHAGYLEIRGVGRALHL---GQRVDAIG-SGLVFRFTALTSTFA--DSPAIITGDTI 121

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R R + L L++LGA ++C PV VN GGL GG+ + G++SSQ+++A+L
Sbjct: 122 LRTRVMKPLFDALDELGARIIEGIEGAKAPV-VNWGGGLRGRCTVPGNVSSQFITALIF 180

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AAPLA VEI I +L+SI Y+ T+ + G++ + +D + ++ G Y++ +
Sbjct: 181 AAPLADKPVEIAIEGELLSISYIRQTIATLRHSGIQVDVTDDFSILRVQPG-NYQAAEYR 239

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTW--TETSVT 306
+ GD +S+SY + AA+ GT + G+ SLQG+ +V++ +G V + T +T
Sbjct: 240 -IGGDYTSSSYLIGAAALFPGTFVLNGLGSESLQGERAIIDVQALGLSVHFDTRNELT 298

Query: 307 VTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ + G A D P++ TLA + + G + + R+ ++ R+ A
Sbjct: 299 LVNSHSQLTGDYEFDASD-----FPNIVPTLAAIGAYVKGTFRVVGGSITRLHKSPIKA 353

Query: 367 IRTELTKLGASVE-----EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
+ +EL K+G ++ +G + P V + ++ DHR+ M+ +A+ A
Sbjct: 354 MVSELGKMGVDIKGLFKDGVYDGFIEIRGTGEYPGGVD-LSSWGDHRIFMSLFIASLRAR 412

Query: 418 VPVTI---RDPGCTRKTFFPDYF 436
P + RD C +FPD+F
Sbjct: 413 QPNRLEGYRDVNC---SFPDFF 431

>gb|AAR92125.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis]
Length = 426

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 123/444 (27%), Positives = 227/444 (51%), Gaps = 33/444 (7%)

Query: 10 QPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ ++++ GT+++PG KS+S+R ++ +L++G T N+L EDV + R LG+ +E
Sbjct: 5 RSVEKLGKGTIRVPGDKSISHRSIIFGSLAKGVTRFHNILRGEDVLSTMQVFRDLGVKIED 64

Query: 70 DKAARKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ VG G + P D L +GN+G ++R ++ + AG + + G
Sbjct: 65 NGDIVEVHGVGFDGLQAPKND-----LDMGNSGTSIRLISGVL--AGQDFEATMFGDDS 116

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + + L Q+G ++ D PP+ + G L + +L + S+Q SAL+
Sbjct: 117 LSKRPMDRVTIPLSQMGVEISGQTERDLPPLTIKGNKLPKIRYQLPVA-SAQVKSALIF 175

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G E I++K ++ + E ++ +FG + E + R I+GGQ++ + +
Sbjct: 176 AALQAEG--ESVIVEKELTRNHT---DMIVQFGGLEVNKGKIR--IQGGQEFIA-QEI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V GD SSA+++L AG I G + +E G + + +V++ MG K+T +
Sbjct: 228 TVPGDISAFAFWLAVGLIIPGSKIVLENVGINETRTGI--LDVIKAMGGKMTLSNIDELA 285

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVN-MNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
S T+T E + ID + ++++P + ++A A G T IRD +VKET
Sbjct: 286 KSATITVETSELKATGDCRRIDSSVIDELP----IITLLATQAHGTTIIRDAEELKVKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ + L +GA++E D II P L+ I+T+ DHR+ M ++AA +
Sbjct: 342 DRIQVVADALNSMGATIEPTEDGMIIHGPTALHGAEINTFGDHRIGMMTAIAALLAKDGE 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +F+ L++ +
Sbjct: 402 VVLERAEAINTSYPAFFEHLNSLM 425

>ref|ZP_06808626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aerococcus viridans
ATCC 11563]
gb|EFG48990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aerococcus viridans
ATCC 11563]
Length = 434

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 126/437 (28%), Positives = 217/437 (49%), Gaps = 27/437 (6%)

Query: 15 ISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+ +PG KS+S+R ++ A++++GTT ++ L++ED + R G V+ D+ A
Sbjct: 18 LEGTITIPGDKSISHRAIMFASIAKGTTKIEGFLHAEDCISTMNIFRDFG--VQIDEAD 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V+V G + L GN+G MR L + G + G + +RP+
Sbjct: 76 GSVIVHKGKIEGLTAPNH--ALDAGNSGTTMRLLAGLFS--GFPFKIKMTGDESLSKRPM 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+Q+GA + G++ P+ + + L + + + S+Q SA+L+A A
Sbjct: 132 NRVMPLRQMGASISGSEGSEFAPLYIQPVDHLNAIEYDMPVA-SAQVKSAILLAGLSAK 190

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G I +K S + E +++ FG+V + D Y++GGQ + + V D
Sbjct: 191 GTTIIH--EKERSRDHTE---NMLKNFGVELKVDDK--DIYLEGGQSL-TATDITVPADI 242

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+ A + G+ + + G + + + EVL MGA + ETS+ G +
Sbjct: 243 SSAAFFIVAALLVKGSKLHMPNVGLNPTRAGI--IEVLHNMGANI---ETSLHEGGLSGD 297

Query: 314 -PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
LKA + + +P + + ++AL A +G T IR+ +VKET+R+
Sbjct: 298 LTVSASDLKATEFGGDIIPALIDEIPIIALAATQAEGRTVIRNAEELKVKETDRIQVTAK 357

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA++EE D IIT P L+ +D+Y DHR+ M +AA E V + P
Sbjct: 358 ELNKMGANIEETKDGMIITGPTPLHAADVDSYGDHRIGMMLQVAALLVKEGTVNLARPEA 417

Query: 428 TRKTFPDYFDVLSTFVK 444
+FP +FD L+ K
Sbjct: 418 VNISFSPFFDDLAALSK 434

>gb|EFS91309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Propionibacterium
acnes HL044PA1]
Length = 429

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 221/439 (50%), Gaps = 31/439 (7%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++G V +PGSKS +NR L+LAAL +G +++D +L S D M L+ LG +++
Sbjct: 15 HRLAGRVVVPKSGSKQTNRALVLAALGDGPSILDGVLTSRDSLLMSAGLQRLGADIQSVGP 74

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ VV A+ + G AG MR L G+ +V D P R R
Sbjct: 75 SSVRVVPR-----ARPAGPIECGLAGTVMRFLPVVAALVPGSTQFVGD-EPASR-R 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG ++ GL+QLG +VD +D P + L G +V + + SSQ++SALL+A
Sbjct: 125 PIGPVLNGLRQLGVEVD----SDQLPFSLRAPDRLGGEVETIDSAASSQFISALLLAGAR 180

Query: 193 ALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-- 249

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      +++      + S P++ MT  ++  GV   SD   + ++ G   P +A+
Sbjct: 181 FPRGIDLRHDGASVPSAPHIAMTCAMLADRGVTVV-SDEPCHWVVRPG-----PIHAFDD 234

Query: 250 -VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
      +E D ++A+ FLA A + GG+VTV      S+Q   +F  + + MGA+++ T+ S+T+T
Sbjct: 235 AIEPDLTNAAVFLAAALVVGGSVTVPAWPADSIQPGAQFVGIADKMGARISRTDDSMIT 294

Query: 309 GPPREPFGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      G + L+ IDV++++ ++  +AVVA A G + IR VA R ET+R+ A+
Sbjct: 295 AQ-----GWQELRPIDVDLHEASELTPVAVVASVAFGRSRIRGVHIRGHETDRLAALA 349

Query: 369 TELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
      EL LG +++ D IT   +K +      Y DHRMA A +L      + + D
Sbjct: 350 HELANLGEVIQQTDDGLDITGQGADKPHGAKFRICYADHRMAHAGALLGLVIDGIELDDIA 409

Query: 427 CTRKTFPDYFDVLSTFVKN 445
      C KT P + + + V+
Sbjct: 410 CASKTMPQFPQMWADLVQE 428

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>ref|ZP_05224153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium intracellulare ATCC 13950]
Length = 419

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 139/428 (32%), Positives = 207/428 (48%), Gaps = 32/428 (7%)

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Query: 15  ISGTVKLPGSKSLSNRILLALLSEG----TTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      + TV +PGSKS +NR L+LAAL+      T +   L S D   M+GALRTLGL V+ D
Sbjct: 1   MHATVTVPGSKSQTNRTLVLALAAAGQGQGTPTISGALRSRDTLDMIGALRTLGLRVDGD 60

Query: 71  KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      +   G P   +   Q+ G AG  +R +      AA   +   DG  + R
Sbjct: 61  GTE----LTVSGRVVP----EPMAQVDCGLAGTVLRFVPP--LAALAESIVEFDGDEQAR 110

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM-A 189
      RPI L+ L+ LG +D   G+   P RV G G +PGG V++ S SSQ++S LL+ A
Sbjct: 111 ARPIAPLLDALRGLGVRID---GSGL-PFRVLGTGAVPGGTVEIDASASSQFVSGLLLCA 166

Query: 190 APLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
      A A G      L S P++ MT+ ++ + GV  + S   +R+ ++ G   + ++
Sbjct: 167 ASFAEGLTVRHTGSALPSAPHIAMVTMLRQAGVDVDDSVN-NRWRVRPGP--VAARHWV 223

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTG 309
      VE D ++A FLA A +TGG V + G   S+Q      VL  + A VT  ++ +
Sbjct: 224 VEPDLTNAVFPFLAAAVVTGGAVRITGWPANSVQPAEHILAVLGKLNNAVVTQHDSHL---- 279

Query: 310 PPREPFGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIR--DVASWRVKETERMVAI 367
      E G      DV++ + ++ ++A +A A   + R   +A R ET+R+ A+
Sbjct: 280 ---EARGSGDYGDFVDLRAVGELTPSVAALAAALAPGSVSRLSGIAHLRGHETDRLAAL 336

Query: 368 RTELTCLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
      E+ +LG   E PD +IT   L      Y DHRMAMA ++      V + D G
Sbjct: 337 SAEINRLGGDCTETPDGLVIT-ATPLRPGVWRAYADHRMAMAGAIVGLRVAGVEVDDIGA 395

Query: 428 TRKTFPDY 435
      T KT PD+
Sbjct: 396 TTKTLPDF 403

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>ref|ZP_07824432.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pseudoporcinus SPIN 20026]
gb|EFR44022.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pseudoporcinus SPIN 20026]
Length = 427

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 127/434 (29%), Positives = 219/434 (50%), Gaps = 33/434 (7%)

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Query: 13  KEISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K + G + +PG KS+S+R ++  A++EGTT ++ LL S DV+   + + R +G+ +E  +

```

Sbjct: 8 KPLRGCLTMPGDKSISHRAIIFGAIAEGTTEIEGLLKSHDVNATISSFRKMGVLE--ET 65

Query: 73 AKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
++ +V G G K P E L +GN+G ++R L + AG + T L G +

Sbjct: 66 DQKVIVHGQGFSGGLKRPQEP-----LDMGNSGTSIRLLCGLI--AGQDWTVTLLKGDASL 117

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + + L+ +GA++ PP+ + G L L + S+Q SA+L+A

Sbjct: 118 SKRPMDRVAIPLLEMGAEISGQGPVKQPPITIKGQSHLKAITYHLPVA-SAQVKSAILLA 176

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKNAY 249
A G + ++++K I+ + E +R+ FG + I+G Q K K

Sbjct: 177 ALQTKG--QTKLVEKAITRNHTEEMIRV---FGGQVHQLGK--EITIQQPQLKGQK-IK 228

Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-TSVTV 307
V GD SSA+++L AG I G + +E G + EV++ MG +VT S

Sbjct: 229 VAGDISSAAFVLVAGLIIPGSDIRLENVGINETRTGI--LEVIKMMGGQVTIENYDSKNQ 286

Query: 308 TGPPREPFRGRHLKKAIDVNMNMKMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
+ R + L+A +++ +P + L ++AL A G T I+D A R+KET+R+

Sbjct: 287 SAHLRVYS--ELRATEISGTLIPRLIDELPIALLATQAKGQTVIKDAAELRLKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTI 422
+ L K+GA VEE D IIT ++L D DHR+ M ++AA + +T+

Sbjct: 345 AVVADILKKMGAKVEEKADGMIITGGQELVACQADAQMDHRIGMMAAIAALLVKKGTMTL 404

Query: 423 RDPGCTRKTFPDYF 436
+ ++P++F

Sbjct: 405 KGAEAIATSYPNFF 418

>ref|YP_003994197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halanaerobium sp.
'sapolanicus']
gb|ADQ13843.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halanaerobium sp.
'sapolanicus']
Length = 428

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 132/458 (28%), Positives = 237/458 (51%), Gaps = 52/458 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++ ++SG +K+PG KS+S+R L+LA+++EG + ++ LL +ED + ++ LG+

Sbjct: 2 DLIVERKRKVSGEIKVPKDKSISHRSLILASIAEGVSKIEGLEAEDCLSTMQIMKDLGI 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E K A+ + V G +E+A + L GN+G +MR LT + A + V+ G

Sbjct: 62 KIE--KTAEGSYQVHGKGLDGLLEADD--VLDCGNSGTSMRLLTGLL--ASQDFYSVVTG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R+RP+ ++ L ++GA + R NG+ + SI Q L A

Sbjct: 116 DHSLRKRPQRIIGPLSRMGAQIWS-----RKNGLAPM-----SIRGQKLDA 157

Query: 186 LLMAAPLALGDVEIEII-----DKLISIPYV--EMTLRLMERFGVKAHSDSWDRFY 235
+ P+A ++ I+ + +I+ P V + T R+++ GV+ + + DR

Sbjct: 158 IEYTLPVASAQLKSSILLAALKSEGETIINEPAVSRDHTEMLKGAGVEIDIEE--DRIV 215

Query: 236 IKGGQYKSPKNAY---VEGDASSASYFLAGAAITG--GTVTVEGCGTTSLQGDVKFAEV 290
+K +K K N++ V GD SSA++F+ AA+T G + ++ G Q F EV

Sbjct: 216 LKAAEKRL--NSFEIKVPGDISSAAFFIT-AALTADEGELIKNVGLN--QTRSGFIEV 270

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFRG-KHLKAIDVNMNMKMP--DVAMTLAVVALFADG 346
++ MG +++ P + + LKA +V+ +P D +AV+A A+G

Sbjct: 271 VQAMGGEISLLNKKDQGGEPADILVKASDLKACEVSGEIIIPRLIDEIPIIAVLA AAAEG 330

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-EKLNVTADITYDDHR 405
T I+D RVKET+R+ A+ +E KLG +EE PD I P E +++Y DHR

Sbjct: 331 KTLIKDAEELRVKETDRIAAVVSEFKLGIIEEHPDGMTINGPVEVEGGIEVESYHDHR 390

Query: 406 MAMAFS-LAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+AM+ + LA + +TI+ +FP + ++L++

Sbjct: 391 IAMS L AVLALRTKKGLTIKGSEIINTSFPSFEELLASI 428

>ref|ZP_04234235.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-28]
gb|EEL34244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-28]
Length = 429

Score = 147 bits (370), Expect = 4e-33, Method: Compositional matrix adjust.
Identities = 132/452 (29%), Positives = 218/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QPI ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPINSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VEITQNGDEVTVVGKG----IEGLQEPKAVLDVGNSTTIRLMSGILA----NTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA +D P+ + G GGL + +S S+
Sbjct: 112 SCVQGDASIAPKPMKRVNPLKQMGAKIDGREGGTFPTLTIRG-GGLKAIEY-ISPVASA 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGV + + G
Sbjct: 170 QVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVNV--TREGKTVKLAG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQK + + V GD SSA++FL AGA I + ++ G + + +VLE MGA
Sbjct: 221 GQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEKMGAT 277

Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L + +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGSTVNSYGDHRIGMMLAIA 397

Query: 414 AC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
C AE TI D ++P +F+ L K
Sbjct: 398 GCLAEGKTTIEDAEAVGVSYPTFFFEELQKLAK 429

>ref|ZP_03932948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49725]
gb|EEI14284.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49725]
Length = 433

Score = 147 bits (370), Expect = 5e-33, Method: Compositional matrix adjust.
Identities = 129/435 (29%), Positives = 205/435 (47%), Gaps = 35/435 (8%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G ++PGSKS++NR +LAAL++ +++ L S D M AL +G+ D
Sbjct: 21 VTGEHQVPGKSITNRAFILAALADSPSILHAPLVSRDTQLMEDALSAMGVRFTHD---- 76

Query: 75 RAVVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
G V+ K + G AG MR + A G +DG + RP
Sbjct: 77 -----GADIHVQPGKLHGATVDCGLAGTVMRFPVPPVAALADGPVR--VDGDKQAYNRP 127

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APL 192
+ + L+ LG DV D P V+ GGV + S SSQ++S LL++ A
Sbjct: 128 MSTTLDALRSLGVDVKG---DSLPTVSANDVPEGKVTIDASGSSQFVSGLLLSGARF 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG---GQKYKSPKNAY 249
+ G +L S+P+VEMT+ ++ + GV+ + SD G G+++ +
Sbjct: 184 SQGIQLTHEGGQLPSMPHVEMTVGMLRQAGVRVD-SDGTTWTVHPGPIAGREW-----F 236

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+E D S+A+ FLA AA+TGG +T++ + Q ++L MG VT SVT G

Sbjct: 237 IEPDLSNATPFLAAAVTGGRLTIKNWPANTTQPGDAIRQILLDMGVMVTQEHNSTVAEG 296

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
P G+ L+ I+ NM + ++ T+A + A+ P+ + +A R ET+R+ +

Sbjct: 297 ---NPAGK--LQGIERNMGDIGELTPTVAALCALAETPSRLTGIAHLRGHETDRLQTLAA 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
+ LG V E D +I P E L+ Y DHRMA A ++ + I D T

Sbjct: 352 NINALGGRVTELDGGLVIEPAE-LHGGNWPCYADHRMATAGAILGLKVPDIQIEDISTTS 410

Query: 430 KTFPDYFDVLSTFVK 444
KT P + + T +

Sbjct: 411 KTLPGFARMWETMLH 425

>ref|ZP_04568170.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
mortiferum ATCC 9817]
gb|EEO34616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
mortiferum ATCC 9817]
Length = 422

Score = 146 bits (369), Expect = 5e-33, Method: Compositional matrix adjust.
Identities = 114/433 (26%), Positives = 201/433 (46%), Gaps = 39/433 (9%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V LP SKS+++R ++ A+L++G + ++N+ S+D+ + ++ LG + +K +

Sbjct: 12 GKVNLPPSKSMAHRSIICASLAQGKSKLENIAYSDDIIATIEGMKKLGAKISKEKDS--- 68

Query: 77 VVVGCGGKFPVEDAKEEVQLF-----LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VE K QL +G +R + + G R+ +

Sbjct: 69 -----LIVEGIKNFSQLTNSIIDCNESGSLTRFFIPIFSLTDKKIEF--RGKNRLLQ 118

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP +++ + F D + ++G L G+ ++G+ISSQ++S LL P

Sbjct: 119 RP---QKIYEEIFKKQNLFFYYQDNNKIEIDG--KLKSGEYIINGNISSQFISGLLFTLP 172

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L D I+II S Y+++T+ +++FG++ D IKG QKY + + VE

Sbjct: 173 LLTEDSIKIIPPFESKSYIDLITIDMLKKFGIEVLFLDDL-TLTIKGNQKYIAT-DYKVE 230

Query: 252 GDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV-TGP 310
GD S +F AI +T EG S QGD + E+L+ G K+ E + G

Sbjct: 231 GDFSQGLFFAVLGAIN-NDLTCEGLDINSKQGDREIIEILKNCGIKIEELENGYKIFRGL 289

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
P KA ++N+ PD+ L V++ + DG I + R KE++R+ A+ E

Sbjct: 290 P-----KAYNINLENCPLGLPILTVLSAYGDGEFKIYNAQRLRYKESDRIEAMENE 340

Query: 371 LTKLGASVEEGPDYCIITPPEK-LNVTADITYDDHRMAMAFSL-AACAEVPTIRDPGCT 428
L KLG + I K ++ + + DHR+ M+ ++ A + P+ I

Sbjct: 341 LKKLGQVISSDESNIYIKGNSKYISCNFVFGHKDHRIVMSLAIFATLLDSPLIIEGAIAI 400

Query: 429 RKTFPDYFDVLST 441
K++P++F+ L

Sbjct: 401 SKSYPNFFEDLKN 413

>ref|ZP_04279363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
m1550]
gb|EEK88992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
m1550]
Length = 432

Score = 146 bits (369), Expect = 5e-33, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 219/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPGLSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +

Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118

Sbjct: 61 + +G VE + VVG G +E +E + L +GN+G +R ++ + N
FKEMG--VEITQNGDEVTVVGK-----LEGLQEPKAVLDVNSGTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K

Sbjct: 111 TPFFSCVQGDSEIAKRPKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +

Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +

Sbjct: 216 GKTVKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVQLNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +

Sbjct: 273 VLEKMGATFTVDLINEGASEPAANITIETSSLKIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II+ L +++Y DHR

Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIISGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K

Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPFFDELQKLAK 432

>ref|ZP_06900730.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 15912]
gb|EFH17983.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 15912]
Length = 436

Score = 146 bits (369), Expect = 5e-33, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 217/446 (48%), Gaps = 41/446 (9%)

Query: 13 KEISGTVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GT+++PG KS+S+R ++ +L++G T V ++L EDV + R LG+S++ D

Sbjct: 17 KGLKGTIRVPGDKSISHRSIIFGSLAKGETKVYDILRGEDVLSTIQVFRDLGVSIIQDDGD 76

Query: 73 AKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R VG G + P L +GN+G ++R ++ + AG + + G + +

Sbjct: 77 VIRIQGVGFQGLQAPT-----APLDMGNSGTSIRLISGVL--AGQDFAVAMVGDDSLSK 128

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ DCP+ G L +L + S+Q SAL+ AA

Sbjct: 129 RPMDRVAIPLRQMGVEIAGQGERDCPLHEKGTHQLQPIHYRLPVA-SAQVKSALIFAAL 187

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +R +FG E I+GGQ+++ + V

Sbjct: 188 QAEG--ESTIIEKEKTRDHTEDMIR---QFG--GEIQVDGKTIRIQGGQEFQG-QEVIVP 239

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----T 303
GD SSA+++L AG + + +E G Q EV++ MG +T +

Sbjct: 240 GDISSAAFVLVAGLILPESVIKIENVGIN--QTRTGILEVIQEMGGDLTMEDRDEKAVSA 297

Query: 304 SVTVTGPPREPFPGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
S+TV LK I ++ +P + L ++AL A +G T I D RVKE

Sbjct: 298 SLTVK-----TSSLKGIRIDGELIPLRIDLPIALLATQANGQTVIADAEELRVKE 349

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEV 418
T+R+ + L +GA+V D IIT P L+ ++T+ DHR+ M ++AA +

Sbjct: 350 TDRIQVVADSLNAMGANVVPTEGDMIIITGPTPLHGADLETFGDHRIGMMATIAALLVRDG 409

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
V + ++P +F+ L T +

Sbjct: 410 NVVLDRAEAINTSYPSFFEDLETLH 435

>ref|ZP_04970608.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium

nucleatum subsp. polymorphum ATCC 10953]
gb|EDK88692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. polymorphum ATCC 10953]
Length = 420

Score = 146 bits (369), Expect = 5e-33, Method: Compositional matrix adjust.
Identities = 110/439 (25%), Positives = 209/439 (47%), Gaps = 49/439 (11%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADK 71
+ ++ G V P SKS+ +R ++ ++L++G + ++N+ S D+ + A++ LG +E
Sbjct: 8 VDKLVGEVSPPPSKSILHRYIIGSSSLAKGISKIEINISFSNDIIATIEAMKKLGAKIEK-- 65

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+++ F E ++ +G +R L + G ++ +
Sbjct: 66 -KDNYLIDGSKTDFDKEYLNNNSEIDCNESGSTLRFLFPLSIVKENKILF--KGKGKLFK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLSGSISSQYLSAL 186
RP L F VNG G L G+ ++ G+ISSQ+++ L
Sbjct: 123 RP-----LSPYFKNFDKYQIKYSHVNGNEILLDGLKSGEYEDGNISSQFITGL 172

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L + PL G+ ++ I KL S Y+++TL + +FGVK ++S+ F I+G Q YKS
Sbjct: 173 LFSPLPLNGNSKVIKKGKLESSYIDITLDCCLKFGVKI-INNSYQEFIEGNQTYKSG- 230

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
N VE D S ++FL +I G + + G SLQGD K +++ + WT+
Sbjct: 231 NYEVEADYSQVAFFLVANSI-GSDIKINGLNVNSLQGDKK---IIDFISEIDNWTNEKL 286

Query: 307 VTGPPPEPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ ++ ++ PD+ L++ A + I ++A R+KE++R+ A
Sbjct: 287 I-----LDGSETPDIIPIILSLKACISKKEIEIVNIARLRIKESDRLKA 329

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKL-----NVTADITYDDHRMAMAFSLAA-CAEVPV 420
EL+KLG + E D +I + + ++ ++ DHR+AM ++A+ C E +
Sbjct: 330 TVQELSKLGFDLMEKEDSILINSRKNYTHNSKEIISLSSHSDHRIAMTVAIASTCYEGEI 389

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
+ + C +K++P+++V
Sbjct: 390 ILDNLDCKVKSYPNFWFV 408

>ref|YP_001516633.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acaryochloris marina
MBIC11017]
sp|B0C218.1|ARO_AACAM1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABW27319.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acaryochloris marina
MBIC11017]
Length = 446

Score = 146 bits (369), Expect = 6e-33, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 207/446 (46%), Gaps = 31/446 (6%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V+Q + G +PG KS+S+R L+L AL+ G T + LL ED R LG +
Sbjct: 18 VIQSEGVLQGKTTIPGDKSISHRALMLGALASGETTIQGLLLGEDPRSTAHCFRALGAEI 77

Query: 68 -EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E + R +G G + +V L GN+G +R L + A+ + + + G
Sbjct: 78 SELNTEHVRVQIGLGHLL-----EPDVVLDAGNSGTTLR-LMLGILASHPDRLFTVTGD 131

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+G ++ L+Q+GA + P+ + G P + I+S + +
Sbjct: 132 TSLCSRPMGRVIKPLQQMGAHIWGRQSDTLAPLAIRGQQLQP---IHYPSPIASAQVKSC 188

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+M A L + + + I + +S + E R+ FG + G + +
Sbjct: 189 IMFAGL-MAEQGTTITEPALSRDHSE---RMFAAFGANIIVDPDTCVTVTGPAQLHG-Q 243

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V GD SSA+++L AAI G+ + +E G + V EVLE MGAK+T

Sbjct: 244 AIIVPGDISSAAFVLVAAAIVPGSDIWIENVGVNPTRTGV--LEVLEQMGAKMTLANQR- 300

Query: 306 TVTGPPREPFGKRHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWR 357
TV G EP H++ ++ + ++ D LAV ALFA GPT IRD A R

Sbjct: 301 TVAG---EPVADIHIQHSQLHGTVIEGAVIPRLVDEVPILAVAALFAQGPTTIRDAEELR 357

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-A 416
VKE++R+ A+ T+L K+GA++ E PD I L +D++ DHR+ M+ ++AA A

Sbjct: 358 VKESDRLTAMATQLQKMGANITEQPDGLEIQGGASLQGADVDSFGDHRVGMSLAIAALNA 417

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTF 442
TI ++P++ L

Sbjct: 418 TGSTTIHRAEAAAISYPNFVATLQQL 443

>ref|YP_003329889.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
VS]
gb|ACZ61561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dehalococcoides sp.
VS]
Length = 420

Score = 146 bits (369), Expect = 6e-33, Method: Compositional matrix adjust.
Identities = 138/429 (32%), Positives = 204/429 (47%), Gaps = 31/429 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-GLSVEADKAAKR 75
G + +P SKS + R L+ AA + G + + + L ++D L + L GL ++ + +

Sbjct: 12 GEIAVPSSKSYTIRGLVAAAQANGQSHIISPLVADDT--LATRQVLSGLDIDINTKTED 68

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMREPIG 135
G F K E LF + +R +AV A ++L G MR RP+

Sbjct: 69 GSWQITGNTF----KKPEGNLFCSRESAATLR-FMSAVCARLLFECHLLAGHSLMR-RPML 122

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
L+ L QLG +++ T + G G + KV L G+ISSQY+SAL++ AP

Sbjct: 123 PLIQALHQLGIEIETRGNTTV---IKG-GEITRSKVSLPGNISSQYVSALMLMAPACKN 177

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKNAYVEGDAS 255
+EI + S+PY++MT + +E FG+K S +W I Q Y P VEGD S

Sbjct: 178 GLEIHLATPPASLPYLKMTQTLESFSGIKVFSSINWQEISIP-PQPYL-PARYRVEGDWS 235

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPF 315
SAS FLA AI V V T S Q D + L MGA+ + V V+ P

Sbjct: 236 SASSFLALGAI-AAPVFVSNLDTDSFQADRIKYLTEMGAEAESGQNWVKVSPKP---- 290

Query: 316 GRKHLKAIDVN MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
L AI+ ++ D+ LAV A A G + + V R+KE+ R+ A+ L +G

Sbjct: 291 ----LSAINADLTHSIDLLPALAVAAACAKGQSILSGVRQARIKESNRIRAVSQGLVAMG 346

Query: 376 ASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
+V E D II P+ T ID++ DHR+AMAF + I D C KT+P

Sbjct: 347 INVTEEDRLIIDGGYPKG---TEIDSGFDHRIAMAFGVLGAVVGETHISDAECVSKTYP 403

Query: 434 DYFDVLSTF 442
+++ L +

Sbjct: 404 GFWEQLESL 412

>ref|ZP_04289791.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
R309803]
gb|EEK78462.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
R309803]
Length = 429

Score = 146 bits (368), Expect = 6e-33, Method: Compositional matrix adjust.
Identities = 132/452 (29%), Positives = 218/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +

Sbjct: 2 KERTIQPVNNGLNIGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122

G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111
Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA +D P+ + G G L + + S S+
Sbjct: 112 SCVQGDASIARPMQVRVTPNPLKQMGAKIDGREGTFTPLTIRG-GDLKAIEYR-SPVASA 169
Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGK + + G
Sbjct: 170 QVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRVGKTVKLAG 220
Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
GQK S + V GD SSA++FL AGA I + +E G + + +VLE MGA
Sbjct: 221 GQKLTS-TDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEKMGAT 277
Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVESINEGASEPAANITITETSSLKGIEIGDIIPLRIDEIPVIALAATQAEGITVIKDA 337
Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMIYKGSALKGNTVNSYGDHRIGMMLAIA 397
Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
C AE TI D ++P +F+ L T K
Sbjct: 398 GCIAEGKTTIEDAEAVGVSYPTFFFEELQTLAK 429

>ref|NP_972290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Treponema denticola
ATCC 35405]
gb|AAS12201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Treponema denticola
ATCC 35405]
Length = 449

Score = 146 bits (368), Expect = 6e-33, Method: Compositional matrix adjust.
Identities = 124/438 (28%), Positives = 218/438 (49%), Gaps = 30/438 (6%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGL--LSVEADKAAKRA 76
+++P SKS S R L+LA +EG + + NLL S D + +LG +E +
Sbjct: 16 IEVPPSKSHSMRALVLATFAEGPSQIKNLLMSGDTKTAVSVFESLGVKFKIEQKNISSAD 75
Query: 77 VVV--GCGKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++V G K +E K+ +++ GN+G L + ++ + ++L G + +RP
Sbjct: 76 IIVFPPKEGLKKRIEKQKQ- IKIDAGNSGTLFYFLGSILSLMSSD--FILTDGSSILKRP 132
Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRV---NGIGGLPGGKVKLSGSISSQYLSALLMA 189
L+ ++LG + G + P+RV + I L G + L G S Q +S LL+
Sbjct: 133 AKPLIEIYEELGLKYEFLDGF EKAPIRVLPGSSSIKNLKGKTLCEGDFS-QVVSGLLLG 191
Query: 190 APLALGDVEIEI-IDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A L D ++I + + +PY++MTL ++ G+K + SD + F I QK +A
Sbjct: 192 A--GLLDFPLQINLKRAGELPYLKMTHLWLKTCGIKFDVSDDFKTFKIIIESQKILG-FSA 248
Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++ +A A IT T++++ +QGD + +VL+ M A + + E S T+
Sbjct: 249 GIPADWSSAAFPALALITASTISIKNIDINDVQGDARIVKVLKEMNADIRFEEKSOTLK 308
Query: 309 GPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LK + + +PD L+ +A FA G T +++ R KE +R+ I
Sbjct: 309 IFPSS-----LKGTFDCSDIPDAVPALSAIACFAKGETILKNIEICRYKECDRLSVIS 362
Query: 369 TELTKLGASVEEGPD--YCIITPEKLNVTADITYDDHRMAM-----AFSLAACAEVPVT 421
+EL KLGA + EG D + I + L+ ++D++ DHR+AM F + T
Sbjct: 363 SELKKLGADITEGRDVLHIIGNAGKNLSPASVDSHKDHRIAMMLTIIGFGIDDKDGTVFT 422
Query: 422 IRDPGCTRKTFPDYFDVL 439
+++ C ++P + + L
Sbjct: 423 LKNAECFDISYPSFLEDL 440

>ref|YP_002140051.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter

bemidjiensis Bem]
sp|B5E9T1.1|ARO_A_GEOBB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACH40255.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
bemidjiensis Bem]
Length = 429

Score = 146 bits (368), Expect = 7e-33, Method: Compositional matrix adjust.
Identities = 128/448 (28%), Positives = 211/448 (47%), Gaps = 27/448 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ ++P K + G + +PG KS+S+R ++ +++ G T V L ED L A R +G
Sbjct: 2 QNYTVRPAKSVRGEISVPGDKSISHRSIMFGSIASGVTTVTGFLRGEDALATLEAFRAMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D G G D L GN+G +MR LT + AG N VL
Sbjct: 62 VQIDDDGETVTIQGRGLHGLSEPTDV-----LDCGNSGTSMRLLTGLL--AGQNFFSVLS 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+ +V L Q+GA + G + P+ + G L G ++ +SS +
Sbjct: 115 GDKYLRARPMPKRVVGLAQMGAIRISGRAGGEKAPLAIQG-SKLKG--IEYDSPVSSAQVK 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+ +M A L G E + + +S + E R++ FG E ++GG + +
Sbjct: 172 SAIMLAGLYAGG-ETVREPHLSRDHSE---RMLRAFGAHVETFPGG--VKVRGGAEL-T 224

Query: 245 PKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++ V GD SSA++FL AG + G + + G G + +VL+ MG +
Sbjct: 225 GRDIVVPGDISAFAFLVAGLIVPGSDLLIRGVGNPTR--TGIIDVLKMGMGDLELINQ 282

Query: 304 SVTVTGPPREPFGFRKH--LKVIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+G P +H L A++++ + +P D + V A A G T +RD A RV
Sbjct: 283 R-DESGEFVADIRVRHSLKTAMEISGDVVPRAIDFPAICVAASLAQGTTVVRDAEELRV 341

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KET+R+ A+ L + G S+ E PD IT L A D++ DHR+AM+ +A A+
Sbjct: 342 KETDRISAMADNLKRAVGSIVETPDGMEITGVSSSLKGCAADSFGDHRIAMSMVAGLVAQ 401

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
++ D C +FP + ++L V+
Sbjct: 402 NETSVSDVECIATSFPGFVNLLLEGVVQR 429

>ref|YP_175399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
sp|Q5WGR7.1|ARO_A_BACSK RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAD64438.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
Length = 430

Score = 146 bits (368), Expect = 7e-33, Method: Compositional matrix adjust.
Identities = 130/440 (29%), Positives = 214/440 (48%), Gaps = 37/440 (8%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ +PG KS+S+R ++ A++ GTT V L +D + R +G+++E +
Sbjct: 15 LSGTIVVPGDKSISHRAVMFGAMANGTTTNVSGFLPGDDCLSTIACFRQMGVAIEQE--GD 72

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ V G G ++ KE + +GN+G +R L ++ ++ V D + +RP
Sbjct: 73 KVTVEGKG---LDGLKEPNGVLDVGNSTTIRLLLVLSGRPFHVVVVD--DSIGKRP 126

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI----SSQYLSALLMA 189
+ + L+Q+GA +D + P+ + G G+ K S+Q SALL+A
Sbjct: 127 MARVTAPLRQMQAQIDGRETGNKTPLSIRG-----GQTKAIEYTMPVASAQVKSALLLA 180

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G E + + + + E R++ FGKV + + I+GGQ ++ +
Sbjct: 181 GLQAEG--ETSTPEPQTTRDHTE---RMLHAFGVKV--TTAGKTISIQQGQSLQA-ADV 232

Query: 250 VEGDASSASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FL AG + G V ++ G + + EVL+ GAK++ E VT
Sbjct: 233 VPGDISSAAFFLVAGCIVPGSRVHLKVNGLNPTRAGI--LEVLKRSKAKLSIDE-QVTTG 289

Query: 309 GPPRE--PFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G PR L + ++P D LAV+A G T IRD +VKET R
Sbjct: 290 GEPRGDMTISTSELSPPFVIEGEEVPTLIDEIPVLAVLATQISGTTIIRDAEELKVKETNR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVTI 422
+ + EL KLGA +E D II + L +D++ DHR+ MA +A+ CA PV +
Sbjct: 350 IDTVVGELAKLGADIEATDDGMIIRGGKPLTGGKVDSDHHRIGMALVIASLCANGPVEL 409

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
+ G ++P +F+ L +
Sbjct: 410 ANIGAISVSYPQFFEHLQSL 429

>ref|ZP_04102639.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar berliner ATCC 10792]
ref|ZP_04133556.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar thuringiensis str. T01001]
ref|ZP_04139874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis Bt407]
gb|EEM28478.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis Bt407]
gb|EEM34818.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar thuringiensis str. T01001]
gb|EEM65728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar berliner ATCC 10792]
Length = 432

Score = 146 bits (368), Expect = 7e-33, Method: Compositional matrix adjust.
Identities = 132/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPGSKSLSNRILLALALSEGTTVVNDLLNSEDEVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNNGNLGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFVFCVQGDSEIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGK
Sbjct: 165 YISPVAQAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKVTREGK 217

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAE 289
R + GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 218 TVR--LSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVLVQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPE--PFGRKHLKAIDVNMNKM---DVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +
Sbjct: 273 VLEKMGATFTVDIINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K
Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPTFFDELQKLAK 432

>ref|ZP_07464879.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
gallolyticus subsp. gallolyticus TX20005]
gb|EFM29262.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus

gallolyticus subsp. gallolyticus TX20005]
Length = 461

Score = 146 bits (368), Expect = 8e-33, Method: Compositional matrix adjust.
Identities = 126/449 (28%), Positives = 227/449 (50%), Gaps = 37/449 (8%)

Query: 8 VLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+L + ++ GT+++PG KS+S+R ++ +L++GTT V ++L EDV + R LG+ +
Sbjct: 37 LLTNVSQLKGTLRVPGDKSISHRSIMFGSLAKGTTTVDILRGEDVLSTMQVFRDLGVDI 96

Query: 68 EADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D VG G K P + +L +GN+G ++R ++ + AG + T + G
Sbjct: 97 QDDGNIVTITGVGFDGLKAP-----KNKLDMGNSGTSIRLISGVL--AGQDFTVEMFGD 148

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ +++ L+Q+G +V D PP+ + G L +L + S+Q SAL
Sbjct: 149 DSLSKRPMDRVIIPLRQMGVEVSGQTDRLPLPLTMRGSKALKPIHYQLPVA-SAQVKSAL 207

Query: 187 LMAAPLAGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA A D E II+K + + E ++ +FG + + R IKGGQ++ + +
Sbjct: 208 IFAALQA--DGESVIEKEKTRNHT---DMIVQFGGAIDVNGKEIR--IKGGQEF-TGQ 259

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303
+ V GD SSA+++L AG + VT+E G + + +V++ MG K+T +
Sbjct: 260 DVVVPGLDISAFAFLVAGLIVPNAKVTLENGINETRGTI--IDVIKEMGGKMTISNVDE 317

Query: 304 ---SVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWR 357
S T+T E L +++ +P + L ++AL A+G T IRD +
Sbjct: 318 IAKSATITVETSE-----LHGVEIGGEIIPRLIDELPIALLATQANGTTIIRDAEELK 371

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--C 415
VKET+R+ + L +GA + D II L+ ++T+ DHR+ M ++AA
Sbjct: 372 VKETDRIQVVADALNAMGADITPTDDGMIKKTPLHGAKVNTFGDHRIGMMTAIAALLV 431

Query: 416 AEVPTVIRDPGCTRKTFFPDYFDVLSTFVK 444
++ V + ++P +F+ L +
Sbjct: 432 SDGDVELERAEAINTSYPSFFNDLEVLRSR 460

>ref|ZP_04115329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar kurstaki str. T03a001]
gb|EEM52957.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar kurstaki str. T03a001]
Length = 432

Score = 146 bits (368), Expect = 8e-33, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 219/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T++ L D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTIIRGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGK-----LEGLQEPKAVLDVNSGTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFFFCVQGDSEIAKRPKRVNTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVK--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 216 GKTVKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVLVQVGMNPTRTGTI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +
Sbjct: 273 VLEKMGATFTVDLINEASEPAANITETSSLKIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYKKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K
Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPTTFDELQKLAK 432

>ref|YP_001843922.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus fermentum IFO 3956]
sp|B2GCR0.1|AROA_LACF3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAG27442.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus fermentum IFO 3956]
gb|ADJ41326.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Lactobacillus fermentum CECT 5716]
Length = 432

Score = 146 bits (368), Expect = 8e-33, Method: Compositional matrix adjust.
Identities = 136/437 (31%), Positives = 217/437 (49%), Gaps = 37/437 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++G + +PG KS+S+R L++ ALSEGTTV+D+ L ED L AL+ LG VE ++
Sbjct: 11 RGLNGELAVPGKKSISHRALMIGALSEGTTVIDHFLVGEDCLSTLRALQDLG--VEIERK 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V+G G VE A L + N+G + R L + AG + T L G + R
Sbjct: 69 GEHVEVIGRGIAGLVEPAAP---LQMNSGTSTRLLMGIL--AGQSFTSQLVGDASLSRR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L +LGA + P V L G +VKL + S+Q SA+++AA
Sbjct: 124 PMKRVQGPLARLGAQIGLSEAGTLPATVVG--HPLQGARVKLEVA-SAQIKSAVILAALQ 180

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G + +P + T RL++ FG + + + G + + V G
Sbjct: 181 AQGSTTVS-----EPLPTRDHTERLLKAFGANLTVDRAANSITVTPGARLVG-QEVLVPG 234

Query: 253 DASSASYFL-AGAAITGGTVTVVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++FL AGA I +TV+ C + G ++ VL+ MGA+++ ET+
Sbjct: 235 DPSSAAFFLVAGAVIANSHLTVKDVCLNPTRTGLIR---VLKMKGARLSIKETASG---- 287

Query: 311 PREPFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
EP G L+A+ V +PD+ L +VAL ADG + I RVKET+
Sbjct: 288 -GEPLGDVVTIQTSQLRAVTVTAKDVPDLIDELPLVALLAACADGVSEISGAGELRVKETD 346

Query: 363 RMVAIRTELTKLGASVEEGPD-YCIITPPE-KLNVT AIDTYDDHRMAMAFSLAAC-AEVP 419
R+ + +LG VEE PD + I+ P ++ ++++ DHR+ M ++AA + P
Sbjct: 347 RIQTVAELFLQLGVDVEERPDPGWRIVGRPNWQVQKPNLNSHGDHRLGMLAAVAALRSTTP 406

Query: 420 VTIRDPGCTRKTFPDYF 436
+ + DP ++P +F
Sbjct: 407 LFLIDPDAVAVSYPSFF 423

>ref|ZP_05645736.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus casseliflavus EC30]
ref|ZP_05652067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus casseliflavus EC10]
gb|EEV29069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus casseliflavus EC30]
gb|EEV35400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus casseliflavus EC10]
Length = 429

Score = 146 bits (368), Expect = 8e-33, Method: Compositional matrix adjust.
Identities = 127/446 (28%), Positives = 212/446 (47%), Gaps = 34/446 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+ + GT+ +P KS+S+R ++ AL+EGTT V N L ED + L A ++LG+ +
Sbjct: 3 LKKATHLKGITIAVPADKSISHRSIMFGALAEGTTTVRNFLRGEDCYSTLHAFQSLGVPIH 62

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D G G P ++ +GN+G +R + + AG T L G
Sbjct: 63 DDGQTITIEGQGFNGLKPADEP-----IDIGNSGTTIRLMMGIL--AGQPFTTTLFGDDS 115

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ +++ L+++GA+V T+ PP+ +NG L ++ + S+Q SAL+
Sbjct: 116 LNRPMNRMVMLPLREMGANVRGHEQTEFPFITINGTASLHPINYQMPVA-SAQVKSALIF 174

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G I I+K S + E +R +FG + + G Q + +
Sbjct: 175 AALQAQGTSTI--IEKETSRNHTEEMIR---QFG--GVITTQGKTITVTGPQTLQG-QEV 226

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET---- 303
V GD SSA++FL AGA + + ++ G + + +VLE MGA + ++
Sbjct: 227 VVPGDISAFAFLTAGAIMPESEIVLKNVGINPRTGI--LDVLEEMGASIAFSNQDDQN 284

Query: 304 -SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTAIRDVASWRVK 359
S +T L+A+ + + +P + L ++AL A G T I+D +VK
Sbjct: 285 QSADLT-----VQSSTLQAVTIAGDIIPRLIDELPIALLATQAHGKTVIKDAEELKVK 338

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418
ET R+ A ELTKLGA + D II P L+ + + DHR+ M +AA +
Sbjct: 339 ETNRIDATAEELTKLGADITPTEDGLIINGPTPLHGGRVSSRGDHRIGMMLQIAALLTDE 398

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
V + ++PD+F+ ++ K
Sbjct: 399 EVELEKAEAVAVSYPDFFEDVARLAK 424

>ref|YP_003920757.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvoylshikimate-3-phosphate synthase) [Bacillus
amyloliquefaciens DSM 7]
emb|CBI43287.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvoylshikimate-3-phosphate synthase) [Bacillus
amyloliquefaciens DSM 7]
Length = 428

Score = 146 bits (368), Expect = 8e-33, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 216/447 (48%), Gaps = 34/447 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ + ++G + +PG KS+S+R ++ AL+EGTT V N L D + R +G+S+E
Sbjct: 4 EKVTSLNGEIIHPGDKSISHRSVMFGALAEGTTTVKNFLPGADCLSTIACFRKMGSIEQ 63

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + G G E + L +GN+G +R + + AG + G +
Sbjct: 64 N--GSDVTIHNGNIDALCE---PDSLLDVGNSGTTIRLMLGIL--AGRPFHSTVAGDESI 116

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + LKQ+GA +D + P+ V GG G +S S+Q SA+L+A
Sbjct: 117 AKRPMKRVTEPLKQMGAVIDGRADGEFTPLSVR--GGQLKGIDYVSPVASAQIKSAVLLA 174

Query: 190 APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G + K + T R++ FG AE +++ + GGQK ++ + +
Sbjct: 175 GLQAEGTTTTEPHK-----SRDHTEMLNAGF--AELAETETSASVTGGQKLRAA-DIF 226

Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FL AGA + G + ++ G + + +VL+ MGA + +
Sbjct: 227 VPGDISAFAFLAAGAVVPGSRIVLKNVGLNPRTGI--IDVLKQMGATLEV----ILSK 280

Query: 309 GPPREPGF-----RKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKE 360
EP+G LKA ++ +P + + ++AL A+G T I+D A +VKE
Sbjct: 281 ADSAEPYGDVLIETSAKAAEIGGEIIPRLIDEIPIIALLATQAEGTTVIKDAEELKVK 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ADITYDDHRMAMAFSLAAC-AEV 418
T R+ + +EL K+GA +E D I + L A + ++ DHR+ M +A+C E
Sbjct: 341 TNRIDTVVSELKIGADIEATEDGMKIHGKKTLAGGAGVSSHGDHRIGMMLGIASCLTEE 400

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 445
P+ I D R ++P +F+ L K
Sbjct: 401 PIEIHDTDAIRVSYPTFFEHLDQLSKK 427

>ref|ZP_04192296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH676]
ref|ZP_04239968.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Rock1-15]
gb|EEL28408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Rock1-15]
gb|EEL75990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH676]
Length = 432

Score = 145 bits (367), Expect = 9e-33, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVVGK-----LEGLQEPKAVLDVGNSTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TFFFSCVQGDSEIAKRP MKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYL SALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISR DHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 216 GKTIVKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLV LQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +
Sbjct: 273 VLEKMGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K
Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPTFFDELQKLAK 432

>ref|YP_037018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27]
sp|Q6HHF8.1|AROABACH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAT61256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27]
Length = 429

Score = 145 bits (367), Expect = 9e-33, Method: Compositional matrix adjust.
Identities = 132/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EGTT + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGAIAEGTTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + D VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQD--GDEVTVVGK-----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ V G G +K S
Sbjct: 112 SCVQGDASIAKRPMKRVNPLKQMGANIDGREGTFTPLTVRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVITGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITIETSSSLKGIIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +F+ L K
Sbjct: 394 LAIAGCIAEGKTIIEDAEAVGVSYPPTFFEELQKLAK 429

>gb|ABZ07600.1| putative EPSP synthase (3-phosphoshikimate
1-carboxyvinyltransferase) [uncultured marine
microorganism HF4000_ANIW137K11]
Length = 183

Score = 145 bits (367), Expect = 9e-33, Method: Compositional matrix adjust.
Identities = 87/188 (46%), Positives = 113/188 (60%), Gaps = 7/188 (3%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + L ++ GTVKLPGSKS+SNR LLLAAL++G T + LL S+D ML ALR LG
Sbjct: 2 ESLTLPAVRHAYGTVKLPGSKSISNRITLLAALAQGDTEIHELLASDDTQRMLDALRIL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + V G G+FPV+ A LFLGNAG A R LTAA+ + GN Y L
Sbjct: 62 VKLE-QTGLHQVQVHGTGCEFPVKQAA---LFLGNAGTAFRPLTAALALSHGN--YELS 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G+ RM ERPIGDLV L GA ++ PP+ + +++ G +SSQ+L+
Sbjct: 115 GIARMHERPIGDLVDTLNAAGAAIEYLQNPGFPPLHIRPATLNTSEALRVRGDVSSQFLT 174

Query: 185 ALLMAAPL 192
ALLMA PL
Sbjct: 175 ALLMALPL 182

>ref|YP_002123076.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equi
subsp. zooepidemicus MGCS10565]
sp|B4U246.1|ARO_A_STREM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACG62063.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Streptococcus
equi subsp. zooepidemicus MGCS10565]
Length = 427

Score = 145 bits (367), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 126/432 (29%), Positives = 219/432 (50%), Gaps = 29/432 (6%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++PG KS+S+R ++ A++EG TV+ LL +DV + A R LG+++ ++
Sbjct: 8 KALRGRRLRVPDGKSISHRAVIFGAIAEGQTVIHGLLRGQDVLATIQAFRDLGVITIY--ES 65

Query: 73 AKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A ++ G G G P + L +GN+G +MR L + A ++ L G +
Sbjct: 66 ADSLIIIEGRGFKGLKPAQKP-----LDMGNSGTSMRLLAGLLAAQ--DFSVQLFGDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + + L +GA++ + PP+ V G GL +L + S+Q SA+L+AA
Sbjct: 119 RRPMDRITIPLSLMGAELSGQGEKELPPLIVKGCQGLRPIHYQLPVA-SAQVKSAILLAA 177

Query: 191 PLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G E I++K ++ + E ++E+FG K S + + IKG Q+ + + +
Sbjct: 178 LQTQG--ETVILEKELTRNHE--EMIEQFGGKL--SVAGKQISIKGPQRLQG-QTLQI 229

Query: 251 EGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++LA G + G + +E G + EV+E MG ++++ +
Sbjct: 230 PGDLSSAAFwLAAGLIVPGSDLVLENVGINPTR--TGLLEVIEKMGGQLSYQAVDKDIQT 287

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVA 366
+ LK I+++ + +P + L V+AL A G T IRD RVKET+R+ A
Sbjct: 288 ATLK-VSYSTLKGIEISGDLIPRLIDELPVIALLATQAQGTYYIRDAQELRVKETDRIQA 346

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ L ++GA ++ D +I L+ A+ T DHR+ M ++AA E VT+
Sbjct: 347 VTDVLQMGADIQATEDGMVIRGKTPHGAAVSTCGDHRIGMMTAIAALLVEEGQVTLER 406

Query: 425 PGCTRKTFFPDYF 436
++PD+F
Sbjct: 407 AEAILTSYPDDF 418

>ref|YP_003900684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vulcanisaeta
distributa DSM 14429]
gb|ADN49633.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vulcanisaeta
distributa DSM 14429]
Length = 429

Score = 145 bits (367), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 218/439 (49%), Gaps = 33/439 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTL- 64
++++ K G V+ P SK+L+ R LL +ALS + L +D M+ ++ +
Sbjct: 3 KLIVNGFKAREGVVEAPPSKALTRLRYLLASALSRTWVSLRKLNWGDDTWSMIRGVKPISE 62

Query: 65 LSVEADKA-AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ V D +R ++V +F V D +G +G +R LT + G +
Sbjct: 63 IEVRDDYVRTRRGMMVE---RFRVID-----VGESGFTLRVLTGVYSGIDGTTLLIP 111

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RP+ +L+ LK LGA VD LG+ +RV G L GG V +SGS+SSQY+
Sbjct: 112 RG--SLIGRPMDLGLGALKNLGAKVDR-LGS---IIRVVG-SKLVGGYVMISGSVSSQYI 164

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL APL G +E+ I + S PY++ T+ ++ FG+ AE SD D Y+ G Q+++
Sbjct: 165 SALLYLAPLTEGGIEVSIKPKIKSRPYIDATISVLRDFGINAERSD--DTIYVSGSQEFR 222

Query: 244 SPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWT 301
+ + V GD S A+Y++A + +TG + + +++ + F + + +G ++
Sbjct: 223 AVNEEFIVPGDYSLAAYIALSVLTGIDLRIMNLHRDRAIESEYSFIKYAKEIGVEIEEY 282

Query: 302 ETSVTVTGPPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
E SV V G K L+ ++ +++ PD+ M LA++ G + I V+ KE+
Sbjct: 283 EDSVMVKGS-----TKSLRPLNADLSDSPDIVMPLALLLTRVQGRSRLGVSHLVYKES 337

Query: 362 ERMVAIRTELTKLGA--SVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAA-CAE 417
R+ + L LGA SV+E I ++ ID +DHR+ M + A A
Sbjct: 338 NRLRGVAAVLKCLGAGVSDEANGIIIEIEGTHEIKGGCEIDALNDHRIVMMGVIGALSAR 397

Query: 418 VPVTIRDPGCTRKTFFPDYF 436
PV I + K++P +
Sbjct: 398 EPVEIINWEGVSKSWPTFI 416

>ref|ZP_06804840.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevibacterium
mcbrellneri ATCC 49030]
gb|EFG48370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevibacterium
mcbrellneri ATCC 49030]

Length = 392

Score = 145 bits (367), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 131/418 (31%), Positives = 201/418 (48%), Gaps = 33/418 (7%)

Query: 33 LLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE 92
+LAALS ++V + L S D M+ AL LG + +V GG DA
Sbjct: 1 MLAALSNAPSIVRSPLVSRDTELMMRALDALGATFTP-HGNDISVEPIMGGDNSASDATI 59

Query: 93 EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC-- 150
+ G AG MR + V A G A + DG P+ R RP+ ++ L LGA VD
Sbjct: 60 DC----GLAGTVMRFPVPPVLTATGTRAHF--DGDPQARVRPMQTILDALTALGATVDSDD 113

Query: 151 -FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SI 208
FL P + G G V + S SSQ++S LL++A + ++ + + S
Sbjct: 114 GFL-----PFSIT-TGDHVGNTVTIDASQSSQFVSGLLLSAARFPDGLTVKHLGETVPSK 167

Query: 209 PYVEMTLRLMERFGVKAHSD--SWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAI 266
P+++MT+ ++++GVK D +W ++ G + + VE D S+A+ FL I
Sbjct: 168 PHIDMTVATLKQYGVKVTQPDPTW---VVEPGVIQAT--DVTVEPDLNAATFLGVPLI 222

Query: 267 TGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREPFGFRKHLKAIDVN 326
GG+VTV + Q F ++ G T +TVTG ++ +D++
Sbjct: 223 AGGSVTVPHWPERTDQAGHAFMDIARAFGGTAELTPAGLTVTG-----SGTVQPVLDL 275

Query: 327 MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 386
++++ ++ +A +A A G + +R + R ET+R+ A+ TELTK GA VEEGPDY
Sbjct: 276 LSQVGELTPVVAIAAHAGHTSHLRGIGHLRGHETDRLTALATELTKAGAQVEEGPDYLT 335

Query: 387 ITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
IT A +Y DHRM MA +L + VTI DP KT P + D+ V
Sbjct: 336 ITSTVSTGC-AWSSYADHRMVMAGALVGLTQ-DVTIEDPDTVAKTLQFTDMFERVVS 391

>gb|EGC83183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerococcus
hydrogenalis ACS-025-V-Sch4]
Length = 409

Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 108/436 (24%), Positives = 222/436 (50%), Gaps = 49/436 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
++I++ P K ++G + SKS ++R+L++A LS +T + S+D++ + L+ LG
Sbjct: 4 DDILIHPSK-LTGQIDAISSKSFARHVLIMAGLSNNSTNIYINEFSKDINVTIDGLKNLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E ++ + + P E+ ++ + + +G ++R T + N +
Sbjct: 63 VGIEKNENFVKII-----PPEEKIDQATIDMYESGSSLRFFTGVSSHFSKNTKII-- 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G R+ +RP +L+ L++ G ++ +D P + G L G+ + + SSQY++
Sbjct: 113 GEKRLAQRPNLELINLRKHGLEI----SSDKIPYTIKG--KLKAGQFEFLENKSSQYIT 166

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGV---KAEHSDSWDRFYIKGGQK 241
A+++AA G I++ +K SI Y+++T ++++ F V K +HS YI +
Sbjct: 167 AIMLAASKLKGTIYIKLSEKPEISIGYIDITRVLKDFNVVDVKKDKHS-----YIENPE 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWT 301
KSPKN VEGD S+A++F GA + G + + SLQ D + E+ + +
Sbjct: 221 IKSPKNYIVEGDWSNAFFY-GANLLGSKIEISNLDENSLQKDREIVEICQKIKE----- 274

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+K K + ++++++PD+ +A++ + D + I + R+KE+
Sbjct: 275 -----CKKEGKELKIDISQIPDLCPIVAILLTYLDKTSYIINGERLRLKES 320

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPV 420
+R+ + L LGA+ + D I+ K++ +D+++DHR+ MA S+ + A+ +
Sbjct: 321 DRLESTSKMLNDLGANCQILGDGLKISG--KISGGKVDSFNDHRIVMAASIGSLLAKEDI 378

Query: 421 TIRDPGCTRKTFPDYF 436
I++ K++P +F

Sbjct: 379 IIKNYKAVNKSYPSFF 394

>ref|YP_002537816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. FRC-32]
sp|B9LZG2.1|AROA_GEOSF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACM20715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. FRC-32]
Length = 429

Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 129/437 (29%), Positives = 209/437 (47%), Gaps = 25/437 (5%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+P K + G + +PG KS+S+R ++L +L+ G T V L ED L A R +G+ V
Sbjct: 7 KPAKTVRGEITVPGDKSISHRSIMLGSLARGITTVKGFLRGEDNLATLNAFRAMGIIIVHD 66

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
D + G G D L GN+G +MR +T ++ G VL G +
Sbjct: 67 DGETLKIENGLHGLGEPADV-----LDCGNSGTSMLMTGLLS--GQRFFSVLTGDQYL 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R+RP+ ++ L +GA V G D P+ + +G G S +Q SA+L+A
Sbjct: 120 RKRPMKRVLEPLNLMGATVFGRAGGDKAPLAI--VGTSKGIAYQSPVSSAQVKSAILLA 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A D E ++ + +S + E R++ FG E R I+GG++ + +
Sbjct: 178 GMYA--DGETQVTEPHLSRDHSE---RILRYFGADIETYSGGTR--IRGGRELEG-REII 229

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVWTETSVTVT 308
V GD SSA++F+ A I G + ++G G + + ++L+ MG +T +
Sbjct: 230 VPGDISAAFFMVAALIVPGSELLIKGVGVNPTRTGI--IDILQAMGGDITLQNCRESSG 287

Query: 309 GPPREPFGFRK-HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + + LK I+V + +P D + V A A+G T IRD RVKET+R+
Sbjct: 288 EPVADILVKSSRLKGIIEVGGDLVPRAIDFVPICVAASLAEGKTVIRDAKELRVKETDRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIR 423
A+ L K G +V E + +T EKL +++ DHR+AM+ +A A +T+
Sbjct: 348 KAMAFNLQKAGVAVVETENGMDVTGMEKLEGCTAESFGDHRIAMSMLIAGLAARDQITVN 407

Query: 424 DPGCTRKTFPDYFDVLS 440
D C +FP++ +L
Sbjct: 408 DTECIGTSFPNFTALLQ 424

>ref|YP_004204016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
BSn5]
gb|ADV92989.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus subtilis
BSn5]
Length = 428

Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 129/448 (28%), Positives = 220/448 (49%), Gaps = 36/448 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ ++ + G + +PG KS+S+R ++ AL+ GTT V N L D + R +G+ +E
Sbjct: 4 EKVQTLHGEIHIPGDKSISHRSVMFGALAAAGTTTVKNFLPGADCLSTIDCFRKMGVHIE- 62

Query: 70 DKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ V+ G G ++ KE E L +GN+G +R + + AG + G
Sbjct: 63 -QSGSDVVIHGKG---IDALKEPESLLDVNGSGTTIRLMLGIL--AGRPFYSAVAGDES 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + LK++GA +D G + P+ V+G L G +S +Q SA+L+
Sbjct: 116 IAKRPMKRVTEPLKKMGAKIDGRAGGEFTPLSVSG-ASLKGIDY-VSPVASAQIKSAVLL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G + K + T R++ FGVK S I GGQK + +
Sbjct: 174 AGLQAEGTTTTEPHK-----SRDHTERMLSAFGVKL--SADQTSVSIAGGQKL-TAADI 225

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+V GD SSA++FL AGA + + ++ G + + +VL+ MGAK+ ++ +
Sbjct: 226 FVPGDISAFAFLAAGAMVPSRIVLKNVGLNPTRTGI--IDVLQNMGAKLEIKPSADSG 283

Query: 308 TGPPREPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
EP+G LKA+++ + +P + + ++AL A G T I+D A +VK
Sbjct: 284 A----EPYGDIIETSSLKAVEIGGDIIPRLIDEIPIIALLATQAKGTTVIKDAELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAAC-AE 417
ET R+ + +EL KLGA +E D + + L A+ ++ DHR+ M +A+C E
Sbjct: 340 ETNRIDTVVSELRKLGAEIEPTADGMKVYKGQTLKGGAAVSSHGDHRIGMMLGIASCITE 399

Query: 418 VPVTIRDPGCTRKTTPDYFDVLSTFVKN 445
P+ I ++P +F+ L+ K
Sbjct: 400 EPIEIEHTDAIHVSYPTEFFHLNKLKSKK 427

>ref|ZP_00052321.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase
[Magnetospirillum magnetotacticum MS-1]
Length = 398

Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 128/394 (32%), Positives = 191/394 (48%), Gaps = 28/394 (7%)

Query: 48 LNSVDHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS 107
L S D M+ ALR LG+ +E + V + PV+ + G AG MR
Sbjct: 11 LRSRDADLMIAALRALGVGIEEGASPTLHVTPGTLRGPVD-----VDCGLAGTVMRF 63

Query: 108 LTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP---PVRVNGI 164
L A G + DG R RP+G +V L L V G P P V G
Sbjct: 64 LPPVAALADGAVRF--DGDEGARVRPMGPVVAALSALDVPVAGDDGGSPLTTLPTFTVRGR 121

Query: 165 GGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGV 223
G + GG V + S SSQ++S LL+AA + + + L S+P++EMT+ ++ GV
Sbjct: 122 GRVRRGGSVDIDASASSQFVSGLLLAARYDQGLTVRHVGHTLPSMPHIEMTVEVLREVG 181

Query: 224 KAEHSDS--WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 281
+ S W ++ G + ++ VE D S+A+ FLA A + GGTV V G T +
Sbjct: 182 VVDDSRPAIW---RVEPGPI--AARDVQVEPDLNAAPFLAALVAGGTVRVTGWPTATT 236

Query: 282 QGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVA 341
Q E+LE MGA + +TVTG ++ +DV+++ ++A T+A +A
Sbjct: 237 QPGAMPELLETMGATSSLDGDLTVTG-----TGEVRGVDVLDHAAGELAPTIAALA 289

Query: 342 LFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTY 401
ADGP+ +R +A R ET+R+ A+ TE+T+LG EE D +IT P L+ TY
Sbjct: 290 ALADGPSRLRGIAHLRGHETDRLAALATEITRLGGQAEETRDGLVIT-PRPLHGAVFR 348

Query: 402 DDHRMAMAFSLAACAEVPVTIRDPGCTRKTTPDY 435
DHRMA + ++ V + + T KT P +
Sbjct: 349 HDHRMATSAAVIGLRVPGVGVENVATTAKTLPGF 382

>ref|ZP_04203661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
F65185]
gb|EEL64644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
F65185]
Length = 432

Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPGSKSLSNRIILLALSEGTTVDNLLNSVDHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNNGLNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGK----LEGLQEPKAVLDVGNSTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK--- 173


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      +   + G   + +RP+   +   LKQ+GA++D           P+ + G           G +K
Sbjct: 111 TPF FSCVQGD ESI AKRPMKRV TNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
      +S   S+Q   SA+L+A   A G   +           + P++   + T R++E FGVK   +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISR DHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
      + GGQK   +   + V GD SSA++FL AGA I   + ++ G   +   +   +
Sbjct: 216 GKT VKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKM P DVAMTLAVVALFA---D 345
      VLE MGA T   +   + P           LK I++   + +P +   + V+AL A   +
Sbjct: 273 VLEKMGATFTVDLINEEASEPAANIT IETSS LK GIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHR 405
      G T I+D   +VKET R+   + ELTKLGA +E   D II   L   +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGN TVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
      + M   ++A C AE   I D   ++P +FD L   K
Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYP TFFDELQKLAK 432

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>ref|ZP_05666868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,141,733]
gb|EEV50201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,141,733]
Length = 431

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Score = 145 bits (366), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 211/441 (47%), Gaps = 24/441 (5%)

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Query: 8   VLQPIKEISGTVKLP GSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
      +LQ I   + GTV++P   KS+S+R ++   A++EGTT + N L +ED   L A + LG+ +
Sbjct: 3   LLQQIHLGRGTVRIPADKSIHRSIMFGAIAEGTTTIQNFLRAEDCLSTLHAFQQLGVEI 62

Query: 68   EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      E ++   +   G   P   +   + +GN+G   R L   + AG   T L G
Sbjct: 63   EEEEEVIKI HGRGSHSFVPPTPEP-----IDMGNSGTTSRLLMGIL--AGQPFTTTTLFGDA 115

Query: 128 RMRERP IGD LVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      + +RP+G ++   L+++GAD+   C P+ V G   L   +   +   + S+Q   SALL
Sbjct: 116 SLSKRPMGRVMEPLREMGADLQGNENDQCLPITVTGT HSLSPIRYNMPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      AA A G   I   ++K S   + E +R   +FG +   D   + G QK   +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IMVTGPQKLTG-QQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      V GD SSA++FLA G   +   + ++ G   +   +   +VLE MGA +T T   +
Sbjct: 227 ITVPGDISSAAFFLAAGLLVPESQLLLKNVGVNPNTRTGI--LDVLEEMGAAITQTNHNKQ 284

Query: 307 VTGPPREFFGRKHLKAIDVNMNKM P ---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      HLK   ++   +P   D   LA+VA A+G T I+D   +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIDGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTI 422
      + A+ EL K+GA ++   D II P L+   + + DHR+ M   +AA A+ P   +
Sbjct: 344 IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFFPDYFDVLSTFV 443
      ++P +FD L+   V
Sbjct: 404 EGAEAVSISYPAFFDDLAELV 424

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>ref|ZP_02082253.1| hypothetical protein CLOLEP_03742 [Clostridium leptum DSM 753]
gb|EDO59692.1| hypothetical protein CLOLEP_03742 [Clostridium leptum DSM 753]
Length = 377

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Score = 145 bits (365), Expect = 1e-32, Method: Compositional matrix adjust.

Identities = 112/352 (31%), Positives = 182/352 (51%), Gaps = 21/352 (5%)

Query: 90 AKKEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADV 149
A + L G +G +R L A G A + G R+ ERPIG + L Q G V
Sbjct: 31 APSQAVLDCGESGSTLRFLIPTAAAGGVRAEFTGRG--RLPERPIGVYLDCLPQAG--VA 86

Query: 150 CFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIP 209
C P ++ G L G +L G+ISSQ+++ LL+A P+ G EI + L S
Sbjct: 87 CRTQGGPLP--LSISGALRPGAFRLPGNISSQFITGLLLALPILNGGSEIRLTSPLESAG 143

Query: 210 YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT-- 267
YV+MT+ +M+RFGV + + + + G Q Y P++ +EGD S A++FLA A++
Sbjct: 144 YVDMTIEMMKRFGVTVTPVE--NGWLVPGNQSY-VPRDLAIEGDWSQAFFLAAGALSQA 200

Query: 268 -GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVN 326
G ++ + G S QGD + + + GAK++W + ++ P + + AID +
Sbjct: 201 QGSSILLRGLQKHSTQGDRQAFSLFQRFQAKLSWEPEGLRIS-----PGALRPIPADAS 255

Query: 327 MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 386
++PD+ LAV A G T+I A R+KE++R+ A+ + LG ++E PD +
Sbjct: 256 --QIPDLVPILAVTAALCPGITSITGAARLRIKESDRKAVAQGVAAALGGEIKELPDGLV 313

Query: 387 ITPPEKLNVTADITYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFFPDYFD 437
+T L+ + +DHR+ MA ++A+ E PV I D K++P +F+
Sbjct: 314 VTGKPMLSGGRAEGCNDHRIVMAMAVASLGCEKPVEITDAQSVSKSYPGFFE 365

>ref|YP_003436313.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ferroglobus placidus
DSM 10642]
gb|ADC66038.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ferroglobus placidus
DSM 10642]
Length = 408

Score = 145 bits (365), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 127/433 (29%), Positives = 209/433 (48%), Gaps = 41/433 (9%)

Query: 14 EISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E++G VK P SKS ++R L ALS + L++ + + ++ + + AA
Sbjct: 6 EVNGEVKAPPSKSYTHRALFAGALSRRARIYSPLISDDTLATAFSCCKSGSIFLRKGDAA 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ GG + N+G +R L + A G ++ +LDG +R RP
Sbjct: 66 IVGGLRKFGGYNYCM-----NSGTTLRILISLAAALGDHS--ILDGDESLRNP 112

Query: 134 IGDVLVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+L +K+LGA+V +G + P+++ G + G+V++SG SSQ++++LL A P
Sbjct: 113 NKELCEAVKKGAEV---IGGEEFKAPLKIRG--RIKAGEVEISGK-SSQFVTSLLFALP 166

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L +GD + + D L S PYV++TL ++E VK E + Y +YK + V
Sbjct: 167 L-VGDSVVRVD-LKSKPYVDVTLHVLEESNVKVEVEGNEYHVY---DSEYK-LREFQVP 220

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SS SY +A A + GG V+++ S QGD +++ MG +V W +
Sbjct: 221 PDFSSISYLIA-AGVVGGKVSINKV-VDSRQGDKVIVDLVREMGGRVEWRNDEIVAE--- 275

Query: 312 REPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+ L+ I+ + + PD+ T+AV+A A G T I + R+KET+R+ I L
Sbjct: 276 -----KSELEGIEFDASNNPDLPVTIAVLA AVAKGKTRIYNAEHLRLKETDRITTICENL 330

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFS-LAACA-EVPVTIRDPGCTR 429
+LG V+ G ++ +D++ DHR+AMAFS L E V I C
Sbjct: 331 RRLGVDVKCEGEIVVEGKGFREFKGVVDSFQDHRIAMAFSVLGLLGE--VRILKAECVS 388

Query: 430 KTFPDYFDVLSTF 442
++P +F L
Sbjct: 389 VSYPKFFQDLKKL 401

>ref|YP_002508788.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halothermothrix
oreonii H 168]

gb|ACL69793.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halothermothrix orenii H 168]
Length = 430

Score = 145 bits (365), Expect = 1e-32, Method: Compositional matrix adjust.
Identities = 128/454 (28%), Positives = 223/454 (49%), Gaps = 40/454 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+ ++ + G + +PG KS+S+R ++ +L+EG +++ L SED L A + +G+
Sbjct: 2 ELKIKKSNPLKGEINIPGDKSISHRSVIFTSLAEGRSLIRGFLESEDCLNLTIRAFQMMGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
++E K + +V G + +++ + + GN+G MR L + A VL G
Sbjct: 62 NIEKIKPGE--YIVNGVGLYGLKEPGDVIDC--GNSGTGMRLLCGLL--APQPFYSVLTG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R RP+G +V L+Q+GA + C G P+ + G L G L + S+Q S+
Sbjct: 116 DNSLRNRPMPGRVNVPLRQMGASIWCRDG-GYAPLSIKG-EKLEGISYTLPPVA-SAQVKSS 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A + GDV + P + T R+++ FGVK + + K +P
Sbjct: 173 LLLAGLYSQGDVFLTEPG-----PSRDHTERMKGFGVKVYKKGNSIKLPHSEDTKL-TP 226

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + GD SSA++F+ + IT G+ + ++ G + + +V+ MG +
Sbjct: 227 QEVLIPGDISSAAFFIVASLITPGSEILLKNVGLNPTRCGI--IDVVRQMGGNLELLNV- 283

Query: 305 VTVTGPPREPFGGRK-----HLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD 352
RE G K L+ + ++ + +P D +AV+A A G T IRD
Sbjct: 284 -----REVNGEKSADILVKYSELEGVHIDGDIIPRLIDEIPVIAVLASQARGETVIRD 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-EKLNVTATIDTYDDHRMAMAFS 411
A +VKET+R+ A TEL K G +EE PD +I P + +++Y DHR+AM+ +
Sbjct: 337 AAELKVKETDRIKATVTELKSGVDIEELPDGMVIKGPCSIIGGVKLESYKDHRIAMSLA 396

Query: 412 LAA-CAEVPVTIRDPGCTRTKTFPDYFDVLSTFVK 444
+A AE +TI++ C +FP + +L ++
Sbjct: 397 VAGLLAEEQITIKNSECINTSFPQFNKLLQKLIQ 430

>ref|ZP_04257264.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus BDRD-Cer4]
ref|ZP_04306583.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus 172560W]
ref|ZP_04318033.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC 10876]
gb|EEK50270.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC 10876]
gb|EEK61594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus 172560W]
gb|EEL10999.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus BDRD-Cer4]
Length = 432

Score = 145 bits (365), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFFSCVQGDESIAPKRPKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +

Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +

Sbjct: 216 GKTVKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVLVNVMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +

Sbjct: 273 VLEKMGATFTVDLINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR

Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYIGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSFVK 444
+ M ++A C AE I D ++P +FD L K

Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPTFFDELQKLAK 432

>ref|YP_872950.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
gb|ABK52964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
Length = 1004

Score = 145 bits (365), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 127/440 (28%), Positives = 224/440 (50%), Gaps = 27/440 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
IV + + E++G + +P SK ++R L+LA+L++GT+ + L ++ V Y +GALR LG

Sbjct: 4 IVKETVGELTGELAIPNSKYHAHRALILASLADGTSYIHGLSDAGHVRYTIGALRALGTR 63

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ D VV G P + +G++G + LT A +A + G

Sbjct: 64 IDVD---GNTFVVRGGPYRP-----RRADVSVGSSGTTLYFLTG--LAGLADAPVRIVGQ 113

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLP-GGKVKLSGSISSQYLSA 185
+ RPI L+ L+ LG V T CPP+ V G P GG+V ++G++ SQ++S

Sbjct: 114 RYFQRRPIRPLAALQALGMQVGS--ATGCPPIEVR--PGRPRGGRVTIAGTL-SQWISG 168

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+ AP A IE+ +L Y+++T+R+M FG+ + + RF + Q + P

Sbjct: 169 LLLLAPFAAATTVIEVDGELNERSYIDLTIRMMREFGLHVDAAPDGRRFEVPPNQTPR-P 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL-QGDVKFAEVLEM---MGAKVTWT 301
+ D +A++ LA A+ V G S + D A++L++ MG +

Sbjct: 228 ATVTLPDPVGAAAFGLAVTALHPSDVLFRGLPALSASETDHPHADLLDIVAGMGLPMRID 287

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ V R L IDV+ +PD+ L+V+A FA G + +R++A R+KE+

Sbjct: 288 PDAGVV---RVTHHGIDLAPIDVDCRSVPDMLPILSVLATFAKGRSRLRNIAHVRLKES 343

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ A+ +L ++G +E+ D + ++L + +++DHR+ MA ++AA AE

Sbjct: 344 DRVAAM-LQLNRMGGRLEQRGDELVCDDVLDLVGADLSSFNDRVLMALAVAASRAEGET 402

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
+ P R ++P + D ++

Sbjct: 403 RLTPPNAYRISYPRFLDEM 422

>ref|YP_003430849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
gallolyticus UCN34]
emb|CBI13925.1| Putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Streptococcus gallolyticus UCN34]
Length = 427

Score = 145 bits (365), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 126/449 (28%), Positives = 225/449 (50%), Gaps = 37/449 (8%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67

Sbjct: 3 +L + ++ GT+++PG KS+S+R ++ +L++GTT V ++L EDV + R LG+ +
LLTNVSQKLGTLRVPDGKSIHSRISIMFGSLAKGTTTVHDILRGEDVLSTMQVFRDLGVDI 62

Query: 68 EADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D VG G K P + +L +GN+G ++R ++ + AG + T + G

Sbjct: 63 QDDGNIVTITGVGFDGLKAP-----KNKLDMGNSGTSIRLISGVL--AGQDFTVEMFGD 114

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + + L+Q+G +V D PP+ + G L +L + S+Q SAL

Sbjct: 115 DLSLSKRPMDRVITPLRQMGVEVSGQTDRLDPLPLTMRGSKALKPIHYQLPVA-SAQVKSAL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA A D E II+K + + E ++ +FG + + R IKGGQ++ + +

Sbjct: 174 IFAALQA--DGESVIEKEKTRNHT---DMIVQFGGAIDVNGKEIR--IKGGQEF-TGQ 225

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303
+ V GD SSA+++L AG + VT+E G + +V++ MG K+T +

Sbjct: 226 DVVVPGLDISAFLVAGLIVPNAKVTLENVGINETR--TGIIDVIKEMGGKMTISNVDE 283

Query: 304 ---SVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWR 357
S T+T E L +++ +P + L ++AL A+G T IRD +

Sbjct: 284 IAKSATITVETSE-----LHGVEIGGEIIPRLIDELPIIALLATQANGTTIIRDAEELK 337

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--C 415
VKET+R+ + L +GA + D II L+ ++T+ DHR+ M ++AA

Sbjct: 338 VKETDRIQVADALNAMGADITPTDDGMIKGTPLHGAKVNTFGDHRIGMMAIAALLV 397

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++ V + ++P +F+ L +

Sbjct: 398 SDGDVELERAEAINTSYPSFFNDLEVLRSR 426

>ref|ZP_04212655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock4-2]
gb|EEL55709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock4-2]
Length = 432

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 131/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEIEVLQPIKE-ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +

Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N

Sbjct: 61 FKEMG--VEITQNGDEVTVVGK-----LEGLQEPKAVLDVGNSGTTIRLMSGILA----N 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K

Sbjct: 111 TPFFSCVQGDSEIAKRPMKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +

Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +

Sbjct: 216 GKTVKLSGGQKL-TAADIQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +

Sbjct: 273 VLEKMGATFTVDLINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR

Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYIGKSALKGNVTNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K

Sbjct: 393 IGMLAIAGCLAEGKTIIEDAEAVGVSYPTFFDELQKLAK 432

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>ref|NP_845288.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Ames]
ref|YP_019596.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. 'Ames Ancestor']
ref|YP_029002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Sterne]
ref|ZP_00393186.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase [Bacillus
anthracis str. A2012]
ref|ZP_02213109.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0488]
ref|ZP_02396235.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0193]
ref|ZP_02895329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0389]
ref|ZP_02932431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0174]
ref|ZP_03017987.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
Tsiankovskii-I]
ref|YP_002814250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. CDC 684]
ref|YP_002867201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0248]
ref|ZP_05195670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Western North America USA6153]
ref|ZP_05204320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Vollum]
ref|ZP_05212823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Australia 94]
sp|Q81P64.1|AROABACAN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|C3NZR4.1|AROABACAA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|C3LF06.1|AROABACAC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAP26774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Ames]
gb|AAT32071.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. 'Ames Ancestor']
gb|AAT55053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Sterne]
gb|EDR20692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0488]
gb|EDR89872.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0193]
gb|EDS99525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0389]
gb|EDT69561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0174]
gb|EDV18347.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
Tsiankovskii-I]
gb|ACPI6234.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. CDC 684]
gb|ACQ49969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0248]
Length = 429
```

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 218/456 (47%), Gaps = 44/456 (9%)

```
Query: 5 EEIVLQPIKE-ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EGTT + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISRRAVMFGAIAEGTTTIKGFPLGADCLSTISCFKEM 61
```

```
Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N ++
```

Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTGTTIRLMSGIL----ANTPFL 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S

Sbjct: 112 SCVQGDTSIAKRPMKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +

Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE

Sbjct: 217 KLAGGQKL-TATDVQVPDGVSSAAFFLVAGAIIPNSKLVLENVGMNPRTGTI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T

Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M

Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDRMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +F+ L K

Sbjct: 394 LAIAGCIAEGKTTIEDAEAVGVSYPYTFEELQKLAK 429

>ref|ZP_04228425.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-29]
ref|ZP_04245856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock1-3]
gb|EEL22432.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock1-3]
gb|EEL39880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-29]
Length = 429

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 131/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QPI ++G + +PG KS+S+R ++ A++EG T + L D + + +

Sbjct: 2 KERTIQPINSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +

Sbjct: 62 G--VEITQNGDEVTVVGKG----IEGLQEPKAVLDVGNSTGTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA +D P+ + G G +K +S

Sbjct: 112 SCVQGDASIAGRPMKRVTNPLKQMGAKIDGREGTFTPLTIRG-----GDLKAIEYISP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGV +

Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVNV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE

Sbjct: 217 KLAGGQKL-TATDVQVPDGVSSAAFFLVAGAIIPNSKLVQNVGMNPRTGTI--IDVLET 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T

Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L + +++Y DHR+ M

Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGSTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K

Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPYTFEELQKLAK 429

>emb|CBL28511.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synergistetes
bacterium SGP1]
Length = 428

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 136/433 (31%), Positives = 215/433 (49%), Gaps = 32/433 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++GTV P SKS ++R+L+ AALS+ T + SED+ LR+LG V ++
Sbjct: 8 RPLAGTVTAPASKSEAHRLICAALSDRPTRTLNGTSEDIDATADCLRSLGAEVLHEEG 67

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + + P+ D +E +G +R L A A + G R+ ER
Sbjct: 68 SLVVTPIRRVPDPLDCRE-----SGSTLRFLLPVAAALAEERFTGSG--RLPER 117

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PIG L + + G D P R +G L G L G +SSQY++ LL+ PL
Sbjct: 118 PIGALQAAMARHGV-----FSADRLPFRTPSGR--LQAGAFDLPGDVSSQYVTGLLLTLPL 171

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHE-----SDSWDRFYIKGGQKYKSPKNA 248
GD + + L S Y+++TL + RFGV+ +D RF + G Q + +P
Sbjct: 172 LSGDSLTVHPPLRSAYLDITLAALRRFGVRPREEGGADLPRRFQLSGPQAFHTPGVL 231

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD S A++FLA A+T G V+V G S QGD + + L+ GA+V+ + +VTV
Sbjct: 232 EVGGDWSGAFFFLAAGALT-GPVSVRGLDPASPQGDRLRILDFLKAFGAEVSLRKDAVTVA 290

Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P + L+ +++ PD+ LA A +ADG TA + R+KE++R+ +
Sbjct: 291 -----PGSLRGLGECPLDVDATPDLLPVLAATAAWADGRTAFVNGGRLRLKESDRIASTL 345

Query: 369 TELTKLGASVEEGP--DYCIITPPEKLNVTATIDTYDHRMAMAFSLAA--CAEVPVTIRD 424
+ + LG EE P D I+ + TA + + DHR+ MA ++AA C + VT+ D
Sbjct: 346 SLIRSLGGRAEETPEGDLIVQGGGLVGGTA-EGFHDHRIVMAAAVAASRCPQG-VTVTD 403

Query: 425 PGCTRKTFPDYFD 437
K++P +F+
Sbjct: 404 AEACSKSYPAFFE 416

>ref|ZP_02920877.1| hypothetical protein STRINF_01760 [Streptococcus infantarius subsp.
infantarius ATCC BAA-102]
gb|EDT46756.1| hypothetical protein STRINF_01760 [Streptococcus infantarius subsp.
infantarius ATCC BAA-102]
Length = 427

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 224/447 (50%), Gaps = 37/447 (8%)

Query: 8 VLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+L + ++ GT+++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +
Sbjct: 3 LLTNVSKLQGTLRIPGDKSISHRSIMFGSLAKGKTTVRDILRGEDVLSTMQVFRDLGVDI 62

Query: 68 EADKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D VG G K P + +L +GN+G ++R ++ + AG + T + G
Sbjct: 63 QDDGDLVTITGVGFDGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFTVEMFGD 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + + L+Q+G +V D PP+ ++G L +L + S+Q SAL
Sbjct: 115 DSLSKRPMDRVITPLRQMGVEVSGQTERDLPPLTMHGSKNLKIHYQLPVA-SAQVKSAL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHESDSWDRFYIKGGQKYKSPK 246
+ AA A D E II+K + + E ++ +FG K + + R IKGGQ++ + +
Sbjct: 174 IFAALQA--DGESVIEKEKTRNHT---DMIVQFGGKIDVNGKEIR--IKGGQEF-TGQ 225

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303
+ V GD SSA++L AG + VT+E G + + +V+ MG K+T ++
Sbjct: 226 DVVVPGDISSAAFVLVAGLIVPNAKVTLENGINETRTGI--LDVILAMGGKMTISDVDE 283

Query: 304 ---SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWR 357
S T+T E L ++ +P + L ++AL A+G T IRD +
Sbjct: 284 VAKSATITVETSE-----LSGTEIGGEVIPRLIDELPIIALLVLTQANGTTVIRDAEELK 337

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--C 415
VKET+R+ + L +GA + D II L+ I+T+ DHR+ M ++AA
Sbjct: 338 VKETDRIQVADALNAMGADITPTDDGMIKGTPLHGAKINTFGDHRIGMMAAIAALLV 397

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+E V + ++P +F L
Sbjct: 398 SEGDVELERAEAINTSYPSFFSDLEVL 424

>ref|ZP_08047105.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
C150]
gb|EFX54680.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
C150]
Length = 427

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 123/444 (27%), Positives = 222/444 (50%), Gaps = 37/444 (8%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++ + G+++PG KS+S+R ++ +L++G T V ++L EDV + R LG+++E D
Sbjct: 7 VQGLHGSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVTIEDDG 66

Query: 72 AAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
R VG G K P + +L +GN+G ++R ++ + AG + + G +
Sbjct: 67 DVVRIHVGFGDLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFEVEFMFGDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + + L+Q+G +V D PP++++G L +L + S+Q SAL+ AA
Sbjct: 119 KRPMDRVITIPLRQMGVEVSGQTDRDLPLKMHGSKSLKPIHYQLPVA-SAQVKSALIFAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A D E II+K + + E ++++FG + + R I GGQ + + K V
Sbjct: 178 LQA--DGESVIIKEKTRNHT---DMIQQFGGQLQVDGKEIR--ISGGQSFTAQK-VVV 229

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE-----TS 304
GD SSA+++L AG + + +E G + +V++ MG K+T ++ S
Sbjct: 230 PGDISSAAFVLVAGLVVPSKIVLENVGINETR--TGIIDVIKDMGGKITLSDIDQVAKS 287

Query: 305 VTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
T+T E LK ++ + +P + L ++ L A G T IRD +VKET
Sbjct: 288 ATITVETSE-----LKGTEIGGDIIPRLIDELPIITLLATQAQGKTVIRDAEELKVKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
+R+ + L +GA + D II+ L+ I+T+ DHR+ M ++AA +
Sbjct: 342 DRIQVADALNAMGADIVPTEDGMIISGKTALHGAEINTFGDHRIGMMAIAALLVQDGE 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
V ++ ++P +F L +
Sbjct: 402 VDLQRAEAINTSYPSFFSDLEGLI 425

>ref|ZP_00144747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. vincentii ATCC 49256]
gb|EAA23660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. vincentii ATCC 49256]
Length = 423

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 109/449 (24%), Positives = 208/449 (46%), Gaps = 48/449 (10%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M G + +++ ++G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A+
Sbjct: 1 MRGMNKKIIKA-NRLTGEVTPPPSKSILHRYIIASSLAKGISKIENISYSDDIATIEAM 59

Query: 61 RTLGLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LG +E +++ F + ++ +G +R L +
Sbjct: 60 EKLGAKEK---KDNLYLLIDGSKTFDKYLNNAEIDCNESGSTLRFLFPLSIVKKNKIS 116

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGS 177
+ G ++ +RP+ + + N I G L GK ++ G+
Sbjct: 117 F--KGKGLFKRPLNPYFENFDKYKIKY-----SYINENEILLDGLKSGKYEIDGN 166

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
ISSQ+++ LL + PL + +I I KL S Y+++TL + +FG+ +S+ F IK
Sbjct: 167 ISSQFITGLLFSPLLNENSKI I I K G L E S S Y I D I T L D C L N K F G I N I - I K N S Y K E F I I K 225

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Q YKS + VE D S ++FL +I G + + G T SLQGD K + + +
Sbjct: 226 GNQNYKSG-DYEVEADYSQVAFFLVANSI-GSNIKINGLNTNSLQGDKKIIDFISQID-- 281

Query: 298 VTWT-ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASW 356
W E + + G + PD+ L++ A + I ++A
Sbjct: 282 -NWNKEEKLILDGS-----ETPDIIPILSLKACTSKKEIEIVNIARL 322

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----VTAIDTYDDHRMAMAFS 411
R+KE++R+ A EL+KLG + E D +I + N + + ++ DHR+AM +
Sbjct: 323 RIKESDRLKATVKELSKLGFDLLEKESILINSRKDFNKINNSLVYLSSHSDHRIAMTIA 382

Query: 412 LA-ACAEVPVTIRDPGCTRKTFPDYFDVL 439
+A C + + + C +K++P++++V
Sbjct: 383 IALTCYNGEIIILDNLDCKVKSYPNFWVEVF 411

>ref|ZP_04223137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-42]
gb|EEL45190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
Rock3-42]
Length = 429

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 130/452 (28%), Positives = 218/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTL 63
+E ++QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERIIQPVNSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTGTTIRLMSGILA---NTPFF 111

Query: 123 --LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L + S S+
Sbjct: 112 SCVQGDASIARPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-GDLKAIEYN-SPVASA 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGK + + G
Sbjct: 170 QVKSAILLAGLAEVGTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTVKLAG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQK + + V GD SSA++FL AGA I + +E G + + +VLE MGA
Sbjct: 221 GQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEKMGAT 277

Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVEPINESSEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMI IYGKSALKGNTVNSYGDHRIGMMLAIA 397

Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
C AE TI D ++P +F+ L K
Sbjct: 398 GCIAEGKTTIEDAEAVGVSYPTFFFEELQKLAK 429

>ref|YP_001421669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
amyloliquefaciens FZB42]
sp|A7Z612.1|ARO_A_BACA2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAL26234.1| 5-enolpyruvylshikimate-3-phosphate synthase [Bacillus
amyloliquefaciens FZB42]
gb|ABS74438.1| AroE [Bacillus amyloliquefaciens FZB42]
Length = 428

Score = 144 bits (364), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 213/447 (47%), Gaps = 34/447 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ + ++G + +PG KS+S+R ++ AL+EGTT V N L D + R +G+S+E
Sbjct: 4 EKVTSNLGEIHIPGDKSISHRSVMFGALAEAGTTTVKNFLPGADCLSTIACFRKMGSIEQ 63

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + G G E + L +GN+G +R + + AG + G +
Sbjct: 64 N--GSDVTIYGKIDALCE---PDSLDDVGNSTTIRLMLGIL--AGRPFHSTVAGDESI 116

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + LKQ+GA +D P+ V GG G +S S+Q SA+L+A
Sbjct: 117 AKRPMKRVTEPLKQMGAAIDGRADGGFTPLSVR--GGQLKGIDYVSPVASAQIKSAVLLA 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G + K + T R++ FG AE +++ + GGQK + + +
Sbjct: 175 GLQAEGTTTVPTEPHK-----SRDHTERMLNAGF--AELAETETSASVTGGQKLRG-ADIF 226

Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FL AGA + G + ++ G + +VL+ MGA + +
Sbjct: 227 VPGDISSAAFFLAAGAVVPGSRIVLKNVGLNPTR--TGMIDVLKQMGASLEVIPSEADSA 284

Query: 309 GPPREPF-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKE 360
EP+G LKA ++ +P + + ++AL A+G T I+D A +VKE
Sbjct: 285 ----EPYGDVLIETSALKAAEIGGEIIPRLIDEIPIIALLATQAEGTTVIKDAAELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT- IDTYDDHRMAMAFSLAAC-AEV 418
T R+ + +EL K+GA +E D I + L A + ++ DHR+ M +A+C E
Sbjct: 341 TNRIDTVSELKRGADIEPTEDGMKIHGKKTLAGGADVSSHGDHRIGMMLGVASCLTEE 400

Query: 419 PVTIRDPGCTRTFPDYFDVLSTFVK 445
P+ IRD ++P +F+ L K
Sbjct: 401 PIDIRDTEAIHVSYPTEFFEHLQDLAKK 427

>ref|ZP_07727814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis F0405]
gb|EFQ54909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis F0405]
Length = 427

Score = 144 bits (363), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 218/446 (48%), Gaps = 41/446 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GT+++PG KS+S+R ++ +L++G T V ++L EDV + R LG+S++ D
Sbjct: 8 KGLKGTIRVPGDKSISHRSIIFGSLAKGETKVYDILRGEDVLSTIQVFRDLGVSIQDDGD 67

Query: 73 AKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R VG G + P L +GN+G ++R ++ + AG + + G + +
Sbjct: 68 VIRIQGVGFQGLQAPT-----APLDMGNSGTSIRLISGVL--AGQDFAVTMVGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ DCP+ G L +L + S+Q SAL+ AA
Sbjct: 120 RMDRVAIPLRQMGVEIAGQGDRDCPLHEKGTHQLKPIHYRLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +R +FG + R IKGGQ+++ + V
Sbjct: 179 QAEG--ESTIIEKEKTRDHTEDMIR---QFGGEILMDGKIIR--IKGGQEFQG-QEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTE-----T 303
GD SSA+++L AG + + +E G Q +V++ MG +T +
Sbjct: 231 GDISSAAFWLVAGLILPESAKIENVGIN--QTRTGILDVIQEMGGDLTIEDRDEKAVSA 288

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
S+TV LK I ++ +P + L ++AL A +G T I D RVKE
Sbjct: 289 SLTVK-----TSSLKGIRIDGELIPRLIDELPIALLATQANGQTVIADAEELRVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEV 418
T+R+ + L +GA+V D IIT P L+ ++T+ DHR+ M ++AA +
Sbjct: 341 TDRIQVADSLNAMGANVVP TKDGM IITGPTPLHGADLETFGDHRIGMMAAIAALLVRDG 400

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
V + ++P +F+ L T +
Sbjct: 401 NVMLDRAEAINTSYPSFFEDLETLH 426

>ref|ZP_03981696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX1330]
ref|ZP_05664085.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,501]
ref|ZP_05675405.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
Com12]
ref|ZP_06623826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
PC4.1]
ref|ZP_06682847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E980]
gb|EEI60182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX1330]
gb|EEV47418.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,501]
gb|EEV58738.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
Com12]
gb|EFF37391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E980]
gb|EFF61758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
PC4.1]
Length = 431

Score = 144 bits (363), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 210/441 (47%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSIHSRISIMFGAIAEGTTTQNFLEADCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + G P + + +GN+G R L + AG T L G
Sbjct: 63 EEEEEVIKIHRGSHSFVPPTPEP-----IDMGNSGTTSRLLMGIL--AGQPFTTTLFGDA 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ C P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMGRVMEPLREMGADLQGNENDQCLPITVTGTRSLSPIRYNMPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IMVTGPQKLTG-QQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAFAFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNNHKQ 284

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAELV 424

>ref|ZP_04175135.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH1273]
ref|ZP_04180899.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH1272]
gb|EEL87397.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH1272]
gb|EEL93159.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus AH1273]
Length = 429

Score = 144 bits (363), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 130/453 (28%), Positives = 222/453 (49%), Gaps = 38/453 (8%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +Q + ++GT+ +PG KS+S+R ++ A++EG T + L D + ++
Sbjct: 2 KETTIQTVTNGLTITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + + V+G G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VEITQNGEEVTVIGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA +D P+ + G G L ++ + ++S
Sbjct: 112 SCVQGDASIAKRPMKRVTNPLKQMGAKIDGREEGTFTPLTIRG-GDLQA--IEYTSPPVAS 168

Query: 181 -QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK 237
Q SA+L+A A G + + P++ + T R++E FGVK + +
Sbjct: 169 AQVKSAILLAGLRAEGVTAV-----TEPHISRDRHTERMLEAFGVKV--TREGTKVKLA 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE MGA
Sbjct: 220 GGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVQNVGMNPTRTGI--IDVLEKMG 276

Query: 297 KVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRD 352
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 277 MFTVEPINESSEPAANITITETSSLGIEIGDIIPLRIDEIPVIALAATQAEGITVIKD 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSL 412
+VKET R+ + ELTKLGA +E D II L +A++++ DHR+ M ++
Sbjct: 337 AHELKVKETNRIDTVVAELTKLGARIEATDDGMIYKGSALKGSASVNSHGDHRIGMMLAI 396

Query: 413 AAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
A C AE TI D ++P +F+ L T K
Sbjct: 397 AGCIAEGETTIEDAEAVGVSYPTFFEELQTLAK 429

>gb|ABM75230.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. NATL1A]
Length = 422

Score = 144 bits (363), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 131/434 (30%), Positives = 211/434 (48%), Gaps = 26/434 (5%)

Query: 19 VKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+K+PG KS+S+R LL A+++G T+++ LL +ED LR++G+ + K +
Sbjct: 1 MKVPGDKSISHRALLFGAIAKGKTLIEGLLPAEDPLSTAECRLSMGVKISPIKKGDIIIEI 60

Query: 79 VGCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
G G + +E Q L GN+G MR L + A + ++L G +R RP+
Sbjct: 61 EGVG-----LNLGLQEPQDILNCGNSGTTMR-LIMGLLAGQKDHFFILTGDKSLRNRPMKR 114

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ LK +GA V G D P+ + IG G V + S+Q SA+L+AA A G
Sbjct: 115 VGQPLKMMGAKVFGRCGGDLAPLSI--IGNKLRGAVIGTPVASAQIKSAILLAALNAEGS 172

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ S + E R+++ FG E R K ++ V GD SS
Sbjct: 173 TTV--IEPARSRDHSE---RMLKAFGANLEVGEMGRHITVSPGKDLKGQSIIVPGDISS 227

Query: 257 ASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR--- 312

A+++L AG+ I G + VE G + + +VLE M A + V G P
Sbjct: 228 AAFWL VAGSIIPGSELVVENVLNPTRTGI--LDVLEAMEANINVINKR-DVAGEPVGDI 284
Query: 313 EPFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
E F +++LK ++ MP D L+V A F +G + I+ + RVKET+R+ +
Sbjct: 285 EVFYKENLKPFIKIDDEIMPRLVDEIPILSVGACFCNGISQIKGASELRVKETDRLAVMAR 344
Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCT 428
+L ++GASV+E D I + L +D+ DDHR+AM+ ++A+ A T+R
Sbjct: 345 QLKRMGASVDEHQDGLTIYGGKSLEGCELDSEDDHRIAMSLAIASIMANSNSTLRRSEAA 404
Query: 429 RKTFFPDYFDVLSTF 442
++PD++ L
Sbjct: 405 AISYPDFWSDLKRL 418

>ref|ZP_02390652.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0442]
ref|ZP_02876744.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0465]
ref|ZP_05149370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. CNEVA-9066]
ref|ZP_05184703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A1055]
ref|ZP_05200545.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. Kruger B]
gb|EDR95259.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0442]
gb|EDT21619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
str. A0465]
Length = 429

Score = 144 bits (363), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 218/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRIILL AALSEGTTVVNDNLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EGTT + L D + + +
Sbjct: 2 KERTIQPVNNGNLNGNITIPGDKSISHRAVMFGAIAEGTTTIGKFLPGADCLSTISCFKEM 61
Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N ++
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTGTTIRLMSGIL----ANTPFL 111
Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDTSIAKRPMKRVTNPLQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165
Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216
Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPDVSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEK 273
Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393
Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +F+ L K
Sbjct: 394 LAIAGCIAEGKTIIEDAEAVGVSYPPTFFELQKLAK 429

>ref|NP_856901.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium bovis
AF2122/97]
sp|Q7TWY4.1|ARO_A_MYCBO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD95348.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE AROA
(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP
SYNTHASE) (EPSPS) [Mycobacterium bovis AF2122/97]
Length = 450

Score = 144 bits (362), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 211/439 (48%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPKSGKSLNRIALLAAL----SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL G + + L S D ML AL+TLGL V+
Sbjct: 13 VRATVTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTLMMLDALQTLGLRVD-- 70

Query: 71 KAAKRAVVVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
G G + V E ++ G AG +R + AA G+ DG
Sbjct: 71 -----GVGSELTVSGRIEPPGARVDCLAGTTLRFVPP--LAALGSVPVTFDGDQ 119

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ R RPI L+ L++LG VD GT P RV+G G L GG V + S SSQ++S LL
Sbjct: 120 QARGRPAPLLDALRELGVAVD---GTGLP-FRVHNGSLAGGTVAIDASASSQFVSGLL 175

Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++A + ++ L S P++ MT ++ + GV + S +R+ ++ G +
Sbjct: 176 LSAASFTDGLTVQHTGSSLPAPHIAMTAAMLQAGVDIDDSTP-NRWQVRPGPVAA--R 232

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+E D ++A FL+ A ++GGTV + G S+Q +L + A V ++S+
Sbjct: 233 RWDIEPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLNAVVIHADSSLE 292

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDAMTLAVVALFADGPTAIR--DVASWRVKETERM 364
V GP DV++ + ++ ++A +A A + R +A R ET+R+
Sbjct: 293 VRGP-----TGVDGFDVLDRAVGELTPSVAALALASPGSVSRSLGIAHLRGHETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TE+ +LG + E PD +IT L Y DHRMAMA ++ V + D
Sbjct: 346 AALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAIIGLRVAGVEVDD 404

Query: 425 PGCTRKTFFPDYFDVLSTFV 443
T KT P++ + + V
Sbjct: 405 IAATTKTLPEFPRLWAEMV 423

>ref|ZP_03109499.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
NVH0597-99]
gb|EDX65562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
NVH0597-99]
Length = 429

Score = 144 bits (362), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 130/452 (28%), Positives = 217/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E ++QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERIIQPVNSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGILA----NTPFF 111

Query: 123 --LDGVP RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L K S S+
Sbjct: 112 SCVQGDASIAPKRPKRVNPLKQMGANIDGREGTFTPLTIRG-GDLKAIKYN-SPVASA 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGK + + G
Sbjct: 170 QVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTVKLAG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQK + + V GD SSA++FL AGA I + +E G + + +VLE MGA
Sbjct: 221 GQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEKMGAT 277

Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITIIKDA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMMLAIA 397

Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
C AE I D ++P +F+ L K
Sbjct: 398 GCIAEGKTIIEDAEAVGVSYPTFFFEELQKLAK 429

>ref|ZP_04072541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus thuringiensis IBL 200]
gb|EEM95759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus thuringiensis IBL 200]
Length = 432

Score = 144 bits (362), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 129/460 (28%), Positives = 219/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNNGLNGLDITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE ++ VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQSGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGILA----N 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFVFCVQGDSEIAKRPKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYL SALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 216 GKTVKLSGGQKL-TATDIQVPBGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
V+E MGA T + + P LK I++ + +P + + ++AL A +
Sbjct: 273 VIEKMGATFTVDLINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPIIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +FD L K
Sbjct: 393 IGMMLAIAAGCLAEGKTIIEDAEAVGVSYPSFFDELQKLAK 432

>ref|ZP_04217934.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Rock3-44]
gb|EEL50362.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Rock3-44]
Length = 429

Score = 144 bits (362), Expect = 3e-32, Method: Compositional matrix adjust.
Identities = 127/453 (28%), Positives = 220/453 (48%), Gaps = 38/453 (8%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 63
+E +QP+ ++GT+ +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGLNGLTITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + +V G G +E +E + L +GN+G +R ++ + N +

Sbjct: 62 GVDITQN--GDEVIVSGKG----IEGLQEPKAVLDVGNSTGTTIRLMSGILA---NTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D G P+ + G G L ++ + ++S

Sbjct: 112 SCVQGDASIARKRPMKRVTDPLKQMGANIDGREGGTYTPTLIRG-GDLKA--IQYTSPVAS 168

Query: 181 -QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK 237
Q SA+L+A A G + + P++ + T R++E FGV + ++

Sbjct: 169 AQVKSALLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TREGKTVKLE 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GGQK + V GD SSA++FL AGA I + ++ G + + +VLE MGA

Sbjct: 220 GGQKLIG-TDVQVPGDVSSAAFFLVAGAIIPNSKLVQNVGMNPTRTGI--IDVLERMGA 276

Query: 297 KVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPVAMTLAVVALFA---DGPTAIRD 352
T + + P LK I++ + +P + + ++AL A +G T I+D

Sbjct: 277 TFTVEPINEGASEPAANITITETSSLKGIEIGDMIPRLIDEIPIIALAATQAEGITVIKD 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSL 412
+VKET R+ + ELTKLGA +E D II L + +Y DHR+ M ++

Sbjct: 337 AHELVKETNRIDTVVAELTKLGARIEATEDGMIIYGKSALTGNEVHSYGDHRIGMMLAI 396

Query: 413 AAC-AEVPVTIRDPGCTRKTFFDYFDVLSTFVK 444
A C AE TI+D ++P +F+ L K

Sbjct: 397 AGCIAEGKTTIQDAEAVGVSYPTFFEELQKLAK 429

>ref|YP_003020815.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. M21]
sp|C6E2B1.1|ARO_A_GEOSM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACT17057.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. M21]
Length = 429

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 130/451 (28%), Positives = 209/451 (46%), Gaps = 33/451 (7%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E +QP K + G + +PG KS+S+R ++ ++S G T V L ED L A R +G

Sbjct: 2 ENYTVQPAKSVRGEISVPGDKSISHRSIMFGSISGVTGVTGFLRGEDALATLQAFRAMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ ++ D G G D L GN+G +MR LT + AG N VL

Sbjct: 62 VQIDDDGETVTIQGRGLHGLSEPTDV-----LDCGNSGTSMRLLTGLL--AQQNFFSVLS 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNG---IGGLPGGKVKLSGSISSQ 181
G +R RP+ +V L +GA + G + P+ + G IG ++ +SS

Sbjct: 115 GDKYLRLRPMKRVVGPLALMGARISGRAGGEKAPLAIQGSKLIG-----IEYDSPVSSA 168

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+ + +M A L G E + + +S + E R++ FG E ++GG +

Sbjct: 169 QVKSAILLAGLYAGG-ETVVREPHLSRDHSE---RMLRAFGAHVETFPGG--VKVRGGAE 222

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ ++ V GD SSA++FL A I G+ + + G G + +VL+ MG +

Sbjct: 223 L-TGRDIVVPGDISAFAFLVAALIVPGSDLLIRGVGNPTR--TGIIDVLKGMGGDLEL 279

Query: 301 TETSVTVTGPPREPFRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVAS 355
T +G P +H L A+++ +P D + V A A G T +RD A

Sbjct: 280 TNQR-DESGEPVADIRVRHSLTAMEICGEVVPRAIDFPAICVAASLAQGTTVVRDAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
RVKET+R+ A+ L + G ++ E PD IT L A D++ DHR+AM+ +A

Sbjct: 339 LRVKETDRISAMADNLRRAGVNIVETPDGMQITGVASLKGCAADSFGDHRIAMSMVAGL 398

Query: 415 CAEVPVTIRDPGCTRKTFFDYFDVLSTFVK 445
A+ ++ D C +FP + ++L V+

Sbjct: 399 VAQGETSVSDVECIATSFPGFVNLLDGVVQR 429

>ref|ZP_04572355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.]

4_1_13]
gb|EEO39734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
4_1_13]
Length = 424

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 109/434 (25%), Positives = 208/434 (47%), Gaps = 48/434 (11%)

Query: 17 GTVKLPQSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A++ LG +E +
Sbjct: 16 GEVTPPPSKSILHRYIIASSLAKGISKIENISYSDDITATIEAMKKLGAKIEKNN---NY 72

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F E ++ +G +R L ++ N + G ++ +RP+
Sbjct: 73 LLIDGSKTFDKEYLNNNAEIDCNESGSTLRFL-FPLSIVKENKI-LFKGKGKLFKRPLSP 130

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + N I G L + ++ G ISSQ+++ LL + PL
Sbjct: 131 YFENFDKYQIKY-----SYINENEILLDGEKLSVEYEIDGDISSQFITGLLFSPLPL 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ +I I KL S Y+++TL + +FG+K ++S+ F I+G Q YKS + VE D
Sbjct: 183 NGNSKISIKGKLESSYIDITLDCLNFKGIKI-INNSYQEFIEGNGQNYKSG-DYEVEAD 240

Query: 254 ASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ETSVTVTGPPR 312
S ++FL +I G + + G T SLQGD K +++ + W E + + G
Sbjct: 241 YSQVAFFLVANSI-GSNIKINGLNTNSLQGDKK---IIDFISQIDNWNKEEKILIDGS-- 294

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ PD+ L++ A + I ++A R+KE++R+ A EL+
Sbjct: 295 -----ETPDIIPILSLKACTSKKEIEIVNIARLRIKESDRKATVKELS 338

Query: 373 KLGASVEEGPDYCIITPPE---KLN---VTAIDTYDDHRMAMAFSLA-ACAEVPVTIRDP 425
KLG + E D +I + K+N + + ++ DHR+AM ++A C + + +
Sbjct: 339 KLGFDLLEKEDSILINSRKDFYKINNNSLVYLSSHSDHRIAMTIAIALTCYNGEIIIDNL 398

Query: 426 GCTRKTFPDYFDVL 439
C +K++P++++V
Sbjct: 399 DCVKKSYPNFWVEF 412

>ref|YP_003563454.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
QM B1551]
gb|ADE70020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
QM B1551]
Length = 423

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 125/443 (28%), Positives = 219/443 (49%), Gaps = 36/443 (8%)

Query: 12 IKEISGTVKLPQSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+++PG KS+S+R ++ +++EGTT ++ L +D + + LG+ ++
Sbjct: 3 VKALRGTIQIPGDKSISHRSVMFGSIAEGTTTNGFLPGDDCLSTISCFQKLGVDIQM-- 60

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+++VVV G ++ KE + +GN+G +R + + ++T + D +
Sbjct: 61 IDEQSVVVGKGG---IQALKEPSDILDVGNSTTIRLMMGILANTPFHSTMIGD--ESIA 115

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ + +D + P+ + G G G S S+Q SA+L+A
Sbjct: 116 KRPMKRVGTGLRDMNIHLDGRKDANFTPLVIRG--GQAKGIHYTSPVASAQVKSAILLAG 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + K + T R++E FGVK E + I+GGQ + + V
Sbjct: 174 LQAEGTTSVTEPAK-----SRDHTERMLEAFGVKVE--EEGLTVSIEGGQTLRG-THVEV 225

Query: 251 EGDASSASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKV-TWTETSVTVT 308
GD SSA++FL AGA I + ++ G + + +VL MGA + T ET T
Sbjct: 226 PGDISSAAFFLVAGAIANSRIEIQKVGMPNPTRTGI--LDVLSNMGASIEVTKETKETA- 282

Query: 309 GPPREPFGFR-----KHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360

EP+ HLK +V + +P + + ++AL A +G T I+D A +VKE
Sbjct: 283 ----EPYADLVVEASHLKGTVEGGDLIPRLIDEIPIIALAATQAEGITVIKDAAELKVKE 338
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVP 419
T R+ + ELTK+GA++E D II KL+ ++++ DHR+ M ++A+C AE
Sbjct: 339 TNRIDTVVNELTKMGANIEATEDGMIIHGGTKLHGANVNSHGDHRIGMMLAVASCIAEGE 398
Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
I + ++P +F L +
Sbjct: 399 TIIENRDAVSVSYPQFFAHLESL 421

>ref|YP_001952384.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter lovleyi SZ]
gb|ACD95864.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter lovleyi SZ]
Length = 434

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 131/444 (29%), Positives = 221/444 (49%), Gaps = 28/444 (6%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ I + P + + G + +PG KS+S+R ++L AL++GT+ + N L ED + A R +
Sbjct: 5 AQPISVLPARAVRGELAI PGDKSISHRSIMLGALAQGTSRITNFLRGEDNFMKAFRAM 64
Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYV 122
G+ +E D + +V G G + KE + GN+G +R +T ++ G + V
Sbjct: 65 GVPIEDD--GQTIIVHGVG----LHGLKEPGDVLDCGNSGTTIRLMTGLLS--GQSFFSV 116
Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G +R+RP+ +V L ++GA + G P+ + G G L G + S S+Q
Sbjct: 117 LTGDQYLKRKRMKRVVEPLARMGARIAGRGGTLAPLAITG-GNLTGIDYQ-SPIASAQV 174
Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SAL++A A G E + + +S + E R+ FG + S ++GG++
Sbjct: 175 KSALMLAGLYASG--ETRVTEPSLSRDHSE---RMFTFFGADLDRSSHG--VTVRGGREL 227
Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + V GD SSA++FL A I G + + G + V ++L+ MG +T
Sbjct: 228 QG-QEICVPGDISAFAFLVAALIVPGSELLIRNVGVNPTRTGV--IDILQAMGGDITLQ 284
Query: 302 ETSVTVTGPPPREPFGR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
+ P + R LK +++ + +P D + V A A+G T I+D R
Sbjct: 285 DQREVSSEPVADLLVRSSRLKGVEIGGDVVPRAIDFPAICVAAVAEGTTTIKDAKELR 344
Query: 358 VKETERMVAIRTELTKLGA-SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-C 415
VKET+R+ A+ L +GA ++E D II E L+ ++ +Y DHR+AM+ S+AA
Sbjct: 345 VKETDRIAAMAANLRIVGAGQIDETEDGMIIQGVESLSGGSVTSYGDHRIAMSLSVAALV 404
Query: 416 AEVPVTIRDPGCTRKTFPDYFDVL 439
V I D C +FP ++++L
Sbjct: 405 CRHQVEIDDVACVATSFPGFYELL 428

>ref|ZP_01906772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Plesiocystis pacifica
SIR-1]
gb|EDM80216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Plesiocystis pacifica
SIR-1]
Length = 269

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 104/245 (42%), Positives = 132/245 (53%), Gaps = 24/245 (9%)

Query: 213 MTLRLMERFGVKA-----EHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAG 263
MTLR++ FG A E + S + + VE DAS+ASY LA
Sbjct: 1 MTLRVLGAFGGSAAWLPTDELPEGASSTTEIIRVESRNL RPCTRYIVEPDASAASYLLAL 60
Query: 264 AAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPFPREPFGRKHLKAI 323
+ GG VTV G+ SLQGD +F VLE G + E+ + GP L+
Sbjct: 61 PVLYGGVEVTPDLGSESLQGDAQFWRVLEAFGGRGQEDESRTVMRGPDPDTP---GQLRGQ 116
Query: 324 DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD 383
++++ MPD+ +T AVVA FA GPT IR V R E++R+ A TEL KLGA VEE D

Sbjct: 117 ELDLTDPMDMTLTAAVVAAFATGPTRIRGVGILRHESDRIAAGATELRKLGAKVEEHED 176

Query: 384 YCIITPP-----EKLNV-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYF 436

I PP E+L+ IDTY+DHRMAMAF+LA VTI DPGC KTFP YF
Sbjct: 177 GLDIEPPTPEALRERLDAGVVIDTYEDHRMAMAFALAG----DVTIADPGCVAKTFPRYF 232

Query: 437 DVLST 441

+VL +
Sbjct: 233 EVLDS 237

>pdb|2BJB|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Unliganded
State
Length = 462

Score = 144 bits (362), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 211/439 (48%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLAL----SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70

+ TV +PGSKS +NR L+LAAL G + + L S D ML AL+TLGL V+
Sbjct: 13 VRATVTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTLMLDALQTLGLRVD-- 70

Query: 71 KAAKRAVVVCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127

G G + V E ++ G AG +R + AA G+ DG
Sbjct: 71 -----GVGSELTVSGRIEPPGARVDCGLAGTVLRFVPP--LAALGSVPVTFDGDQ 119

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187

+ R RPI L+ L++LG VD GT P RV G G L GG V + S SSQ++S LL
Sbjct: 120 QARGRPPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDASASSQFVSGLL 175

Query: 188 MAAPLALGDVEIEIII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

++A + ++ L S P++ MT ++ + GV + S +R+ ++ G + +
Sbjct: 176 LSAASFTDGLTVQHTGSSLPSAPHIAMTAAMLRQAGVIDDDSTP-NRWQVRPGPV--AAR 232

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306

+E D ++A FL+ A ++GGTV + G S+Q +L + A V ++S+
Sbjct: 233 RWDIEPDLTNAVAFLSAAVSGGTVRITGWPRVSVQPADHILAILRQLNAVVIHADSSLE 292

Query: 307 VTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPFAIR--DVASWRVKETERM 364

V GP DV++ + ++ ++A +A A + R +A R ET+R+
Sbjct: 293 VRGP-----TGVDGFDVDLRAVGELTPSVAALALASPGSVSRLSGIAHLRGHETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424

A+ TE+ +LG + E PD +IT L Y DHRMAMA ++ V + D
Sbjct: 346 AALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAIIGLRVAGVEVDD 404

Query: 425 PGCTRKTFFPDYFDVLSTFV 443

T KT P++ + + V
Sbjct: 405 IAATTKTLPEFPRLWAEMV 423

>ref|ZP_05655369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
casseliflavus EC20]
gb|EEV38702.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus
casseliflavus EC20]
Length = 429

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 126/446 (28%), Positives = 211/446 (47%), Gaps = 34/446 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68

L+ + GT+ +P KS+S+R ++ AL+EGTT V N L ED + L A ++LG+ +
Sbjct: 3 LKKATHLKGTIAVPADKSISHSIMFGALAEGTTTVRNFLRGEDCYSTLHAFQSLGVPIH 62

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128

D G G P ++ + +GN+G +R + + AG T L G
Sbjct: 63 DDGQTITIEGQGFNGLKPADEP-----IDIGNSGTTIRLMMGIL--AGQPFTTTLFGDDS 115

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

+ RP+ +++ L+++GA+V T+ PP+ +N L ++ + S+Q SAL+
Sbjct: 116 LNRRPMMNRVMLPLREMGANVRGHEQTEFPFITINSTASLHPINYQMPVA-SAQVKSALIF 174

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G I I+K S + E +R +FG + + G Q + +
Sbjct: 175 AALQAQGTSTI--IEKETSRNHEEMIR---QFG--GVITTQVKTTITVTGPTLQG-QEV 226

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET---- 303
V GD SSA++FL AGA + + ++ G + + +VLE MGA + ++
Sbjct: 227 VVPGDISAFLTAGAIMPESEIVLKNVGINPRTGTI--LDVLEEMGASIAFSNQDDQN 284

Query: 304 -SVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
S +T L+A+ + + +P + L ++AL A G T I+D +VK
Sbjct: 285 QSADLT-----VQSSTLQAVTIAGDIIPRLIDELPIIALLATQAHGKTVIKDAEELKVK 338

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEV 418
ET R+ A ELTKLGA + D II P L+ + + DHR+ M +AA +
Sbjct: 339 ETNRIDATAEELTKLGADITPTEDGLIINGPTPLHGGRVSSRGDHRIGMMLQIAALLTDE 398

Query: 419 PVTIRDPGCTRTKTFPDYFDVLSSTFVK 444
V + ++PD+F+ ++ K
Sbjct: 399 EVELEKAEAVAVSYDPDFEDVARLAK 424

>ref|ZP_05915865.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevibacterium linens
BL2]
Length = 438

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 126/431 (29%), Positives = 209/431 (48%), Gaps = 38/431 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKSL+NR L+LAAL+E +V+ L S D M+ AL+ LG ++ +
Sbjct: 24 VTATVSVPGSKSLTNRYLVLAALAESNSVIRGWLRSRDTLLMVEALKALGADIDEVDGSL 83

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ F + + + G AG MR + A G +LDG + R RP+
Sbjct: 84 HITPI----DFSAQREGPPITIDCGLAGTVMRFVPPPLAAATGRE--VILDGDAQARVRPM 137

Query: 135 GDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
++ L LG + D L P+ ++ L GG +++ S SSQ++S +L+ AP
Sbjct: 138 SVIIDALTHLGVSITAEDNLL-----PMTIHAQSHLRGGHLEIDASASSQFVSGMLLTAP 192

Query: 192 -LALGDVEIEIIDKLISIP---YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+ LG IE++++ +P +V+MTL ++ GV + + ++ G +
Sbjct: 193 AMPLG---IELVNRGETVPSRAHVDMTLEVLADAGVDVTEPQP-EHWIVEPG--LPRGLD 246

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+A+ F+A A T G VTV + Q F ++E G VT + V
Sbjct: 247 VQVEPDLSNAAAFVAAALATEGDVTVLDWPAHTTQAGDGFRSIVEAFGGTVTLDRHGLRV 306

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GP K L+A+D++++ + ++ +A +A A+G + + + R ET+R+ A+
Sbjct: 307 QGP-----KVLQAVDLDLAIGELTPVVAALAAMAEGTSRLTGIGHLRGHETDRLSAL 359

Query: 368 RTELTKLGASVEEGPDYCIIT---PPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
EL+ +G V E P IT P L TY+DHRM MA +L + I +
Sbjct: 360 HRELSAIGIHVVEQPTSLTITGANPHSGL---WHTYNDHRMVMAGALLGLRVDGLVIEN 415

Query: 425 PGCTRTKTFPDY 435
KT P++
Sbjct: 416 ADTVAKTLPEF 426

>ref|YP_003634887.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira murdochii
DSM 12563]
gb|ADG72688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira murdochii
DSM 12563]
Length = 420

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 130/438 (29%), Positives = 221/438 (50%), Gaps = 51/438 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVV---DNLLNSEDVHYMLGALRTL----- 63
EI G+V + SKS ++R L+ +ALS+ ++ DN+ S D+ A+
Sbjct: 9 EIFGSVYIQMSKSDAHRALIASALS KSPNI IKPWIDNV--SIDIEVTKDAVSNFADLELI 66

Query: 64 --GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
GL V K K+ + + DAKE +G ++R L V+A G N T+
Sbjct: 67 DDGLKVVPKKEYKKELTI-----DAKE-----SGTSLRLLIPIVSALGLNCTF 109

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
+ G ++ RP+ K+ G ++ L D V G L G+ +++G++SSQ
Sbjct: 110 I--GSKKLF SRPMEVYKNIWKEQG--LEFSLNEDSLKVS---GKLKSGEFRVAGNVSSQ 161

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++S LL A PL GD +I I +L S PYV MTL+ ++ ++ S D + G Q+
Sbjct: 162 FVSGLLFALPLLEGDSKIVIEGELESAPYVMMTLTKLKHANIELTRKGS-DVIEVYGNQE 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y S + VE D S A++ A A GG VT+ G S+QGD + +L+ MGA + +
Sbjct: 221 Y-SLTDYEVESDWSHAAF-FAAAGALGGEVTLYGLNKYSIQGDKEILNILKFMGAPIYN 278

Query: 302 E-TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ S+T+ R L A+D++++ +PD+A + +A A G T + + + R KE
Sbjct: 279 DDNSITIKKANR-----LNAMDIDISNIPDLAPIITSLASTAKGRTKLYNASRLRYKE 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACA-EVP 419
++R+ ++ +K+GA +E + I EKL +++DHR+AM+ ++A+ A P
Sbjct: 332 SDRINDLKDSFSKIGAKIEVTENEIFIEGIEKLEGGKTTSHNDHRIAMSLAVASIASNNP 391

Query: 420 VTIRDPGCTRKTFPDYFD 437
+TI D K+ ++ +
Sbjct: 392 ITIDDAQSINKSSFNFI 409

>ref|YP_001799884.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
urealyticum DSM 7109]
emb|CAQ04450.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
urealyticum DSM 7109]
Length = 467

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 141/448 (31%), Positives = 210/448 (46%), Gaps = 47/448 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++ TV +PGSKS++NR L+LAAL++G + N L S D ML ALRTL G+ VE +
Sbjct: 18 VTATVPVPGSKSITNRALVLAALADGPATITNTLISRDELMLDALRTLGVGVEILSSEG 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A V PV+ V L AG MR + AA A DG P+ R RP+
Sbjct: 78 AAATVRI--TPPVQFTGGHVDCGL--AGTVMRFVPP--IAALATAPVSFDGDPQARRRPM 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCCP-----PVRVN-----GIGGLPGGKVKL 174
+ ++ LGA + GTD P N G GG+V++
Sbjct: 132 DQTLDSIRGLGAGIGE--GTDATEPSSDTASLPFTVLPAAANTEQGSAGSTTPTGGEVRI 189

Query: 175 SGSISSQYLSALLM-AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV----KAEHSD 229
S SSQ++S LL+ A A G + + S P+++MT+ ++ GV E +
Sbjct: 190 DASGSSQFVSGLLLVGARFADGVRIVHTGQSVSPKPHIDMTIDMLAEAGVVVETGTTEEAT 249

Query: 230 SWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAE 289
+ ++ G + +E D S+A+ FLA A+T G V+V T+ Q +
Sbjct: 250 GNPTWTVPQGPPIKA--VDWVIEPDLSNATPFLAAGALTQGA VSVPHWPATTTPQPGDQIRP 307

Query: 290 VLEMMGAKVTWTETSVTVT--GPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGP 347
+LE MGA VT E ++T + GP L+ +D +M + ++ T+A +A A
Sbjct: 308 ILEAMGATVTLNEGTLTASAAGP-----LQGVWDWMDIGELTPTVAALAAALATTE 358

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMA 407
T +R +A R ET+R+ A+ E+ LG +V E D IT P L +Y DHRMA
Sbjct: 359 TRLRGIAHLRGHETDRLHALAAEINALGGNVAETEDGLHIT-PVPLAGARWRSYADHRMA 417

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDY 435

A ++ V + D T KT P +
Sbjct: 418 TAGAIIIGLLVPGVEEDVATTAKTMPGF 445

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>ref|ZP_03099981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus W]
ref|YP_002451903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH820]
ref|ZP_04091040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pondicheriensis BGSC 4BA1]
ref|ZP_04097046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar andalousiensis BGSC 4AW1]
ref|ZP_04108870.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar monterrey BGSC 4AJ1]
ref|ZP_04251704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
95/8201]
ref|YP_003792672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus anthracis
CI]
sp|B7JSV5.1|AROA_BACCO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EDX59272.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus W]
gb|ACK90121.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH820]
gb|EEL16679.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
95/8201]
gb|EEM59474.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar monterrey BGSC 4AJ1]
gb|EEM71169.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar andalousiensis BGSC 4AW1]
gb|EEM77277.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pondicheriensis BGSC 4BA1]
gb|ADK05534.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
biovar anthracis str. CI]
Length = 429
```

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

```
Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EGTT + L D + ++
Sbjct: 2 KERTIQPVNNGNLGNITIPGDKSISHRAVMFGAIAEGTTTIKGFPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAKRPMKRVNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIETYSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSSLKGIIGDIIPLRIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +F+ L K
Sbjct: 394 LAIAGCIAEGKTIIEDAEAVGVSYPYTFEELQKLAK 429
```

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>ref|ZP_04079131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pulsiensis BGSC 4CC1]
gb|EEM89249.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pulsiensis BGSC 4CC1]
Length = 429

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 130/452 (28%), Positives = 217/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EGTT + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGAIAEGTTTIKGFPLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGILA----NTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L + S S+
Sbjct: 112 SCVKGDASIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-GDLKAIEYN-SPVASA 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGK + + G
Sbjct: 170 QVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTVKLAG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQK + + V GD SSA++FL AGA I + +E G + + +VLE MGA
Sbjct: 221 GQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEKMGAT 277

Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKVIDNMNMKMPDVAMTLAVVALFA--DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVEPINEGASEPAANITITETSSLKIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMIYKGSALKGNTVNSYGDHRIGMMLAIA 397

Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
C AE I D ++P +F+ L K
Sbjct: 398 GCIAEGKTIIEDAEAVGVSYPTFFFEELQKLAK 429

>ref|ZP_04197981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH603]
gb|EEL70251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH603]
Length = 429

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 126/442 (28%), Positives = 216/442 (48%), Gaps = 37/442 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EG T + L D + + +G+ + ++
Sbjct: 13 LNGTITIPGDKSISHRAVMFGAIAEGKTTIKGFPLPGADCLSTISCFKEMGVEITQNR--D 70

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATY--VLDGVPRMRE 131
V+G G +E +E + L +GN+G +R ++ + N + + G + +
Sbjct: 71 EVTIVGTG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFFSCVQGDASIAK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAA 190
RP+ + LKQ+GA +D P+ + G G L ++ + ++S Q SA+L+A
Sbjct: 123 RPMQRTVNPLKQMGAKIDGRKEGTFTPLTIRG-GNLKA--IEYTSPVASAQVKSAILLAG 179

Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G + + P++ + T R++E FGV + + GGK + +
Sbjct: 180 LRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TRVGKTVKLAGGQKL-TATDV 229

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL AGA IT + + G + + +VLE MGA T + +
Sbjct: 230 QVPGDVSSAAFFLVAGAIITNSKLLQNVMNPTRTGI--IDVLEKMGATFTVEQINEGA 287
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Query: 308 TGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
+ P LK I++ + +P + + ++AL A DG T I+D +VKET R
Sbjct: 288 SEPAANITITETSPKLGIEIGGDIIPRLIDEIPIIALAATQADGITVIKDAHELKVKETNR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ + ELTKLGA +E D II KL T + ++ DHR+ M ++A C AE TI
Sbjct: 348 IDTVVAELTKLGARIEATDDGMIIYGKCKLKGTTVHSHGDHRIGMMLAIAGCIAEGETTI 407

Query: 423 RDPGCTRKTFFPDYFDVLSTFVK 444
D ++P +F+ L K
Sbjct: 408 EDAAEVGVSYPTFFFEELQMLAK 429

>ref|ZP_08058944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
cristatus ATCC 51100]
gb|EFX53473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
cristatus ATCC 51100]
Length = 432

Score = 143 bits (361), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 224/456 (49%), Gaps = 37/456 (8%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M GA + K ++G +++PG KS+S+R ++ +L++G TVV ++L EDV +
Sbjct: 1 MKGASMKLRTEAKGLNGRIRVPGDKSISHRSIMFGSLAKGLTVVHDILRGEDVLSTMQVF 60

Query: 61 RTLGLSVEADKAAKRAVVVCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
R LG+ +E D + VG G K P +L +GN+G ++R ++ + AG +
Sbjct: 61 RDLGVKIEDDGKTVKIHGVDGLKAPYN-----KLDMGNSGTSIRLISGVL--AGQDF 112

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSIS 179
+ G + +RP+ + + L Q+G D+ D PP+ ++G L +L + S
Sbjct: 113 AAEMFGDDSLSKRPMRVTPLPSQMGVDIWGQTERDLPLHIHGRKDLKPIHYQLPVA-S 171

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+Q SAL+ AA A G E II+K I+ + E ++ +FG + E R ++GG
Sbjct: 172 AQVKSALIFAALQAQG--ESVIEKEITRNHTE---DMIVQFGGQIEVKGKEIR--VQGG 224

Query: 240 QKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
Q + + + V GD SSA+++L AG + + +E G + + +V++ MG K+
Sbjct: 225 QTF-TGQAVRVPGDISSAAFVLVAGLILPHSKIVLENGINDTRTGI--LDVIKAMGGKM 281

Query: 299 TWTE-----TSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAI 350
T + S T+T E LK ++ +P + L ++AL A +G T I
Sbjct: 282 TLSNIDEVAKSATITVETSE-----LKGTEIGGEIIPRLIDELPIIALLATQAEGRTVI 335

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF 410
RD +VKET+R+ + L +GA++ D II L+ I+T+ DHR+ M
Sbjct: 336 RDAEELKVKETDRIQVVADALNSMGAITPTADGMIIDGKTPLHGATINTFGDHRIGMMA 395

Query: 411 SLAA--CAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
++AA ++ V + ++P +F L V
Sbjct: 396 AIAALLVSDGEVELERAEAINTSYPSFFSDLEDLVN 431

>ref|ZP_04120862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pakistani str. T13001]
ref|ZP_04273919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST24]
gb|EEK94434.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST24]
gb|EEM47470.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar pakistani str. T13001]
Length = 432

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 130/460 (28%), Positives = 218/460 (47%), Gaps = 44/460 (9%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL---AN 110

Query: 119 ATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + G G +K
Sbjct: 111 TPFFFCVQGGDESIKRPMPKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAE 289
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +
Sbjct: 216 GKTVKLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVQLNVGMNPRTGI--ID 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---D 345
VLE MGA T + + P LK I++ + +P + + V+AL A +
Sbjct: 273 VLEKMGATFTVDLINEGASEPAANITETSSSLKGIEIGGDIIPRLIDEIPVIALAATQAE 332

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHR 405
G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR
Sbjct: 333 GITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHR 392

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ M ++A C AE I D ++P +F+ L K
Sbjct: 393 IGMMLAIAGCLAEGKTIIEDAEAVGVSYPTFFEEQLKLAK 432

>ref|ZP_03417422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis 02_1987]
ref|ZP_06506424.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis 02_1987]
gb|EFD55062.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis 02_1987]
Length = 450

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 210/439 (47%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LALL G + + L S D ML AL+TLGL V+
Sbjct: 13 VRATVTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTLMMLDALQTLGLRVD-- 70

Query: 71 KAAKRAVVVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
G G + V E ++ G AG +R + AA G+ DG
Sbjct: 71 -----GVGSELTVSGRIEFGPGARVDCGLAGTVLRFVPP--LAALGSVPVTFDGDQ 119

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ R RPI L+ L++LG VD GT P RV G G L GG V + S SSQ++S LL
Sbjct: 120 QARGRPAPIPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDASASSQFVSGLL 175

Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++A + ++ L S P++ MT ++ + GV + S +R+ ++ G +
Sbjct: 176 LSAASFTDGLTVQHTGSSLPASPHIAMTAAMLRQAGVDIDDSTP-NRWQVRPGPVAA--R 232

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+E D ++A FL+ A ++GGTV + G S+Q +L + A V ++S+
Sbjct: 233 RWDIEPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLNAVVIHADSSLE 292

Query: 307 VTGPPREFFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIR--DVASWRVKETERM 364
V GP DV++ + ++ ++A +A A + R +A R ET+R+
Sbjct: 293 VRGP-----TGYDGFVDLRAVGELTPSVAALALASPGSVSRLSGIAHLRGHETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ TE+ +LG + E PD +IT L Y DHRMAMA ++ V + D
Sbjct: 346 AALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWPAYADHRMAMAGAIIGLRVAGVEVDD 404

Query: 425 PGCTRKTFPDYFDVLSTFV 443
T KT P++ + + V

Sbjct: 405 IAATTKTLPEFPRLWAEMV 423

>ref|YP_003598217.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
DSM 319]
gb|ADF39867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
DSM 319]
Length = 423

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 125/443 (28%), Positives = 219/443 (49%), Gaps = 36/443 (8%)

Query: 12 IKEISGTVKLPGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+++PG KS+S+R ++ +++EGTT ++ L +D + + LG+ ++
Sbjct: 3 VKALRGTIQIPGDKSISHRSVMFGSIAEGTTTNGFPLPGDDCLSTISCFQKLGVDIQM-- 60

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPFMR 130
+++VVV G ++ KE + +GN+G +R + + ++T + D +
Sbjct: 61 IDEQSVVVKGK---IQALKEPSDILDVGNSTTIRLMMGILANTPFHSTLIGD--ESIA 115

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ + +D + P+ + G G G S S+Q SA+L+A
Sbjct: 116 KRPMKRVGTGPLRDMNIHLDGRKDANFTPLVIRG--GKAKGIHYTSPVASAQVKSAILLAG 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + K + T R++E FGVK E + I+GGQ + + V
Sbjct: 174 LQAEGTTSVTEPAK-----SRDHTERMLEAFGVKVE--EEGLTVSIEGGQTLRG-THVEV 225

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV-TWTETSVTVT 308
GD SSA++FL AGA I + ++ G + + +VL MGA + T ET T
Sbjct: 226 PGDISSAAFFLVAGAIANSRIEIQVGMNPTRTGI--LDVLSNMGASIVTKETKETA- 282

Query: 309 GPPREPFGFR-----KHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
EP+ HLK +V + +P + + ++AL A +G T I+D A +VKE
Sbjct: 283 ----EPYADLVVEASHLKGTEVGGDLIPRLIDEIPIIALAATQAEGITVIKDAAELKVKE 338

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
T R+ + ELTK+GA++E D II KL+ +++++ DHR+ M ++A+C AE
Sbjct: 339 TNRIDTVVNETKMGANIEATEDGMIHGGAKLHGANVNSHGDHRIGMMLAVASCIAEGE 398

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
I + ++P +F L +
Sbjct: 399 TIIENRDAVSVSYPQFFAHLESL 421

>ref|NP_217744.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Rv]
ref|NP_337853.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis CDC1551]
ref|YP_979341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium bovis
BCG str. Pasteur 1173P2]
ref|YP_979433.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium bovis
BCG str. Pasteur 1173P2]
ref|YP_001284613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Ra]
ref|YP_001289183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis F11]
ref|ZP_02550256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Ra]
ref|ZP_03421808.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 94_M4241A]
ref|ZP_03426628.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis T92]
ref|ZP_03434282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis T85]
ref|ZP_03538362.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
tuberculosis T17]
ref|YP_002646298.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium bovis
BCG str. Tokyo 172]
ref|YP_003033270.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis KZN 1435]

ref|ZP_04927166.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis C]
ref|ZP_05142778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis '98-R604 INH-RIF-EM']
ref|ZP_05219491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_05765750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis CPHL_A]
ref|ZP_05769877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis T46]
ref|ZP_05774070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis K85]
ref|ZP_06434548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis T46]
ref|ZP_06438660.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis CPHL_A]
ref|ZP_06444716.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis KZN 605]
ref|ZP_06451680.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis T17]
ref|ZP_06456175.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis K85]
ref|ZP_06511298.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis T92]
ref|ZP_06518744.1| 5-enolpyruvylshikimate-3-phosphate synthase [Mycobacterium tuberculosis T85]
ref|ZP_06799524.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis 210]
ref|ZP_06953660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis KZN 4207]
ref|ZP_06961995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis KZN R506]
ref|ZP_07014114.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis 94_M4241A]
ref|ZP_07433290.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu005]
ref|ZP_07437489.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu006]
ref|ZP_07481984.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu009]
ref|ZP_07817089.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis KZN V2475]
sp|P22487.1|ARO_A_MYCTU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|A5U7Q1.1|ARO_A_MYCTA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|C1AH01.1|ARO_A_MYCBT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
pdb|200B|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Complex With S3p (Partially Photolyzed)
pdb|200D|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Complex With S3p
pdb|200E|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Complex With S3p And Pep
pdb|200X|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Complex With Intermediate
pdb|200Z|A Chain A, Mycobacterium Tuberculosis Epsp Synthase In Complex With Product (Eps)
pdb|2015|A Chain A, Mycobacterium Tuberculosis Epsp Synthase After Partial Products Withdrawal
gb|AAA25356.1| key enzyme from the shikimate biosynthesis pathway [Mycobacterium tuberculosis]
emb|CAA36510.1| unnamed protein product [Mycobacterium tuberculosis]
emb|CAB08328.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE AROA (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) [Mycobacterium tuberculosis H37Rv]
gb|AAK47667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis CDC1551]

emb|CAL73246.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium bovis BCG str. Pasteur 1173P2]
emb|CAL73339.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium bovis BCG str. Pasteur 1173P2]
gb|EAY58474.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis C]
gb|ABQ75051.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis H37Ra]
gb|ABR07581.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis F11]
dbj|BAH27530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium bovis BCG str. Tokyo 172]
gb|ACT26375.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis KZN 1435]
gb|EFD14963.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis T46]
gb|EFD19075.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis CPHL_A]
gb|EFD22631.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis KZN 605]
gb|EFD44957.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis K85]
gb|EFD48855.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis T17]
gb|EFD59936.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis T92]
gb|EFD78942.1| 5-enolpyruvylshikimate-3-phosphate synthase [Mycobacterium tuberculosis T85]
gb|EFI31793.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis 94_M4241A]
gb|EFP25620.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu005]
gb|EFP29455.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu006]
gb|EFP42026.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu009]
Length = 450

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 136/439 (30%), Positives = 210/439 (47%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPGSKSLNRIILLAL----SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL G + + L S D ML AL+TLGL V+
Sbjct: 13 VRATVTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTLMMLDALQTLGLRVD-- 70

Query: 71 KAAKRAVVVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
G G + V E ++ G AG +R + AA G+ DG
Sbjct: 71 -----GVGSELTVSGRIEFGPGARVDCGLAGTVLRFVPP--LAALGSVPVTFDGDQ 119

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ R RPI L+ L++LG VD GT P RV G G L GG V + S SSQ++S LL
Sbjct: 120 QARGRPAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDASASSQFVSGLL 175

Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++A + ++ L S P++ MT ++ + GV + S +R+ ++ G +
Sbjct: 176 LSAASFTDGLTVQHTGSSSLPSAPHIAMTAAMLRAQAGVDIDDSTP-NRWQVRPGPVAA--R 232

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+E D ++A FL+ A ++GGTV + G S+Q +L + A V ++S+
Sbjct: 233 RWDIEPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLNAVVIHADSSLE 292

Query: 307 VTGPPREFFGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIR--DVASWRVKETERM 364
V GP DV++ + ++ ++A +A A + R +A R ET+R+
Sbjct: 293 VRGP-----TGYDGFVDLRAVGELTPSVAALASPGSVSRSLGIAHLRGHETDRL 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRD 424
A+ TE+ +LG + E PD +IT L Y DHRMAMA ++ V + D
Sbjct: 346 AALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAIIGLRVAGVEVDD 404

Query: 425 PGCTRKTFPDYFDVLSTFV 443
T KT P++ + + V

Sbjct: 405 IAATTKTLPEFPRLWAEMV 423

>ref|ZP_05677975.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
Com15]
gb|EEV61308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
Com15]
Length = 431

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 209/441 (47%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSIHRSIMFGAIAEGTTTTIQNFLRAEDCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ G P + + +GN+G R L + AG T L G
Sbjct: 63 EEEEEVINIHGRGSHSFVPPTPEP-----IDMGNSGTTSRLLMGIL--AGQPFTTTLFGDA 115

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ C P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMGRVMEPLREMGADLQGNENDQCLPITVTGTRSLSPIRYNMPVA-SAQVKSAALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IMVTGPQKLTG-QQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAAFFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNHNKQ 284

Query: 307 VTGPPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAELQLKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAEVLV 424

>ref|NP_832685.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
14579]
ref|ZP_03232779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1134]
ref|YP_002367664.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
B4264]
sp|Q81C45.1|AROA_BACCR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B7H636.1|AROA_BACC4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAP09886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
14579]
gb|EDZ50388.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1134]
gb|ACK62102.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
B4264]
Length = 429

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGLNNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VEITQNGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K +S
Sbjct: 112 SCVQGDASIARPMKRVNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYISP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVDLINEGASEPAANITIETSSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTaidTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +FD L K
Sbjct: 394 LAIAGCLAEGKTIIEDAEAVGVSYPYTFDELQKLAK 429

>ref|YP_084260.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus E33L]
sp|Q63A07.1|ARO_A_BACCZ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAU17588.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus E33L]
Length = 429

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGNLGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIARPMKRVNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITIETSSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTaidTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSVLKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPYTFEELQKLAK 429

>ref|ZP_05814046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_33]
gb|EEW95577.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_33]
Length = 421

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 105/433 (24%), Positives = 203/433 (46%), Gaps = 46/433 (10%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + P SKS+ +R ++ ++L+ G + ++N+ S+D+ + A+ LG +E
Sbjct: 13 GEITPPPSKSLHRYIIASSLANGVSKNIENISYSDDIATIEAMEKLGAKIEK---KDNV 69

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F + ++ +G +R L + G ++ +RP+
Sbjct: 70 LLIDGSKTFDKKYLNNNAEIDCNESGSTLRFPLSIVKQNRILF--KGKGKLFKRPLSP 127

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + N I G L G+ ++ G+ISSQ+++ LL + PL
Sbjct: 128 YFENFDKYQINYSY-----INENEILLDGELKSGEYEIDGNISSQFITGLLFSPLPL 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ +I I KL S Y+++TL + +FG+K ++S+ F I+G Q YKS N VE D
Sbjct: 180 NENSKIIKKGLESSYIDITLNLNKGFIKI-INNSYREFIIEGNQTYKSG-NYQVEAD 237

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S ++FL +I G + + T SLQGD K +++ + W + +
Sbjct: 238 YSQVAFFLVANSI-GSNIKINELNTNSLQGDKK---IIDFISQIDNWNKKEKLI----- 287

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
++ ++ PD+ L++ A + I ++A R+KE++R+ A ELTK
Sbjct: 288 -----LDGSETPDIIPILSLKACISKKEIEIVNIARLRIKESDRLKATVQELTK 336

Query: 374 LGASVEEGPDYCIITPPEKLVN-----TAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
LG + E D +I E N + ++ DHR+AM ++A+ C + + + +
Sbjct: 337 LGFDLIEREDSILINSRENFNKILNNSPVFLSSHLDHRIAMMIAIASTCYDGEIVLDNSD 396

Query: 427 CTRKTFPDYFDVL 439
C +K++P++++V
Sbjct: 397 CVKKSYPNFWFV 409

>ref|ZP_07723502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
vestibularis F0396]
gb|EFQ59005.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
vestibularis F0396]
Length = 427

Score = 143 bits (361), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 121/434 (27%), Positives = 218/434 (50%), Gaps = 37/434 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++++PG KS+S+R ++ +L+G T V ++L EDV + R LG+++E D
Sbjct: 10 LHGSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVITIEDDGDV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G K P + +L +GN+G ++R ++ + AG + + G + +RP
Sbjct: 70 RIHGVDGDLKAP-----QNKLDMSGTSIRLISGLV--AGQDFDVEFMGDDSLSKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L+Q+G +V D PP++++G L +L + S+Q SAL+ AA A
Sbjct: 122 MDRVITIPLRQMGEVSGQTDRLPPLKMHGSKSLKPIHYQLPVA-SAQVKSALIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E II+K + + E ++++FG + + R I GGQ + + + V GD
Sbjct: 181 --DGESVIEIEKTRNHT---DMIQQFGGQLQVDGKEIR--ISGGQSF-TAQEVVVPD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++L AG + + +E G + +V++ MG K+T ++ S T+

Sbjct: 233 ISSAAFVLVAGLVVPNSKIVLENVGINETR--TGIIDVIKDMGGKITLSIDIDQVAKSATI 290

Query: 308 TGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
T E LK ++ + +P + L ++ L A G T IRD +VKET+R+

Sbjct: 291 TVETSE-----LKGTEIGGDIIPRLIDELPIITLLATQAQKKTIVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +

Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTALHGAEVNTFGDHRIGMMTAIAALLVQDGEVDL 404

Query: 423 RDPGCTRKTFPDYF 436
+ ++P +F

Sbjct: 405 QRAEAINTSYPSFF 418

>ref|YP_003136833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
8802]
gb|ACU99997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
8802]
Length = 448

Score = 143 bits (360), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 218/446 (48%), Gaps = 41/446 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+PG KS+S+R L+L A+++G T+++ LL ED R +G + + ++

Sbjct: 26 LQGTCLKIPGDKSISHRSLMLGAIAQGETIIEGLLLGEDPRSTAACFRAMGAEI-SPLNSQ 84

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G + + +E + + GN+G MR L + A+ + + G +R RP

Sbjct: 85 SITVKGVG---LGNLQEPLDVLDAAGSGTTMR-LMLGLLASHPGRFFCVTGDNSLRSRP 139

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
+ +V L+++GA++ P+ + G P + I+S Q S +L+A +

Sbjct: 140 MSRVVVKPLQEMGANIWRQONSLAPLAIQGNLTP---IHYHSPIASQVKSICILLAGLM 196

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-----GQKYKSPKN 247
G + + + +S + E R+++ FG + E I G GQK P

Sbjct: 197 TEG--KTTVTEPTLSRDHSE---RMLQGFGAQLAIDPETHSVTITGKPTLIGQKVVP-- 249

Query: 248 AYVEGDASSASYFL-AGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
GD SSA+++L AGA + G + +E G + + E LEMM A + E

Sbjct: 250 ----GDISSAAFVLVAGAIVPGSELLIENVGINPTRTGI--LEALEMMEADIKL-ENKRI 302

Query: 307 VTGPP---REFPGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
VTG P R F + LKA + + +P D LAV A+ A G T I+D A RVK

Sbjct: 303 VTGEPVADIRVFSQ--LKACTIONGDLIPRLIDEIPILAVAAVCAQGTIIKDAEELRVK 360

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEV 418
E++R+ + +EL+++GA + E PD IT L +D+Y DHR+AM+ ++A+ A+

Sbjct: 361 ESDRLAVMASELSRMGAKITELPDGLEITGGTLLKGEEVDSYTDHRIAMSLAIASLIAGK 420

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI ++P++ L ++

Sbjct: 421 STTIHRAEAAVSYPEFVTTLQQVIQ 446

>ref|YP_002371268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
8801]
gb|ACK65112.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
8801]
Length = 448

Score = 143 bits (360), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 128/446 (28%), Positives = 218/446 (48%), Gaps = 41/446 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+PG KS+S+R L+L A+++G T+++ LL ED R +G + + ++

Sbjct: 26 LQGTCLKIPGDKSISHRSLMLGAIAQGETIIEGLLLGEDPRSTAACFRAMGAEI-SPLNSQ 84

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

V G G + + +E + + GN+G MR + + + G + + G +R RP
 Sbjct: 85 SITVKGVG----LGNLQEPDLILDAGNSGTTMRLMLGFLASHPGRF-FCVTGDNSLSRSP 139
 Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
 + +V L+++GA++ P+ + G P + I+S Q S +L+A +
 Sbjct: 140 MSRVVKPLQEMGANIWRQONSLAPLAIQGNLTP---IHYSPIASQVKSCILLAGLM 196
 Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-----GQKYKSPKN 247
 G + + + +S + E R+++ FG + E I G GQK P
 Sbjct: 197 TEG--KTTVTPEPLSRDHSE---RMLQGFGAQLAIDPETHSVTITGKPTLIQKVVVP-- 249
 Query: 248 AYVEGDASSASYFL-AGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
 GD SSA+++L AGA + G + +E G + + E LEMM A + E
 Sbjct: 250 ----GDISSAAFVWLAGAIVPGSELLIENVGINPTRTGI--LEALEMMEADIKL-ENKRI 302
 Query: 307 VTGPP---REFPGRKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
 VTG P R F + LKA + + +P D LAV A+ A G T I+D A RVK
 Sbjct: 303 VTGEPVADIRVKSQ--LKACTIGGDLIPRLIDEIPILAVAAVCAQGTIIKDAAELRVK 360
 Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418
 E++R+ + +EL+++GA + E PD IT L +D+Y DHR+AM+ ++A+ A+
 Sbjct: 361 ESDRLAVMAEELSRMGAKITELPDGLEITGGTLLKGEEVDSYTDHRIAMSLAIAASLIAK 420
 Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
 TI ++P++ L ++
 Sbjct: 421 STTIHRAEAAVSYPEFVTTLQQVIQ 446

>ref|ZP_07973206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
 CB0101]
 Length = 435

Score = 143 bits (360), Expect = 6e-32, Method: Compositional matrix adjust.
 Identities = 130/439 (29%), Positives = 215/439 (48%), Gaps = 25/439 (5%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
 + + GTV++PG KS+S+R LL A+++GTT ++ LL +ED LR +G+ V +A
 Sbjct: 11 RSLRGTVRVPGDKSISHRSLFGAIADGTTTIEGLPAEDPLSTAACLAMGVDVSPIEA 70
 Query: 73 AKRAVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
 + V G G ++ +E E L GN+G MR + + G +VL G +R
 Sbjct: 71 GQTVTVQGVG----LDGFREPESVLDGNSGTTMRLMLGLLAGRAGR-HFVLTGDDSLRR 125
 Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
 RP+ + L ++GA + G + P+ + G L G ++ + S+Q SA+L+AA
 Sbjct: 126 RPMKRVGGPLAEMGATIAGRSGGNLAPLAIQG-QTLHGATIR-TPVASAQVKSAILLAAL 183
 Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYV 250
 A G +I+ + S + E R++ FG + + +K GQ+ + + V
 Sbjct: 184 TAEGPT--TVIEPVQSRDHSE---RMLRAFGAELSVGGPGNTEVTVKPGQRLRG-QAVVV 237
 Query: 251 EGDASSASYFLAGAAIT-GGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
 GD SSA+++L AIT G +TVE G + +VLE MGA++ V G
 Sbjct: 238 PGDISSAAFVWLAGAITPGADLTVENVGLNPSR--TGILDVLEQMGARIEVLNQR-DVAG 294
 Query: 310 PPREFPGRKH--LKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 P H LKA ++ + +P D LAV A A+G + + RVKET+R+
 Sbjct: 295 EPVGDRLRVTHGPLKAFEIGADLIPRLVDEIPVLAVAACCAEGVSRVSGAEELRVKETDRL 354
 Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
 + +L +GA +EE D I +L+ +D+ DHR+AM+ ++AA A +
 Sbjct: 355 AVMARQLGAMGARIEEFADGMAIQGGVQLHGAEVDSSETDHRVAMSLAVAAQIATGATQLH 414
 Query: 424 DPGCTRKTFPDYFDVLSTF 442
 P ++P+++ L
 Sbjct: 415 RPEAAVSYPEFWSDLERL 433

>ref|YP_895431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
 thuringiensis str. Al Hakam]
 sp|A0RFD1.1|ARO_A_BACAH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK85924.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis str. Al Hakam]
Length = 429

Score = 143 bits (360), Expect = 7e-32, Method: Compositional matrix adjust.
Identities = 129/452 (28%), Positives = 217/452 (48%), Gaps = 36/452 (7%)

Query: 5 EEIVLQPIKE-ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E ++QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERIIQPVNSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGILA----NTPFF 111

Query: 123 --LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L + S S+
Sbjct: 112 SCVQGDASIAPKRPMTNPLKQMGANIDGREGTFTPLTIRG-GDLKAIEYN-SPVASA 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKG 238
Q SA+L+A A G + + P++ + T R++E FGK + + G
Sbjct: 170 QVKSAILLAGLRAEGVTAV-----TEPHISRDRHTERMLEAFGVKV--TREGKTVKLAG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQK + + V GD SSA++FL AGA I + +E G + + +VLE MGA
Sbjct: 221 GQKL-TATDVQVPGDVSSAAFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEKMGAT 277

Query: 298 VTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDV 353
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 278 FTVEPINEGASEPAANITITETSSLKGEIGGDIIPRLIDEIPVIALAATQAEGITVIKDA 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++A
Sbjct: 338 HELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMMLAIA 397

Query: 414 AC-AEVPVTIRDPGCTRKTFFDYFDVLSTFVK 444
C AE I D ++P +F+ L K
Sbjct: 398 GCIAEGKTIIEDAEAVGVSYPTFFFEELQKLT 429

>ref|ZP_06608175.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
odontolyticus F0309]
gb|EFF80484.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
odontolyticus F0309]
Length = 437

Score = 143 bits (360), Expect = 7e-32, Method: Compositional matrix adjust.
Identities = 134/441 (30%), Positives = 207/441 (46%), Gaps = 32/441 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV++PGSKS++ R L LAA+++ +V+ L++ D AL +G VE + A
Sbjct: 1 MDATVEVPGSKSITARALYLAADVADSPSVIRGALDARDTRLFAAALEVMAHVEDEGAGI 60

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V P+ ++ G AG MR L AA + DG + RP+
Sbjct: 61 LRVTV-----PMSLPPRGRIECLAGTVMRFLPP--LAALSPEETLFDGDEQAYARPL 111

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
G L+ L ++GA V P + G P G + + S SSQ+LSALL+ +PL
Sbjct: 112 GPLLDALVRMGATVTYHGERGHLPTTIQGPPIHTPLGAQAWVDSSSSSQFLSALLLVSPLV 171

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIK--GGQKYKS 244
+ + + S+P+VEMTL + G+ E D +W F + GG
Sbjct: 172 GDPLFVSAPGVIPSMHVEMTLASLAGAGIDLEVVEGRANLSTWHIFPSRPIGG----- 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ VE D S+A FLA A +TGG V + + Q + +L MGA +T E
Sbjct: 227 --DITVEPDLNAGPFLAAMVTGGRVRIAPWPEATTQAGDAWRALLGHMGATITLDEEG 284

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+T+TGP G + I M ++ ++ TLA + +A P+ + +A R ET+R+
Sbjct: 285 LTLTGP-----GAGNYPGIKATMAEVEGELTPTLAAICAYASTPSHLSGIAHLRGHETDRL 339

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDAITYDDHRMAMAFSLAACAEVPTIRD 424
A+ TE+ + G EE D IIT P L+ I +Y DHRMA ++ +T+ D
Sbjct: 340 AALVTEINRAGGQAETEDGLIIT-PRPLHAAQIRSYADHRMAAFGAILGLITPGITVDD 398

Query: 425 PGCTRKTFPDYFDVLSTFVKN 445
CT KT P + + ++ V
Sbjct: 399 IACTSKTLPTFEAMWASLVSE 419

>ref|YP_001035408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK36]
sp|A3CNV3.1|AROASSTRSV RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABN44858.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative
[Streptococcus sanguinis SK36]
Length = 427

Score = 143 bits (360), Expect = 7e-32, Method: Compositional matrix adjust.
Identities = 122/439 (27%), Positives = 220/439 (50%), Gaps = 35/439 (7%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 7 VKGLKGRIRVPGDKSISHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ VG G ++ +L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 NLVKIHGVGFEGQLQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+++ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVITIPLRMGVETIAGRTERDLPLKMKGSRELQPIHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K I+ + E ++ +FG + E R I+GGQ++ + + V
Sbjct: 179 QAQG--ESVIEKEITRNHTE---DMIAQFGGQIEVEGKEIR--IQGGQEF-TAQEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + EV+E MG ++T ++ S
Sbjct: 231 GDISAFAFWLAVGLIVPDSKIVLENVGINETRTGI--LEVIEAMGGRMTLSVDVPAKSA 288

Query: 306 TVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIIALLATQAQGRTVIRDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDAITYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA++ D II L+ ++T DHR+ M ++AA V
Sbjct: 343 RIQVVADALNSMGAAITPTEDGMIIEGKTPLHGAQVNTLGDHRIGMMTAIAALLAQSSQV 402

Query: 421 TIRDPGCTRKTFPDYFDVL 439
+ + ++P++F+ L
Sbjct: 403 ELERSEAIKTSYPNFFNDL 421

>gb|EGD29195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK72]
Length = 427

Score = 142 bits (359), Expect = 7e-32, Method: Compositional matrix adjust.
Identities = 122/439 (27%), Positives = 219/439 (49%), Gaps = 35/439 (7%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 7 VKGLKGRIRVPGDKSISHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ VG G ++ +L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 NLVKIHGVGFEGQLQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAEMFGDDSLSK 119

Sbjct: 67 NLVKIHGVGFEGQLQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAEFMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+++ G L +L + S+Q SAL+ AA

Sbjct: 120 RPYMDRVTIPLRQMGVEIAGRTERDLPPLKMKGSRELKSMHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K I+ + E ++ +FG + E R I+GGQ++ + + V

Sbjct: 179 QAQG--ESVIIKEKTRNHT---DMIVQFGGQIEVKGKEIR--IQGGQEF-TAQEVTV 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + +V+E MG ++T ++ S

Sbjct: 231 GDISAFAFWLVAGLIVPDSKIVLENVGINETRTGI--LDVIEAMGGRMTLSVDVPAKSA 288

Query: 306 TVTGPPREPFGKRLKKAIDVNMNKMPPVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+

Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIALLATQAQGRTVIRDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA++ D II LN ++T+ DHR+ M ++AA V

Sbjct: 343 RIQVVADALNSMGAAITPTEDGMIIEGKTPLNGAQVNTFGDHRIGMMTAIAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFPDYFDVL 439
+ + ++P +F L

Sbjct: 403 ELERSEAIKTSYPRFFSDL 421

>ref|YP_002482018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
7425]
gb|ACL43657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanothec sp. PCC
7425]
Length = 451

Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 207/436 (47%), Gaps = 25/436 (5%)

Query: 15 ISGTVKLPGSKSLSNRIILLALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+ GT+ +PG KS+S+R L+L AL+EG T + LL ED R LG + A +

Sbjct: 30 LRGTLSVPGDKSISHRALMLGALAEGETQIQGLLLGEDPRSTAACFRALGAEISALNSEL 89

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R +G G E+ L GN+G +R L + A+ + + + G +R RP

Sbjct: 90 VRVKIGILGQLLEPEEV-----LDAGNSGTTLR-LMLGILASHPHRFFTVTGDRSLRSRP 143

Query: 134 IGDVVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+++GA + P+ V G ++ S I+S + + L+ A L

Sbjct: 144 MKRVVTPQLQEMGAMIWGRQSGSLAPLAVQG---QQLRSIRYSSPIASQVKSCLLFAGLM 200

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + E + + +S + E R++ FG + E + G K + ++ V GD

Sbjct: 201 I-EGETTVSEPALSRDHSE---RMLRAFGAQIEVDPHSHSVTVVGPAPKLQG-QSVIVPGD 255

Query: 254 ASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L AAI + +E G + V EVLE MGA++ E V G P

Sbjct: 256 ISSAFAFWLVAAAIPDAELVLENVGNPRTGTG--LEVLEQMGAIEK-QENHRLVAGEPV 312

Query: 313 EPFGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ LKA + + +P D LAV A FA G T IRD A RVKE++R+ A+

Sbjct: 313 ADLRVRSSTLKAQIGGDLIPRLIDEIPILAVAATFARGTTVIRDAEELRVKESDRITAL 372

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVT-IRDPG 426
++L+++GA V E PD IT L +D+ DHR+AM+ ++AA T I+

Sbjct: 373 ASQLSRMGAQVRELPGLEITGGTPLTGAEVDSLGDHRIAMSLAIALQARGTTWIKGGE 432

Query: 427 CTRKTFPDYFDVLSTF 442
++PD+ L

Sbjct: 433 VAAISYPDFAPTLQRL 448

>ref|ZP_07094728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus sp.
oral taxon 836 str. F0141]

gb|EFK38674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus sp.
oral taxon 836 str. F0141]
Length = 415

Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 116/429 (27%), Positives = 214/429 (49%), Gaps = 40/429 (9%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLN--SEDVHYMLGALRTLGLSVEADK 71
++ G + SKS +R L+L AL E T + LN S+D+ + AL LG +E +
Sbjct: 9 KLEGDIDAISKSQGHRLILGALCEKTEI--FLNNFSDILVTVKALENLGFVIERKE 66

Query: 72 AAKRAVVVGCGKFPVEDAKE--EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ F ++D + Q+ ++G ++R L A G N Y+ G +
Sbjct: 67 NS-----FLIKDRADVKNPQIDFKDSGSSSLRFLLAIGNFYGENVKYI--GSESL 113

Query: 130 RERPIGLDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ +L+ ++L + F P + G GGK G ISSQY+S +L+A
Sbjct: 114 SKRPLKELI---EELEKNFNSFSQNHLP---LEARGYFKGGKFTFRGDISSQYISGILLA 167

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A + + +I + L S PYV++T+ +++F + + + + + IKGG KSP Y
Sbjct: 168 ASKSPFESQIILKSNLESKPYVDLTINELKKFCIDVKME--NSYKIKGGN-LKSPGKLY 224

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
VEGD S+AS F+ GA + G V + G SLQGD + + + G+K+ +TE ++
Sbjct: 225 VEGDWSNASVFI--GANLLGSKVKIRGLNIDSLQGDKEILTIKKFGSKI--FTEDNILEN- 281

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ ++++++ +PD+A L V+ + + + + R KE++R+ ++
Sbjct: 282 -----SKADIRSMEIDIKNIPDLAPVLCVILAASTEKSRLINAKRLRFKESDRLFSLCK 335

Query: 370 ELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCT 428
+ LGA + D IT K+ +++++DHR+ MA LA+ A+ + I
Sbjct: 336 MINDLGAYGKIVGDSLEITG--KIKGHHVNSFNDHRIVMAACLASTFAKEEIIIDGAQAV 393

Query: 429 RKTFFPDYFD 437
K++ ++F+
Sbjct: 394 EKSYPKFF 402

>ref|ZP_06747931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
1_1_41FAA]
gb|EFG29021.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
1_1_41FAA]
Length = 418

Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 108/430 (25%), Positives = 204/430 (47%), Gaps = 42/430 (9%)

Query: 17 GTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + P SKS+ +R ++ ++L++G + ++N+ SED+ + A++ LG +E ++
Sbjct: 11 GELSPPPSKSVLHRYIIASSLAKGISKIENISFSEDIATIEAMKKGAKIE-----QKE 65

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G + E +++ +G +R L + G ++ +RP
Sbjct: 66 NYLLIDGSDTFKKNLENIEIDCNESGSTLRFLFPLSIVKENKVLF--KGRGKLFKRP--- 120

Query: 137 LVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ K G + D + + G L G K+ G+ISSQ+++ LL + PL G
Sbjct: 121 MTPYFKNFGKHKIKYSYIDENKILLEG--QLKAGIYKIDGNISSQFITGLLFSPLLDGK 178

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+I I KL S Y++++L + +FG+K ++S+ F I+G Q Y++ N E D S
Sbjct: 179 SKIIINGKLESSNYIDISLDCLSKFGIKI-INNSYQEFIEGNQSYRAG-NYRTEADYSQ 236

Query: 257 ASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREFPG 316
A++FL AI G + + SLQGD K +++ + W V
Sbjct: 237 AAFFLVANAI--GSNIKINDLSENSLQGDKK---IIDYISEIDNWNKDTLV----- 283

Query: 317 RKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
++ ++ PD+ L++ A + I +V R+KE++R+ A EL+KL

Sbjct: 284 -----LDGSETPDIIPILSLKAAVSGKKIEIVNVERLRIKESDRLKATVEELSKLNF 335

Query: 377 SVEEGPDYCIITPPEKL-----NVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTR 429
+ E D +I E L + ++ Y DHR+AM ++AA C + + + + C +

Sbjct: 336 DLIEKKDSILINSREALKANKNEKIVLSAYSSDHRIAMMIAAATCYDGEILLDNLDVCVK 395

Query: 430 KTFPDYFDVL 439
K++P++++V

Sbjct: 396 KSYPNFWVEVF 405

>ref|YP_003827622.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetohalobium
arabaticum DSM 5501]
gb|ADL12557.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetohalobium
arabaticum DSM 5501]
Length = 427

Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 133/441 (30%), Positives = 217/441 (49%), Gaps = 25/441 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E+ ++P ++ GT+K+PG KS+S+R ++L AL+EG T V L ED A + +G+

Sbjct: 2 ELKIKPKDKLQGTIKVPGDKSISHRSVMLGALAEGKTEVTGFLTGEDCLNTARAFQKMGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E ++ V+ G G E E L LGN+G +MR + + AG + V+ G

Sbjct: 62 EIEG-LGSEEMVIHGVGLNGLQEP---ESILDGNSGTSMLMLGIL--AGQDFYAVVTG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+ +V L +GA++ G + P+ V IG + S S+Q S

Sbjct: 116 DESLSKRPMARVVEPLGDMGAEIYGRDGGNLAPLTV--IGQNLTNQEYQSPVASAQVKSC 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G + I+ S + E R++E FG + + D + I GQ

Sbjct: 174 ILLAGLYADGTTTV--IEPAKSRDHT---RMLEYFGTEL-NIDGLEVSVI--GQPKLKG 225

Query: 246 KNAYVEGDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
+ V D SSAS+FL A I + +E G + + EVL M A +

Sbjct: 226 QKVVPSPDISASSFFLVAALINQQAELILEDVGLNPTRAGI--LEVLTAEMEADYELLDKR 283

Query: 305 VTVTGPPE-PFGRKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ P + +L+A + + K+ D LAV A A+G T I+D RVKE

Sbjct: 284 LENQEPIADIKVNSSNLQATTIGGAVIPKLI DELPILAVAATQAEGETVIKDAEELRVKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFSLAA-CAEV 418
T+R+ A+ TEL +LG VEE D +I P+ + + +YDDHR+AM+ ++A A+

Sbjct: 344 TDRISAMVTELRLGVEVEEREDGMVPGPQSIKGGCSCRSYDDHRIAMSLAVAGLIAQE 403

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
+ I + C + +FP++ ++L

Sbjct: 404 EIEITNADCIKTSFPNFVELL 424

>ref|ZP_03234463.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
H3081.97]
gb|EDZ59090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
H3081.97]
Length = 429

Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +

Sbjct: 2 KERTIQPVNNGLNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +

Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176

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      + G   + +RP+   +   LKQ+GA++D      P+ + G      G +K      S
Sbjct: 112 SCVQGDASIAKRPMKRVNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
      S+Q  SA+L+A   A G   +      + P++   + T R++E FGVK   +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
      + GGQK  + +   V GD SSA++FL AGA I   + ++   G   + +   +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTA 349
      MGA  T   +   + P      LK I++   + +P +   + V+AL A   +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
      I+D   +VKET R+   + ELTKLGA +E   D II   L   +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
      ++A C AE   TI D      ++P +F+ L   K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPFFFEELQKLAK 429

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>ref|YP_002249558.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermodesulfovibrio
yellowstonii DSM 11347]
sp|B5YH68.1|AROA_THEYD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI20539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermodesulfovibrio
yellowstonii DSM 11347]
Length = 430

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Score = 142 bits (359), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 125/447 (27%), Positives = 218/447 (48%), Gaps = 30/447 (6%)

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Query: 8   VLQPIKEISGTVKLPKSKLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
      +++ K + G + P KS+S+R ++ A+L++G + + N L ++D   L A+++LG V
Sbjct: 4   IIKKAKTLKGEITPPPKSISHRAVMFASLAKGQSRIKNFLWAKDPLSSLNAMKSLG--V 61

Query: 68  EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      E      + ++V G   ++++   +   GN+G +R L+ V AG   VL G
Sbjct: 62  EITITDSKEIIVNGKGLHSLKESDNVIDC--GNSGTTIRLLSGIV--AGQRFLTVLGTDD 117

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      +R RP+ ++ L +GA++      PP+ + G G L G   ++ + S+Q SA+L
Sbjct: 118 SLRYRPMKRIINPLSLMGANIMGRAENKFPPPIVIKG-GFLKGISYEMPIA-SAQVKSAIL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      +A   A G+ +   K      + T ++++ GV   +D+ +   N
Sbjct: 176 LAGLYAKGETTLTEPHK-----SRDHTEKMLKNMGVNI IINDNTVKL-----SPVDHELN 225

Query: 248 AY---VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      +   + D SSA++F+AGA +   + ++      +   F EVL+ MGA +
Sbjct: 226 CFDITIPNDFSSAAFFIAGACLVPDSEILIKQVNLNETR--TGFIEVLKNMGATIEIFNI 283

Query: 304 SVTVTGPPREPFGRK--HLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
      +   P + F +   LK I+V + +P   D   L VVA A+G T I+D   R
Sbjct: 284 TEQGGEPPVGDIFAKSSSELKGINVQGDIIIPKLIDEFPILCVVATQAEGKTVIKDAKDLRA 343

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
      KE++R+ A+ +EL K+G ++E D   I P KL T + +Y DHR+AMA S+A AE
Sbjct: 344 KESDRIKAMTSELKMGVKIKEFEDGVEIEGPKKLIGTEVYSYKDHRIAMALSIAGVIAE 403

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
      TI+D C   +FP+++ +L   K
Sbjct: 404 GETTIKDANCVDISFPFYSLLEMLQK 430

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>ref|ZP_03777933.1| hypothetical protein CLOHYLEM_04987 [Clostridium hylemonae DSM
15053]

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gb|EEG75026.1| hypothetical protein CLOHYLEM_04987 [Clostridium hylemonae DSM 15053]
Length = 432

Score = 142 bits (359), Expect = 9e-32, Method: Compositional matrix adjust.
Identities = 128/438 (29%), Positives = 209/438 (47%), Gaps = 34/438 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV++PG KS+S+R ++L +++ GTT + N L D +G R +G+ +E +
Sbjct: 12 LKGTVRVPGDKSISHRAVMLGSIALGTTEITNFLEGADCLATIGCFRKMGEIEQRQECI 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G G P L +GN+G R ++ + G + T VL G + RP+
Sbjct: 72 LVHGKGLRGLRPPAGI-----LDVGNSGTTTTLISGIL--CGQDFTSVLSGDASLNSRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG---GKVKLSGSISSQYLSALLMAAP 191
G ++ L+ +GA V G C P+++ PG G S S+Q SA+L+A
Sbjct: 125 GRIITPLRNMGASVTSVNGNGCAPLKIE-----PGRIGHIYESPVASAQVKSALLAGL 179

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
A D + + +S + E+ +++ FG A H D + + +
Sbjct: 180 YA--DNTTSVTPEPSLSRNHTEL---MLQNFGAALSAMHPDGRATAELAPCTELYG-RQI 233

Query: 249 YVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+V GD SSA+YF+A G + G + ++ GT + F V + MGA+VT +V
Sbjct: 234 HVPGLDISSAAYFIAAGLTVPGSELLLNKVGNTNFTRAG--FLTVCQNMGARVTRLNETVQ- 290

Query: 308 TGPPPREPF---GRKHLKAIDVNM-NKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G R GR H I+ ++ + D +AV+A A+G T IRD A +VKET+
Sbjct: 291 GGEARADLLVTPGRHLGTVIEGDLIPSLIDEIPVIAVMAACAEGTTVIRDAELKVKETD 350

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ + L +GA V D II L I+++ DHR+AMAF++AA A+
Sbjct: 351 RIATVTENLRAMGACVTPTEDGMIIEGRGGLKGAFIESHMDHRIAMAFAVAALSAGGESR 410

Query: 422 IRDPGCTRKTFPDYFDVL 439
I + C ++P +++ L
Sbjct: 411 INNSQCVDVSYPAFWETL 428

>ref|YP_001733439.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. PCC 7002]
gb|ACA98183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. PCC 7002]
Length = 446

Score = 142 bits (358), Expect = 9e-32, Method: Compositional matrix adjust.
Identities = 131/443 (29%), Positives = 213/443 (48%), Gaps = 35/443 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G V++PG KS+S+R L+L A++EG T+++ LL ED +G ++ E ++
Sbjct: 24 LQGKVRIPGDKSISHRALMLGAIAEGETIIEGLLLGEDPRSTAACFAAMGANISELNETE 83

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G ++ L GN+G MR L + A+ + + + G +R RP
Sbjct: 84 VRVQGVGLGNLQEPDNV-----LDAGNSGTTMR-LMMGLLASSPDRFFAVTGDGSLRSRP 137

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V LK++GA + G P+ + G L G S S+Q S +L+A LA
Sbjct: 138 MSRVVNPLKEMGAQIWGKKGNLAPLAIQG-QQLKGIHYH-SPIASAQVKSCVLLAGLLA 195

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVK-----AEHSDSWDRFYIKGGQKYKSPKNA 248
G + + + +S + E R++ FG HS + D GQK P
Sbjct: 196 EG--QTTVTPEPALSRDHSE---RMLRAFGANLTIDPETHSVTIDPHPTLRGQKVVP--- 247

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
GD SSA++++ AAI + +T+E G + + E ++MMGA +T + + V
Sbjct: 248 ---GDISAFAWMVAAAIVPDSDLTIENVGINPTRTGI--IEAMQMMGADMTL-DNAREV 301

Query: 308 TGPPPREPFGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P ++ LK + +P D LAV A FA G T I+D RVKE++

Sbjct: 302 AGEPVADLRVQYSPLKGCTIGGEIIPRLIDEIPILAVAACFAAGTTIIKDAEELRVKESD 361
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAAC-AEVPVT 421
R+ + ELTK+GA++ E PD I LN +D+Y DHR+AM+ ++AA A+
Sbjct: 362 RLAVMAAELTKMGANIIEHPDGLIIGGASLNGAEMDSYTDHRIAMSLAIAALNAKDETR 421
Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I ++P + + L+ +
Sbjct: 422 IHRAEAASISYPTFVETLTNVCQ 444

>ref|YP_001645575.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
gb|ABY43947.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
Length = 429

Score = 142 bits (358), Expect = 9e-32, Method: Compositional matrix adjust.
Identities = 128/445 (28%), Positives = 218/445 (48%), Gaps = 43/445 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EG T + L D + + +G+ + ++
Sbjct: 13 LNGTITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVEITQNR--D 70
Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV--LDGVPRMRE 131
V+G G +E +E + L +GN+G +R ++ + N + + G + +
Sbjct: 71 EVTIVGTG---LEGLQEPKAVLDVNGSGTTIRLMSGIL---ANTPFFSCVQGDASIAK 122
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAA 190
RP+ + LKQ+GA +D P+ + G G L ++ + ++S Q SA+L+A
Sbjct: 123 RPMQRTVNPLKQMGAKIDGRKEGTFTPLTIRG-GNLKA--IEYTSPPVASAQVKSAILLAG 179
Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G + + P++ + T R++E FGV + + GGQK + +
Sbjct: 180 LRAEGVTAV-----TEPHISRDHTERMLEAFGVTI--TRVGKTVKLAGGQKL-TATDV 229
Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL AGA I + ++ G + + +VLE MGA T + +
Sbjct: 230 QVPGDVSSAAFFLVAGAIIPNSKLLQNVGMNPTRTGI--IDVLEKMGATFTVEQINEGA 287
Query: 308 TGPPR---EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
+ P E F LK I++ + +P + + V+AL A +G T I+D +VKE
Sbjct: 288 SEPAANITITET---SLKGIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDAHLEKVKVE 344
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAAC-AEVP 419
T R+ + ELTKLGA +E D II KL T + ++ DHR+ M ++A C AE
Sbjct: 345 TNRIDTVVAELTKLGARIEATDDGMIYIGKCKLKGTTVHSHGDHRIGMMLAAGCIAEGE 404
Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D ++P +F+ L T K
Sbjct: 405 TTIEDAEAVGSYPTFFEELQTLAK 429

>ref|ZP_08062863.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 903]
gb|EFX39465.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 903]
Length = 436

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 128/446 (28%), Positives = 216/446 (48%), Gaps = 41/446 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++PG KS+S+R ++ +L+ G T V ++L EDV + R LG+S++ D
Sbjct: 17 KGLRGIIRVPGDKSISHRSIIFGSLATGETKVYDILRGEDVLSTIQVFRDLGVSIQDDGD 76
Query: 73 AKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R VG G K P L +GN+G ++R ++ + AG + + + G + +
Sbjct: 77 VIRIQGVGFQGLKAPTS-----PLDMGNSGTSIRLISGVL--AGQDFSVTMVGDDSLSK 128
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191

RP+ + + L+Q+G ++ DCP+ G L L + S+Q SAL+ AA
Sbjct: 129 RMDRVAIPLRQMGVEIAGHGERDCPLHEKGTQQLQPIYYHLPVA-SAQVKSALIFAAL 187

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +R +FG + + + R I+GGQ+++ + V

Sbjct: 188 QAEG--ESTIIEKEKTRDHTEDMIR---QFGGEIQVDEKTIR--IQGGQEFQG-QEVIVP 239

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTE-----T 303
GD SSA+++L AG + + +E G Q +V++ MG +T +

Sbjct: 240 GDISSAAFVLVAGLILPESVIKIENVGIN--QTRTGILDVIQEMGGDLTIEDRDEKAVSA 297

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKE 360
S+TV LK I ++ +P + L ++AL A G T I D RVKE

Sbjct: 298 SLTVK-----TSSLKGIRIDGELIPRLIDELPIALLATQATGQTVIADAEELRVKE 349

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEV 418
T+R+ + L +GA+V D IIT P L ++T+ DHR+ M ++AA +

Sbjct: 350 TDRIQVVADSLNAMGANVVPTEGDMITGPTPLQGADLETFGDHRIGMMAAIAALLVRDG 409

Query: 419 PVTIRDPGCTRTFPDYPFDVLSFVK 444
V + ++P +F+ L T +

Sbjct: 410 NVVLDRAEAINTSYPSFFDELTLLH 435

>ref|ZP_03110090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
03BB108]
gb|EDX65003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
03BB108]
Length = 429

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E ++QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +

Sbjct: 2 KERIIQPVNSGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +

Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGILA---NTPFF 111

Query: 123 --LDGVPRMRRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S

Sbjct: 112 SCVQGDASIAPKRVNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +

Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + +E G + + +VLE

Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLENVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T

Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGDIIPLRIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M

Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYKGSALKGNVTNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRTFPDYPFDVLSFVK 444
++A C AE I D ++P +F+ L K

Sbjct: 394 LAIAGCIAEGKTIIEDAEAVGVSYPTFFELQKLAK 429

>ref|ZP_06291795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
lacrimalis 315-B]
gb|EFA89505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
lacrimalis 315-B]
Length = 415

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 116/429 (27%), Positives = 214/429 (49%), Gaps = 40/429 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLN--SEDVHYMLGALRTLGLSVEADK 71
++ G + SKS +R L+L AL E T + LN S+D+ + AL LG +E +
Sbjct: 9 KLEGDIDAISKSQGHRLILGALCEEKTEI--FLNNFSDDILVTVKALENLGFVIERKE 66

Query: 72 AAKRAVVVGCGGKFPVEDAKE--EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ F ++D + Q+ ++G ++R L A G N Y+ G +
Sbjct: 67 NS-----FLIKDRVDVKNPQIDFKDSGSSSLRFLLAIGNFYGENVKYI--GSESL 113

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ +L+ ++L + F P + G GKG G ISSQY+S +L+A
Sbjct: 114 SKRPLKELI---ELEEKNNFSFSQNHLP---LEARGYFKGGKFTFRGDISSQYISGILLA 167

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A + + +I + L S PYV++T+ ++F + + + + IKGG KSP Y
Sbjct: 168 ASKSPFESQIILKSNLESKPVDLTINELKKFCIDVKME--NSYIKKGN-LKSPGKLY 224

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
VEGD S+AS F+ GA + G V + G SLQGD + + + G+K+ +TE ++
Sbjct: 225 VEGDWSNASVFI-GANLLGSKVKIRGLNIDSLQGDKEILTIKKFGSKI-FTEDNILEN- 281

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ ++++++ +PD+A L V+ + + + R KE++R+ ++
Sbjct: 282 -----SKADIRSMEIDIKNIPDLAPVLCVILAASTEKSRLINAKRLRFKESDRFLSLCK 335

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCT 428
+ LGA + D IT K+ +++++DHR+ MA LA+ A+ + I
Sbjct: 336 MINDLGADGKIVGDSLEITG--KIKGGHVNSFNDHRIVMAACLASTFAKEEIIDGAQAV 393

Query: 429 RKTFFPDYFD 437
K++ ++F+
Sbjct: 394 EKSYKNFFE 402

>ref|ZP_07320814.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Finegoldia
magna BVS033A4]
gb|EFL54469.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Finegoldia
magna BVS033A4]
Length = 398

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 116/425 (27%), Positives = 202/425 (47%), Gaps = 46/425 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ G V SKS ++R L+LA++++ TT++ N S D+ + LR LG+ +E ++
Sbjct: 7 KLQGVDAISSKSFAHRFLILASVADTDTTIIINEF-SNDIMTTIDCLRNGLVEIEINEN 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V F +D + + + ++G R L V+ G R+++
Sbjct: 66 E-----VTVHPSFFQKDVS---INVNDSGSTFRFLPLVSFLSQKTNIQCSG--RLQDR 115

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +LV LK G + P V+G + G +SSQY+SA++M APL
Sbjct: 116 PIKELVDQLKLAGLT----FSEEKLPFTVDG--TFHKIDFEFPGDVSSQYISAIMMIAPL 169

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+G EI++ KL S Y+++T ++ FG+ +E D+ +K G KSP VEG
Sbjct: 170 -IGGCEIKLSSKLESTGYIKITQECLKLFIDSEIL--LDKVIVKPGA-LKSPGKIIVEG 225

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A++FL A+ G + VE S+Q D K E LE + + E
Sbjct: 226 DWSNAAFFLCANAL-GADIKVENLNVNSVQADRKIVFLEKIENNEDYCE----- 274

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+++++ PD+ + LAVV + +++ R+KE++R+ + L
Sbjct: 275 -----IDISQTPDLFVILAVVLSQKCEKSVLKNKRLRLKESDRIQSTYDMLK 322

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432

G + D +I E + +++ DDHR+ MA ++A+ V I+D +K++
Sbjct: 323 SFGVHCDIEGDNLVICKSE-MKPAVNVSCDDHRIVMAAAIASIITKEVEIKDWQAVKKS 381
Query: 433 PDYFD 437
P +FD
Sbjct: 382 PSFFD 386

>ref|ZP_05364937.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
tuberculoostearicum SK141]
gb|EET78282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
tuberculoostearicum SK141]
Length = 433

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 132/435 (30%), Positives = 203/435 (46%), Gaps = 27/435 (6%)

Query: 10 QPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
Q I+ +PGSKS++NR +LAAL++G + + L S D M AL ++G+ E
Sbjct: 16 QAAGPITWAQHVPKSGSITNRAFILAALADGPSTLRAPLVSRDSQLMEKALESMDGVRFEH 75

Query: 70 DKAACKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 129
+ + V G P++ A + L AG MR + A G ++DG +
Sbjct: 76 EG---EDIHVTPG---PLKGATVDCGL---AGTVMRFIPPVAALADG--AVLVDGDEQA 123

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+QLG +VD D P V G GG+V + S SSQ++S LL+A
Sbjct: 124 YARPMSTTLDALRQLGVEVDG---DSLPTVTRSHGVPEGGEVTIDASGSSQFVSGLLLA 179

Query: 190 -APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G L S+P+VEMT+ ++ + GV+ + + + + G +
Sbjct: 180 GARFAKGITVTHEGGPLPSMPHVEMTVGMLRQAGVRVDSGE--NTWTVHPGPIAG--REW 235

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A+ FLA AA+TGG VT++ + Q +L MG VT VT
Sbjct: 236 AIEPDLSNATPFLAAAATGGRVTIKRWPANTTQPGDAIRHILVDMGMVMTQEPGFVTAK 295

Query: 309 GPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G L+ I+ NM + ++ T+A + AD P+ + +A R ET+R+ A+
Sbjct: 296 G-----AKDGALQGIERNMGDIGELTPTVAALCALADTPTSTLTGIAHLRGHETDRLKALA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
+ LG V E D I P L+ Y DHRMA A ++ V + D T
Sbjct: 351 DNINALGGKVTELADGLHID-PAPLHGGGEWPCYADHRMATAGAIIGLRVPGVEVEDIATT 409

Query: 429 RKTFFPDYFDVLSTFV 443
KT P + + T V
Sbjct: 410 AKTLPGFDRMWETMV 424

>ref|YP_901025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelobacter
propionicus DSM 2379]
sp|A1ANP7.1|ARO_A_PELPD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK98967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelobacter
propionicus DSM 2379]
Length = 431

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 127/443 (28%), Positives = 211/443 (47%), Gaps = 27/443 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
I + P + G + +PG KS+S+R ++L A++ G T V L ED + A R +G+
Sbjct: 4 ISITPGSSSLKGLVVPKDKSISHRSIMLGAANGVTTVRGFLRGEDNMATMAAFRAMGVR 63

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
++ D + + G +E+ + L GN+G +MR LT + AG N VL G
Sbjct: 64 IDDDG---HLLSIHGRGLHGLEEPGD--VLDCGNSGTSMLLTGLL--AGQNFFSVLSGD 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSA 185

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      +R+RP+ +V L ++GA + G + P+ ++G G L + +SS Q SA
Sbjct: 117 QYLRKRPKMRVVEPLSRMGARILGRAGGNLAPLAISG-GTL--NAIGYESPVSSAQIKSA 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      +++A A GD + + +S + E R+ FG E + +KGG + +
Sbjct: 174 IMLAGLYADGDTSVR--EPSLSRDHSE--RMFALFGASLE--TFHNGVTVKGGIELHA- 225

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + +V GD SSA++F+ A IT + + G + +VL MG + +
Sbjct: 226 QEIHVPGDISSAAFFIVAALITPDSELLIRNVGVNPNTR--TGIIDVLRSMGGSIELVDER 283

Query: 305 VTVTGPPEPFGGRK-HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      P + R LK + + +P D + V A A+G T+IRD RVKE
Sbjct: 284 EVSAEPVADILVRSSRLKGVRIEGQTVPRIDEFPAICVAACAEGTTSIRDARELRVKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-P 419
      T+R+ A+ L LG +V+E + IT E+L +++ DHR+AM+ S+A
Sbjct: 344 TDRISAMAVNLRTLGVTVDECEGMDITGVERLGGGVAESFGDHRIAMSLSVAGLVSADA 403

Query: 420 VTIRDPGCTRKTFFPDYFDVLSTF 442
      V + D C +FP++F +L F
Sbjct: 404 VRVNDIDCVSTSFNPFSLLERF 426

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>ref|NP_378277.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus tokodaii
      str. 7]
sp|Q96Y91.1|AROASULTO RecName: Full=Probable 3-phosphoshikimate
      1-carboxyvinyltransferase; AltName:
      Full=5-enolpyruvylshikimate-3-phosphate synthase;
      Short=EPSP synthase; Short=EPSPS
dbj|BAB67386.1| 408aa long hypothetical 3-phosphoshikimate
      1-carboxyvinyltransferase [Sulfolobus tokodaii str. 7]
      Length = 408

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Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 120/429 (27%), Positives = 208/429 (48%), Gaps = 39/429 (9%)

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Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
      +I G VK P SKS R++L + L E +DNL+ S+DV+ + ++ LG+SVE
Sbjct: 9 KIYGVKAPQSKSFGIRLVLYSLLKESK--LDNLIPSDDVNVAINVVKQLGVSVEGYTFK 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 133
      + +V KF L+ G + +R ++ G + ++DG +R+RP
Sbjct: 67 REKELVTP--KF-----LYFGGSATTLRMSIPILSVLGVDT--IIDGETLKRKP 112

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      + ++ K L V + P +++G L V++ G SSQY+S + A L
Sbjct: 113 LNAII---KALEGSVS--FSSLLPTKISG--KLKENFVRIEGGESQYISGFIYAFSL- 164

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      +G EIEII + S Y+ +T+ L+ G + ++ Y++ G +K P V GD
Sbjct: 165 VGGGEIEIIPPISSKSYIYLTIELLNSLGGNIKMKG--NKIYVEKGD-FK-PYIGKVPGD 220

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTT-SLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      + AS++ + + ++GG + +E + GD +MMGA+ + V +
Sbjct: 221 YALASFYASSSIVSGGEIVIEDVYELPNFDGDHSIVNFYKMMGAESYVKDNKWIVKSSEK 280

Query: 313 EPFGRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
      L I+VN++ PD+A ++A +A F+ PT I+ + + KE+ R+V I L+
Sbjct: 281 -----LNGIEVNVDDYPDLAPSIASLAPFSSSPTTIKGIKRLKTESNRVVTISETLS 333

Query: 373 KLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFF 432
      K G VE D +I P E + + +DHR+AM S+ + TI C K+
Sbjct: 334 KFGVKVEYDEDKIVIYPSE-VKAGHVICPNDHRIAMLASVLSFKS-GGTIEKAECVNKSN 391

Query: 433 PDYF-DVLS 440
      P+++ D++S
Sbjct: 392 PNFWKDLIS 400

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>sp|Q8FRI2.1|AROACOREF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

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AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC17589.1| 5-enolpyruvylshikimate-3-phosphate synthase [Corynebacterium
efficiens YS-314]
Length = 408

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 128/420 (30%), Positives = 208/420 (49%), Gaps = 31/420 (7%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR L+LAAL+ G + + +L S D M ALR++G+++ + + V
Sbjct: 6 IPGSKSITNRALILAALAAGPSTIHGVLRSRDTDLADALRSMGVITITEAPDRYHV--- 62

Query: 81 CGGKFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
+ P E + + G AG MR + A G + DG + R RP+ ++
Sbjct: 63 ---EPPAELSSGSID--CGLAGTVMRFVPPVAAFADGPVHF--DGDEQARIRPMTSILDA 115

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L+ LG V+ + P V G GG V++ S SSQ++S LL++AP + V +
Sbjct: 116 LRTLGVVRVE----NNRLPFTVTSDGIPGEGVVEIDASASSQFVSGLLSAPRFVNGVTVR 171

Query: 201 II-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
I +L S+P++EMT+ ++ G++ + + +++ + G+ +E D S+A+
Sbjct: 172 HIGGRLPSMPHIEMTVAMLRVIRVDVTP--NQWTVHPGEIRG--HTWRIEPDLSNATP 227

Query: 260 FLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT---VTGPPPREPF 315
FLA AA+T GTVTV + Q +LE MG V + T VTGP
Sbjct: 228 FLAAAATVTRGTVTRVNRWPRDTPQPGDSIRSILEDGCTVEFISNGATFDLEVTGP----- 282

Query: 316 GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
LK I ++M+ + ++ T+A +A A + + +A R ET R+ A+ E+ +LG
Sbjct: 283 --AELKGIHLDMSDIGELTPTVAALAAALATTESRLTGIAHLRGHETNRLEALTAENRLG 340

Query: 376 ASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
+ E D IT P L+ +Y DHRMA A ++ V + D T KTFP +
Sbjct: 341 GNCTELDDGLHIT-PAPLHGGVWHSYADHRMATAGAIIGLVIKDVGVEDIQTTSKTFPGF 399

>ref|ZP_07726162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus downei
F0415]
gb|EFQ56568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus downei
F0415]
Length = 427

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 118/441 (26%), Positives = 219/441 (49%), Gaps = 29/441 (6%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++++ G +++PG KS+S+R ++ +L++G T++ ++L EDV + A R +G+++E D
Sbjct: 7 VQQLQGNLVRPGDKSISHRSIMFGSLAQGGQTLIRDLRGEDVLSTMQAFRDMGVNIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R VG G P + L +GN+G ++R ++ + AG + + + G + +
Sbjct: 67 DVIRIEGVGFQGLRPPQKP-----LNIGNSGTSIRLISGVL--AGQDFSVMQMGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+ ++G L L + S+Q SAL+ AA
Sbjct: 120 RPMDRISIPLRQMGVEIAGRSEKDLPLNIHGSRLKPIHYHLPIA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++E+FG E S +++GGQ + + V
Sbjct: 179 QANG--ESIIIEKEKTRNHT---DMIEQFGGHLEI--SGKEIHVQGGQIL-TGQEVVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + + +E G + +V++ MG K++ ++ S
Sbjct: 231 GDISSAAFVLVAGLIMPDSKIILENVGINETR--TGILDVIKAMGGKISLSQIDEGAKSA 288

Query: 306 TVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
T+T E G + I + ++ D +A++A A G T I D +VKET+R+
Sbjct: 289 TITVESSELHGTRIAGDI---IPRLIDELPIALLATQAQGGQTVIADAEELKVKETDRIQ 345

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIR 423
+ L +GA +E D II L+ ++T DHR+ M ++AA E V +
Sbjct: 346 VVADALNSMGADIEPTADGMIIQGTKALHGAKVNTLGDHRIGMMVAIAALLVKEGEVDLE 405

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
++P +F+ + +
Sbjct: 406 RAEAINTSYSPSFEDMKGLIN 426

>ref|ZP_07466969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus bovis
ATCC 700338]
gb|EFM27179.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus bovis
ATCC 700338]
Length = 461

Score = 142 bits (358), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 125/449 (27%), Positives = 225/449 (50%), Gaps = 37/449 (8%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+L + ++ GT+++PG KS+S+R ++ +L++GTT V ++L EDV + R LG+ +
Sbjct: 37 LLTNVSQKGLTRVPGDKSISHRSIMFGSLAKGTTTVDILRGEDVLSTMQVFRDLGVDI 96

Query: 68 EADKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ D VG G K P + +L +GN+G ++R ++ + AG + T + G
Sbjct: 97 QDDGNIVTITGVGFDGLKAP-----KNKLDMSGSGTSIRLISGVL--AGQDFTVEMFGD 148

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + + L+Q+G +V D PP+ + G L +L + S+Q SAL
Sbjct: 149 DSLSKRPMDRVITPLRQMGVEVSGQTDRLPLTMRGSKALKPIHYQLPMA-SAQVKSAL 207

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA A D E II+K + + E ++ +FG + + R IKGGQ++ + +
Sbjct: 208 IFAALQA--DGESVIEKEKTRNHT---DMIVQFGGAIDVNGKEIR--IKGGQEF-TGQ 259

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303
+ V GD SSA+++L AG + VT+E G + + +V++ MG K+T
Sbjct: 260 DVVVPGLDISSAAFVLVAGLIVPNAKVTLENVGINETRTGI--IDVIKEMGGKMTILNVDE 317

Query: 304 ---SVTVTGPPPREPFGRKHLKAIDVNMKMPDVAMTLAVVALF---ADGPTAIRDVASWR 357
S T+T E L +++ +P + L ++AL A+G T IRD +
Sbjct: 318 IAKSATITVETSE-----LHGVEIGGEIIPRLIDELPIIALLATQANGTTIIRDAEELK 371

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--C 415
VKET+R+ + L +GA + D I+ L+ + + T+ DHR+ M ++AA
Sbjct: 372 VKETDRIQVVVDALNAMGADITPTDDGMIVKGKTPHSGSVSTFGDHRIGMMTAVAALLV 431

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
++ V + ++P +F+ L +
Sbjct: 432 SDGDVELERAEAINTSYSPSFNDLEVLRS 460

>ref|YP_004203174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus scotoductus
SA-01]
gb|ADW22625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus scotoductus
SA-01]
Length = 441

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 144/451 (31%), Positives = 214/451 (47%), Gaps = 38/451 (8%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P + G +++PG KS+++R L+L ALSEG + L + D LR LG +
Sbjct: 8 LGPCVPLRGVLRVPGDKSVTHRGLMLLALSEGGRFLFYPLKAGDTLSTARVLRALGAEIL 67

Query: 69 ADKAAKRAVVVGC-GGKFPVEDA-----KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+K + A + G F V + E L GNAG +R L + A V
Sbjct: 68 EEKGPEGARLAREEGPHFRVRGQGLRLKEPEDVLDGNGAGTLIR-LILGILAGQEGFLFAV 126

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G +R RP+G +V L+ +GA +D G P+ V G G L G L S+Q
Sbjct: 127 LTGDASLRRRPMGRVVEPLRAMGASIDGREGGRAPLAVRGRG-LKGVSYTLP-VPSAQV 184

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SALL+A A ++ + + +P + T RL FG+ E R + +
Sbjct: 185 KSALLLAGLFA-----EDVTEVVEPVPTRDHTRERLFRHFGLETEGP--RIRTHRAEPF 237

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ ++ V GD SSA++FL A +T G+ VTVEG G + +VL+ MGA + W
Sbjct: 238 PA-RDLTVPGDFSSAAFFLVAALLTPGSEVTVVEGVLNPTTR--TGLLKVLQAMGADLEWQ 294

Query: 302 ETSVTVTGPPREPFPG-----RKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDV 353
V G EP G LK + V+ +P D LA A +A+G T I +
Sbjct: 295 ----VVEGESGEPVGVWIRARYSPLKGVSVDPGLIPLMVDEVVLA AAAAWEGETYIPGL 350

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLA 413
+ RVKE++R+ AI L LG VEEGPD+ I + ++ + DHR+AMAF++A
Sbjct: 351 SELRVKESDRVAIAHNLRALGVGVVEGPDWLRIG-GGGVKPGEVEPFHDHRIAMAFAVA 409

Query: 414 ACAEVPVTIR--DPGCTRKTFPDYFDVLSTF 442
A +PV +R +P ++P +F L
Sbjct: 410 A---LPVGVRVWEPHWAEISYPGFFQDLKRL 437

>ref|YP_002750296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
03BB102]
sp|C1EYX7.1|AROABACC3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACO27272.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
03BB102]
Length = 429

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGLNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAILDVGNSGTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIARKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITITETSLKGIIEGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPPTFFELQRLTK 429

>emb|CBW27913.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Bacteriovorax marinus SJ]
Length = 410

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 121/435 (27%), Positives = 208/435 (47%), Gaps = 49/435 (11%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K V +P SKS +NR ++LAALS+ ++NL S DV +L LR +GL +
Sbjct: 13 KSFDAENVNVPSSKSYANRAIILAALSKDAITENLPLSHDVTNLLNVLREVLRI---VE 69

Query: 73 AKRAVVVGCGGKFPVED--AKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +++ FP + + E++++ G+ G R L + A G +Y ++ RMR
Sbjct: 70 VENGIIE--ENSFPECERPSSEKIKIYPGDGGTTTRFLIPFL--AMGKNSYQIEPEGRMR 125

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCPP--VRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
ERP+ DL+ L +LGA ++ C + + G K+K S ++Q+ +AL +
Sbjct: 126 ERPVADLLEVLAEELGASIN-----QCDTWLTIRGPLSFQTNKLKADASKTTQHATALALC 180

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
LA ++E++ +D S Y +MT+ L++ F KG +K+ Y
Sbjct: 181 --LAFQNIIEVQPVDMKYSKSYWDMTMSLIQDFK-----KGQKKF-----Y 218

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGC--GTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D SS SY LA A G V V+ C + Q D F EVL+ MG VT ++ + V
Sbjct: 219 VPVDFSSMSYVLALGA--DRGKVLVKNCDIDTFQSDSIFVEVLKNMGYSVTLSDKGLEVK 277

Query: 309 GPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+E + I+++ + PD+ TLA DG + + +++ + KE++R++ ++
Sbjct: 278 SSEKE-----ITPINLDCSNCPDLVPTLAFTCSRIDGESKLSNLSVLKYKESDRLELVQ 331

Query: 369 T--ELTKLGASVEEGPDYCIITPPEKLNVTIDTY--DDHRMAMAFSLAACAEVPTIRD 424
+L + + E D I +K A + Y DDHR+ M L A +
Sbjct: 332 KLLDLYSIENTYNEKEDVLHIKSGSKRIDKAKEIYPPDDHRIVMVSYLFLRAHGGGVLNS 391

Query: 425 PGCTRKTFPDYFDVL 439
K+F ++F+V+
Sbjct: 392 IHSVSKSFGNFFEVV 406

>ref|ZP_07713645.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
gb|EFQ80953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
Length = 433

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 132/435 (30%), Positives = 203/435 (46%), Gaps = 27/435 (6%)

Query: 10 QPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
Q I+ +PGSKS++NR +LAL++G + + L S D M AL ++G+ E
Sbjct: 16 QAAGPITWAQHVPGSKSITNRAFILAALADGPSTLRAPLVSRDSQLMEKALESMSGVRFEH 75

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + V G P++ A + L AG MR + A G ++DG +
Sbjct: 76 EG---EDIHVAPG---PLKGATVDCGL---AGTVMRFIPPVAALADG--AVLVDGDEQA 123

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+QLG +VD D P V G GG+V + S SSQ++S LL+A
Sbjct: 124 YARPMSTTLDALRQLGVEVDG----DSLPTVRSHGVPEGGEVTIDASGSSQFVSGLLLA 179

Query: 190 -APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G L S+P+VEMT+ ++ + GV+ + + + + G +
Sbjct: 180 GARFAKGITVTHEGGPLPSMPHVEMTVGMLRQAGVRVDSGE--NTWTVHPGPIAG--REW 235

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+E D S+A+ FLA AA+TGG VT++ + Q +L MG VT VT
Sbjct: 236 AIEPDLSNATPFLAAAAVTGGRVTIKRWPANTTQPGDAIRHILVDMGMVMVTQEPGFVTAK 295

Query: 309 GPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G L+ I+ NM + ++ T+A + AD P+ + +A R ET+R+ A+
Sbjct: 296 G-----TKGGALQGIERNMGDIGELTPTVAALCALADTPSILTGHILRGHETDRLKALA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
+ LG V E D I P L+ Y DHRMA A ++ V + D T

Sbjct: 351 DNINALGGKVAELADGLHID-PAPLHGGEWPCYADHRMATAGAIIGLRVPGVEVEDISTT 409

Query: 429 RKTFPDYFDVLSTFV 443

KT P + + T V

Sbjct: 410 AKTLPGFDRMWETMV 424

>emb|CBZ48633.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
gallolyticus subsp. gallolyticus ATCC BAA-2069]
Length = 427

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 125/449 (27%), Positives = 224/449 (49%), Gaps = 37/449 (8%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67

+L + ++ GT+++PG KS+S+R ++ +L++GTT V ++L EDV + R LG+ +

Sbjct: 3 LLTNVSQKGLTRVPGDKSISHRSIMFGSLAKGTTTVHDILRGEDVLSTMQVFRDLGVDI 62

Query: 68 EADKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126

+ D VG G K P + +L +GN+G ++R ++ + AG + T + G

Sbjct: 63 QDDGNIVTITGVGFDGLKAP-----KNKLDMGNSGTSIRLISGVL--AGQDFTVEMFGD 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

+ +RP+ + + L+Q+G +V D PP+ + G L +L + S+Q SAL

Sbjct: 115 DSLSKRPMDRVITPLRQMGVEVSGQTDRLPLPLTMRGSKALKPIHYQLPVA-SAQVKSAL 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

+ AA A D E II+K + + E ++ +FG + + R IKGGQ++ + +

Sbjct: 174 IFAALQA--DGESVIEIEKEKTRNHT---DMIVQFGGAIDVNGKEIR--IKGGQEF-TGQ 225

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-- 303

+ V GD SSA+++L AG + VT+E G + +V++ MG K+T +

Sbjct: 226 DVVVPGLDISSAAFVLVAGLIVPNAKVTLENVGINETR--TGIIDVIKEMGGKMTISNVDE 283

Query: 304 ---SVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWR 357

S T+T E L +++ +P + L ++AL A+G T IRD +

Sbjct: 284 IAKSATITVETSE-----LHGVEIGGEIIPRLIDELPIIALLATQANGTTIIRDAEELK 337

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--C 415

VKET+R+ + L +G + D II L+ ++T+ DHR+ M ++AA

Sbjct: 338 VKETDRIQVVADALNAMGTDITPTDDGMIIGKKTPLHGAKVNTFGDHRIGMMTAIAALLV 397

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444

++ V + ++P +F+ L +

Sbjct: 398 SDGDVELGRAEAINTSYPSFFNDLEVLRS 426

>ref|ZP_04570784.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
2_1_31]
gb|EE037367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
2_1_31]
Length = 418

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 108/435 (24%), Positives = 206/435 (47%), Gaps = 52/435 (11%)

Query: 17 GTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAKRA 76

G + P SKS+ +R ++ ++L++GT+ ++N+ SED+ + A++ LG +E K+

Sbjct: 11 GELSPPPSKSVLHRYIIASSLAKGTSKIENISFSEDIATIEAMKKGAKIE-----KKD 65

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136

+ G ++ E +++ +G +R L + G ++ +RP+

Sbjct: 66 NYLLIDGSDTFKNLNENIEIDCNESGSTRFLRFLPLSIVKENKVLF--KGRGKLFKRPMT 123

Query: 137 LVVG-----LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191

+K L D + L G L G ++ G+ISSQ+++ LL + P

Sbjct: 124 YFQNFEEKYIKHLYIDENAILLE-----GKLKAGIYEIEGNISSQFITGLLFSLP 173

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251

L G+ +I I KL S Y++++L + +FG+K ++S+ F I+G Q Y++ N E

Sbjct: 174 LLDGESKIIINGKLESSNYIDISLDCLNKFGIKI-INNSYQEFIEGNISSQSYRAG-NYRTE 231

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVWTETSVTVTGPP 311
D S A++FL AI G + + SLQGD K +++ + W V
Sbjct: 232 ADYSQAFFLVANAI-GSKIKINDLSEDSLQGDKK---IIDYISEIDNWNKDTLV---- 283

Query: 312 REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
++ ++ PD+ L++ A + I ++ R+KE++R+ A EL
Sbjct: 284 -----LDGSETPDIIPILSLKAAVSGKKIEIVNIERLRIKESDRLKATVEEL 330

Query: 372 TKLGASVEEGPDYCIITPPEKLNVT-----AIDTYDDHRMAMAFSLAA-CAEVPVTIRD 424
+KL + E D +I E V ++ + DHR+AM ++AA C + + + +
Sbjct: 331 SKLNFDLIEKKDSILINSRENFEVKNKVVSLSAHSDHRIAMMIAAATCYDGEILLDN 390

Query: 425 PGCTRKTFFPDYFDVL 439
C +K++P+++V
Sbjct: 391 LDCVKKSYPNFWVEVF 405

>gb|ADY22175.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar finitimus YBT-020]
Length = 429

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 128/453 (28%), Positives = 218/453 (48%), Gaps = 38/453 (8%)

Query: 5 EEIVLQPIKE-ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L ++ + ++S
Sbjct: 112 SCVQGDASIAKRPMKRVTNPLKQMGANIDGREGTFTPLTIRG-GDLKA--IQYTSPVAS 168

Query: 181 -QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK 237
Q SA+L+A A G + + PY+ + T R++E FGVK + +
Sbjct: 169 AQVKSAILLAGLRAEGVTAV-----TEPYISRDHTERMLEAFGVKVTREGKTVK--LA 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGA 296
GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE MGA
Sbjct: 220 GGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEKMG 276

Query: 297 KVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRD 352
T + + P LK I++ + +P + + V+AL A +G T I+D
Sbjct: 277 TFTVEPINEEASEPAANITITETSSLGIEIGGDIIPRLIDEIPVIALAATQAEGITVIK 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSL 412
+VKET R+ + ELTKLGA +E D II L +++Y DHR+ M ++
Sbjct: 337 AHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMMLAI 396

Query: 413 AAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
A C A TI D ++P +F+ L K
Sbjct: 397 AGCLAGGKTTIEDAEAVGVSYPTFFEELQKLAK 429

>ref|ZP_04063025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
salivarius SK126]
gb|EEK09366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
salivarius SK126]
Length = 427

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 121/434 (27%), Positives = 218/434 (50%), Gaps = 37/434 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++++PG KS+S+R ++ +L++G T V ++L EDV + R LG+++E D
Sbjct: 10 LHGSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVITIEDDGDVV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G K P + +L +GN+G ++R ++ + AG + + G + +RP
Sbjct: 70 RIHGVGFDGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFDVFEMFGDDSLSKRP 121

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L+Q+G +V D PP++++G L +L + S+Q SAL+ AA A
Sbjct: 122 MDRVVTIPLRQMGEVSGQTDRLPPLKMHGSKSLKPIHYQLPVA-SAQVKSALIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E II+K + + E +++++FG + + R I GGQ + + + V GD
Sbjct: 181 --DGESVIEIEKTRNHT---DMIQQFGGQLQVDGKEIR--ISGGQSF-TAQEVVVPD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++L AG + + +E G + +V++ MG K+T ++ S T+
Sbjct: 233 ISSAAFWLVAGLVVPSKIVLENVGINETR--TGIIDVIKDMGGKITLSIDIDQVAKSATI 290

Query: 308 TGPPREPFPGRKHLK AIDVNMNMKMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
T E LK ++ + +P + L ++ L A G T IRD +VKET+R+
Sbjct: 291 TVETSE-----LKGTEIGGDIIPRLIDELPIITLLATQAQKTVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +
Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTALHGAEVNTFGDHRIGMMAIAALLVQDGEVDL 404

Query: 423 RDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 405 QCAEAINTSYPSFF 418

>ref|NP_737389.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
ref|ZP_05749429.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
gb|EEW50501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
Length = 431

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 128/420 (30%), Positives = 208/420 (49%), Gaps = 31/420 (7%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PGSKS++NR L+LAAL+ G + + +L S D M ALR++G+++ + + V
Sbjct: 29 IPGSKSITNRALILAAALAGPSTIHGVLRSRDTDLADALRSMGVTTITEAPDRYHV--- 85

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP IGD LVVG 140
+ P E + + G AG MR + A G + DG + R RP+ ++
Sbjct: 86 ---EPPAELSSGSID--CGLAGTVMRFVPPVAAFADGPVHF--DGDEQARIRPMTSILDA 138

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L+ LG V+ + P V G GG V++ S SSQ++S LL++AP + V +
Sbjct: 139 LRTLGRVVE---NNRLPFTVTS DGIPEGGVVEIDASASSQFVSGLLLSAPRFVNGVTVR 194

Query: 201 II-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
I +L S+P++EMT+ ++ G++ + + +++ + G+ +E D S+A+
Sbjct: 195 HIGGRLPSPHIEMTVAMLRVGVIRVDVTP--NQWTVHPGEIRG--HTWRIEPLSNATP 250

Query: 260 FLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVT----VTGPPREPF 315
FLA AA+T GTVTV + Q +LE MG V + T VTGP
Sbjct: 251 FLAAAATVTRGTVTRNWRPDTTQPGDSIRSILEDGCTVEFISNGATFDLEVTGP----- 305

Query: 316 GRKHLK AIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
LK I ++M+ + ++ T+A +A A + + +A R ET R+ A+ E+ +LG
Sbjct: 306 --AELKGIHLMSDIGELTPTVAALAAALATTESRLTGIAHLRGHETNRLEALTAEINRLG 363

Query: 376 ASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAAEVPTIRDPGCTRKTFPDY 435
+ E D IT P L+ +Y DHRMA A ++ V + D T KTFP +
Sbjct: 364 GNCTELDDGLHIT-PAPLHGGVWHSYADHRMATAGAIIGLVKIDVGVEDIQTTSTKTFPGF 422

>ref|ZP_07051859.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
fusiformis ZC1]

gb|EFI66755.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
fusiformis ZC1]
Length = 428

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 132/440 (30%), Positives = 209/440 (47%), Gaps = 28/440 (6%)

Query: 6 EIVLQPIK-EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E VLQ K + G++ +PG KS+S+R ++ A++ GTT V+ L ED + + LG
Sbjct: 3 EKVLQYNKPSLQGSALTVPQDKSVSHRSVMFGAIAAGTTTVEGFLLEDCLSTIDCFQKLG 62

Query: 65 LSVEADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E + G GG + P E L+ GN+G R + + AG V+
Sbjct: 63 VQIEVEGTNVTIHSPGMGGWQEPTE-----VLYTGNSGTTTRLMLGIL--AGSTVHSVM 114

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + +RP+ ++ L+Q+GA + P+ + G L K+ + S+Q
Sbjct: 115 TGDASIGKRPMRVIDPLRQMGAIITGRADGQYTPLAIQGTK-LQAIDYKMPVA-SAQVK 172

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+L+A A G + +D +S + E R++ +FG + E + I+GGQ
Sbjct: 173 SAILLAGLRAEGTTIVREMD--VSRDHE---RMLRQFGAQVEVDNGV--VSIEGGQALN 225

Query: 244 SPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+ V GD SSA++FL AGA +T+ G + + EVL+ MGA +T T
Sbjct: 226 G-THVSVPGLDISSAAFFLVAGAICKNSQLTLNNVGINPTRDGI--IEVLQKMGATMTVTP 282

Query: 303 TSVTVTGPPRE-PFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
P L + + +P D LA++A A G T I+D +V
Sbjct: 283 NDDNQAEPTATIQTATSSLTGTIIEGDIIPRLIDEIPILALLATQAHGQTIKDAEELKV 342

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KET+R+ A+ TEL KLGA +E D II P L + TY DHR+ M ++AA +
Sbjct: 343 KETDRITAVVTELKKGAIQIEATDDGMIIEGPTPLKGANLQTYGDHRIGMMGAVAALLTD 402

Query: 418 VPVTIRDPGCTRKTFPDYFD 437
VT+ D C ++P +F+
Sbjct: 403 GAVTLDDAQCIASVSPSFFE 422

>ref|NP_681133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosynechococcus
elongatus BP-1]
sp|Q8DLY3.1|ARO3_THEEB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC07895.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosynechococcus
elongatus BP-1]
Length = 440

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 140/440 (31%), Positives = 209/440 (47%), Gaps = 33/440 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R L+L A++EGTT + LL ED R LG + A
Sbjct: 21 LRGTLLQVPGDKSISHRALMLGAMAEGTTQITGLLVGEDTCSTASCFRALGAEISPLNAT- 79

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLVDGVPRMRERPI 134
AV V G +++ + + GN+G MR L + A G + L G +R RP+
Sbjct: 80 -AVTVQGLGMGRLLQEPGDVMNA--GNSGTTMRLLLGVLAQTGR-FFTTLTGASLRSRPM 135

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLA 193
+V L Q+GA + P+ I G P + I+S Q SALL+AA
Sbjct: 136 ARVVTPLQLMGAIQWGRQHHSRAPL---AILGQPLEPITYYSPIASQVKSALLLALHT 192

Query: 194 LGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G LI P+ + + R+++ FG + ++ ++G K K V
Sbjct: 193 EGT-----LIREPHRSRDHSERMLQAFGARLSVDEATCTVSLEGPVLLKQK-VIVP 244

Query: 252 GDASSASYFLAGAAITGGT---VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SSA+++L A+I + +T G T +VL MGA++T E VT
Sbjct: 245 GDISSAAFWLVAASIIIPDSELLLTVNGVNPTR----TGILDVLWAMGAEITL-ENERLVT 299

Query: 309 GPPREPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P + LK+ + +P D LAV A FA+G T IRD A RVKE++R
Sbjct: 300 GEPVADLRVRSARLKSTRIGGELIPRLIDEIPILAVAAFAEGVTEIRDAAELRVKESDR 359

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ TEL K+GA V E D I L T ++TY DHRMAM+ ++AA A+ I
Sbjct: 360 LKAVATELQKMGAKVTLESDGLDIQGGGPLQGTHLETYGDHRMAMSLAIAALNAKGTSEI 419

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
+ ++P++ VL
Sbjct: 420 HNASAAVSYPEFVTVLQQI 439

>ref|YP_003665177.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis BMB171]
gb|ADH07457.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis BMB171]
Length = 429

Score = 142 bits (357), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ +++EG T + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VETIQNGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K +S
Sbjct: 112 SCVQGDESIAKRPMKRVTNPLKQMGANIDGREGGTFPTLTIRG-----GDLKAIEYISP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLSGGQKL-TATDIQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVDLINEGASEPAANITIETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE I D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTIIEDAEAVGVSYPTFFFEELQKLAK 429

>ref|ZP_07268112.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Finergoldia
magna ACS-171-V-Col3]
gb|EFK94530.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Finergoldia
magna ACS-171-V-Col3]
Length = 398

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 117/425 (27%), Positives = 201/425 (47%), Gaps = 46/425 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTILGLSVEADKA 72
++ G V SKS ++R L+LA++++ TT++ N S D+ + LR LG+ +E ++
Sbjct: 7 KLQKGKVAISSKSFAHRFLILASVADTDTTIIINEF-SNDIMTTIDCLRNLGVEIEINEN 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V F +D + + + ++G R L V+ G R+++R

Sbjct: 66 E-----VTVHPSFFQKDVSD---INVNDSGSTFRFLPLVVSFLSQKTNIQCSG--RLQDR 115

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +LV LK G + P V+G + G +SSQY+SA++M APL

Sbjct: 116 PIKELVDQLKLSGLT----FSEELPFTVDG--TFHKIDFEFPGDVSSQYISAIMMIAPL 169

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+G EI++ KL S Y+++T ++ FGV +E D+ +K G KSP VEG

Sbjct: 170 -IGGCEIKLSSKLESTGYIKITQECLKLFGVDSEIL--LDKVIKPGA-LKSPGKIIVEG 225

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A++FL A+ G + VE S+Q D K E LE + + E

Sbjct: 226 DWSNAAFFLCANAL-GADIKVENLNVNSVQADRKIVEFLEKIENNEDYCE----- 274

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
++++ PD+ + LAVV + +++ R+KE++R+ + L

Sbjct: 275 -----IDISQTPDLFVILAVVLSQKCEKSVLKNKRLRLKESDRIQSTYDMLK 322

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432
G + E D +I E + +++ DDHR+ M ++A+ V I+D K++

Sbjct: 323 SFGINCEIEGDNLVICKSE-MKPAVNVSCDDHRIVMTAAIASIVTKEVEIKDWQAVSKSY 381

Query: 433 PDYFD 437
P +FD

Sbjct: 382 PSFFD 386

>ref|YP_002997062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
dysgalactiae subsp. equisimilis GGS_124]
dbj|BAH81848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
dysgalactiae subsp. equisimilis GGS_124]
Length = 430

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 126/440 (28%), Positives = 214/440 (48%), Gaps = 25/440 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + GT+ +PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +

Sbjct: 10 VGRLLQGTICVPGDKSISHRAVILGAIAKGETRVKGLLKGEDVLSTIQAFRNLGVRIE--E 67

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ V+ G G F A + L +GN+G +MR + + AG + + G + +

Sbjct: 68 KDDQLVIEGQG--FEGLTAPHQT-LDMGNSGTSMLRIAGLL--AGQSFDVTMSGDDSLSK 122

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +V+ L+Q+GAD+ PP+++ G L L + S+Q SA+L+AA

Sbjct: 123 RPMDRIVLPLRQMGADITGEGSRHLPPLKLGKSRELNPITYALPVA-SAQVKSAILLAAL 181

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E+ I+K I+ + E ++++FG + + ++ G Q + V

Sbjct: 182 QANGTTEV--IEKEITRNHTE---DMIQQFG--GQLRVDGKKIWLTPQTTLIG-QEVTVP 233

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
GD SSA+++L AG + G + +E G + + EV+E MG +VT+ E T

Sbjct: 234 GDISSAAFVLVAGLIVPGSAILLENGINPRTGI--LEVIEQMGQVQTY-EAVNPQTQS 290

Query: 311 PREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D RVKET+R+ +

Sbjct: 291 ANLGVAYSQLKGTITISGQLIPRLIDELPIIALLATQAQGVTHIKDAQELRVKETDRIQVV 350

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA++E D II P L+ T+ DHR+ M ++AA + V +

Sbjct: 351 TDILKSMGATIEATADGMIIIEGPTALHAAQTSTFGDHRIGMMTAIAALLVKQGEVHLDRE 410

Query: 426 GCTRKTFFPDYFDVLSTFVKN 445
++P +F L +

Sbjct: 411 EAIMTSYPTFFKDLERLCHD 430

>ref|YP_002950111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
WCH70]

gb|ACS24845.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
WCH70]
Length = 428

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 132/452 (29%), Positives = 217/452 (48%), Gaps = 41/452 (9%)

Query: 9 LQPIK----EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+QP++ + GT+ +PG KS+S+R ++L A++ GTT + N L ED + R LG
Sbjct: 1 MQPLRTNISSLRGTINVPKDKSISHRAVMLGAIANGTITIANFLQGEDCLSTIDCFRKL 60

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+S+E + VV G G K E + L +GN+G R L + AG L
Sbjct: 61 VSIEQN--GSDVVVEGKGLKGLKEPSD---ILNVGNSGTTARLLLGIL--AGCPFHSLI 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI-SSQYL 183
G + +RP+G + LK +GA +D + P+ + G P + S+ S+Q
Sbjct: 114 GDESIARPMGRVTKPLKMMGAHIDGREHGNYPPLSIRGGELQP---IHYESSVASAQVK 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+L+A + + + S + E +RL FG D I G Q+
Sbjct: 171 SAILLAG--LTNNGTTVTPEHRSDHTERMIRL---FGGSVTVDLT--VSITGPQQLI 223

Query: 244 SPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
N YV GD SSA++FL AGA + +T++ G + + +VL+ MGA++T
Sbjct: 224 G-ANIYVPGDISAFLVAGAIVPNSEITLKNVGLNPTRTGI--IDVLQKMGAEMTIEN 280

Query: 303 TSVTVTGPPREPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVA 354
+ EP G +L A +++ +P + + ++AL A+G T I+D +
Sbjct: 281 ----IRNEQTEPLGDITIRTSNLTATEISGALIPRLIDEIPIIALLATQAEGETTVIKDAS 336

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSL 412
+VKET R+ + TEL KLGA ++ D +I L +D+Y DHR+ M ++
Sbjct: 337 ELKVKETNRIDTVVTELRLKLGADIKATADGMVHKGSAKAKDVVVDSYGDHRIGMMLAI 396

Query: 413 AAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
AAC + V ++ P ++P +FD L + +
Sbjct: 397 AACITQGTVCCLKRPEAVAVSYPSFFDHLHSLM 428

>ref|YP_001277962.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseiflexus sp. RS-1]
sp|A5UZ9.1|AROAROSS1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ92012.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseiflexus sp. RS-1]
Length = 433

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 209/445 (46%), Gaps = 35/445 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + G + LPG KS+S+R +LL A++ G+ + N L D + ++ LG+ +E
Sbjct: 6 ITPPHRLRGIIDLPGDKSISHRAILLNAVAAGSAEITNFLTGADCLSTIACVQALGVHIE 65

Query: 69 ADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY-VLDGV 126
R G G + PV+ L GN+G +R L + AG + VL G
Sbjct: 66 RQGTTVRVGDAGLRGLREPVD-----VLDCGNSGTTLRLLAGMI--AGQEGMFAVLTD 117

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R RP +V L+ LGA +D +C P+ V G L GG +L + S+Q SAL
Sbjct: 118 SSLRSRQQRIVAPLRALGASLDGRQQGNCAPLAVRG-AHLHGGAYELPIA-SAQVKSAL 175

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+AA GD + + + + E R++ GV+ + R P
Sbjct: 176 LLAA--LFGDAPLTLTGRTDGRDHTE---RMLAAMGVEITVNTPVIRLTPPAHSDALRPL 230

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ GD SSA+++ AAI +T G C + G + + L MGA++ T
Sbjct: 231 SLRAPGDPSSAAFVWVAAAIHPDAELTTTGVCNLNPTRTGAL---DALRAMGAQIEVTNQR 287

Query: 305 VTVTGPREPFG-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356

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      + +   EP G           L+ I +   +P   D   LA+ A   A+G T   IRD
Sbjct: 288 IEGS----EPVGDVTVRSSQLRGITIEGALIPRLIDELPVLALAAACAEGETIIRDAQEL 343

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-C 415
      RVKET+R+   + LT LGA+VE   D +I+   +L   ++D++ DHR+AM   +++A
Sbjct: 344 RVKETDRIATAASGLTALGATVEPTSDGMVISGGARLRGASLDSHGDRHLAMTWAIAGLV 403

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLS 440
      A   T+R   G   ++P+++ VL+
Sbjct: 404 ASGETTLRGAGAVDVSYPEFWGVLA 428

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>emb|CAN73015.1| hypothetical protein VITISV_004387 [Vitis vinifera]
Length = 74

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 62/72 (86%), Positives = 69/72 (95%)

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Query: 374 LGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
      LGA+VEEGPDYC+ITPPEKLNVT+IDTYDDHRMAMAFSLAAC+VPVTI+DPGCTRKTFP
Sbjct: 3   LGATVEEGPDYCVITPPEKLNVTSIDTYDDHRMAMAFSLAACADVPTIKDPGCTRKTFP 62

Query: 434 DYFDVLSSTFVKN 445
      DYF+VL   F K+
Sbjct: 63 DYFEVLQRFTKH 74

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>gb|ABX11283.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured bacterium]
Length = 454

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 136/456 (29%), Positives = 232/456 (50%), Gaps = 44/456 (9%)

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Query: 6   EIVLQP-IKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E+   QP   K + G +++PG KS+S+R ++   +++ GTT + N L S+D   + L A R+LG
Sbjct: 27   EVKFQPTKGLLGEMEVPGDKSISHRAIMFGSMATGTTKITNFLQSDCLHTLEAFRSLG 86

Query: 65   LSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
      + +E   +++   + G G   ++ KE   V ++ GN+G A R +   + A   V+
Sbjct: 87   VEIEHKESS--ITIYGKG----IDAFKEPTVPVYFGNSGTAAARLMLGLL--ASLPFYTVI 138

Query: 124   DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI----S 179
      G P +   RP+   ++V LK++GA +D   P+   G+ G ++K   I   S
Sbjct: 139   HGDPHLTIRPMDRVIVPLKEMGASIDGRGEGSLLPL-----GIRGKQLKGIDYILPVKS 192

Query: 180   SQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGG 239
      +Q   SA+L+A   LA G ++ ID   + T R++ FG + H +   + I+G
Sbjct: 193   AQVKSAILIAGLADGVTKVTEIDT-----SRDHTERMLTAFGAEV-HVEGLE-ISIQGK 245

Query: 240   QKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      QK +   N +V GD SSA++F+   AAI   T+T++ G   +   + +VL+ MG +
Sbjct: 246   QKL-TGTNVHVPGLDISSAAFFIVAAAIVPNSTLTIKNVGLNETRTGI--IDVLQQMGGNI 302

Query: 299   TWTETSVTVTGPPEPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAI 350
      T +   + + G   E FG   HL+ I++N   +P +   + ++AL A   DG T I
Sbjct: 303   TISNEQM-IGG---EHFGDVTVKHSHLRGIEINGKIIPRLIDEIPIIALLATQADGKTVI 358

Query: 351   RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
      D   RVKET+R+ A   LT LGA +E   D II   L+   + +Y DHR+AM
Sbjct: 359   TDAEELRVKETDRIDATVDVLTTLGAKIEPLEDGMIIHGNTNLSGGKVKSYSDHRIAMMG 418

Query: 411   SLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSSTFVKN 445
      ++A+   A+   V + D   ++P++ + L   ++
Sbjct: 419   AIASLIAKDEVILDDSSISVSYPNFLEDLHQLTQS 454

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>ref|NP_897098.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH
8102]
sp|Q7U7H8.1|AROASYNPX RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

emb|CAE07520.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Synechococcus sp. WH 8102]
Length = 441

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 129/450 (28%), Positives = 202/450 (44%), Gaps = 51/450 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG VK+PG KS+S+R LL A++EGTT +D LL +ED LR +G+ + +AA
Sbjct: 19 LSGHVKVPKDKSISHRSLLFGAIAEGTTTIDGLLPAEDPISTAACLAMGVLISPIEAAG 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G ++ +E ++ GN+G MR + + G +VLDG +R RP
Sbjct: 79 LVTVEGVG----LDGLQEPAEILDGNSGTTMRLMLGLLAGRAGR-HFVLDGDASLRRRP 133

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L +GADV G + P+ V G Q L ++ P+A
Sbjct: 134 MRRVVGQPLASMGADVGRDGNLAPLAVQG-----QSLRGTVIGTPVA 176

Query: 194 LGDVE-----IEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGG 239
V+ +I+ S + E R++ FG + R ++ G
Sbjct: 177 SAQVKSALLLAALTADGTTTVEIPAQRDHS---RMLRAFADLQVGGEMGRHITVRPG 233

Query: 240 QKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
K + V GD SSA+++L AGA + G +T+E G + EVLE M A++
Sbjct: 234 NTLKG-QQVVVPGDISAFAFWLVAGALVPGADLTIEVGLNPTR--TGILEVLEQMNAQI 290

Query: 299 TWTETSVTVTGPPREPFGKHK--LKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
V G P H L+ + MP D L+V A F DG + I
Sbjct: 291 EVLNRD-DVAGEPVGDLRITHGPLQPFSGIEEIMPRLVDEVPILSVAACFCDESIRISGA 349

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLA 413
+ RVKET+R+ + +L +GA +EE D I L A+D+ DHR+AM+ ++A
Sbjct: 350 SELRVKETDRLAVMARQLKAMGAEIEEHEDGMTIHGGRPLKGAALDSETDHRVAMSLAVA 409

Query: 414 A-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ A T++ ++P ++D L
Sbjct: 410 SLLASGDSTLQRSDAAAVSYPFWDDLRL 439

>ref|YP_001550922.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9211]
gb|ABX08968.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9211]
Length = 445

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 127/447 (28%), Positives = 221/447 (49%), Gaps = 32/447 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P ++ G +K+PG KS+S+R LL +++EG T++ LL +ED LR +G+ +
Sbjct: 16 VKPGGKLIGKLVKPGDKSISHRALLFGSIAEGETIIKGLLPAEDPISTANCLAMGVKIS 75

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ ++ K + G G ++ KE + L GN+G MR L + G +VL+G
Sbjct: 76 SIESDKVVSIIQGVG---LDGLKEPSEVLNCGNSGTTMRLLLGLLVGRKGRH-FVLNGDK 130

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + LK +GA+++ D P+ + +G G V + S+Q SA+L
Sbjct: 131 SLNKRPMQVRQPLKLMGAEINGRSDGDLAPLSI--VGRNLHGAVIGTPVASAQVKSAIL 188

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPK 246
+AA A G ++ I+ S + E R+++ FG E S R + G K +
Sbjct: 189 LAALTAEGSTKV--IEPTSSRDHSE---RMLKAFGANLEVSGERGRHISVWPGSKLLG-Q 242

Query: 247 NAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V GD SSA+++L AG I +T+E G + + +V+E M A + +
Sbjct: 243 SIVVPGDISAFAFWLIAGTIIPNSELTIENVGLNPTRTGI--LKVMEQMEANIEL----I 296

Query: 306 TVTGGPPREPFG-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
+ EP G LK ++ + +P D L+V A F DG T I +

Sbjct: 297 NIRDVAGEPVGDIKVIHNDQLKPFKIDSSLVPSLVDEIPILSVAACFCGTTKITGASEL 356

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-C 415

RVKET+R+ + +L ++GA++EE PD I + L +D+ DHR+AM+ ++A+

Sbjct: 357 RVKETDRLKVMTRQLLRMGANIEEHPDGLTIHGVDHLKGNHLDSETDHRVAMSLAIASIV 416

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442

A+ TI ++P++++ L

Sbjct: 417 AKGTSTIERSNAAAVSYPEFWNDLERL 443

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>ref|ZP_00604575.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
DO]
ref|ZP_05662518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,502]
ref|ZP_05669009.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,410]
ref|ZP_05674021.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,408]
ref|ZP_05713805.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
DO]
ref|ZP_05832212.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
C68]
ref|ZP_06446330.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
D344SRF]
ref|ZP_06676490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1162]
ref|ZP_06700249.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
U0317]
ref|ZP_07845126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133a04]
ref|ZP_07848525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133C]
ref|ZP_07852261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0082]
ref|ZP_07854057.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133A]
ref|ZP_07858387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133B]
ref|ZP_07861481.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133a01]
gb|EAN09098.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
DO]
gb|EEV45851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,502]
gb|EEV52342.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,410]
gb|EEV57354.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,231,408]
gb|EEW62193.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
C68]
gb|EFD10208.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
D344SRF]
gb|EFF30396.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
U0317]
gb|EFF35496.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1162]
gb|EFR68265.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133a01]
gb|EFR71359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133B]
gb|EFR75690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133A]
gb|EFR78379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133C]
gb|EFS07420.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0133a04]
gb|EFS09262.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TX0082]
Length = 431
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Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 214/441 (48%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSIHRSIMFGAIAEGTTTQNFRLAEDCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + + +GN+G +R L + AG T L G
Sbjct: 63 EEEEEVIK--IHGRGSHSFVQPTES---IDMGNSGTTIRLLMGIL--AGQPFTTTLFGDA 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMGRVMEPLREMGADLQGEENDQYLPITVTGTRSLSPIRYNMPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK + +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IIVTGPQKL-TGQQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAAFFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNHNEQ 284

Query: 307 VTGPPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAEV 424

>ref|YP_002744816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equi
subsp. zooepidemicus]
sp|C0MCK4.1|AROA_STRS7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAW99831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equi
subsp. zooepidemicus]
Length = 427

Score = 141 bits (356), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 127/438 (28%), Positives = 220/438 (50%), Gaps = 29/438 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++PG KS+S+R ++ A++EG TV+ LL +DV + A R LG+++ +A
Sbjct: 8 KALRGRRLRVPDGKSIHRAVIFGAIAEGQTVIHGLLRGQDVLATIQAFRDLGVTIY--EA 65

Query: 73 AKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A ++ G G G P + L +GN+G +MR L A + AA + +L G +
Sbjct: 66 ADSLIIIEGRGFGLKPAQKP-----LDMGNSGTSMR-LLAGLLAAQDFSQQLL-GDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + + L +GA++ + PP+ V G L +L + S+Q SA+L+AA
Sbjct: 119 RRPMDRITIPLSLGMAGELSGQGEKELPPLIVKGCQELRPIHYQLPVA-SAQVKSAILLAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G E I++K ++ + E ++E+FG K S + + IKG Q+ + + +
Sbjct: 178 LQTQG--ETVILEKELTRNHT---EMIEQFGGKL--SIAGKQISIKGPQRLQG-QILQI 229

Query: 251 EGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++LA G + G + +E G + EV+E MG ++++ +
Sbjct: 230 PGDISAAFWLAAGLIVPGSDLVLENVGINPTR--TGLLEVIEKMGQQLSYQAVDKDIQS 287

Query: 310 PPREFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVA 366
LK ++++ + +P + L V+AL A G T IR+ RVKET+R+ A
Sbjct: 288 ASLR-VSYSSLKVEISGDLIPRLIDELPVIALLATQAQGTYYIRNAQELRVKETDRIQA 346

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ L ++GA ++ D +I L+ A+ T DHR+ M ++AA E VT+
Sbjct: 347 VTDVLGQMGADIQATEDGMVIRGKTPHGAAVSTCGDHRIGMMAIAALLVEEGQVTLER 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
++PD+F L
Sbjct: 407 AEAILTSYPDFFKDLERL 424

>ref|ZP_06808915.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus
thermoglucosidasius C56-YS93]
gb|EFG53995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus
thermoglucosidasius C56-YS93]
Length = 428

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 131/447 (29%), Positives = 215/447 (48%), Gaps = 41/447 (9%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + GT+ +PG KS+S+R ++L A++ GTT + N L ED + R + +S+E +
Sbjct: 8 VSALQGTNLNVPKDKSISHRAVMLGAIANGTTTIANFLPGEDCLSTIDCFRKMVSIEQN- 66

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
VV G G + KE L +GN+G R L + AG L G +
Sbjct: 67 -GSDVVVEGKG---LNGLKEPTDILHVGNSGTTARLLLGL--AGCPFHSLIGDESIA 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+G + LK +GA +D + P+ + G G L + S S+Q SA+L+A
Sbjct: 120 KRPMGRVTKPLKMMGAHIDGREQGNYPPLSIRG-GELQPIHYE-SPVASAQVKSAILLAG 177

Query: 191 PLALGDVEIEIIDKLISIPY--VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
G ++ P+ + T R++ FG + + + G Q+ + N
Sbjct: 178 LATEGTTA-----VTEPHRSRDHTERMIRLFG--GDVTVDGRTVSVTGPQQL-TGTNI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
YV GD SSA++FL AGA + +T++ G + + +VL+ MGA +T V
Sbjct: 228 YVPGDISSAAFFLVAGAIVPNSIITLKNVGLNPTRTGI--IDVLQQMGADITIEN---V 281

Query: 308 TGPPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
EPFG +L A+++ +P + + V+AL A+G T I+D +VK
Sbjct: 282 RNEQTEPFGDITVRTSNLTAVEIGGALIPRLIDEIPVIALLATQAEGTTVIKDAGELKVK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAAC-A 416
ET R+ + TEL KLGA++E D II L +D++ DHR+ M ++AAC
Sbjct: 342 ETNRIDTVVTELRLKGANIEATGDGMIHGAALTAKEAVVDSDHGRIGMMLAIAACIT 401

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+ V ++ P ++P +FD L + +
Sbjct: 402 QGTVHLKRPEAVAVSYPSFFDHLHSLM 428

>ref|YP_003108586.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri SMDSEM]
gb|ACU52913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Sulcia
muelleri SMDSEM]
Length = 413

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 115/424 (27%), Positives = 199/424 (46%), Gaps = 40/424 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + + GSKS SNR+L+L AL + N+ NS+D +++ AL T K
Sbjct: 13 LKGKINITGSKSESNRLLILKALYPNIINIKNISNSDDTYFLKKALFT-----TK 62

Query: 75 RAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ + + ++G AMR LTA + N +L G RM+ERPI
Sbjct: 63 KVININ-----HSGTAMRFLTAFFSIKK-NKEIILTGSYRMQERPI 102

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
LV LK+LG + PP+R+ G L GG + + ++SSQY+SA+++ A

Sbjct: 103 SILVETLKKLGKIFYEKKKGYPPLRIIG-SNLLGGTISIDANLSSQYISAIMLIASQFK 161

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
++I + K+ S+ Y++MT ++++ G+ + K +E D

Sbjct: 162 NGLKIFLSKKITSLSYIKMTFNILKKIGINVYWKKNLII---INKNNIFKNKKILIESDW 218

Query: 255 SSASYFLAGAAI-TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSASY+ + A+ + ++ S+QGD + T+ + +

Sbjct: 219 SSASYYYSLVALCKKANLNLKFFTKKSIQGDKVITNIYNSFFNVKTFFKKKKLILKKKII 278

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+K+ I +++N PD+A T+ V + + + ++KET+R+ A++ EL K

Sbjct: 279 KRKKKY---IFLDLNPDIQTIVVTCAGLKIKCFLTGLETLKIKETDRLKALKIELFK 335

Query: 374 LG-ASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTF 432
LG S++ + K I TYDDHRMAM+FS + P++I DP K++

Sbjct: 336 LGIKSIKTNNSLLLNPNFKNMYIYTYDDHRMAMSFSTLSII-YPISILDYPYVVSXSY 394

Query: 433 PDYF 436
P+++

Sbjct: 395 PNFW 398

>gb|ADX24900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
dysgalactiae subsp. equisimilis ATCC 12394]
Length = 427

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 126/440 (28%), Positives = 214/440 (48%), Gaps = 25/440 (5%)

Query: 12 IKEISGTVKLPKSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + GT+ +PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +

Sbjct: 7 VGRLQGTICVPGDKSISHRAVILGAIAGKGETRVKGLLKGEDVLSTIQAFRNLGVRIE--E 64

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V+ G G F A + L +GN+G +MR + + AG + + G + +

Sbjct: 65 KDDQLVIEGQG--FEGLTAPHQT-LDMGNSGTSMLRIAGLL--AGQSFDVTMSGDDSLSK 119

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +V+ L+Q+GAD+ PP+++ G L L + S+Q SA+L+AA

Sbjct: 120 RPMDRIVLPLRQMGADITGEGSRHLPLPLKGSRELNPIYALPVA-SAQVKSAILLAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E+ I+K I+ + E ++++FG + + ++ G Q + V

Sbjct: 179 QANGTTEV--IEKEITRNHTE---DMIQQFG--GQLRVDGKKIWLTPQTTLIG-QEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + G + +E G + + EV+E MG +VT+ E T

Sbjct: 231 GDISSAAFWLVAGLIVPGSAILLENGINPRTGI--LEVIEQMGQVQTY-EAVNPQTQS 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D RVKET+R+ +

Sbjct: 288 ANLGVAYSQLKGTITISGQLIPRLIDELPIALLATQAQGVTHIKDAQELRVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA++E D II P L+ T+ DHR+ M ++AA + V +

Sbjct: 348 TDILKSMGATIEATADGMIIIEGPTALHAAQTSTFGDHRIGMMTAIAALLVKQGEVHLDRE 407

Query: 426 GCTRKTFPDYFDVLSTFVKN 445
++P +F L +

Sbjct: 408 EAIMTSYPTFFKDLERLCHD 427

>ref|ZP_04151690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
pseudomycoides DSM 12442]
gb|EEM16578.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
pseudomycoides DSM 12442]
Length = 434

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 125/451 (27%), Positives = 219/451 (48%), Gaps = 38/451 (8%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 63
+E +QP+ ++GT+ +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGNLNGTITIPGDKSISHRAVMFGAIAEGRTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + +V+G G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIMQN--GDEVIVIGKG----IEGLQEPKAVLDVGNSTTIRLISGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + +RP+ + LKQ+GA++D P+ + G G L ++ + ++S
Sbjct: 112 SCVQGDASIARKPMKRVNPLKQMGANIDGREDGTYTPTLIRG-GALKA--IQYTSPVAS 168

Query: 181 -QYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK 237
Q SA+L+A A G + + P++ + T R++E FGV + + +
Sbjct: 169 AQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TREGKTVKLA 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
GGQK + + V GD SSA++FL AGA + + ++ G + + +VLE MGA
Sbjct: 220 GGQKL-TGIDVQVPGDVSSAAFFLVAGAILPNSKIQLQNVGMNPTRTGI--IDVLERMGA 276

Query: 297 KVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRD 352
T + + + P LK I++ + +P + + ++AL A +G T I+D
Sbjct: 277 TFTIEPNEGASEPAANITITETSSLKGIEIGDIIPLRLIDEIPIIALAATQAEGITVIKD 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSL 412
+VKET R+ + ELTKLGA +E D II L + +Y DHR+ M ++
Sbjct: 337 ARELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSTLKGNTVHSYGDHRIGMMLAI 396

Query: 413 AAC-AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A C AE TI+D ++P +F LS
Sbjct: 397 AGCIAEGKTTIQDAEAVGVSYPTFFQELSKL 427

>ref|YP_001017896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9303]
sp|A2CAX1.1|AROAX_PROM3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM78631.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9303]
Length = 441

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 141/446 (31%), Positives = 214/446 (47%), Gaps = 39/446 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R LL A++EG T ++ LL +ED LR +G ++ A +
Sbjct: 19 LSGTVRVPKSGKSLSHRALLFGAIAEGITTIEGLLPAEDPMSTAACLAMGATISPIHAGQ 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G D +E Q L GN+G +R + + A+ G +VL G +R R
Sbjct: 79 IVRVEGVG-----LDGLQEPQDVLDCGNSGTTIRLMGLLAASKGR-HFVLSGDSSLRRR 132

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMA 189
P+ + L +GA + D P+ V+G GG+ G V S+Q SALL+A
Sbjct: 133 PMNRVGQPLTMMGAKIKGRSNGDFAPLAVSGQKLRGVIGTPVA-----SAQVKSALLLA 187

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNA 248
A A D +I+ S + E R++ FG E R + GQK +N
Sbjct: 188 ALTA--DGATTVIEPAHSRDHSE---RMLRAFADLEVGGEMGRHIRVSPGQKLYG-QNI 241

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA+++L AG + G + VE G + EVL+ M A++ V
Sbjct: 242 VVPGDISSAAFVWLVAGVLPVGAELVVENVGLNPTR--TGILEVLQQMEARIEVLNRH-EV 298

Query: 308 TGPPREPF-----RKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G EP G + LK +N + +P D LAV A F DG + I D + RVK
Sbjct: 299 AG---EPVGDRLVRVQGPLKPSINGDIIPLRVDEVPIILAVAACFCDESKITDASELRVK 355

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEV 418

ET+R+ + +LT +GA ++E D I L T +D+ DHR+AM+ ++AA AE
Sbjct: 356 ETDR LAVMTRQLTAMGADIDEHADGLTIRGGRTLRTGTELDSETDHRVAMSLAVAALLAEG 415

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
+ ++P+++D L +
Sbjct: 416 NSRLTGSEAAAVSYPNFWDDLERLHR 441

>ref|ZP_04262650.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST196]
gb|EEL05540.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST196]
Length = 429

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 125/442 (28%), Positives = 215/442 (48%), Gaps = 37/442 (8%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EG T + L D + + +G+ + ++
Sbjct: 13 LNGTHITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVEITQNR--D 70

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATY--VLDGVPRMRE 131
V+G G +E +E + L +GN+G +R ++ + N + + G + +
Sbjct: 71 EVTVIGTG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFFSCVQGDASIAK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAA 190
RP+ + LKQ+GA +D P+ + G G L ++ + ++S Q SA+L+A
Sbjct: 123 RPMQVRVTPNPLKQMGAKIDGRKEGTFPLTIRG-GNLKA--IEYTSPPVASAQVKSAILLAG 179

Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G + + P++ + T R++E FGV + GGQK + +
Sbjct: 180 LRAEGVTAV-----TEPHISRDRHTERMLEAFGVTV--TRVGKTVKLAGGQKL-TATDV 229

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL AGA I + ++ G + + +VLE MGA T + +
Sbjct: 230 QVPGDVSSAAFFLVAGAIIPNSKLLQNVGMNPTRTGI--IDVLEKMGATFTVEQINEGA 287

Query: 308 TGPPRE-PFGRKHLKKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
+ P LK I++ + +P + + V+AL A +G T I+D +VKET R
Sbjct: 288 SEPAANITITETSSSLKGIEIGDIIPLRLIDEIPVIALAATQAEGITVIKDAHELKVKETNR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ + ELTKLGA +E D II KL + ++ DHR+ M ++A C AE TI
Sbjct: 348 IDTVVABELTKLGARIEATDDGMIIYGCKLKGNTVHSHGDHRIGMMLAIAAGCIAEGETTI 407

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
D ++P +F+ L T K
Sbjct: 408 EDAAEAVGVSYPTFFFEELQTLAK 429

>ref|YP_001849633.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Mycobacterium
marinum M]
sp|B2HES1.1|ARO_A_MYCMM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACC39778.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Mycobacterium
marinum M]
Length = 431

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 137/442 (30%), Positives = 221/442 (50%), Gaps = 42/442 (9%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEG---TTVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL+ ++ + L S D M+ AL+TLGL V+
Sbjct: 16 VHATVTVPGSKSQTNRTLVLAAALAAQGGSTITGALRSRDTLMI EALQTLGLRVD-- 73

Query: 71 KAAKRAVVVGCGGKFPVED---AKEEVQLFLGNAGIAMRSLT--AAVTAAGGNATYVLDG 125
G G + V E ++ G AG +R + AA++AA DG
Sbjct: 74 -----GTGSELTVSGRIRPGPEARVDCGLAGTVLRFVPLAALSAA----PITFDG 120

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185

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      + R RPI L+ L+ LG VD G P RV G G + GG V + S SSQ++S
Sbjct: 121 DEQARARPIAPLLDALRGLGVPVD---GAGLP-FRVQGTGSVAGGTVAIDASASSQFVSG 176

Query: 186 LLMA-APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      LL++ A G +L S P++ MT++++ + GV + S +R+ ++ G
Sbjct: 177 LLLSGASFTDGLTVQHTGSELPSAPHIAMTVQMLRQAGVDVDDSDIP-NRWLVRPGALR-- 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      P++ VE D ++A FLA A +TGGTVT+ G S+Q ++L+ + + V ++
Sbjct: 234 PRHWDVEPDLTNAVAFLAAAVVTGGTVTITGWPADSVQPAKNILDILQTLNSTVRHIDSC 293

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIR--DVASWRVKETE 362
      + V GP + + DV++ + ++ ++A +A A + R +A R ET+
Sbjct: 294 LQVQGP-----QTYRGFDVLDLVDVGLTPSVAALAALASPGSVSRLAGIAHLRGHETD 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
      R+ A+ TE+ +LG + E+ D +IT L + Y DHRMAMA ++ V +
Sbjct: 347 RLAALSTEINRLGGNCEQTSGLVIT-ATPLRPGSWRAYADHRMAMAGAIIVGLRVAGVEV 405

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
      D G T KT P++ + + V+
Sbjct: 406 DDIGATSKTLPEFPQLWTEMV 427

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>ref|YP_001692549.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Finegoldia magna ATCC
29328]
dbj|BAG08659.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Finegoldia magna ATCC
29328]
Length = 401

```

Score = 141 bits (355), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 117/425 (27%), Positives = 202/425 (47%), Gaps = 46/425 (10%)

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Query: 14 EISGTVKLPGSKSLSNRILLLAALSE-GTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      ++ G V SKS ++R L+LA++++ TT++ N S D+ + LR LG+ +E ++
Sbjct: 10 KLQGVDAISSKSFAHRFLILASVADTDTTIIINEF-SNDIMTTIDCLRNLGVEIEINEN 68

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
      V F +D + + + ++G R L V+ G R+++R
Sbjct: 69 E-----VTVHPSFFQKDVSD---INVNDSGSTFRLLPLVSFLSQKTNIQCSG--RLQDR 118

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      PI +LV LK G + P V+G + G +SSQY+SA++M APL
Sbjct: 119 PIKELVDQLKLSGLT----FSEKLPFTVDG--TFHKIDFEFPGDVSSQYISAIMMIAPL 172

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
      +G EI++ KL S Y+++T ++ FGV +E D+ +K G KSP VEG
Sbjct: 173 -IGGCEIKLSSKLESTGYIKITQECLKLFGVDSEIL--IDKVIVKPGA-LKSPGKIIVEG 228

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 312
      D S+A++F A+ G + VE S+Q D K E LE + + E
Sbjct: 229 DWSNAAFFWCANAL-GADIKVENLKKDSVQADRKIVEFLEKIENNEVYCE----- 277

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
      +++++ PD+ + LAVV + +++ R+KE++R+ + L
Sbjct: 278 -----IDISQTPDLFVILAVVLSQKCDKSVLKNALRLKESDRIKSTYDMLK 325

Query: 373 KLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIIRDPGCTRKTF 432
      G + E D +I E + +++ DDHR+ MA ++A+ V I+D +K++
Sbjct: 326 SFGVNCEIEGDNLVIIYKSE-MKPAVNVSCDDHRIVMAATIASIITKEVEIKDWQAVKKS 384

Query: 433 PDYFD 437
      P +FD
Sbjct: 385 PSFFD 389

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>ref|ZP_04186657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1271]
gb|EEL81637.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1271]
Length = 429

```

Score = 141 bits (355), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 128/456 (28%), Positives = 216/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGNLGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GNLKAIEYTS 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKVTREGKIVK- 217

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AAI + ++ G + + +VLE
Sbjct: 218 -LAGGQKL-TATDVQVPGDVSSAAFFLVAAAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYKGSPLKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCIAEGKTTIEDAEAVGVSYPPTFFELQKLAK 429

>ref|YP_001230236.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
uraniireducens Rf4]
sp|A5GE08.1|ARO_A_GEOUR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ25663.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
uraniireducens Rf4]
Length = 428

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 131/446 (29%), Positives = 208/446 (46%), Gaps = 36/446 (8%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P + + G + +PG KS+S+R ++L +++ GTT V L ED L A R +G+ V
Sbjct: 6 IKPAQSVRGEIAVPGDKSISHRSIMLGSIAAGTTTVCGLRGEDNMATLNAFRAMGVDVR 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D R G G D L GN+G +MR +T + AG VL G
Sbjct: 66 DDGETLRIEGKGLAGLSEPTDV-----LDCGNSGTSMRLMTGLL--AGQRFSSVLTGDQY 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALL 187
+R RP+ ++ L ++GA + G D P+ V G GL G V + +SS Q SA+L
Sbjct: 119 LRNRPMKRVLEPLSRMGATIFGRAGDKAPLAVVG-RGLTG--VTYASPVSSAQVKSAIL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK---- 243
+A A D E E+ + +S + E R++ FG E GG K +
Sbjct: 176 LAGLYA--DGETEVTEPHLSRDHSE---RMLRYFGADIE-----TFAGGVKVRGREL 222

Query: 244 SPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ ++ V GD SSA++F+ A I G + ++G G + + ++L MG +
Sbjct: 223 TGRDITVPGDISAAFFIVAALIVPGSELLIKGVGNPTRTGI--IDILTAMGGSIELLN 280

Query: 303 TSVTVTGPPREPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
P + R LK I++ + +P D + V A A+G T IRD RV

Sbjct: 281 CREISGEFVADLLVRASELKGIEIGDLPVRAIDFPPVICVAASCAEGRTVIRDARELRV 340

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KET+R+ A+ L K G V E + + E+L +++ DHR+AM+ +A A

Sbjct: 341 KETDRIAAMAVNLRKAGVDVETENGMEIGVERLEGCTAESFGDHRIAMSMLIAGLAAR 400

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFV 443
+T+ D C +FP++ +L V

Sbjct: 401 GEITVNDTECIATSFNFIALLEKVV 426

>ref|ZP_05347009.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]
gb|EET60243.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]
Length = 425

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 128/442 (28%), Positives = 206/442 (46%), Gaps = 39/442 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AL+EGTT + N L D + R LG+ +E +
Sbjct: 9 LRGEITVPGDKSISHRAVMFGALAEGTTEITNFLQGADCLSTIHCFRMLGIDIE--NTPE 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R ++ G G A L GN+G R ++ + AG + L+G ++ RP+
Sbjct: 67 RILIHGKGLHGLSAPAD---TLDGTGSGTTTTLISGIL--AGQPFSCTLNGDASIQRPM 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLA 193
++ L Q+GAD+ C P+R+ G L G + S ++S Q S +L+A A
Sbjct: 122 KRIMEPLSQMGADIVSLKDNGCAPLRICG-SHLHG--IHYSSPVASAQVKSCILLAGLYA 178

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFVGKAEHSDSWDRFY---IKGGQKYKSPKNAYV 250
D + + +S + E+ ++ FG + + + G K P
Sbjct: 179 --DAPTSVTEPQLSRNHTL---MLAGFGADVQSHGTTATILPEPVLSGMKITVP----- 228

Query: 251 EGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+YF+A G I G + + G + + V+ MG VT V+ G
Sbjct: 229 -GDISSAAYFIAAGLMIPGSEILIRNVGINPTRDGI--LRVVRDMGGDVTVLNEKVS-GG 284

Query: 310 PPREFPGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P KH L D+ +P D +AV+A A+G T IRD +VKE++R+
Sbjct: 285 EPVADLLVKHSAHGTDIGGGIIPTLIDELPVI AVLACMAEGTTVIRDAQELKVKESDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA---EVPVT 421
+ LT +GA V D II L+ ID++ DHR+AM+F++AA A E +T
Sbjct: 345 AVMTENLTAMGAHVATATDDGMIIEGGHPLHGAVIDSHLDHRIAMSFAVAALAADGETEIT 404

Query: 422 IRDPGCTRKTFPDYFDVLSTFV 443
D C R ++PD+++ L +
Sbjct: 405 GAD--CVRISYPDFYETLKALM 424

>ref|ZP_03497830.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus aquaticus
Y51MC23]
gb|EED08984.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus aquaticus
Y51MC23]
Length = 429

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 143/440 (32%), Positives = 214/440 (48%), Gaps = 40/440 (9%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P + G +++PG KS+++R L+L AL+EG + + L + D LR LG +E
Sbjct: 8 LGPCGPLRGALRVPGDKSVTHRGLMLLALAEGEGRLYHPLKAGDTLSTARVLRALGAEIE 67

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ R G K P ED L GNAG MR L + A VL G
Sbjct: 68 EEGPHFRVRGRGLRLKEP-EDV-----LDCGNAGTLMR-LVLGILAGQEGLFAVLTDGAS 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

+R RP+ + L+ +GA +D G P+ V G G L G + L S+Q SALL+
Sbjct: 121 LRRRPMARVAEPLRAMGARIDREGGGKAPLAVRG-GPLRGIRYTLTP-VPSAQVKSALLL 178

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP-KN 247
A A G+ E+E +P + T RL FG+ + + ++ + P K+

Sbjct: 179 AGLFAEGETEEVEE-----PVPTRDHTERLFRHFGLPLWVAGN----RVRTAKTGPFPAKD 229

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FL A I+ G+ V VEG G + +VL+ MGA+V W

Sbjct: 230 LTVPGDFSSAAFFLVAAALISPGSEVVVEGVGLNPTR--TGLLQVLKAMGAEFWEVR----V 283

Query: 307 VTGPPREPFGR---KH--LK AIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ G EP G +H LK + V+ +P D LA A +A+G T I ++ RV

Sbjct: 284 LEGEAGEPVGVRARHSPLKGVAVDEGLIPLMVDEVPIAAAAWAEGETFIPGLSELRV 343

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEV 418
KE++R+ AI L LG VEEGPD+ + + ++ + DHR+AMAF++A +

Sbjct: 344 KESDRVAAIAQNLRALGVEVEEGPDW-LRIRGGGVRRGEVEPFHDHRIAMAFVAVAG---L 399

Query: 419 PVTIR--DPGCTRKTTPDYF 436
PV +R +P ++P +F

Sbjct: 400 PVGVRVWEPEWAEISYPGFF 419

>ref|YP_003121639.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chitinophaga pinensis
DSM 2588]
gb|ACU59438.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chitinophaga pinensis
DSM 2588]
Length = 426

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 128/426 (30%), Positives = 204/426 (47%), Gaps = 27/426 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISGTV SKS R + A LS GT+++ N S D L LG + K +

Sbjct: 10 ISGTVTANPSKSAHQRAVAAALLSNGTSIIRNPGLSNDCLAALDVAGKLGAEI---KRNE 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ + G PV + ++ G +G+ +R T AA ++G + RP+

Sbjct: 67 DHIEITSKGIHPVSE-----EINCGESGLGIRMFTP--IAALSEKAITINGHGSGLTVRPM 119

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L QL DV C P+ + G L + + GS+SSQ+L+ LLMA A

Sbjct: 120 DFFQEVLPQL--DVKCSTREGRLPLNIQG--PLQPKNITIDGSLSSQFLTGLLMAYGAAA 175

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
DV I + D L S PY+ +TL+LM++FGV+ + + +++F+ Q YK+ + VEGD

Sbjct: 176 EDVTITVKD-LKSKPYIALTLQLMQFQGVQVK-EEQYEQFHFGKRQSYKAGEYT-VEGDW 232

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPREP 314
S A++ L AA+ G V T S Q D E LE GA + +V V

Sbjct: 233 SGAFFLLVAAAVAG-KAEVHHLNTQSAQSDKAILEALEKAGAGLLPGVFTTVVVE----- 285

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
++ L+A D + PD+ L +A G T I V KE++R ++ E K+

Sbjct: 286 --KQQLQAFDFDATDCPDLFPPLVALAANCQGTTKIIGVNRLAHKESDRGKTLQEEFGKM 343

Query: 375 GASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTTP 433
G +++ D ++ + + +++DHR+AMA ++AA A+ PV + D K++P

Sbjct: 344 GIAIDLHGDEMLVHGGTGIGAVVSSHNDHRIAMACAVAALTADAPVIVEDAEAINKSY 403

Query: 434 DYFDVL 439
+++D L

Sbjct: 404 EFDYDL 409

>ref|ZP_02410091.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
pseudomallei 14]
Length = 434

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.

Identities = 116/437 (26%), Positives = 202/437 (46%), Gaps = 43/437 (9%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+++P SK + R ++ A+L+ GT++V N L + M A R LG ++ D+ A + +
Sbjct: 1 MRVPASKPETQRAIVAASLAHGTISVRNDRCIETETMKAACRKLGIATI--DETADQLTI 58

Query: 79 VGCGGKFPVE---DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G GG+F + DAK +G+ R++ A + G +L G +R R +
Sbjct: 59 TGTGGRFSTDVHVIDAK-----GSGLVFRTMMALSSMRG--IPTILTGDATLRRRV 108

Query: 135 GDLVVLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L L LGA+ +LG D +N L G L+G ISSQ+++ALLMAAPL
Sbjct: 109 KPLFDALHALGANF-SYLGDDGKAPVINWGKALDGSHTLAGDISSQFVTALLMAAPLQ 167

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKNAYVEGDA 254
V+I + ++S Y++ TL M R G+ + S + + G+ Y++ + ++ D
Sbjct: 168 RSVDIRLTPPVLSQSYIDQTLFMRAGIDVQASPDYATYRASPGE-YQA-FDTHINADF 225

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
+S SY L A+ GT + G +LQG+ F +V+E +G ++ + V
Sbjct: 226 TSLSYLLMACALFPGTYRIAGIQERTLQGEKLFVDVVEALGVRLRYAPGHVLEVDSSNAG 285

Query: 315 FGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ +++ P++ TL ++LF G +R + R ++ R+ ++ E+ KL
Sbjct: 286 LDGN---FEFVSSGPNIIPTLVALSLFVKGKLTVRGGSVTRFHKSSRIESMVGEVRKL 341

Query: 375 GASVE--EGPD-----YCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTIRDPGC 427
GA++E PD + + + DHR M+ +AA D C
Sbjct: 342 GANIEIIRHPDGHDTGFTVTRGRDRYAGGVTLSSNGDHRNFMSLFVAALRF-----DNAC 395

Query: 428 TRK-----TFPDYFD 437
+ +FPD+ D
Sbjct: 396 SLDGYADVSCSFPDFID 412

>ref|ZP_05965183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
gallicum DSM 20093]
gb|EFA23522.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bifidobacterium
gallicum DSM 20093]
Length = 476

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 139/460 (30%), Positives = 204/460 (44%), Gaps = 42/460 (9%)

Query: 13 KEISGTVKLPKSGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + V +PGSKSLSNR L+LAAL + +L S D ML ALR LG+S D
Sbjct: 29 EPLEAEVTIPGSKSLSNRYLILAAALGTSPVSLVGMRLSRDTRLMLDALRALGVSCIEDPF 88

Query: 73 AKRAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V G+F V +F G AG MR + A G + DG +
Sbjct: 89 EGTTVQVNPVVDGRF-----HGVDVFCGLAGTVMRFVPGALFADGPVRF--DGDAQAY 141

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGI-GGLPGGKVKLSGSISSQY 182
RP+ L+ GL QLGA V F G T PP + G G P V + S SSQ+
Sbjct: 142 ARPMEPLLDGLVQLGAQV-SFDGQPGRLPFTVTPPAELAGSDGARP--VVSIDASSSSQF 198

Query: 183 LSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGG 239
+S LL+ +E+ + + L S+P++ MT+ + + G V W +
Sbjct: 199 VSGLLLIGSKLPSGLELRHVGESLPSMPHIRMTMEDIRQAGGSVSMPEPGVW----VVEP 254

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
P VE D S+A+ FL A I GG+V+V + Q +L MGA VT
Sbjct: 255 HALAMPLEVVVEPDLNAAPFLGAALIAGGSVSVPNWPAHTTQPGGLLPFMLANMGATVT 314

Query: 300 WTETSVTVT-----GPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPT 348
+ T G G + L +M+ ++A ++A +A A
Sbjct: 315 LDDRPFNSTEDMALFPNGYSGLLTVSAGERLLGLGSFDMASAGEIAPSIAALATLASSDM 374

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDYDDHRM 406
A+ + R ET+R+ A+ TE+ ++G EE D I P L+ +DTY DHRM
Sbjct: 375 ALHGIGHLRGHETDRLAALVTEIRRVGGIAEELEDGIAIHAVPASALHGAVMDTYADHRM 434

Query: 407 AMAFSLAACAEVP-VTIRDPGCTRKTFPDYFDVLSTFVKN 445
A F+ +P + ++D TRKT PD+ + + ++
Sbjct: 435 A-TFAAMLGLRIPGIQVKDVLTTTRKTIPDFVGLWTRMLEQ 473

>gb|ABO69382.1| 5-enolpyruvylshikimate 3-phosphate synthase [uncultured soil
bacterium]
Length = 429

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 210/441 (47%), Gaps = 39/441 (8%)

Query: 12 IKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G + +PG KS+S+R ++ A++EG T + + L ED + +G+S++ +
Sbjct: 10 LSSLQGEISIPGDKSISHRAVMFGAMAEKTTINHFAGEDCLSTISCFEKMGVSIK--R 67

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V G G +E E + +GN+G R + + AG L G +
Sbjct: 68 EGEYVEVEGKG---IEGLSEPTSILDVNGSGTTTTRLMLGIL--AGVPFHTSLIGDESIA 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + V L+ +GA +D P+ G G L S S+Q SA+L+A
Sbjct: 122 KRPMRSRVTVPLRSMGAKIDGREHGQYTPLSTRG-GALKAIHYH-SPVASAQVKSAILLAG 179

Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G ++ + P+ + T R++ FGV E + I+GGQ + +
Sbjct: 180 LHAEGTTKV-----TEPFSTRDHTERMLRAFGVDVEVDGTT--VSIEGGQSLRG-TDV 229

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
YV GD SSA++FL AGA + + ++ G + + +VL+ MGA++T + +
Sbjct: 230 YVPGDISSAFFLVAGAIVPNSRIVLKNVGLNPTRTGI--IDVLQQMGARLTISNERIQ- 286

Query: 308 TGPPPEPFG-----RKHLKAIDVNMNMPDVAMTLAVVALFAD---GPTAIRDVASWRVK 359
EP G LK I++ + +P + + V+AL A G T I+D +VK
Sbjct: 287 ---NGEPIGDLTIETSQLKGIEIGGDLIPRLIDEIPVIALLATQATGKTVIKDAEELKVK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDAITYDDHRMAMAFSLAAC-AEV 418
ET R+ + TEL+KLGASV D II L +D+Y DHR+ M ++AA A
Sbjct: 344 ETNRIDTVATELSKLGASVTPADGLIIEGKTALRSGEVDSYGDHRIGMMLAVAAAIATG 403

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
VT+ ++P +F+ L
Sbjct: 404 EVTLNRSDAIHVSYPFFEDL 424

>ref|NP_979297.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
10987]
sp|Q736A7.1|AROABACCI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAS41905.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
10987]
Length = 429

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 128/456 (28%), Positives = 217/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGLNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLEQEPKAVLDVNGSGTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAKRPMPKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIETYSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234

S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216
Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVQNVGMNPTRTGI--IDVLEK 273
Query: 294 MGA KVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITIETSSSLKGIIEGGDIIPRLIDEIPVIALAATQAEGITV 333
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393
Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C A+ TI D ++P +F+ L K
Sbjct: 394 LAIAGCIAKGKTTIEDAEAVGVSYPYTFEELQKLAK 429

>ref|YP_003830415.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Butyrivibrio
proteoclasticus B316]
gb|ADL33833.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Butyrivibrio
proteoclasticus B316]
Length = 442

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 127/453 (28%), Positives = 212/453 (46%), Gaps = 49/453 (10%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL---- 65
+P + G V +PG KS+S+R ++ AL+EGTT + L S D + + LG+
Sbjct: 6 KPSHPLKGDVFPVPGDKSISHRSIMFGALAEAGTEITGFLESADCLSTIDCFKKGIIIDH 65
Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V+ + V G G + K L+ GN+G R ++ + A ++ +
Sbjct: 66 TVKPTNGVPKITVHGRG---LHGLKASASTLYTGNSGTTTRLMSGILVAQPFDSN---IT 119
Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGS-----I 178
G + +RP+ ++ L Q+GAD+ +G DC P+ + GG KL G
Sbjct: 120 GDSSIEKRPMRSRIIKPLSQMGADISSVMGNDCAPLHI-----GGGCKLRGINYRNPIA 172
Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFY 235
S+Q SA+L+A A D E + + +S + E+ ++ FG + + D
Sbjct: 173 SAQVKSAILLAGLYA--DGETVVYEPALSRNHSEI---MLASFGADVHNEIARDGSAAAI 227
Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
+ G K V GD SSA+YF+A A + G + + G + + VL+ M
Sbjct: 228 LHPGMPLHGIK-INVPGDISSAAYFIAAALMVPGSELLIRNVGVNKRSGI--LTVLKQM 284
Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNK-----MPDVAMTLAVVALFA 344
GA +T ++ +G PR K+ + NK M D +AV+A A
Sbjct: 285 GADITLL--NMNESGEPRADILVKYSELHGNQNNKFEIGGKDIPTMIDELPMVAULAATA 342
Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDH 404
+ T I+D A +VKE++R+ + LT +GA +E D II + L+ I+T++DH
Sbjct: 343 NCDTIKDAELKVKESDRIATVVENLTAMGADIEATDDGMIHGGKPLHGADINTHNDH 402
Query: 405 RMAMAFSLAACAEVPVT-IRDPGCTRKTFPDYF 436
R+AM F++AA + +T I D C ++P +F
Sbjct: 403 RLAMCFIAIALSADGITRILDDACVGISYPTFF 435

>ref|ZP_02207983.1| hypothetical protein COPEUT_02810 [Coproccoccus eutactus ATCC 27759]
gb|EDP24872.1| hypothetical protein COPEUT_02810 [Coproccoccus eutactus ATCC 27759]
Length = 425

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 128/445 (28%), Positives = 218/445 (48%), Gaps = 39/445 (8%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ +K ++G + +PG KS+S+R ++ ++++G T V LN D + R +G+ ++

Sbjct: 3 INRVKSLNGEITIPGDKSISHRSIMFGSIADGITEVHGFLNGADCISSMNCFRQMGIDID 62

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D + +V GK +K E L +GN+G R L + + AA A+ ++ G

Sbjct: 63 YDGS-----IVTVYGKGLNGLSKPEGTLDVGNSTTTR-LISGILAAQPFASRLI-GDAS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ ++ L +GAD+ LG DC P+ +NG L G S S+Q S +L+

Sbjct: 116 ICKRPMKRIMTPLSMMGADITSELGNDCAPLLING-KELHGIHYN-SPVASAQVKSCVLL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSW---DRFYIKGGQKY 242
A A D E + + +S + E+ ++E FG +K E + + D+ GQK

Sbjct: 174 AGLYA--DGETSVTEPYVSRNHTL---MLESFGGNIKTEGTATVKPVDKLV---GQKI 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
P GD SSA+YFL IT +T++ G + + EV++ M + ++

Sbjct: 226 IVP-----GDISSAAYFLVAGLITPNSCITIKNVGINPTRDGI--LEVIKAMCGDMEYS 277

Query: 302 ETSVTVTGPPREPFGGRK--HLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASW 356
V+ G P K LK + + +P D +AV+A FADG T IRD

Sbjct: 278 NV-VSGCGEPTADITVKTSSLKGCVIEGSIIPKLIDEIPAIAVLACFADGETIIRDAQEL 336

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC- 415
+VKE+ R+ + L+ +GA + D II + L+ ID++ DHR+AM+F++A

Sbjct: 337 KVKESNRIDVMVNALSAMGADITATDDGMIIRGGKPLHGAVIDSHLDHRIAMSFAIAGLN 396

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLS 440
A+ I C ++P ++D L+

Sbjct: 397 ADGDTEITGAECVNISYPGFYDDLA 421

>gb|EFV82379.1| 5-enolpyruvylshikimate-3-phosphate synthase [Achromobacter
xylosoxidans C54]
Length = 447

Score = 140 bits (354), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 119/444 (26%), Positives = 210/444 (47%), Gaps = 38/444 (8%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
++PIKE+ + +P SK + R +L A L++GT+++ N L + M A LG +E

Sbjct: 5 VEPIKELGTRMNVPAKSPETQRAILAATLADGTSIIRNDRCTETETMKIACQLGAKIE 64

Query: 69 ADKAAKRAVVVCGCGKFP----VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+AA V G GG+F V DAK +G+ R++ A + + +L

Sbjct: 65 --EADVLFVFTGTGGRFASGIEVIDAK-----GSGLVFRMTMA--LSCMKSTPTILT 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R R+ + L+ GL+ LGA+ +LG + +N L G +L+G ISSQ+++

Sbjct: 113 GDATLRRVMQPLLDGLRHLGANF-AYLGDEGKAPVINWGASLTGRHCRLAGDISSQFIT 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+LMAAPL + +E+ ++S Y+ T+ + + G+ A+ + + R+++ G

Sbjct: 172 AILMAAPLTRQGISLEVTPPVLSQSYLAQTETLRQCGIDAQVNPEYTRYHVAPG--VYQ 229

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + D +S SY L A+ G + G +LQG+ FA++++ +GA++ + +

Sbjct: 230 PFETRINADYTSLSYLLMACALFPGRYRIGGIEQETLQGEKLFADIVQALGAQLRYEAGA 289

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
+ V G D P+V TL ++LF G + + R ++ R+

Sbjct: 290 LHV DSTSARLEGN YTFDVRD-----GPNVIPTLVALSLFVRGTFTVTGGSVTRFHKSSRV 344

Query: 365 VAIRTELTKLGASVE-----EGPDYCIIT--PPEKLNVTATIDYDDHRMAMAFSLAA--C 415
++ E+ KLGA ++ +G +T P + + DHR M+ +A+ C

Sbjct: 345 ESMIGEVKRLGADIDMIRNIDGHIDGTVTRGRPRYAGGVTLSSRGDHRNFMSLFVASLRC 404

Query: 416 AEVPVT--IRDPGCTRKTFFPDYFD 437
E D C +FPD+ D

Sbjct: 405 EEACHLDGYADVIC---SFPDFID 425

>ref|YP_003564759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
QM B1551]
gb|ADE71325.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
QM B1551]
Length = 429

Score = 140 bits (353), Expect = 3e-31, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 211/441 (47%), Gaps = 39/441 (8%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G + +PG KS+S+R ++ A++EG T +++ L ED + +G+S++ +
Sbjct: 10 LSSLQGEISIPGDKSISHRAVMFGAMAEKTTINHFLAGEDCLSTISCFEKMGSVSIK--R 67

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V G G +E E + +GN+G R + + AG L G +
Sbjct: 68 EGEYVEVEGKG---IEGLSEPTSILDVGNSTTTRLMLGIL--AGVPFHTSLIGDESIA 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + V L+ +GA +D P+ G G L S S+Q SA+L+A
Sbjct: 122 KRPMRSRVTVPLRSMGAKIDGREHGQYTPLSTRG-GALKAIHYH-SPVASAQVKSAILLAG 179

Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G ++ + P+ + T R++ FGV E + I+GGQ + +
Sbjct: 180 LHAEGTTRKV-----TEPFTSRDHTERMLRAFGVDVEVDGTT--VSIEGGQSLRG-TDV 229

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
YV GD SSA++FL AGA + + ++ G + + +VL+ MGA++T + +
Sbjct: 230 YVPGDISSAFFLVAGAIVPDSRIVLKNVGLNPTRTGI--IDVLQQMGAARLTISNERIQ- 286

Query: 308 TGPPREPFPG-----RKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTAIRDVASWRVK 359
EP G LK I++ + +P + + V+AL A +G T I+D +VK
Sbjct: 287 ---NGEPIGDLTIETSQLKGIEIRGDLIPRLIDEIPVIALLATQANGKTVIKDAEELKVK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAAC-AEV 418
ET R+ + TEL+KLGASV D II L +D+Y DHR+ M ++AA A
Sbjct: 344 ETNRIDTVATELSKLGASVTPADGLIIEGKTALQSGEVDSDYGDHRIGMMLAVAAAIATG 403

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
VT+ ++P +F+ L
Sbjct: 404 EVTLMRSEAIHVSYPPTFFEDL 424

>ref|YP_004151127.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermovibrio
ammonificans HB-1]
gb|ADU96486.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermovibrio
ammonificans HB-1]
Length = 430

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 135/444 (30%), Positives = 214/444 (48%), Gaps = 36/444 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ G +++P KS+S+R ++L +L+ G VV + L SED L A LG V
Sbjct: 9 KKLKGELRVPSDKSISHRCIMLGSLSNRGEVVVKHFLRSEDCLNTLKAFVELGADVT--DT 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATY-VLDGVPRMR 130
++ G G + KE + LGN+G ++R L A + A G Y VL G +R
Sbjct: 67 GTELIKKGKGR---SLKEPFNVIDLGNSTGTSIR-LMAGILA--GQPFYSVLTGDRYLR 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + V L+ +GA + G PP+ + G L G K S S+Q S++L+A
Sbjct: 120 RRPMDRVAVPLRMMGAQIYGREGGKYPLTIIGKEKLRGISYK-SPKASAVKSSILLAG 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
D +E+ + S + E R++ FGV E + R + ++ + V
Sbjct: 179 LFT--DETVEVTEPAKSRDHTE--RMLRAFGVDVEENGLTVR--LGKNRELAADLEIDV 231

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++F+ GA IT G+ V ++ + + +V MGA +T +V+G
Sbjct: 232 PADISSAAFFIVGALITPGSEVLLKSVILNPTRTGI--LDVASRMGADITVLNRR-SVSG 288

Query: 310 PPREFPG-----RKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
E G HLKA + ++P + L V+AL A +G T IRD A RVKE
Sbjct: 289 ---EEVGDLLVRFTPHLKATVIEGEEIPRLIDELPVIALLATQAEGETVIRDAEELRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAA-CAEVP 419
++R+ + L +GA VEE PD +I L + ++ DHR+AM ++A+ E P
Sbjct: 346 SDRIKSTVENLNAIGACVEELPDGMVIRGKTPLKGGTVSSFGDHRIAMTLAVASLITEEP 405

Query: 420 VTIRDPGCTRKTFFPDYFDVLSTFV 443
V I + ++P +FD LS +
Sbjct: 406 VVIDEVDVSVTSYPSFFDLSRL 429

>emb|CBL06985.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Megamonas hypermegale
ART12/1]
Length = 447

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 119/449 (26%), Positives = 216/449 (48%), Gaps = 38/449 (8%)

Query: 9 LQPIKE-ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+QPIK + G + +PG KS+S+R ++ A L + + N L++ D + +R LG+ V
Sbjct: 21 IQPIKTGLKGEILIPGDKSVSHRSVMFAGLCDSEVKITNFLHAADCMSTVNCMRALGVKV 80

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + + ++V G +++ + + GN+G +R + + AG G
Sbjct: 81 K--ELDENTLIVKGNFHLQEPQSIIDA--GNSGTTLRLLMMGIL--AGQKFLTTFTGDA 134

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-----SISSQ 181
+ RP+G ++ L Q+GA++ P+ V +P K L G S+Q
Sbjct: 135 SLSRRPMGRVINPLSQMGANIVGRKENKLLPITV-----IPA-KESLQGIDYQMPMASAQ 188

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGG 239
SA+L+A A G + + PY + T R++E FGVK E S + I
Sbjct: 189 VKSAILLAGMNAEGRTTV-----TEPYTSRDHTERMLEGFGVKLEKSGT--SITISKV 239

Query: 240 QKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+K +PK +V GD SSA+++L AG+ I + ++ G + + +VL+ MGA +
Sbjct: 240 EKMTAPKEIHVPGDISAFAFWLVAGSIIEDSDIILKDVGINETRTGI--IDVLKAMGANI 297

Query: 299 TWTET--SVTVTGPPREFPGRKHLKAIDVN-MNKMPDVAMTLAVVALFADGPTAIRDVAS 355
V R + + H + + M ++ D + V ++FA+G T I
Sbjct: 298 ELLNVRDEVEPIADIRVRYAKLHGTSFGADIMPRIDEIPIITVASMFAEGETIITGAGE 357

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI--DTYDDHRMAMAFSLA 413
RVKET+R+ I E K+ ++ D IIT ++ N+ + +++DDHR+AMA ++
Sbjct: 358 LRVKETDRLQVITDEFNKVCPICKGTQDGLIITGSQRNNLQKVVCNSHDDHRIAMALAIL 417

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
+ V + I + C ++P +++L+ F
Sbjct: 418 GASGVGIEIENSECVNISYPTFYEILTRF 446

>ref|YP_003318133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermanaerovibrio
acidaminovorans DSM 6589]
gb|ACZ19851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermanaerovibrio
acidaminovorans DSM 6589]
Length = 436

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 138/452 (30%), Positives = 207/452 (45%), Gaps = 48/452 (10%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G +++PG KS+S+R L ALS+ VDN + ED L L LG SV
Sbjct: 15 PCSGLKGELRVPGDKSISHRAAFLGALSDEGIRVDNFSSGEDCASTLRCLFALGFSV-VR 73

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
+ +V G G P E L+ GN+G R L ++A G V+ G +R
Sbjct: 74 SGGRVSVSRGSGPSDPAE-----PLYAGNSGTTARLLCGLMSAVPG-LFGVITGDGSLR 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190

RP+G +V L+ LGA +D G P+ + G L GG+++L S+Q +AL+++A
Sbjct: 127 GRPMGRVVEPLRSLGARIDGRDGGRLPLLSIRG-ARLSGGRLELR-VPSAQVKTALILAG 184
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY- 249
L GDV + + + +S + E+ ++E GV + Y + P A+
Sbjct: 185 -LMGGDV-LTVAEPHLSRDHTEV---MLEHLGVPVRRNGLSVTVY----PVDRVPGGAW 235
Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA+++L AGA + + V G +G + L MG V
Sbjct: 236 VPGDMSSAAFVLVAGAVVPRSDLVVRGVCLN--RGRTGLLDALRAMGCHVEVH----- 286
Query: 309 GPPREPFPG-----RKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVAS 355
PR P G +L+ I V +++P D LAV A A G T IR
Sbjct: 287 --PRSPQGGAEVGDVVRHNSLRGIKQPHQVPSMVDELPLVAVAASLAQGGTEIRGAGE 344
Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLA 413
R KE +R+ A+ L+ +G + E D +I L+ +D+Y DHR+AMA ++
Sbjct: 345 LRHKECDRIGAMAQGLSAMGVRIREVEDGWVIQNGGAPLSPARVDSYGDHRIAMALAVG 404
Query: 414 A-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
A A PV IR C ++P++FD L V
Sbjct: 405 ALAASGPVEIRGASCVSISYPEFFDHLKGLVS 436

>ref|NP_906026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas
gingivalis W83]
gb|AAQ66925.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas
gingivalis W83]
Length = 419

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 142/440 (32%), Positives = 209/440 (47%), Gaps = 68/440 (15%)

Query: 18 TVKLPGSKSLSNRILLALS-----EGTTVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+++LP SKS R+LLL A+S EG D + VH +L +
Sbjct: 18 SLRLPPSKSEWIRLLLRAMSGEVLAPLEG----DAPTDVVRTVHRILTS----- 62
Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
D +EV + +AG AMR LTA + A + L G RM
Sbjct: 63 -----DISDEVNV--RDAGTAMRFLTAYM-ARFASRPVRLYGTERMC 101
Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L+ LGADV D PP+ + + GG V + +SSQ++SALL+ A
Sbjct: 102 ARPIRPLVEALRSLGADVIERVEDFPPLLRIP-AAMRGGTVCVDAGVSSQFVSALLLIA 160
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P G + I++ ++ +S PY +MT RL+ FG++ E S+ D + G + + +P Y
Sbjct: 161 PTLRGGLSIKLENREVSAPYTDMTCLRLTAFGIEVERSE--DSITV-GERPFVAPTEWYP 217
Query: 251 EGDASSASYFLAGAAI--TGTVTVEGC--GTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
D S+A Y A+ G+V++ G S+Q D + A + +G T++ +T
Sbjct: 218 SADWSAAGYIYNMVAVGELSGSVSLPGLLPPEESMQADSRAATLFGRLGVVTEKTDSGIT 277
Query: 307 VTGPP---REPFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
++ P + FG + ++ PD+ TLAV L P + V R+KE +R
Sbjct: 278 LSYSFVRCTDDFGTE-----DVRDCPDLPVTLAVCCLLKRVFPCLTGVGHLRLKECDR 330
Query: 364 MVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAAC-AEV 418
+ AI TE KLG V D + PE+L V I YDDHRMAMAF+ AA ++
Sbjct: 331 LAAICTEARKLGYVVRSDKDALLWDGERCTPEELPV--IRVYDDHRMAMAF+AAAVLSKK 388
Query: 419 PVTIRDPGCTRKTFPDYFDV 438
V I D G K+FP +F V
Sbjct: 389 GVMIEDAGVVGKSFPGFFSV 408

>ref|ZP_04323863.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
m1293]
gb|EEK44434.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
m1293]
Length = 429

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 128/456 (28%), Positives = 216/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNNGNLGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + V G G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVAGKG---LEGLQEPKAVLDVGNSGTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATEDGMIYKSVLKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPPTFFELQRLTK 429

>ref|YP_003897787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halomonas elongata
DSM 2581]
emb|CBV42602.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halomonas elongata
DSM 2581]
Length = 756

Score = 140 bits (353), Expect = 4e-31, Method: Compositional matrix adjust.
Identities = 137/455 (30%), Positives = 215/455 (47%), Gaps = 58/455 (12%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P E+ G +++PG KS+S+R ++L AL+EG T V L ED L A R +G+++E
Sbjct: 318 PGGEVRGRIRVPGDKSVSHRAIMLGALAEGITEVSGFLEGEDSLATLQAFREMGVAIEGP 377

Query: 71 KAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G K P L++GNAG AMR + AG L G
Sbjct: 378 HQGRVTIHGVGLHGLKAPAG-----PLYVGNAGTAMRLFAGLL--AGQAFDTELTDGVS 429

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+G + L+++GA ++ G PP+++ G L G + + S+Q S LL+
Sbjct: 430 LTKRPMGRVADPLREMGAVIETAEGGR-PPLKLRGGQALKGITYDMPMA-SAQVKSCLLL 487

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY-KSPKN 247
A A G+ + P + T R++ FG + E D +++GG K +P +
Sbjct: 488 AGLYAEGETRVR-----EPAPTRDHTERMLGGFGYRVER--EGDTCWLEGGKLTAAPID 540

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL AAIT G + +E G + + +L++MGA + E
Sbjct: 541 --VPSDISSATFFLVAAAITPGADLVLEHVGVNPNTR--IGVINILKLMGADLRL-ENERE 595

Query: 307 VTGPPREFFGRKH--LKVIDNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P +H LK ID+ ++++P D L V A A+G T +RD A RVKE+
Sbjct: 596 VGGEFVADLHIRHAPLKIDIPVDQVPLAIDEFPALFVAAANAEGVTRLRDAAELRVKES 655

Query: 362 ERMVAIRTELTKLG-----ASVEEGPDYCIITPPEKLNVTIAIDTYDDH 404

+R+ A+ LG +EGP Y +D+ DH
Sbjct: 656 DRLQAMADGFAVLGIEHRLYEDGIDIVGRHEGQSDEGPSY-----GGGRVDSLGDH 706

Query: 405 RMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDV 438
R+AMAF++AA A V + D +FP + ++

Sbjct: 707 RIAMAFAVAALRASEAVVDDCANVATSFPGFIEL 741

>ref|YP_002746075.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equi
subsp. equi 4047]
sp|COA42.1|AROA_STRE4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAW93107.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus equi
subsp. equi 4047]
Length = 427

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 127/438 (28%), Positives = 219/438 (50%), Gaps = 29/438 (6%)

Query: 13 KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++PG KS+S+R ++ A++EG TV+ LL +DV + A R LG+++ ++
Sbjct: 8 KALRGRRLRVPDGKSIHRAVIFGAIAEGQTVIHGLLRQDVLATIQAFRDLGVITIY--ES 65

Query: 73 AKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMR 130
A ++ G G G P + L +GN+G +MR L A + AA + +L G +
Sbjct: 66 ADSLIIEGRGFKGLKPAQKP----LDMGNSGTSMR--LLAGLLAAQDFSVQLL--GDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + + L +GA++ + PP+ V G L +L + S+Q SA+L+AA
Sbjct: 119 RRPMDRITIPLSLMGAELSGQGEKELPPLIVKGCQELRPIHYQLPVA-SAQVKSAILLAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G E I++K ++ + E ++E+FG K S + + IKG Q+ + + +
Sbjct: 178 LQTQG--ETVILEKELTRNHT---EMIEQFGGKL--SVAGKQISIKGPQRLQG-QTLQI 229

Query: 251 EGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++LA G + G + +E G + EV+E MG +++
Sbjct: 230 PGDLSSAAFWLAAGLIVPGSDLVLENGVINPTR--TGLLEVIEKMGGGRISYQAVDKDRQA 287

Query: 310 PPREFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVA 366
+ LK I+++ + +P + L V+AL A G T IRD RVKET+R+ A
Sbjct: 288 ATLK-VSYSTLKGIEISGDLIPRLIDELPVIALLATQAQGTTYIRDAQELRVKETDRIQA 346

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ L ++GA ++ D + L+ A+ T DHR+ M ++AA E VT+
Sbjct: 347 VTDVLGQMGAADIQATEDGMVTRGKTPHGAAVSTCGDHRIGMMTAIAALLVEEGQVTLER 406

Query: 425 PGCTRKTFPDYFDVLSTF 442
++PD+F L
Sbjct: 407 AEAILTSYPDFDKDLERL 424

>ref|ZP_04301143.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus MM3]
gb|EEK67261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus MM3]
Length = 429

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 216/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E ++P+ + G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIEPVNGLKGIIITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 G--VEIVQNGDEVTVVGKG----LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAPKPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTS 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVNQVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGSSEPAANITITETSTLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPPTFFEELQKLAK 429

>ref|YP_003718208.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
ATCC 43063]
gb|ADI66714.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus curtisii
ATCC 43063]
Length = 463

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 139/454 (30%), Positives = 216/454 (47%), Gaps = 50/454 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-----A 69
+ G V+LPGSKSLS R LLL+A+ + + +L + D M+ ALR+LG +
Sbjct: 15 VFGAVRLPGSKSLSARELLLSAIGDAEANLTGVLFARDTDLMVQALRSLGAVIAPWPPVV 74

Query: 70 DKAAKRAVVVGCGGKFPVEDAK-----EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
D+ + + P +DA + + G AG MR + A A G +V
Sbjct: 75 DQPVQIKPLPQLWTGAPAQDASGGPSGGAPITVDCGLAGTVMRFIPALAVAGRAVRVFA 134

Query: 124 DGVPRMRERPIGDLVVGLKQLGA-----DVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
D + RP+ L+ L QLGA D D F T PP G +V +
Sbjct: 135 DS--QANARPMRPLLDALVQLGARIEYESPDGDFVFPYTIYPPAERL-----GAEVTVDA 186

Query: 177 SISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLRLMERFGVKAH--SDSWDR 233
+ SSQ++SALL+AAPL I L S+P++EMT++ + + G+ E SD
Sbjct: 187 TASSQFISALLAAPLLPDGCTIRSKTVALPSLPHIEMTMQCLSQHGITVEQGLSDDGKP 246

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
F+ + ++ ++E D S+A FLA I GG ++V ++Q + ++L +
Sbjct: 247 FWNVSEPFVFG-QDVFIEPDLNAGPFLALVGIAGGRISVPAWPAKTMQAGAAWLQILPL 305

Query: 294 MGAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDV 353
MG +V W +TV+ P L+ +D +++ + ++ +A +A FA+G + +R +
Sbjct: 306 MGLRVEWNCGLTVSRP-----GPLQPLDADLSAVGELVPAVAALAAFAEGTSHLRGL 358

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGP-DYCIIT----PPEKLNVTATID-----TY 401
R ET+R+ A+R ELT +G S E P D +IT P + ID +Y
Sbjct: 359 HHLRGHETDRLEALRAELTAIGISCEITPEDDLVITGKPVTPSWRDTPTIDAEPLLLHSY 418

Query: 402 DDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
DHR+A F PV I D G T KT PD+
Sbjct: 419 QDHRLA-TFGALLGLYYPVQIDDIGATTKTLPDF 451

>gb|EGD36849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK150]
Length = 427

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 121/439 (27%), Positives = 219/439 (49%), Gaps = 35/439 (7%)

Query: 12 IKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++ + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 7 VRGLKGRIRVPGDKSISHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ VG G ++ +L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 NLVKIHGVGFEGQLQAPKN-----RLDMGNSGTSIRLISGVL--AGQDFEAEFMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+++ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVITPLRQMGVEIAGRTERDLPLKMKGSRELQPIHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISSIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K I+ + E ++ +FG + E R I+GGQ++ + + V
Sbjct: 179 QAQG--ESVIEKEITRNHTE---DMAQFGGQIEVKGKEIR--IQGGQEF-TAQEVTV 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + EV+E MG ++T ++ S
Sbjct: 231 GDISAFAFWLAVGLIVPDSKIVLENGINETRTGI--LEVIEAMGGRMTLSDVDQVAKSA 288

Query: 306 TVTGGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIALLATQAQGRTVIRDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA+++ D II L+ ++T DHR+ M ++AA V
Sbjct: 343 RIQVVADALNSMGAAIKPTEDGMIIEGKTPLHGARVNTLGDHRIGMMTAIAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
+ + ++P +F L
Sbjct: 403 ELERSEAIKTSYPSFFSDL 421

>ref|NP_301607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium leprae
TN]
ref|YP_002503238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium leprae
Br4923]
sp|Q9CCI3.1|AROAMYCLE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAC30301.1| putative 3-phosphoshikimate 1-carboxyvinyl transferase
[Mycobacterium leprae]
emb|CAR70886.1| putative 3-phosphoshikimate 1-carboxyvinyl transferase
[Mycobacterium leprae Br4923]
Length = 430

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 137/437 (31%), Positives = 216/437 (49%), Gaps = 32/437 (7%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALS----EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ V +PGSKS +NR L+LAAL+ +GT+ + L S D M+ ALRTLGL V D
Sbjct: 15 VQANVTIPGSKSQTNRALMLAALAAAGQGQSTIGGALRSRDTLMISALRTLGLHV--D 72

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+A +V+ G P EDA Q+ G AG +R + + T+ DG + R
Sbjct: 73 EAG--SVLTVNGRITPGEDA----QVDCGLAGTVLRFVPLAALSANPVTF--DGDEQAR 124

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI L+ L+ LG VD P +V G G + GG V + S SSQ++S LL+ A
Sbjct: 125 ARPITPLLDALRGLGVPVDGV----GLPFQVQGSQSVAGGTVAIDASASSQFVSGLLLCA 180

Query: 191 PLALGDVEIEIIDKLI-SIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
V ++ + S P++ MT+ ++ + GV+ + S +R+ ++ G + ++
Sbjct: 181 ASFTQGVTVQHTGSPVPSAPHIAMTVMMLRQAGVQVDDSVG-NRWQVRPG--TVAARHWV 237

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
VE D ++A FLA AA++GGTV + G TS+Q +L + V T++ + V
Sbjct: 238 VEPDLTNAVAFLAAAVSGGTVRITGWPKTSVQPADNILNILFRLNVVVNQTSFLEVQ- 296

Query: 310 PPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMVAI 367
G DV++ + ++ ++A +A A + + +A R ET+R+ A+

Sbjct: 297 -----GSTVYDGFVDLRLDVGELTPSVAALALATPGSVSQLHGIAHLRGHETDRLAAL 350

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
TE+ +LG +E D IIT L Y DHRMAMA ++ V + D G

Sbjct: 351 STEINRLGGDCQETSGLIIT-ATPLRPGVWVAYADHRMAMAGAIVGLRVSGVEVDDIGA 409

Query: 428 TRKTFPDYDFVLSTFVK 444
T KT P + + + +K

Sbjct: 410 THKTLPQFPQLWANMLK 426

>ref|NP_875440.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
gb|AAQ00093.1| 5-enolpyruvylshikimate-3-phosphate synthase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
Length = 444

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 133/445 (29%), Positives = 212/445 (47%), Gaps = 34/445 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + G VK+PG KS+S+R LL +A++EG T ++ LL +ED L+ +G+ +

Sbjct: 15 ITPGGSGLIGNVKVPKDKSISHRSLFSAVAEGETTIEGLLPAEDPISTANCLKAMGVKIS 74

Query: 69 ADKAAKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ V G G G +D L GN+G MR L + G +VL G

Sbjct: 75 PISKGEIVKVQGVGLDGLNEPDDV----LDCGNSGTTMRLLLGLIVGREGRH-FVLTGD 128

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
++ RP+ + LK +GA V+ D P+ + +G G V + S+Q SA+

Sbjct: 129 NSLKS RPMKRVGHPLKMMGAHVNGRAKGDFAPISI--VGKQLHGA VIGTPVASAQIKSAI 186

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSP 245
L+AA A G + I+ S + E R+++ FG E S R +K G K K

Sbjct: 187 LLAALTAEGSTTV--IEPANSRDHTE---RMLKAFGANLEISGEMGRHITLPGVKLKG 241

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVWTWETS 304
+ V GD SSA+++L AG+ I +T+E G + + EVL+ MGA +

Sbjct: 242 Q-IVVPGDISSAAFVLIAGSIIPKSDITIENIGLNPTRTGI--LEVLDNMGANIQLLNKR 298

Query: 305 VTVTGPFPREPFG-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
V G EP G + LK+ ++ MP D L V A F DG + I +

Sbjct: 299 -EVAG---EPVGDIVTYSEQLKSFTLDNEIMPRLIDEVPILIVAACFCDGISQITGASE 354

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA- 414
R+KET+R+ + +L K+GA +EE D I + L+ +D+ DHR+AM+ +A+

Sbjct: 355 LRIKETDRLQVMTRQLKMGAKIEEKADGLTINGSQSLHGANLDSSESDHRIAMSLGIASL 414

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVL 439
A+ +I ++P+++ L

Sbjct: 415 LADSNSSIFRSDAASVSYPEFWSDL 439

>ref|YP_383831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
metallireducens GS-15]
sp|Q39XB8.1|AROAG_EOMG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB31106.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
metallireducens GS-15]
Length = 429

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 206/437 (47%), Gaps = 25/437 (5%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P K I G + +PG KS+S+R ++L +++ G T V L ED L A R +G+ ++

Sbjct: 6 VRPAKGIRGEITVPKDKSISHRSIMLGSIGARGETTIVRGFLRGEDNIATLNAFRAMGVVID 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D R G G D L GN+G +MR LT + A VL G

Sbjct: 66 DDGETLRIAGKGLRGLAEPTDV-----LDCGNSGTSMRLLTGLL--APQRFYSVLSGDQY 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+ +V L ++GA + G + P+ + +G G S S+Q SAL++

Sbjct: 119 LRRRPMRRVVEPLSRMGACIHGREGGEKAPLAI--VGRDLKGISYSSVASAQVKSALML 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G E + + +S + E R+ FG E+ + ++GG++ + ++

Sbjct: 177 AGLYAE--ETRVTEPHLSRDHSE---RMFRHFGADIENGPAG--VVVRGGRELEG-RDI 228

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++F+ A I G + + G G + ++L MG + +

Sbjct: 229 IVPGDISSAAFFMVAALIVPGSELLIRGVGNPTR--TGIIDILTAMGGSLELLDQREVS 286

Query: 308 TGPPREPFGRK-HLK AIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P + R LK I++ +P D + V A A+G T +R+ RVKET+R

Sbjct: 287 GEPVADILVRSSRLKGIEIAGEVVPRAIDFPPVICVAAAVAEGRTVREARELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ T L +G +V E D I E++ ++++ DHR+AM+ +A A +T+

Sbjct: 347 IAAMATNLRAVGVTVTESEDGMDIEGAEQIAAGTVESFGDHRIAMSMLIAGLTAGGDITV 406

Query: 423 RDPGCTRKTFPDYFDVL 439
D C +FP +F +L

Sbjct: 407 TDTECIGTSFPTFFPLL 423

>ref|YP_003988776.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y4.1MCl]
gb|ADP74165.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y4.1MCl]
Length = 428

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 215/447 (48%), Gaps = 41/447 (9%)

Query: 12 IKEISGTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + GT+ +PG KS+S+R ++L A++ GTT + N L ED + R + +S+E +

Sbjct: 8 VSALQGTNLNVPBGDKSISHRAVMLGAIANGTTTIANFLPGEDCLSTIDCFRKMRSVIEQN- 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
VV G G + KE L +GN+G R L + ++ + D +

Sbjct: 67 -GSDVVVEGKG---LNGLKEPTDILHVGNSGTTARLLLGLACCPFHSCSLIGD--ESIA 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+G + LK +GA +D + P+ + G G L + S S+Q SA+L+A

Sbjct: 120 KRPMGRVTKPLKMMGAHIDGREQGNYPPLSIRG-GELQPIHYE-SPVASAQVKSAILLAG 177

Query: 191 PLALGDVEIEIIDKLISIPY--VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
G ++ P+ + T R++ FG + + + G Q+ + N

Sbjct: 178 LATEGTTA-----VTEPHRSRDHTERMIRLFG--GDVTVDGRTVSVTGPQQL-TGTNI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
YV GD SSA++FL AGA + +T++ G + + +VL+ MGA +T V

Sbjct: 228 YVPGDISSAAFFLVAGAIVPNSEITLKNVGLNPTRTGI--IDVLQQMGADITIEN----V 281

Query: 308 TGPPREPFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
EPFG +L A+++ +P + + V+AL A+G T I+D +VK

Sbjct: 282 RNEQTEPFGDITVRTSNLTAVEIGGALIPRLIDEIPVIALLATQAEGTTVIKDAGELKVK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAAC-A 416
ET R+ + TEL KLGA++E D II L +D++ DHR+ M ++AAC

Sbjct: 342 ETNRIDTVVTELQKLGANIEATGDGMIHGAALTAKEAVVDSHGDRHIGMMLAIAACIT 401

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+ V ++ P ++P +FD L + +

Sbjct: 402 QGTVHLKRPEAVAVSYPSFFDHLHSLM 428

>ref|ZP_02420864.1| hypothetical protein ANACAC_03511 [Anaerostipes caccae DSM 14662]
gb|EDR95836.1| hypothetical protein ANACAC_03511 [Anaerostipes caccae DSM 14662]

Length = 426

Score = 140 bits (352), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 120/440 (27%), Positives = 208/440 (47%), Gaps = 29/440 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+ ++ + GT+ +PG KS+S+R ++ +L++GTT + N L+ D + R +G+ +E
Sbjct: 3 LKKVEGLKGTISIPGDKSISHRAVMFGSLAKGTTHTITNLSGADCLATIDCFRAGVRIE 62

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ VV G K E QL +GN+G R ++ ++ G + L G
Sbjct: 63 -----QEGTVTVVHGNLRLGLKKPEKQLDVGNSGTTTRLISGILS--GQDFEVTLSGDAS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALL 187
+ +RP+G ++ L +GA+++ G C P+++ G P V+ ++S Q SA+L
Sbjct: 116 LNKRPMPGRIMKPLSMMGAIEESVNGDGCAPLKITG---KPLKAVRYESPVASAQVKSAYL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A D + + +S + E+ L+ FGV+ + K + +
Sbjct: 173 LAGLYA--DGRSTVTEPALSRNHTLMK---SFGVQVLSEGTASVM---PPKEMTATD 224

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++F+A +T +T++ G + + +V E MGA +T +
Sbjct: 225 IAVPGDISAFAFFIAAGLVTPDSCITLKVGINPTRNGI---IKVCEAMGADLTMSNVKDD 282

Query: 307 VTGPPPREPFGRK--HLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRVKET 361
G P K LK ++ +P + + V+AL FA+G T I++ A +VKE+
Sbjct: 283 -NGEPTADITVKTSLRKGTEIGGELIPTLIDEIPVIALMAAFAEGETVIKNAELKVKE 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAAC-AEVPV 420
R+ L K+GA E D II L I DHR+AM FS+A A+
Sbjct: 342 NRIDLTVNVLKMGADAEATDDGMIIRGGNPLRGATIHCKYDHRIAMTFSVAGINAGTT 401

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
I D C ++P++++ L
Sbjct: 402 VIEDAECVDVSYPNFYEQQLQ 421

>ref|ZP_04169387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides DSM
2048]
gb|EEL98899.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides DSM
2048]
Length = 429

Score = 140 bits (352), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 125/445 (28%), Positives = 212/445 (47%), Gaps = 43/445 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EG T + L D + + +G+ + ++
Sbjct: 13 LNKGITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVEITQNR--D 70

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATY--VLDGVPRMRE 131
V+G G +E +E + L +GN+G +R ++ + N + + G + +
Sbjct: 71 EVTIVGTG---LEGLQEPKAVLDVGNSGTTIRLMSGIL---ANTPFFSCVQGDASIAK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALL 187
RP+ + LKQ+GA +D P+ + G G +K S S+Q SA+L
Sbjct: 123 RPMQRTVNPLKQMGAKIDGRKDGTFTPLTIRG-----GNLKAIEYTSPPVASAQVKSAIL 176

Query: 188 MAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+A A G + + P++ + T R++E FGV + + GGQK +
Sbjct: 177 LAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TRVGKTVKLAGGQKL-TA 226

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA++FL AGA I + ++ G + + +VLE MGA T + +
Sbjct: 227 TDVQVPGDVSSAAFFLVAGAIIPNSKLLLQNVGMNPTRTGI--IDVLEKMGATFTVEQIN 284

Query: 305 VTVTGPPE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
+ P LK I++ + +P + + ++AL A DG T I+D +VKE
Sbjct: 285 EGASEPAANITITETSPLKGIIEGGDIIPRLIDEIPIIALAATQADGITVIKDAHELKVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
T R+ + ELTKLGA +E D II KL + ++ DHR+ M ++A C AE
Sbjct: 345 TNRIDTVVAELTKLGARIEATDDGMIYIGKCKLKGNTVHSHGDHRIGMMLAIAGCIAEGE 404

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D ++P +F+ L T K
Sbjct: 405 TTIEDAEAVGVSYPTFFFEELQTLAK 429

>ref|YP_357296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelobacter
carbinolicus DSM 2380]
sp|Q3A3D1.1|AROA_PELCD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABA89126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelobacter
carbinolicus DSM 2380]
Length = 431

Score = 140 bits (352), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 127/449 (28%), Positives = 214/449 (47%), Gaps = 34/449 (7%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E V++P + G V++PG KS+S+R ++L AL EG TVV LL ED L A R++
Sbjct: 2 SENQVIKPGGRLVGEVQVPGDKSISHRAIMLGALGEGETTVVRGLLRGEDNLATLEAFRSM 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G++ D A+ + G +++ ++ + GN+G MR +T + AG V+
Sbjct: 62 GVAFCE--GDGALRIAGRGLHGLQEPQDVDC--GNSGTTMLMTGLL--AGQQFFSVM 115

Query: 124 DGVRPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G +R+RP+ +V L +GA + G + P+ + G G S S+Q
Sbjct: 116 TGDRFLRKRPKRVVGLPTAMGAHILGRAGGEYAPLALQG--KTLQGITHHSAVASAQVK 173

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY----IKGG 239
SALL+ A G + + + + R++ FG + + +KGG
Sbjct: 174 SALLLGGLYAEGPTTVHEPHR-----SRDHSERMLTWFGADVVRPFEGGVTLHPGSCLKGG 228

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ V GD SSA++F+ A I G+ ++ G + V ++L MG +
Sbjct: 229 E-----VIVPGDISAAFFMVAALIVPGSELLIRQGVNPNTRSGV--IDILRQMGGNI 279

Query: 299 TWTETSVTVTGPPREPFRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
+G P K LK +++ +P D ++V A FA+G T IRD
Sbjct: 280 ELLNER-DCSGEPVADILVKASDLKGEIGGAVIPRAIDFEPVISVAAFAEGRTVIRDA 338

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
RVKET+R+ ++ +++ LGA VE D +IT L + + DHR+ M+ ++A
Sbjct: 339 RELRVKETDRIASMCQMGALGALVEPREDGMVITGGPSLGAAKVSSLGDHRIGMSMAVA 398

Query: 414 AC-AEVPVTIRDPGCTRKTFPDYFDVLST 441
A A PVT+ D CT +FP ++++ ++
Sbjct: 399 ALRASAPVTVTDTECTATSFPGFWELFNS 427

>ref|ZP_04284624.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
4342]
gb|EEK83665.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus ATCC
4342]
Length = 429

Score = 140 bits (352), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 128/456 (28%), Positives = 216/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + ++
Sbjct: 2 KERTIQPVNNGLNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL----ANTPFF 111

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASI AKRPMKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGV +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGAMFTVEPINEGASEPAANITIETSSLKGI EIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYP TFFEEQLKLAK 429

>ref|ZP_07445888.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu007]
ref|ZP_07495102.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu012]
gb|EFP33393.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu007]
gb|EFP53310.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis SUMu012]
gb|EGB27278.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium tuberculosis CDC1551A]
Length = 434

Score = 140 bits (352), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 134/435 (30%), Positives = 209/435 (48%), Gaps = 38/435 (8%)

Query: 19 VKLPGSKSLSNRILLAL----SEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ +PGSKS +NR L+LAAL G + + L S D ML AL+TLGL V+
Sbjct: 1 MTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTEMLDALQTLGLRVD----- 54

Query: 75 RAVVVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
G G + V E ++ G AG +R + AA G+ DG + R
Sbjct: 55 -----GVGSELTVSGRIEPPGARVDCGLAGTVLRFVPP--LAALGSVPVTFDGDQQARG 107

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI L+ L++LG VD GT P RV G G L GG V + S SSQ++S LL++A
Sbjct: 108 RPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDASASSQFVSGLLLSAA 163

Query: 192 LALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+ ++ L S P++ MT ++ + GV + S +R+ ++ G + + +
Sbjct: 164 SFTDGLTVQHTGSSLP SAPHIAMTAAMLRQAGVDIDDSTP-NRWQVRPGPV--AARRWDI 220

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
E D ++A FL+ A ++GGTV + G S+Q +L + A V ++S+ V GP
Sbjct: 221 EPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLNAVVIHADSSLEV RGP 280

Query: 311 PREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMVAIR 368
DV++ + ++ ++A +A A + R +A R ET+R+ A+
Sbjct: 281 -----TGYDGFVDLRAVGELTPSVAALALASPGSVSRLSGIAHLRGHETDRLAALS 333

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
TE+ +LG + E PD +IT L Y DHRMAMA ++ V + D T
Sbjct: 334 TEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAIIGLRVAGVEVDDIAAT 392

Query: 429 RKTFFPDYFDVLSTFV 443
KT P++ + + V
Sbjct: 393 TKTLPEFPRLWAEMV 407

>ref|ZP_01739541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter sp.
ELB17]
gb|EAZ97562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter sp.
ELB17]
Length = 444

Score = 140 bits (352), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 126/437 (28%), Positives = 209/437 (47%), Gaps = 28/437 (6%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP I G +++PG KS+S+R ++L AL+EG T V+ L ED + A R LG+++E
Sbjct: 14 QPAGPIVGDIRVPGDKSMSHRSIMLGALAEIGTEVNGFLEGEDSLATVQAFRDLGVITIEG 73

Query: 70 -DKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
D R VG G ++LGN+G MR + + A ++ V D
Sbjct: 74 PDNGFVRIHGVGMNGL-----QAPRGPIYLGNSGTGMRLFSGLLAAQAFDSELVGDA--S 126

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+G + L+ +GA +D G PP+++ G L G + + S+Q S LL+
Sbjct: 127 LTKRPMGRVADPLRAMGAVIDTAEGGR-PPLKIRGSQPLTGIHYDMPVA-SAQVKSCLLL 184

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G + P + T R++E FG +D+ + GG K + N
Sbjct: 185 AGLYADG-----VTSVTEPAPTRDHTERMLEGFYHVYRADATSS--VSGGKLVACNI 236

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++FL AG+ G +T+ G + V +L +MGA + + +
Sbjct: 237 DVPADISSAAFFLVAGSIAPGSDLTLRHVGMNPT--VGVINILRLMGANIDVSNER-AI 293

Query: 308 TGPPPREPFRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P ++ LK ID+ ++P D L + A FA+G T +R RVKE++
Sbjct: 294 GGEVADVRVRYAPLKGIDIPEREVPLAIDEFPVLFIAATFAEGRITLRGAEEELRVKESD 353

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVT 421
R+ + L +G PD II + + +++++ DHR+AM+F++A+ A+ +
Sbjct: 354 RIQVMADGLAAGVVKTTVTPDGIIDGGQAMTGGIVNSHGDHRIAMSFVAVSLRAKGEIV 413

Query: 422 IRDPGCTRKTFPDYFDV 438
I D +FP + ++
Sbjct: 414 INDCANVATSFPGFVEL 430

>ref|ZP_01628336.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nodularia spumigena
CCY9414]
gb|EAW46915.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nodularia spumigena
CCY9414]
Length = 450

Score = 139 bits (351), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 126/439 (28%), Positives = 209/439 (47%), Gaps = 25/439 (5%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+L A+++G T + LL ED + +G + ++ +
Sbjct: 29 LQGRIRVPGDKSISHRALMLGAIAQGETQIQGLLLGEDPRSTASCFQAMGAQI-SELNTE 87

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V G G + +E V L GN+G +R L + A+ + + G +R RP
Sbjct: 88 LVTVQGIG----LGQLQEPVDVLNAGNSGTTLR-LMLGLLASHPGRFFTVTGDSSLSRSP 142

Query: 134 IGDVVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+Q+GA++ G P+ + G P S S+Q S +L+A L
Sbjct: 143 MSRVVVKPLQQMGAIEWGRKGNLAPLAIQGGQALKP--THYHSPIASAQVKSILLAGLLT 200

Query: 194 LGDVEIEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + + + +S + E R++ FG + + + G + + K V GD
Sbjct: 201 AG--KTTVTPEPALSRDHSE---RMLRAFGAELTIDPETNSVTVIGPAQLRGQK-VIVPGD 254

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPR 312
SSA+++L AGA + G + VE G + + E LE+MGA + E V G P

Sbjct: 255 ISSAAFVLVAGAIVPGSELVVENVGVPNPTRTGI--LEALELMGADIQL-ENQREVAGEPV 311

Query: 313 EPFGRK--HLKAIDVN--MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367

+ LK+ + + +M D LAV A+FA+G T IRD RVKE++R+ +
Sbjct: 312 ADIRVRSSRLKSCTIAGDIIPRMIDEIPILAVAAVFAEGTTIIRDAEELRVKESDRITVM 371

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVVPV-TIRDPG 426

+L K+GA V E PD IT L T +D+Y DHR+AM+ ++A+ + TI
Sbjct: 372 AQQLNKGAKVSELPDGMETGGTPLVGTVDVSYTDHRIAMSLAIASLVSTGITTIIHRAE 431

Query: 427 CTRKTFPDYFDVLSTFVK 445

++PD+ L +
Sbjct: 432 AAAISYPDFTATLQKVLNT 450

>ref|NP_894231.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9313]
sp|Q7V8F4.1|ARO_A_PROMM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE20573.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9313]
Length = 441

Score = 139 bits (351), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 141/446 (31%), Positives = 213/446 (47%), Gaps = 39/446 (8%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+SGTV++PG KS+S+R LL A++EG T ++ LL +ED LR +G ++ +
Sbjct: 19 LSGTVRVPKDKSISRALLFGAIAEGVTTIEGLLPAEDPMSTAACLRAMGATIGPIHVGQ 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132

V G G D +E Q L GN+G +R + + A G +VL G +R R
Sbjct: 79 IVRVEGVG-----LDGLQEPQDVLDCGNSGTTIRLMLGLLAARKGR-HFVLSGDASLRER 132

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMA 189

P+ + L +GA + D P+ V+G GG+ G V S+Q SALL+A
Sbjct: 133 PMNRVGPPLTMMGAKIKGRSNGDFAPLAVSGQKLKRGVIGTPVA-----SAQVKSALLLA 187

Query: 190 APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNA 248

A A D +I+ S + E R++ FG E R + GQK +N
Sbjct: 188 ALTA--DGATTVIEPAHSRDHSE--RMLRAFADLEVGGEMGRHIRVSPGQKLYG-QNI 241

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307

V GD SSA+++L AGA + G + VE G + EVL+ M A++ V
Sbjct: 242 VVPGDISSAFVLVAGALVPGAELVVENVGVLNPT--TGILEVLQMEARIEVLNRH-EV 298

Query: 308 TGPPREPF-----RKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVK 359

G EP G + LK +N + +P D LAV A F DG + I D + RVK
Sbjct: 299 AG---EPVGDRLVRQSLKPFSGINGDIIPRLVDEVPILAVAACFCDGESKITDASELRVK 355

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418

ET+R+ + +LT +GA ++E D I L T +D+ DHR+AM+ ++AA AE
Sbjct: 356 ETDRLAVMTRQLTAMGADIDEHADGLTIRGGRTLRTGLDSETDHRVAMSLAVAALLAEG 415

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444

+ ++P+++D L +
Sbjct: 416 NSRLTGSEAAAVSYPNFWDDLRLHR 441

>ref|ZP_08070009.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
vestibularis ATCC 49124]
gb|EFX95786.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
vestibularis ATCC 49124]
Length = 427

Score = 139 bits (351), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 119/434 (27%), Positives = 215/434 (49%), Gaps = 37/434 (8%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G++++PG KS+S+R ++ +L++G T V ++L EDV + R LG+++E D

Sbjct: 10 LHGSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVTIEDDGDVV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G K P + +L +GN+G ++R ++ + AG + + G + +RP

Sbjct: 70 RIHGVGFDGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFDVEFMFGDDSLSKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L+Q+G +V D PP++++G L +L + S+Q SAL+ AA A

Sbjct: 122 MDRVVTIPLRQMGVEVSGQTDRDLPLPKMHGSKSLKPIHYQLPVA-SAQVKSALIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E II+K + + E ++++FG + + I GGQ + + V GD

Sbjct: 181 --DGESVIEIEKEKTRNHT---DMIQFG--GQLQVDGNEIRISGGQTL-TAQEVVVPD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++L AG + + +E G + +V++ MG K++ ++ S T+

Sbjct: 233 ISSAAFWLAVGLVMPNSKIVLENVGINETR--TGIIDVIKDMGGKISLSDIDQVAKSATI 290

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
T E LK + + +P + L ++ L A G T IRD +VKET+R+

Sbjct: 291 TVETSE-----LKGTKIGDIIPLRIDELPIITLLATQAQKTVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +

Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTALHGAEVNTFGDHRIGMMAIAALLVQDGEVNL 404

Query: 423 RDPGCTRKTFFPDYF 436
+ ++P +F

Sbjct: 405 QRAEAINTSYPSFF 418

>ref|ZP_05550675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_36A2]
gb|EEU32331.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_36A2]
Length = 421

Score = 139 bits (351), Expect = 6e-31, Method: Compositional matrix adjust.
Identities = 106/436 (24%), Positives = 207/436 (47%), Gaps = 48/436 (11%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A+ LG +E

Sbjct: 11 LTGEVTPPPSKSILHRYIIASSLAKGISKIENISYSDDIIATIEAMEKLGAKIEK---KD 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 134
+++ F + ++ +G +R L ++ G ++ +RP+

Sbjct: 68 NYLLIDGSKTDFDKYLSNNAEIDCNEGSGSTLRFLFPLSIVKKNKISF--KGKGKLFKRPL 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLMAAP 191
+ + N I G L G+ ++ G+ISSQ+++ LL + P

Sbjct: 126 NPYFENFDKYIKY-----SYINENEILLDGEKSGEYIDGNISSQFITGLLFSLP 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L + +I I KL S Y+++T+ + +FG+K ++S+ F I+G Q YKS + VE

Sbjct: 178 LLNENSKIIIRKGLESSYIDITVDCLNKFGIKI-INNSYQEFIEGNQNYKSG-DYEVE 235

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ETSVTVTGP 310
D S ++FL +I G + + G T SLQGD K +++ + W E + + G

Sbjct: 236 ADYSQVAFFLVANSI-GSNIKINGLNTNSLQGDKK---IIDFISQIDNWNKEEKLILDGS 291

Query: 311 PREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
+ PD+ L++ A + I ++A R+KE++R+ A E

Sbjct: 292 -----ETPDIIPILSLKACTSKKEIEIVNIARLRIKESDRLKATVKE 333

Query: 371 LTKLGASVEEGPDYCIITPPE---KLN---VTAIDTYDDHRMAMAFSLA-ACAEVPVTIR 423
L+KLG + E D +I + K+N + + ++ DHR+AM ++A C + +

Sbjct: 334 LSKLGFDDLLEKEDSILINSRKDFYKINNNSLVYLSSHSDHRIAMTIAIALTCYNGEIIID 393

Query: 424 DPGCTRKTFFPDYFDVL 439
+ C +K++P+++V

Sbjct: 394 NLDCVKKSYPNFWVEF 409

>ref|YP_003599482.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
DSM 319]
gb|ADF41132.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus megaterium
DSM 319]
Length = 429

Score = 139 bits (351), Expect = 7e-31, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 210/441 (47%), Gaps = 39/441 (8%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G + +PG KS+S+R ++ A++EG T + + L ED + +G+S++ +
Sbjct: 10 LSSLQGEISIPGDKSISHRAVMFGAMAEKTTISHFLAGEDCLSTISCFEKMGSVSIK--R 67

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V G G +E E + +GN+G R + + AG L G +
Sbjct: 68 EDEYVEVEGKG---IEGLSEPASILDVGNSTTTRMLMLGIL--AGVPFHTSLIGDESIA 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDPCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + V L+ +GA +D P+ G G L S S+Q SA+L+A
Sbjct: 122 KRPMRSRVTVPLRSMGAKIDGREHGQYTPLSTRG-GALKAIHYH-SPVASAQVKSAILLAG 179

Query: 191 PLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G ++ + P+ + T R++ FGV E + I+GGQ + +
Sbjct: 180 LHAEGTTRKV-----TEPFTSRDHTERMLRAFGVDVEVDGTT--VSIEGGQSLRG-TDV 229

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
YV GD SSA++FL AGA + + ++ G + + +VL+ MGA++T + +
Sbjct: 230 YVPGDISAFLVAGAVVPNSRIVLKSIVGLNPTRTGI--IDVLQQMGAARTISNERIQ- 286

Query: 308 TGPPREPFPG-----RKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
EP G LK I++ + +P + + V+AL A +G T I+D +VK
Sbjct: 287 ---NGEPIGDLTIETSQLKGIEIGGDLIPRLIDEIPVIALLATQANGKTVIKDAEELKVK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATD'TYDDHRMAMAFSLAAC-AEV 418
ET R+ + TEL+KLGASV D II L +D+Y DHR+ M ++AA A
Sbjct: 344 ETNRIDTVATELSKLGASVTPTADGLIIEGKTALKSGEVDVSYGDHRIGMMLAVAAAIATG 403

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
VT+ ++P +F+ L
Sbjct: 404 EVTLMRSEAIHVSYPFFEDL 424

>ref|ZP_04295406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH621]
gb|EEK72883.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH621]
Length = 429

Score = 139 bits (351), Expect = 7e-31, Method: Compositional matrix adjust.
Identities = 125/445 (28%), Positives = 212/445 (47%), Gaps = 43/445 (9%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EG T + L D + + +G+ + ++
Sbjct: 13 LNGKITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVEITQNR--D 70

Query: 75 RAVVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATY--VLDGVPRMR 131
V+G G +E +E + L +GN+G +R ++ + N + + G + +
Sbjct: 71 EVTIVIGTG---LEGLQEPKAVLDVGNSTTIRLMSGIL---ANTPFFSCVQGDASIAK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDPCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALL 187
RP+ + LKQ+GA +D P+ + G G +K S S+Q SA+L
Sbjct: 123 RPMQVRVNPLKQMGAKIDGRKEGTFTPLTIRG-----GNLKAIEYTSVPVASAQVKSAIL 176

Query: 188 MAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+A A G + + P++ + T R++E FGV + + GGQK +
Sbjct: 177 LAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVTV--TRVGKTVKLAGGQKL-TA 226

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA++FL AGA I + ++ G + + +VLE MGA T + +

Sbjct: 227 TDVQVPGDVSSAAFFLVAGAIIPNSKLLQLNVGMNPTRTGI--IDVLEKMGATFTVEQIN 284
Query: 305 VTVTGPPE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKE 360
+ P LK I++ + +P + + ++AL A DG T I+D +VKE
Sbjct: 285 EGASEPAANITIETSPKLGIEIGGDIIPRLIDEIPIIALAATQADGITVIKDAHELKVKE 344
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVP 419
T R+ + ELTKLGA +E D II KL + ++ DHR+ M ++A C AE
Sbjct: 345 TNRIDTVVAELTKLGARIEATDDGMIYGGCKLKGNTVHSHGDHRIGMMLAAGCIAEGE 404
Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D ++P +F+ L T K
Sbjct: 405 TTIEDAEAVGVSYPTFFFEELQTLAK 429

>ref|YP_002338950.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH187]
ref|ZP_04268155.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST26]
sp|B7HVH9.1|AROABACC7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACJ77163.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH187]
gb|EEL00392.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST26]
Length = 429

Score = 139 bits (351), Expect = 7e-31, Method: Compositional matrix adjust.
Identities = 128/456 (28%), Positives = 216/456 (47%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61
Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG----LEGLQEPKAVLDVNSGTTIRLMGIL----ANTPFF 111
Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVK----LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIARKPMKRVTNPLKQMGANIDGREGTFTPLTIRG-----GDLKAIEYTSP 165
Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + + P++ + T R++E FGVK +
Sbjct: 166 VASAQVKSAILLAGLRAEGVTAV-----TEPHISRDHTERMLEAFGVKV--TREGKTV 216
Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPGDVSSAAFFLVAGAIIPNSKLVQLNVGMNPTRTGI--IDVLEK 273
Query: 294 MGAKVTWTETSVTVTGPPE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTA 349
M A T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MDATFTVEPINEGASEPAANITIETSSLKLGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDHRIGMM 393
Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
++A C AE TI D ++P +F+ L K
Sbjct: 394 LAIAGCLAEGKTTIEDAEAVGVSYPTFFFEELQRLTK 429

>ref|ZP_07109493.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oscillatoria sp. PCC
6506]
emb|CBN54641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oscillatoria sp. PCC
6506]
Length = 452

Score = 139 bits (351), Expect = 8e-31, Method: Compositional matrix adjust.

Identities = 126/439 (28%), Positives = 206/439 (46%), Gaps = 24/439 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+L A++ G T ++ LL ED ++G E K
Sbjct: 27 LQGRIRIPGDKSISHRALMLGAIASGETTIEGLLLGEDPRSTAKCFASMG--AEISKLNA 84

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V V G + + K+ L GN+G MR L + A+ + + G MR RP+
Sbjct: 85 ELVRVKGFGLGELREPKD--ILDTGNSGTTMR-LMMGILASHPGRFFTVTGDSSMRSRPM 141

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLA 193
+V L+Q+GA + P+ V G P + I+S Q S +L+A +A
Sbjct: 142 SRVVKPLQMQGAQIWGRESHSLAPLAVLGQRLKP---IHYHSPIASAQVKSCILLAGLMA 198

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G E + + +S + E R+++ FG K + G K + + V GD
Sbjct: 199 EG--ETTVEPALSRDHSE---RMLQAFGAKVSVDPDTCSTVTGTGPAKLQG-QAVIVPGD 252

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPR 312
SSA+++L AGA + +T+E G + + E L MMGA + + P
Sbjct: 253 ISSAAFWLVAGAIVPDELTIENVGVNPTRTGI--LEALAMMGANIELQNQRLVAGEPVA 310

Query: 313 EPFGRK--HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ R LK ++ + +P D LAV A+FA+G T IRD A RVKE++R+ +
Sbjct: 311 DIVVRNSGKLGCTISGDLIPRLIDEIPILAVAAIFAEGTTTIRDAELRVKESDRLAVM 370

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVT-IRDPG 426
++L ++GA + E PD I L T +D++ DHR+AM+ ++AA +T I
Sbjct: 371 ASQLNRMGAQITELPDGLEIAGGTALTGTDLSDHTDHRIAMSLAIAALNASGITAIHRAE 430

Query: 427 CTRKTFPDYFDVLSTFVK 445
++PD+ L +
Sbjct: 431 AASISYPDFTATLKQLTDS 449

>ref|ZP_08086958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis VMC66]
gb|EFX94237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis VMC66]
Length = 427

Score = 139 bits (351), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 217/442 (49%), Gaps = 35/442 (7%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 7 VKGLKGRIRVPGDKSISHRSIIFGSLAQGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++ +L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 NLVEIHGVGFELQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+++ G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVTIPLRQMGVEIAGRTERDLPPLKMGSKELQPIHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A GD I I+K I+ + E ++ +FG + E R I+GGQ++ + + V
Sbjct: 179 QAQGDSVI--IEKEITRNHTE---DMAIQFGGQIEVKGEIR--IQGGQEF-TAQEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + +V+E MG ++T ++ S
Sbjct: 231 GDISAFAFWLVAGLIVPDSKIVLENGINETRTGI--LDVIEAMGGRMTLSVDVPVAKSA 288

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITVETSE-----LKGEIGGEIIPRLIDELPIIALLATQAQGRTVIRDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA++ D II L+ ++T DHR+ M ++AA V
Sbjct: 343 RIQVVADALNSMGAAITPTEDGMIIDGKTPHGAQVNTLGDHRIIGMMAIAAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
+ + ++P +F L
Sbjct: 403 ELERSEAIKTSYPSFFSDLEVL 424

>ref|ZP_02433359.1| hypothetical protein CLOSCI_03637 [Clostridium scindens ATCC 35704]
gb|EDS05028.1| hypothetical protein CLOSCI_03637 [Clostridium scindens ATCC 35704]
Length = 435

Score = 139 bits (350), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 121/439 (27%), Positives = 214/439 (48%), Gaps = 32/439 (7%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ G + +PG KS+S+R ++L A+++GTT + N L D + R +G+ ++ +
Sbjct: 10 KKLKGEITVPGKKSISHRSIMLGAIAGQTTEITNFLTGTADCLATIKCFRKMGIIDICRPS 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++V G + + A + + L +GN+G R ++ + AG + + VL+G + +R
Sbjct: 70 S---ILVHGKGLYGLT-APDGI-LDVGNSGTTTRLMSGIL--AGQDFSCVLNGDDSLNQR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPG---GKVKLSGSISSQYLSALLMA 189
P+ ++ L +GA + C P+++ PG V S S+Q SA+L+A
Sbjct: 123 PMARIMKPLNLSGAHITSIKDNGCAPLKIE-----PGHLHSIVYQSPVASAQVKSAILLA 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPK 246
GD E + + +S + E+ +++ FG A H D Y+ + +
Sbjct: 178 G--LYGDGETSVTEPALSRNHTL---MLQSFASVSAAMHPDGSATAYVHACDELYG-Q 231

Query: 247 NAYVEGDASSASYFLA-GAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETS 304
+V GD SSA+YF+A G + G + V+ GT + F +V + MGA +T ET
Sbjct: 232 QIFVPGDISAAYFIAAGLLVPGSELLVKNVGTNFTFTR--AGFLDVCKAMGADITRVNETF 289

Query: 305 VVTGTPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ G LK + + +P D LAV+A A+G T I+D A +VKET
Sbjct: 290 LGEGRADILVRSSDLKGATIEGDIIPALIDEIPILAVMAAHAEGTTVIKDAEELKVKET 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAA-CAEVPV 420
R+ + L +G ++ D II L+ I ++ DHR+AMAF++A A+
Sbjct: 350 NRIATVTFENLKAMGCNITPTADGMIIEGGSPLSGARIQSHMDHRIAMAFIAGLTAKGET 409

Query: 421 TIRDPGCTRKTFPDYFDVL 439
I D ++P++F+ +
Sbjct: 410 VIEDSQYVDVSYPEFFEAV 428

>gb|EFY02974.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
dysgalactiae subsp. dysgalactiae ATCC 27957]
Length = 427

Score = 139 bits (350), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 123/437 (28%), Positives = 215/437 (49%), Gaps = 25/437 (5%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+ +PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 10 LQGTICVPGDKSISHRAVILGAIAGKETRVKGLLKGEDVLSTIQAFRNLGVRIE--EKDD 67

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G F A ++ L +GN+G +MR + + AG + + G + +RP+
Sbjct: 68 QLVIEGQG--FEGLTAPHQI-LDMGNSGTSMLIAGLL--AGQSFEVTMSGDDSLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V+ L+Q+G D+ P+++ G GL L + S+Q SA+L+AA A
Sbjct: 123 DRIVLPLRQMGVDITGESSRHLSPKLKGSRLNPITYALPVA-SAQVKSAILLAALQAN 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ I+K I+ + E ++++FG + + ++ G Q + V GD
Sbjct: 182 GTTKL--IEKEITRNHTE---DMIQQFGGRLRVDGK--KIWLTPQTLLIG-QEVTVPGLDI 233

Query: 255 SSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPRE 313
SSA+++L AG + G + +E G + + EV+E MG +VT+ E + T

Sbjct: 234 SSAAFWLVLVAGLIVPGSAILLENVGINPRTGTI--LEVIEQMGGQVTY-EAVNSQTQSANL 290

Query: 314 PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTE 370
LK ++ +P + L ++AL A G T I+D RVKET+R+ +

Sbjct: 291 GVAYSQKLGTTISGQLIPRLIDELPIIALLATQAQGVYTIKDAQELRVKETDRIQVVTDI 350

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
L +GA+++ D II P L+ T+ DHR+ M ++AA + V +

Sbjct: 351 LKSMGATIKATADGMIIEGPTALHAAKTSTFGDHRIGMMTAIAALLVKQGQVHLDREEAI 410

Query: 429 RKTFFPDYFDVLSTFVKN 445
++P +F+ L +

Sbjct: 411 MTSYPTFFNDLERLCHD 427

>ref|ZP_05403383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mitsuokella multacida
DSM 20544]
gb|EEX70182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mitsuokella multacida
DSM 20544]
Length = 434

Score = 139 bits (350), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 121/432 (28%), Positives = 207/432 (47%), Gaps = 21/432 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ +AL + N L+++D ++ LG SVE + ++

Sbjct: 14 LHGTIEIPGDKSISHRSVMFSLGSPVHITNFLHAQDCLSTAACMKALGASVEFE--SE 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A+VV G +++A + GN+G +R + + T+ D + +RP+

Sbjct: 72 TALVVCGHGLHGLKEASTIIDA--GNSGTTLRLMMGILAPQPFLLTFTGDA--SLHKRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G ++ L +GA + P+ + G V S S+Q SA+L+A A

Sbjct: 128 GRVIKPLSAMAKIYGRENNTKLPIITIVPAESRLHGMVYESPVASAQVKSAILLAGMYA- 186

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D +++ S + E R++E FGV+ + + I+ +++P+ V GD

Sbjct: 187 -DGPTTVVEPFSTRDHTE---RMLEAFGVETKKEGTA--VTIEPVDSFRAPEAIEVPGDI 240

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT---VTGP 310
SSA+Y+L AG+ + G ++ ++ G + + +VL+ MGA VT V+

Sbjct: 241 SSAAYWLVAGSVVPGSSLLKNVGNVNPRTGTI--LDVLKAMGASVTLENERVSGEAAAD 298

Query: 311 PREPFGKHLKAIDVN-MNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
R + H + M ++ D +AV ALFA+G T I RVKET+R+ AI

Sbjct: 299 IRVEAAKLHGTSFGAEIMPRIDEIPVIAAALFAEGDTVITGAGELRVKETDRLQAITD 358

Query: 370 ELTKLG-ASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCT 428
E KL SVE D +I K+ +YDDHRMAM+ ++ A V I P C

Sbjct: 359 EFNKLAPGSVEASEDGLVIHGKTKVCANCFSYDDHRMAMSLAILGTAGEGVEIERPDCV 418

Query: 429 RKTFFPDYFDVLS 440
++P ++ L+

Sbjct: 419 NISYPAFYGTLA 430

>gb|EGC25868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK405]
gb|EGC26641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK678]
Length = 427

Score = 139 bits (350), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 119/437 (27%), Positives = 216/437 (49%), Gaps = 37/437 (8%)

Query: 12 IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++ + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D

Sbjct: 7 VRGLKGRIRVPDGKSIHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

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      +   VG   G   ++      +L +GN+G ++R ++   +   AG +   +   G   + +
Sbjct: 67  NLVKIHGVGFKGLQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAFMGDDSLSK 119

Query: 132  RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+   + + L+Q+G ++      D PP+++ G   L   +L + S+Q  SAL+ AA
Sbjct: 120  RMDRVTIPLRQMGVEIAGRTERDLPLPKMKGSRELQPIHYQLPVA-SAQVKSALIFAAL 178

Query: 192  LALGDVEIEIIDKLISIPYVE-MTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      A G   E  II+K I+   + E M   +   + VK +   + I+GGQ++ + +   V
Sbjct: 179  QAQG--ESIIIEKEITRNHTEDMIAQFCGQIEVKGKE-----IRIQGGQEF-TAQEVTV 229

Query: 251  EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----S 304
      GD SSA+++L AG   +   + +E G   +   + EV+E MG ++T ++   S
Sbjct: 230  PGDISSAAFVLVAGLIVPDSKIVLENVGINETRTGI--LEVIEAMGGRMTLSVDVPAKS 287

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
      T+T   E   LK ++   +P +   L ++AL A   G T IRD   +VKET
Sbjct: 288  ATITVTETSE-----LKGTEIGGEIIPRLIDELPIIALLATQAQGRTVIRDAEELVKET 341

Query: 362  ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
      +R+   +   L +GA++   D II   L+   ++T+ DHR+ M   ++AA
Sbjct: 342  DRIQVVADALNSMGAAITPTEDGMIIEGKTPHLGAQVNTFGDHRIGMMTAIAALLAQSGQ 401

Query: 420  VTIRDPGCTRKTFPDYF 436
      V +   +   ++P +F
Sbjct: 402  VELERSEAIKTSYPSFF 418

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>ref|ZP_08060961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
      infantis ATCC 700779]
gb|EFX37375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
      infantis ATCC 700779]
Length = 431

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Score = 139 bits (350), Expect = 8e-31, Method: Compositional matrix adjust.
Identities = 122/444 (27%), Positives = 218/444 (49%), Gaps = 37/444 (8%)

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Query: 12  IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADK 71
      +K ++G++++PG KS+S+R ++   +L+EG T V ++L EDV   +   R LG+ +E
Sbjct: 11  VKHLNGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTIQVFRDLGVEIEDKD 70

Query: 72  AAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      VG   G K P   +   L +GN+G ++R ++   +   AG +   +   G   +
Sbjct: 71  GVVTIQGVGMDGLKAP-----QKALDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 122

Query: 131  ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      +RP+   + + LK++G   +   D PP+ + G   L   +L + S+Q  SAL+ AA
Sbjct: 123  KRPMDRVTLPLKMGVSIISGQAERDLPLHLKGTKNLKP IQYELPIA-SAQVKSALIFAA 181

Query: 191  PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      A G   +  II+K   +   + E   ++++FG   + S   +   ++G QK   S +   V
Sbjct: 182  LQAQG--QSVIIEKKCTRNHTE---DMLQQFG--GDLSVDGKKITVQGPQKL-SGQTVVV 233

Query: 251  EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TS 304
      GD SSA+++L AG   +   V ++   G   +   + +V+ MG K+ T+   S
Sbjct: 234  PGDISSAAFVLVAGLIVPNSRVVLKNVGINETRTGI--IDVIRAMGGKLEITDIDPIAKS 291

Query: 305  VVTGTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
      T+T   E   L   I++   +P +   L ++AL A   G T I+D   +VKET
Sbjct: 292  ATLTVETSE-----LNGIEIGGALIPRLIDELPIIALLATQTQGGQTVIKDAEELVKET 345

Query: 362  ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVP 419
      +R+   +   L +GA++   D II   L+   ++T+ DHR+ M   ++AA   A+
Sbjct: 346  DRIQVVADALNSMGATITPTADGMIIEGKSALHGAKVNTFGDHRIGMMTAIAALLVADRE 405

Query: 420  VTIRDPGCTRKTFPDYFDVLSTFV 443
      V +   +   ++P +FD L T +
Sbjct: 406  VVLDRAEAINTSYPSFFDDLETLI 429

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>ref|ZP_06680425.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium

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E1071]
gb|EFF20006.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1071]
Length = 431

Score = 139 bits (350), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 213/441 (48%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSISHRSIMFGAIAEGTTTTIQNFLRAEDCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + + +GN+G +R L + AG L G
Sbjct: 63 EEEEEIMK--IHGRGSHSFVQPTES---IDMGNSGTTIRLLMGIL--AGQPFMTTLFGDA 115

Query: 128 RMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMPGRVMEPLREMGADLQKGENEQYLPITVTGTNSLSPIRYNMPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + S + G QK + +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRI--SVEGKTITVTGPQL-TGQQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAAFFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAATQTNHNEQ 284

Query: 307 VTGPPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAEV 424

>ref|YP_574215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chromohalobacter
saalexigens DSM 3043]
gb|ABE59516.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chromohalobacter
saalexigens DSM 3043]
Length = 750

Score = 139 bits (350), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 135/447 (30%), Positives = 213/447 (47%), Gaps = 38/447 (8%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + G +++PG KS+S+R ++L AL++G T V L ED L A R +G+++E
Sbjct: 311 VSPGGAVRGQIRVPGDKSISHRSIMLGALADGVTEVHGFLEGEDSLATLQAFREMGAIE 370

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 128
R + G G A L++GN+G AMR + AG L G
Sbjct: 371 GPHHG-RVTIHGVGLHGLTAPAGP---LYVGNSGTAMRLFAGLL--AGQAFDTELTGDVS 424

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+G + L+++GA ++ G PP+ + G L G + + + S+Q S LL+
Sbjct: 425 LNKRPMPGRIADPLREMGAVIETAEGGR-PPLTIRGGQALSGIRYDMPMA-SAQVKSCLLL 482

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A G+ + P + T R++ FG V+ + ++W GG+ SP
Sbjct: 483 AGLYAEGETRVR-----EPAPTRDHTERMLNGFGYPVQRDGEAW---LQGGGRLAASPI 534

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL AAIT G+ + +E G + + +L+ MGA +T E
Sbjct: 535 D--VPDISAATFFLVAAAITPGSDLLLEHVGINPTR--IGVINILQAMGADLTLLQEPR- 589

Query: 306 TVTGPPPREPFGRKH--LK AIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360

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      V G P      ++ LK ID+  +++P  D    L V A  A+G T +R      RVKE
Sbjct: 590 EVGGEPVADIRIRYAPLKGDIDPTDQVPLAIDFPALEFVAANAEGVTRLRGAEELRVKE 649

Query: 361 TERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDTYDDHRMAMAFSL 412
      ++R+ A+  LT LG      PD  I      TP      +D+  DHR+AMAF++
Sbjct: 650 SDRIQAMADGLTTLGVDNTVYPDGDIDVGRASADETPAAHYRGGQVDSLGDHRIAMAFV 709

Query: 413 AAC-AEVPVTIRDPGCTRKTFPDYFDV 438
      AA  A   + I D      +FP + D+
Sbjct: 710 AALRASDEIVDDCANVATSFPGFVDL 736

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>ref|YP_003676763.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
      mathranii subsp. mathranii str. A3]
gb|ADH60752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
      mathranii subsp. mathranii str. A3]
Length = 423

```

Score = 139 bits (350), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 128/445 (28%), Positives = 214/445 (48%), Gaps = 34/445 (7%)

```

Query: 6    EIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
      +I ++  K + G + +PG KS+S+R +++ ++EG T + N L  ED   +  +R LG+
Sbjct: 2    DIEVKKKFLKGVISVPGDKSISHRAVMIGSIAEGITEIGNFLLGEDCISTINCMRNLGV 61

Query: 66   SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      VE      +  V  GK   +  E++ L +GN+G  +R L  ++      AT  + G
Sbjct: 62   DVEL-----KGTNVKVYVGKGLYLNKSEKI-LDVGNSGTTIRLLMGILSGQKFEAT--VTG 113

Query: 126  VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSA 185
      ++ RP+G ++  L  +GA ++   G +  P+ V G   L G  K+   I+S  + +
Sbjct: 114  DESIKRRPMPGRVITPLSMMGAKIEAREG-NFAPLTVFG-NKLGKIYYKMP--IASAQVKS 169

Query: 186  LLMAAPLALGDVEIEIIDKLISIPY--VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +M A L   D  I      I  PY   T  +   FG K + + +   Y   G K +
Sbjct: 170  SIMLASLYADDKTI-----IEEPYPSRNHTELMFSSFGAKVDVNGTKITCY--PGYKLQ 221

Query: 244  SPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWT- 301
      K   V GD SSA+YF+  A +   VT++      +  +  +V+E MG  +  T
Sbjct: 222  GQK-IVVPGDISAAYFIVAATLVPNSEVTIKNVNPNTRTGI--IDVIEKMGGDIVLTN 278

Query: 302  ETSVTVTGPPREPFGFRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRV 358
      E ++      LK I++  + +P  D    +AV A+FA+G T I+D  +V
Sbjct: 279  ERTINNEKVADITVKT SRLKGIEIGGSLIPRLIDEIPVIAVAAVFAEGKTVIKDAEELKV 338

Query: 359  KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AE 417
      KE+ R+  I +EL KLGA + E  D  II   L   +++Y+DHR+AM+  +A  AE
Sbjct: 339  KESNRINTITSELKKLGAKIFERDDGMIEGTGFLRGNTVESYNDHRIAMSLWVAGLMAE 398

Query: 418  VPVTIRDPGCTRKTFPDY---FDVL 439
      I++  C   ++PD+  FD+L
Sbjct: 399  GETKIKNAECVNISYPDFYKTFDIL 423

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```

>ref|NP_829586.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
      GPIC]
sp|Q822G0.1|ARO_A_CHLCV RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|AAP05464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
      GPIC]
Length = 446

```

Score = 139 bits (350), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 125/434 (28%), Positives = 211/434 (48%), Gaps = 26/434 (5%)

```

Query: 15   ISGTVKLPKSKLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      ISG+V +P SKS + R +  A+LS GT+ ++N L S D  M+ A + LG      K  K
Sbjct: 11   ISGSVDVPPSKSHTLRAIFWASLSRGTTSTINNPLESPESEMIQACKQLGA-----KIYK 65

Query: 75   RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

```



```

      ++ + G P      +++ + G++GI R TA AA + + G +++ RPI
Sbjct: 66 KSSSLEITGT-PHLRLPKDIAIDAGSSGIVFRFFTA--LAAIFSEKVTITGSSQLQRRPI 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      L+ L+ GA      P V +G + G ++ G SQY SAL MA LA
Sbjct: 123 APLIRALENFGATFSYQRDPYTLPSV--LGPISSGYTEVLGE-DSQYASALAMACSLAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G II+ P+ ++TL +E+ + +S S + Y G+ + V GD
Sbjct: 180 GPFSFTIINPK-ERPWFKLTLWWLEQLAIP--YSQSEENTYSFVGKSRPEGFSYTVGGDF 236

Query: 255 SSASYFLAGAAI--TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      SSA++ A + + + +QGD + +L+ +GA + + E + + P
Sbjct: 237 SSAAFLAVAALLSQSPHPTYLRLNLMQDVQGDKEFLVLLKKLGANIVF-ENDIVIIIFP-- 293

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
      + +++M+ D LAV+ FA P+ + + + KE++R+VAI EL
Sbjct: 294 -----STISGGNIDMPFIDALPILAVLCCFATSPSHLYNARGAKDKESDRIVAITEELQ 348

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
      K+GA ++ D +I P L ++ +++DHR+AMA S+AA A +I D C +KT
Sbjct: 349 KMGACIQPCHDGLLIN-PSPLYGASMFSHNDHRIAMALSIAAMHASGDSSISDTECVKKT 407

Query: 432 FPDYFDVLSTFVK 445
      FP++ +L++ N
Sbjct: 408 FPNFIQILNSLHAN 421

```

>gb|ACN18643.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
Length = 428

Score = 139 bits (350), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 121/436 (27%), Positives = 218/436 (50%), Gaps = 27/436 (6%)

```

Query: 17 GTVKLPKSKSLNRIILLAAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
      G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E +
Sbjct: 12 GAITVPGDKSMHSRIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIEETEEIIV 71

Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
      G G + + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 HGTGFDGL-----KQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMMNR 124

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
      +++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G+
Sbjct: 125 VMLPLQMGAKMHGKDGSEFAPITINGKQTLKRMZYHMPVA-SAQVKSIIFAALQAEGE 183

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
      I +K + T ++ +FG + E D R +KGGQK+ + + V GD SS
Sbjct: 184 TIIHEKEK-----TRDHTHEMIRQFGGEIEMDDLIR--VKGGQKF-TGQEMTVPGDVSS 235

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
      A++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 236 AAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGLLVKDDSSRS-TGKLAGTV 292

Query: 316 GRK--HLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRTE 370
      K LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TE
Sbjct: 293 VVKTSKLGTEIDGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELVKETNRIDAVATE 352

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
      L K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 353 LNKMGADITPTEDGLIHHGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERPEAV 412

Query: 429 RKTFPDYFDVLSTFVK 444
      ++P +F+ + + +K
Sbjct: 413 SVSYPTFFEDIRSLK 428

```

>ref|ZP_07462927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis ATCC 6249]
gb|EFM31180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis

ATCC 6249]
Length = 427

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 122/443 (27%), Positives = 215/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMDGLKAPQNA-----LDMNGSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RMDRVTIPLKKMGVSISGQTERDLPPLHLKGTKNLKPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG + S + ++G QK K V
Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GQLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA++L AG + V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLIVPDSRVELKNVGINETRTGI--LDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK +++ +P + L ++AL A +G T I+D +VKET+
Sbjct: 289 TLTVESSE-----LKGEISGALIPRLIDELPIIALLATQAEGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGAETIPTADGMIKGSLLHGAVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L +
Sbjct: 403 ELDRAEAINTSYSPFFDDLENLI 425

>ref|ZP_06966618.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ktedonobacter
racemifer DSM 44963]
gb|EFH89729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ktedonobacter
racemifer DSM 44963]
Length = 450

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 132/447 (29%), Positives = 211/447 (47%), Gaps = 30/447 (6%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I ++ I G +LP SK + R +L AAL++GT++V S+D + R LG
Sbjct: 16 IAIEEASRIQKPELPSSKYFTLRYVLAALAKGTSMVYYPAQSDDEALFRGCALGAQ 75

Query: 67 ---VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+A++ R VG +P A + V L +GNAG +R L + A T+V
Sbjct: 76 LDWVDAEETILRVQGVG---YP--QAADAVTLNVGNAGAVLR-LLLGLGACLSEITFVT 128

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
D + +RP +L+ L LGA C P+ + G L GKV++SG+ SSQY+
Sbjct: 129 DHPQSLGKRPNRELLEALSTLGATYQAEGAEGCLPITLRG-SALHGKVRISGARSSQYI 187

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL APL +EIEIID L S P+V TL+++ G++ EHS + G Q+Y+
Sbjct: 188 SALLFLAPLLPEGLEIEIIDGLKSQPFVRSTLQVLHEAGIQFEHSADLSHLSVPGKQQYQ 247

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL----EMMGAKVT 299
+ + + GD SA+ ++ A I+ E GD + + L + MGA++
Sbjct: 248 A-REYILPGDYPSAAALIS-ACISATDPASELVNLRLKPGD-EIGDALLVAYQAMGAQLD 304

Query: 300 WTETSVTVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
VTV G L+ + V+ +++ D L A FA G + ++ + K
Sbjct: 305 IAGEQVTVRGGTT-----LQGVVRVDGRIIDCIPVLVAAACFAQGESVFYNIETLHYK 357

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAA--C 415
E++R+ + EL + G V D I+ P +D ++DHR+ MA ++ C
Sbjct: 358 ESDRIDLCAELRRAGCDVTPQRDAIIVRGRPQGIEGGVTVGDHNDHRLLMALAIVGMRC 417

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ + K++P +F L
Sbjct: 418 RH-GLALTGSEHIAKSYPHFFAQLKEL 443

>ref|ZP_05297675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-003]
Length = 428

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 120/435 (27%), Positives = 214/435 (49%), Gaps = 25/435 (5%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G G D L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTGFGGLKQADGP---LDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMPN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI-FDVVKQMGGSLLVVKDSSRSTGKLAGTVV 293

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLKGTEIDGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAADITPTEDGLIIHGKTPHAAANVTSGDHRIGMMLQIAALLVEEGDVLELERPEAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTFFEDIRSLK 428

>ref|YP_002771962.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevibacillus brevis
NBRC 100599]
sp|C0ZCE9.1|AROABREB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAH43458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevibacillus brevis
NBRC 100599]
Length = 426

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 212/439 (48%), Gaps = 29/439 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q K+I GTV++PG KS+S+R ++ AL+EGTT ++ L D + R +G+ +E
Sbjct: 4 VQQAQKQIKGTVRVPDGKSIHRAVMFGALAEGTTTIEGFLPGADCLSTISCFRRMGIEIE 63

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
AV V G + +++ + L +GN+G +R L A + A V++G
Sbjct: 64 QQG---DAVTVQKGWYGLQEPSQ--HLDVGNSGTTIR-LMAGIMATQ-PFHVVMEGDES 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

```

      + +RP+  ++  L+Q+GA +D      +  P+  + G  G  G  S  S+Q  SA+++
Sbjct: 117 IAKRPMRRVIGPLRQMGAKIDGRKDGEYTPLSIRG--GKLQGIAYQSPVASAQVKSAILM 174

Query: 189 AAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      A  A G  +      + P++  + T R+++ FGV+      ++GGQK K  +
Sbjct: 175 AGLQAKGVTSV-----TEPHLSRDHTERMQLQAFGVQVVRDGLT--VSVEGGQKLKG-R 224

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      V GD SSA++ +A  + G ++ +E G  +  +  +V++ MG  +      +
Sbjct: 225 AISVPGDISSAAFLIAAVMVVPGSSLLIENVGINPSRTGI--IDVVKAMGGSLELLNERI 282

Query: 306 TVTGPPPREPF-GRKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
      P  +      L  I++  + +P  D  +AV+A  A G T  IRD  +VKET
Sbjct: 283 VNEEPVADLLVTHSELHGIEIAGDIIPRLIDEIPVIAVMATQAKGQTVIRDAEELVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPV 420
      +R+  + ++L+K GA V  D  II  L  ID+  DHR+ MA ++A  AE
Sbjct: 343 DRIATVVSQLSKFGAKVTPDDGMIIGGKTGLTGAIIDSMGDHRIGMAMAIAGLIAEGET 402

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
      I  +      +FP  + D+L
Sbjct: 403 KIENDEAIDVSFPGFHDL 421

```

>gb|EGD37927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sanguinis SK160]
Length = 427

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 121/439 (27%), Positives = 217/439 (49%), Gaps = 35/439 (7%)

```

Query: 12  IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
      ++  + G +++PG KS+S+R ++  +L++G T V ++L  EDV  +  R LG+ +E D
Sbjct: 7   VRGLKGRIKRVPGDKSISHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72  AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      +  VG G  ++      +L +GN+G ++R ++  +  AG  +      + G  +  +
Sbjct: 67  NLVKIHGVGFELQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAEFMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
      RP+  +  + L+Q+G  +      D PP+++ G  L  +L  + S+Q  SAL+ AA
Sbjct: 120 RPYMDRVTIPLRQMGVKIAGRTERDLPPLKMGSKELQPIHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G  E  II+K I+  + E      ++ +FG  + E      R  I+GGQ++  +  +  V
Sbjct: 179 QAQG--ESVIEKEITRNHTE---DMIAQFGGQIEVKGEIR--IQGGQEF-TAQEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
      GD SSA+++L AG  +      + +E G  +  +  EV+E MG ++T ++      S
Sbjct: 231 GDISSAAFVLVAGLIVPDSKIILENVGINETRTGI--LEVIEAMGGRMTLSIDIDPAKSA 288

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
      T+T  E      LK  ++  +P  +  L  ++AL A  G T  IRD  +VKET+
Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIALLATQAQGRTVIRDAEELVKKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
      R+  +  L  +GA++  D  II  L+  ++T  DHR+ M  ++AA  V
Sbjct: 343 RIQVVADALNSMGAAIAPTEDGMIIEGKTTLHSAQVNTLGDHRIGMMTAIAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
      +      +  ++P  +F  L
Sbjct: 403 ELERSEAIKTSYPSFFSDL 421

```

>ref|ZP_06697675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium El679]
gb|EFF26946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium El679]
Length = 431

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.

Identities = 131/441 (29%), Positives = 213/441 (48%), Gaps = 24/441 (5%)

```
Query: 8  VLQPIKEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3  LLQQIHGLRGTVRIPADKSISHRSIMFGAIAEGTTTQNFRLAEDCLSTLHAFQQLGVEI 62

Query: 68  EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + + +GN+G +R L + AG L G
Sbjct: 63  EEEEEMIK--IHGRGSHSFVQPTES---IDMGNSGTTIRLLMGIL--AGQPFMTTLFGDA 115

Query: 128  RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 116  SLSKRPMPGRVMEPLREMGADLQKGENEQYLPITVTGTNSLSPIRYNMPVA-SAQVKSALL 174

Query: 188  MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + S + G QK + +
Sbjct: 175  FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRI--SVEGKTITVTGPQKL-TGQQ 226

Query: 248  AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227  ITVPGDISAAFFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNHNEQ 284

Query: 307  VTGPPREPFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285  NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344  IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423  RDPGCTRKTFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404  EGAEAVSISYPAFFDDLAELV 424
```

```
>ref|ZP_05658100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,230,933]
gb|EEV41433.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
1,230,933]
Length = 431
```

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 213/441 (48%), Gaps = 24/441 (5%)

```
Query: 8  VLQPIKEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3  LLQQIHGLRGTVRIPADKSISHRSIMFGAIAEGTTTQNFRLAEDCLSTLHAFQQLGVEI 62

Query: 68  EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + + +GN+G +R L + AG T L G
Sbjct: 63  EEEEEVIK--IHGRGSHSFVQPTES---IDMGNSGTTIRLLMGIL--AGQPFMTTLFGDA 115

Query: 128  RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++AD+ P+ V G L + + + S+Q SALL
Sbjct: 116  SLSKRPMPGRVMEPLREMSADLQGEENDQYLPITVTGTSLSPIRYNMPVA-SAQVKSALL 174

Query: 188  MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK + +
Sbjct: 175  FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IIVTGPQKL-TGQQ 226

Query: 248  AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227  ITVPGDISAAFFLAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNHNEQ 284

Query: 307  VTGPPREPFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I+D +VKET R
Sbjct: 285  NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGITIIKDAEELKVKETNR 343

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344  IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403
```

Query: 423 RDPGCTRKTFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAELV 424

>ref|YP_001704276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
abscessus ATCC 19977]
emb|CAM63622.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
abscessus]
Length = 431

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 136/429 (31%), Positives = 206/429 (48%), Gaps = 33/429 (7%)

Query: 14 EISGTVKLPGSKSLNRILLALLAALSE---GTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
I T+ +PGSKS +NR L+LAAL+ GT+ V L S D M+ ALR+LG + D
Sbjct: 14 SICATITMPGSKSQTNRALVLAALAAREGGTSTVSGALRSRDTLMIRALRSLGFDIIGD 73

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G G +D V L AG +R L AA +A V DG + R
Sbjct: 74 -GTDLTVSPGAG-----DDASTVDCGL--AGTVLRFLPP--VAALRHAPTVPFDGDEQAR 123

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA- 189
RPI L+ L+ G +D P V G G + GG+V + S SSQ++S LL++
Sbjct: 124 ARPIAPLLDALRSTGVGIDG----QHLPTFTVTGTGQVQGGVEGVVDASGSSQFVSGLLLSG 179

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A + G + D L S P+V MT+ ++ G+ + S R+ I P + +
Sbjct: 180 AAFSAGLTAMNTADVLPSPGPHVMTVTMLREAGIAVDDSV--GRWRID---PQPIPAHQW 235

Query: 250 V-EGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V E D S+A F+A A TGGTV + G S Q + +V+ V+ T+T + VT
Sbjct: 236 VIEPDLNALAFIAPALATGGTVRITGWPRQSTQPARQIEDVVRQFAQTVSLTDTHLEVT 295

Query: 309 GPPREPFGKRHLKAIDVNMNMPDVMATLAVVALFADGP--TAIRDVASWRVKETERMVA 366
G+ +D+++++ ++ T+A ++ A+ + +R +A R ET+R+ A
Sbjct: 296 -----GQSGYGGVDLDLSEVGELTPTVAALSALAESGAVSTLRGIAHLRGHETDRLKA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
+ E+ LG EE D I + L +Y DHRMA A +L V++ D
Sbjct: 349 LAHEINALGGRCEETQDGLRIVATD-LRGGVWGSYADHRMATAGALVGLKVPGVSVDDIA 407

Query: 427 CTRKTFPDY 435
T KT PD+
Sbjct: 408 TTSKTLPDF 416

>ref|ZP_06068698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter lwoffii
SH145]
gb|EEY90849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter lwoffii
SH145]
Length = 748

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 133/456 (29%), Positives = 216/456 (47%), Gaps = 42/456 (9%)

Query: 5 EEIVLQP-IKEISGTVKLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
++ +QP K+ G +PG KS+S+R ++ A++EGTT V L ED L A R +
Sbjct: 305 QQFTIQPGAKKFQGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDM 364

Query: 64 GLSVEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
G+S+E K + + VG G K P + +++GN+G +MR L+ + A ++
Sbjct: 365 GVSIEGPKNGEVTIHGVMQGLKAP-----QSAIYMGNSGTSMLLSGMLAAQKFDS-- 416

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
V+ G + +RP+ + L+++GA + PPV + G L G + L + S+Q
Sbjct: 417 VMTGDASLSKRPMERIAKPLREMGAIQTTGERGTPPV SITGNQNLKGIQYDLPMA-SAQ 475

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGG 239
S +L+A A G+ + + P + T R++ FG VK E +R ++GG

Sbjct: 476 VKSGILLAGLWAEGETSVTEPE-----PTRDHTERMLRAFGYEVKTE----GNRISLQGG 526

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
K N V D SSA++F+ GAAIT + VT+E G + V E+L+ MGA +

Sbjct: 527 GKLVG-TNIQVPSDISAAFFMVGAATENSVDVLEAVGINPRTGTG--VEILKQMGADI 583

Query: 299 TWTETSVTVTGPPREP---GRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRD 352
T E G P G + LK I + +++P D L + A A+G T +

Sbjct: 584 T-VENERIAGGEPIADIRIRGTRTLKGIHMPEDQVPLAIDFPAALFIAAACAEGQTILTG 642

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHR 405
A RVKE++R+ + L +G D II K I+++ DHR

Sbjct: 643 AAELRVKESDRIQVMADGLQTMGIDCTPTDDGIIIEGKGKSGDWSPIFTGGEIESHHDHR 702

Query: 406 MAMAFSLAACAEV-PVTIRDPGCTRKTFPDYFDVLS 440
+AM+FS+A + I +FP + ++ S

Sbjct: 703 IAMSFSIAGLRNSEQIKIVGTETVATSFPTFTELTS 738

>ref|YP_001654695.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
434/Bu]

ref|YP_001653707.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
L2b/UCH-1/proctitis]

ref|ZP_07224087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
L2tet1]

sp|B0B7T5.1|AROA_CHLT2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

sp|B0BC00.1|AROA_CHLTB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

emb|CAP04061.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
434/Bu]

emb|CAP07015.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
L2b/UCH-1/proctitis]
Length = 440

Score = 139 bits (350), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 121/433 (27%), Positives = 196/433 (45%), Gaps = 29/433 (6%)

Query: 17 GTVKLPKSKSLNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS S R +L A+LS+GT++++N L S D ML A +G V +

Sbjct: 17 GEIAVPPSKSHSLRAILFASLSKGTSIENCLFSPDSQTMLTACEKMGAVHR--RIGDSL 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA T + ++ G ++ RPI

Sbjct: 75 HIQGN----PDPHCHPPYFHMGNISGIALRFLTALSTLSP--TPTLTIGSHTLKRRPIAP 128

Query: 137 LVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ LKQLGA + + P G L G V +SG SQY SAL + A LA

Sbjct: 129 LLSSLKQLGAHRIQKTSSSIP---FTIHGPLSPGHVTISGQ-DSQYASALAITAALAPYP 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + D GGQ +S + V GD SS

Sbjct: 185 LSFS-IENLKERPFDFLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPREP 314
A++ + ++ + + + QGD +L+ +GA + + + + P

Sbjct: 241 AAFLASFGLSSSSKPTILRNLPQSQGDKLLFSLKQLGAHILIEKHHIEMH--PSS- 297

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+++M+ D LAV+ FA P+ + + + KE+ R+ AI EL K+

Sbjct: 298 -----FSGGEIDMPDFDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEIAIAHELQKM 352

Query: 375 GASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTF 432
G SV D I P +L+ +D+++DHR+AMA ++A + + C K+F

Sbjct: 353 GGSVHPTRDGLYIE-PSRLHGAVVDSDHNDHRIAMALAVAGVHASSGQTLNCNTQCINKSF 411

Query: 433 PDYFDVLSTFVKN 445
P + T N

Sbjct: 412 PHFVIAAQTLHAN 424

>ref|YP_139166.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
thermophilus LMG 18311]
sp|Q5M551.1|AROASTRT2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAV60351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
thermophilus LMG 18311]
Length = 427

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 120/434 (27%), Positives = 218/434 (50%), Gaps = 37/434 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+++PG KS+S+R ++ +L+G T V ++L EDV + R LG+++E D
Sbjct: 10 LRGLSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVTIEDDGDVV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G K P + +L +GN+G ++R ++ + AG + + G + +RP
Sbjct: 70 RIHGVGFGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFDVMFGLDGLSKRP 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L+Q+G +V D PP+++G L +L + S+Q SAL+ AA A
Sbjct: 122 MDRVTTIPLRQMGEVSGQTDRLPLPKMHGSKSLKPIHYELPVA-SAQVKSALIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E II+K + + E ++++FG + + R I GGQ + + + V GD
Sbjct: 181 --DGESVIEIEKTRNHT---DMIQQFGGQLQVEGKEIR--ISGGQTF-TAQEVVVPGD 232

Query: 254 ASSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++L AG + + + G + V +V++ MG K+ ++ S T+
Sbjct: 233 ISSAAFWLVLVAGLVVPSKIVLKNVGINETRTGV--IDVIKDMGGKIKLSDIDQVAKSATI 290

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
T E LK ++ + +P + L ++ L A G T IRD +VKET+R+
Sbjct: 291 TVETSE-----LKGTEIGGDIIPRLIDELPIITLLATQAQKTVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +
Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTPHGAEVNTFGDHRIGMMTAIAALLVQDGEVDL 404

Query: 423 RDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 405 QRAEAINTSYPSFF 418

>ref|NP_622666.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
tengcongensis MB4]
sp|Q8RB11.1|AROATHTN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM24270.1| 5-enolpyruvylshikimate-3-phosphate synthase [Thermoanaerobacter
tengcongensis MB4]
Length = 423

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 124/434 (28%), Positives = 219/434 (50%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R +++ +EG T V+N L ++D + +R LG+ ++ ++
Sbjct: 11 LKGVISVPGDKSISHRAVMIGSIAEGLTEVENFLVAKDTLSTVECMRKLGVDIKLER--N 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V G G +K L +GN+G +R L + AG +L G ++ RP+
Sbjct: 69 RVKVYVGKGLYL---SKSSEVLVDGNSGTTIRLLMGIL--AGQEFETILTGDSDIKRRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G ++V L +GA ++ G + PV++ G G L G + K+ + S+Q S++++A+ A
Sbjct: 123 GRVIVPLTLMGAKIEAREG-NFAPVKIRG-GKLRGIEYKMPIA-SAQVKSSIMLASLYAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G IE + +S + E+ +++ FG + E + + G K K K V GD
Sbjct: 180 GRTVIE--EPALSRNHTL---MLQTFGARIEIDGK--KIFCYPGSKLKGQK-IIVPGDI 231

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPR 312
SSA+YF+ A + V ++ + + +VL+ MG V E V
Sbjct: 232 SSAAYFIVAANLLPNSSEVVIKDVNVNPTRTGI--IDVLKGMGGNVELINERYVNNEKIAD 289

Query: 313 EPFGRKHLKVIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
LK I++ + +P D +AV A+FA+G T I++ +VKE+ R+ ++ +
Sbjct: 290 IIVKSSKLKGIEIGDLIPKLIDEIPVIAAFAEGTTVIKNAEELKVKESNRIKSMTS 349

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCT 428
EL K+GA + E D II L +++Y+DHR+AM+ +A AE I+ C
Sbjct: 350 ELGKMGAIFETEDGMIIEGTGFLRGAEVESYNDHRVAMSLWIAGLLAEGRTIikkaecv 409

Query: 429 RKTFFPDY---FDVL 439
++PD+ FD+L
Sbjct: 410 DVSYPDFYKTFDML 423

>ref|ZP_02425601.1| hypothetical protein ALIPUT_01748 [Alistipes putredinis DSM 17216]
gb|EDS02229.1| hypothetical protein ALIPUT_01748 [Alistipes putredinis DSM 17216]
Length = 658

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 134/456 (29%), Positives = 218/456 (47%), Gaps = 48/456 (10%)

Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV +P SKS++ R +L AAL+ G + + N D+ + +R +G + +D
Sbjct: 215 TVAVPCSKSVAQRAVLAAALAGESRLANYAPCNDIVGAVEVIRGMGCRIASDGTTLH-- 272

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT---AAVTAAGGNATYVLDGVPRMRERPI 134
+ G G + +K E G +G+ R LT + ++A G A + G + +R +
Sbjct: 273 IEGVGAERLGRCSKIET---GESGLLTRLLTPLASHISALNGGAPVEISGHGSILKRN 328

Query: 135 GDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ V L++ G V C + P R+ G G+ ++ SG SSQ +S LM PL
Sbjct: 329 HEAVAALREAG--VHCSAREEGYLPFRIEG--GITREIAFSGRESSQTVSGFLMTLPL- 383

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-----FYIKGG 239
L D + + + SIPY+E+TLR + RFG++ + +D F + GG
Sbjct: 384 LQDATVLTVTEPSSIPYLELTLRTLFRGIRLDREAFYDGGCGGRKPGTSPKIVFSVPGG 443

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTT-----SLQGDVKFAEVLEMM 294
Q+Y+ P + +++ D SSA+YF A+ +EG SLQ D K ++L
Sbjct: 444 QEYR-PSDLFLDADWSSAAYFAVAGAVASSLGRIEGITLRNMRDLSLQADEKILDILRSC 502

Query: 295 GAKVTWTETSVTVTG-PR------PFGRKHLKVIDVNMNMKMPDVAMTLAVVALFADG 346
GA V+ V+V G P + GR+ LKA +V+ PD+ LAV+A DG
Sbjct: 503 GADVSVAPADVSRGDMPGDLQNISVTATGRR-LKAFEVDPATHCPDLFPILAVLAACD 561

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTIAIDTYDDHR 405
+ I V KE+ R I E LGA ++ +G + + P L+ + +++DHR
Sbjct: 562 TSRIAGVGRLTQKESNRAETIYAEFRTLGARIDIQGD EFMVTGGP--LHGGDVRSNDHR 619

Query: 406 MAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLS 440
+AM+ +A PV + D C K+FP + D+L+
Sbjct: 620 IAMSLIVAGLFTPEPVRLLDDVKCIDKSFPSFLDLA 655

>ref|ZP_06198713.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
M143]
gb|EFA24327.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
M143]
Length = 427

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 120/438 (27%), Positives = 211/438 (48%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71

Sbjct: 7 I+ + G +++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
IRHLHGNIRVPDGKSIHSRISIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +

Sbjct: 67 GVITIQGVGMDGLKAPQNA-----LDMGNSGTSIRLISGLV--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA

Sbjct: 120 RMDRVTLPLKKMGVSIAGQTERDLPLRLKGTKNLTPIHYELPIA-SAQVKSALMFAAI 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V

Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + V ++ G + + +V+ MG K+ TE +V

Sbjct: 231 GDISSAAFVWVAGLIVPDSRVVLQNVGINETRTGI--IDVIRAMGGKLEVTEID-SVAKS 287

Query: 311 PREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK +++ +P + L +++L A G T I+D +VKET+R+ +

Sbjct: 288 ATLTVESSDLKGEIDGALIPRLIDELPIIISLLATQAHGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGSVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II +L+ ++T+ DHR+ M S+AA + V +

Sbjct: 348 ADALNSMGADITPTADGMIKGSRLHGAVNTFGDHRIGMMSIAALLVKDGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L T +

Sbjct: 408 EAINTSYPSFFDDLETLI 425

>ref|ZP_06598775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oribacterium sp. oral
taxon 078 str. F0262]
gb|EFE91703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oribacterium sp. oral
taxon 078 str. F0262]
Length = 443

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 132/440 (30%), Positives = 218/440 (49%), Gaps = 29/440 (6%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G + +PG KS+S+R L+L+AL+EG T + L D + LR +G+S+E+ +

Sbjct: 10 RALRGELTVPGDKSISHRALMLSALTEGETRIRGFLYGADCISTIRCLREMGVSIESREG 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
++ G A E + L GN+G MR L+ ++A ++ VL G +R R

Sbjct: 70 ESGPELLLRGVLRLGLRAPERI-LDCGNSGTTMRLLSGLLSAQRFDS--VLSGDESIRRR 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G ++ L ++GAD+ G P+ ++G L G + S S+Q SA+L+A

Sbjct: 127 PMGRVIRPLTEMGADIFSERGDGRAPLHIHG-RALRGISYE-SPLASAQVKSAILLAGLY 184

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKS-PKNA 248
A G E +I+ +S + E R++ GV E +D ++ ++ S P

Sbjct: 185 AEG--ESRVIEPGLSRDHSE---RMLRSLGVPIESRTLFDGRTEIRLRPVERLASFPNPL 239

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
++ GD SSA+YFL A I G + + GT + + EV MG ++ +E + +

Sbjct: 240 FIPGDISSAAYFLTAALIVPGSELLRNVTGTPNPTDGI--LEVYRSMGGDIS-SERNRII 296

Query: 308 TGPPREPFGKRH--LKAIDVNMNKMPPDVAMTLAVV---ALFADGPTAIRDVASWRVKETE 362
G +H L ++ +P + L V+ A A+G T I+D A R KE++

Sbjct: 297 AGEVSDLRVRHSLHGTITISGALIPRLIDELPVIAAAAAAEGETLIKDAADLRQKESD 356

Query: 363 RMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVT--TAIDTYDDHRMAMAFSLAACAEVP 419
R+ A+ L LG SVEE D I+ EKL++ ID+ DHR+AM+F++ E P

Sbjct: 357 RISAVAEGLRALGVSVVEEREDGMRIILQGEKLSLREAEIDSRGDHRIAMSFVAVLGLLEEP 416

Query: 420 ---VTIRDPGCTRKTFPDYF 436
+ I C R ++PD+F

Sbjct: 417 GSFLRIHGSDCIRISYPDF 436

>ref|ZP_04156369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock3-17]
gb|EEM11961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock3-17]
Length = 464

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 123/438 (28%), Positives = 214/438 (48%), Gaps = 33/438 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EGTT + N L ED + R LG+ +E D
Sbjct: 50 LNGTIAVPGDKSISHRAVMFGAIAEGTTKISNFFLLGEDCLSTIACFRKLGIMIEEDG--- 106
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+V G +++ KE L +GN+G +R + + A + T + D + +RP+
Sbjct: 107 NDVIVYGKGLAGLQEPKE--VLDVGNSGTTIRLMLGILANAPFHCTIIGD--ESIGKRPM 162
Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+++ A ++ P+ + G G + G S S+Q SA+L+A
Sbjct: 163 KRVTAPLREMDAQIEGREDDGQYTPLSIRG-GNIKGIHYH-SPVASAQVKSAILLAG--LQ 218
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ + + L S + E R++ FG E + ++GGQ + V GD
Sbjct: 219 GEGVTSVTEPLQSRDHTE--RMLRAFG--CEVNVEGRVTVSLQGGQSLVGTE-IEVPGDV 272
Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLOGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++FL AGA + + ++ G + + +VL MGA ++ V E
Sbjct: 273 SSAAFFLVAGAIVPNSKLVLKNVGLNPTRTGI--LDVLSEMGALISIR----NVRNEEFE 326
Query: 314 PFG----RKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMV 365
P G LK I++ + +P + + ++AL A G T I+D +VKET R+
Sbjct: 327 PCGDITITETSELKGIEIGGSLIPRLIDEIPIIALLATQATGTTIKDAEELKVKETNRIN 386
Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIRD 424
+ EL KLGA +E PD II +KL +++++ DHR+ M ++A+C AE + I +
Sbjct: 387 TVVDELRLKLGAEIATPDGMIINGNQKLQGNIVNSHGDHRIGMMLAIASCIAEGEMQIEN 446
Query: 425 PGCTRKTFFPDYFDVLSTF 442
++P++F+ L +
Sbjct: 447 GDAVAVSYPNPFQLESL 464

>ref|ZP_07319485.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium vaginae
PB189-T1-4]
gb|EFL44361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium vaginae
PB189-T1-4]
Length = 447

Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 136/461 (29%), Positives = 209/461 (45%), Gaps = 58/461 (12%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++++P ++SGT++ SKS+++RIL+LAALS+G VD S+D+ + L LG
Sbjct: 2 NVIIIEP-HQLSGTIRAISKSMAHRILILAALS+GIVDVDCITTSQDIDTTVSCLEALGA 60
Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAV 112
+ K R + G ++ KE + L +G R + A
Sbjct: 61 RITKTKRGWR--IRGIRSQYS-SAPKEAISADNTPARLEDMPILNCKESGSTFRFMVAVC 117
Query: 113 TAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP---- 168
A GG+ +V G R+ +RP+ L L G + ++ G P
Sbjct: 118 AALGGSFCFV--GAKRLAQRPLEPLYSLLSNAG-----ITLSEQEFPFPTLT 162
Query: 169 ----GGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK 224
KL G++SSQY+S LL+AA A I + S YV MT++ + FGV+
Sbjct: 163 GALTATTFKLGKGNVSSQYISGLLLAACAAQAFTIVVEAPFESQDYVSMITQALSIFYGVQ 222
Query: 225 AE-----HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278

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      E      SD W  F + G Q      +   VE D S+AS++LA  A+ G  V VEG
Sbjct: 223 VEVTKPENTSDPWI-FAVNGTQMRCPLQPVVVEADWSNASFWLAAGAM-GHNVVRVEGLNL 280

Query: 279 TSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLA 338
      SLQGD +   L   GA V   E +V V           K ++   + +N + D+A  LA
Sbjct: 281 ASLQGDRRILSCLMNFGAHVEQQEHAVEVHA-----KLMRGCTLELNDIIDLAPPLA 332

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTA 397
      A FA G T +       ++KE+ R+VAI  L+ LGA +   D  I   +LN
Sbjct: 333 ATACFAWGNTTTLTGAHRLQLKESNRIVAITRALSALGADITADDDAIYIHGRRLNGAGT 392

Query: 398 IDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFFPDYFD 437
      +   +DHR+AM ++ A +   T+   C  K++P +F+
Sbjct: 393 VSCANDHRIAMMAAICAAGSSRSCTLIGAECVAKSYPSFFE 433

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>ref|ZP_06727521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
      haemolyticus ATCC 19194]
gb|EFF82783.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
      haemolyticus ATCC 19194]
Length = 749

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Score = 139 bits (349), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 133/448 (29%), Positives = 211/448 (47%), Gaps = 41/448 (9%)

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Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K +G   +PG KS+S+R ++  A++EGTT V   L  ED   L A R +G+S+E  K
Sbjct: 314 KTFTGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGTFLEGEDALATLQAFRDMGVSIIEGPKN 73

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
      +   +   VG  G K P           L++GN+G +MR L+  ++A  ++  V+ G   +
Sbjct: 374 GEVTIHHGVGMHGLKVPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      +RP+ +   L+++GA +           PPV + G   L G +   L + S+Q  S +L+A
Sbjct: 426 KRPMERIAKPLREMGAIQITTEGKGTTPPVSTIGSQALKGIQYDLPMA-SAQVKSIGILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
      A G   +   +   P + T R++  FG  VK E   ++   + GG K   N
Sbjct: 485 LWAEGVTSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTV 307
      V  D SSA++F+  GAAIT G  V +E  G   +  V   E+L+ MGA +T  E
Sbjct: 535 QVPSDISSAAFFMVGAAITEGADVLEAVGINPRTGTG--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPFG--GRKHLKAIDVNMNMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
      G P           G + LK I +   +++P  D   L + A  A+G T +   A  RVKE+
Sbjct: 592 GGEPIADIIHKSRTLKGIHMPEDQVPLAIDEFPALFIAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
      +R+ +   L +G   D  II  K           N  I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTDDGIIIEGKGKSGDWSAIFNGGEIESHHDHRIAMSFSIAG 711

Query: 415 CAEV-PVTIRDPGCTRKTFFPDYFDVLST 441
      +TI           +FP + ++ +T
Sbjct: 712 LRTAGAITIHGTETVATSFPTFTELANT 739

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>ref|ZP_08049983.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
      C300]
gb|EFX56773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
      C300]
Length = 427

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Score = 138 bits (348), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 121/443 (27%), Positives = 215/443 (48%), Gaps = 35/443 (7%)

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Query: 12 IKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
      I+ + G++++PG KS+S+R ++  +L+EG T V ++L  EDV   +   R LG+ +E
Sbjct: 7  IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

```

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQGVGMGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLTK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVITPLKKMGVSISGQTERDLPPLHLKGTKKLTPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V
Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLIGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + +V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISAFAFWLAVGLIPNSSVVLQNVGINETRTGI--IDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGGPPREPFGKRHLKAIDVNMNKMPPVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGETVIKDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II +L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVTDALNSMGADITPTADGMIKGSRLHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYSPFFDDLES LI 425

>ref|ZP_06674770.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1039]
gb|EFF31861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1039]
Length = 431

Score = 138 bits (348), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 211/441 (47%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSISHRSIMFGAIAEGTTTTIQNFLRAEDCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + +GN+G R L + AG T L G
Sbjct: 63 EEEEEVIK--IHGRGSHSFVQPT---APIDMGNSGTTSRLLMGIL--AGQPFTTTLVGDA 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMGRVMEPLREMGADLQGNENDQYLPITVTGTSLSTIRYNMPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK + +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IMVTGPQKL-TGQQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FLA G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAFAFLAAGLLVPESQLLLKNVGVNPNTRTGI--LDVLEEMGAAITQTNHNEH 284

Query: 307 VTGPPREPFGKRHLKAIDVNMNKMPPVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGVTIIEDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAELV 424

>ref|ZP_07547402.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
wiegelii Rt8.B1]
gb|EFN49351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
wiegelii Rt8.B1]
Length = 423

Score = 138 bits (348), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 124/443 (27%), Positives = 214/443 (48%), Gaps = 30/443 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I ++ + + G + +PG KS+S+R +++ ++EG T ++N L ED + ++ LG+
Sbjct: 2 DIEVKKRFLKGIISVPGDKSISHRAVMIGSIAEGITEIENFLLGEDCISTINCMKNLGV 61

Query: 66 SVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + + V GK + E++ L +GN+G +R L + AG L G
Sbjct: 62 DIEL-----KGTNVKHGKGLYLKSEKI-LDVGNSTTIRLLMGIL--AGQKFETTLTG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ RP+G ++ L +GA ++ G + P+ V G L G K+ + S+Q S+
Sbjct: 114 DDSIKRRPMGRVITPLSMMGAKIEAREG-NFAPLTVFG-NKLKGIYYKMPIA-SAQVKSS 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSP 245
+++A+ A IE P T + FG K E + + Y G K +
Sbjct: 171 IMLASLYADDKTIEE-----PYPSRNHTELMFSSFGAKVEVTGKITCY--PGYKLQGG 223

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K V GD SSA+YF+ A I VT++ + + +V++ MG V T
Sbjct: 224 K-IVVPGDISAAYFIVAATIVPNSEVTIQDVNVNHTRTGI--IDVIKEMGGNVVLTNER 280

Query: 305 VVTGTGPPRE-PFGRKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V + LK I++ + +P D +AV A+F++G T I+D +VKE
Sbjct: 281 VVNNEKVADITIKTSRLKGIEIGGSLIPRLIDEIPVIAVAADFSEKTVIKDAEELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
+ R+ I +EL K+GA + E D II L +++Y+DHR+AM+ +A AE
Sbjct: 341 SNRINTITSELKMKGAKIFETEDGMIIEGTGFLKGNVTESYNDHRIAMSLWVAGLMAEGE 400

Query: 420 VTIRDPGCTRKTFPDY---FDVL 439
I++ C ++PD+ FD+L
Sbjct: 401 TKIKNAECVNISYPDFYKTFDML 423

>ref|ZP_06341249.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bulleidia extructa
W1219]
gb|EFC06101.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bulleidia extructa
W1219]
Length = 405

Score = 138 bits (348), Expect = 1e-30, Method: Compositional matrix adjust.
Identities = 115/422 (27%), Positives = 196/422 (46%), Gaps = 42/422 (9%)

Query: 18 TVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
++K+P SKS +R L+ A+LS+ + + NL N++D+ + L+ LG+S + +
Sbjct: 15 SLKMPTSKSYGHRSLIAASLSKEVSTIQNLNPNQDIQTTMACLKKLGVSFQEGSQTTI- 73

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+P + V L +G +R L V G+ G R+ ERP
Sbjct: 74 -----YPKWKIQNSVVLDCHESGSTLRFLIPLVLI--GDRIVKFQGTKRLLERP---- 120

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
+ L + + F + V G + G + G+ISSQ+++ LL+A PL GD
Sbjct: 121 QTIYEFLAREKEFFFEKTAHSIFVKG--PIQAGHFVVDGTISSQFITGLLLALPLLKGD 178

Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+EI +L+S YVE+TL ++ G++ E ++ F I G Q Y++ K VEGD SSA
Sbjct: 179 TLEIQGLVSKDYVEITLDVLCLAGIRIERTNHL--FMIPGNQHYQAFKYE-VEGDYSSA 235

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPEPFGR 317
++ A A + ++E + S Q D K LE +
Sbjct: 236 AFLYALAFHLRKELSIENLNSFSKQADFKILAFLEQV----- 272

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
K+ KA ++ PD+ L V+ +G + ++ R KE++R+ A+R EL KLG
Sbjct: 273 KNRKASSFDLEGCPDLGFILMAVSSQLEGTSHFVNIKRLRFKESDRIEAMREELKKLGIE 332

Query: 378 VEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFD 437
++ G + IT + + + DHR+ MA S+ A I +K++P++F+
Sbjct: 333 MKVGENEAFITGGKLRPNQILSGHHDHRIVMALSVLATLTKNTVIEGANAIQKSYPNFFE 392

Query: 438 VL 439
L
Sbjct: 393 DL 394

>ref|ZP_05380739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
70]
ref|ZP_05381662.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
70s]
Length = 440

Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 119/423 (28%), Positives = 194/423 (45%), Gaps = 29/423 (6%)

Query: 17 GTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS S R +L A+LS+GT++++N L S D ML A +G V +
Sbjct: 17 GEIAVPPSKSHSLRAILFASLSKGTSIENCLFSPDSQAMLTACEKMGAVR--RIGDSL 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA T + ++ G ++ RPI
Sbjct: 75 HIQGN----PDPHHCHPRYFHMGNISGIALRFLTALSTLSP--TPTLITGSHTLKRRPIAP 128

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ LKQLGA + + P G L G V +SG SQY SAL + A LA
Sbjct: 129 LLSSLKQLGAHIRQKTSSSIP---FTIHGPLSPGHVTISGQ-DSQYASALAITAALAPYP 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + D GGQ +S + V GD SS
Sbjct: 185 LSFS-IENLKERPWFDLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A++ + ++ + + QGD ++L+ +GA + + + + P
Sbjct: 241 AAFLASFGLSSSSKPTILRNLPQSQDGKLLFSLKQLGAHILIEKHHEM-----HP 295

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+++M+ D LAV+ FA P+ + + + KE+ R+ AI EL K+
Sbjct: 296 ---SSFSGEIDMPFIDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEAIHAHELQKM 352

Query: 375 GASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTF 432
G SV D I P +L+ +D+++DHR+AMA ++A + + + C K+F
Sbjct: 353 GGSVHPTSDGLYIE-PSRLHGAVVDSDHNDHRIAMALAVAGVHASSGQTLCLCNTQCINKSF 411

Query: 433 PDY 435
P +
Sbjct: 412 PHF 414

>gb|ACN18424.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
Length = 428

Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 121/436 (27%), Positives = 217/436 (49%), Gaps = 27/436 (6%)

Query: 17 GTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E +
Sbjct: 12 GAITVPGDKSMHSRIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIEETEEIIV 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
G G + + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 HGTGFDGL-----KQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMMNR 124

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196

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      +++ L+Q+GA +      G++ P+ +NG L + + + S+Q SA++ AA A G+
Sbjct: 125 VMLPLQQMGAKMHGKDGSEFAPITINGKQTLKRMEYHMPVA-SAQVKSALIFAALQAEGE 183

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
      I +K + T ++ +FG + E D R +KGGQK+ + + V GD SS
Sbjct: 184 TIIHEKEK-----TRDHTHEMIRQFGGEIEMDDLTIIR--VKGGQKF-TGQEMTVPGDVSS 235

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
      A++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 236 AAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGTV 292

Query: 316 GRK--HLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTE 370
      K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TE
Sbjct: 293 VVKTSELKGTTEGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELVKETNRIDAVATE 352

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
      L K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 353 LNKMGADITPTDEGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERPEAV 412

Query: 429 RKTFFPDYFDVLSTFVK 444
      ++P +F+ + + +K
Sbjct: 413 SVSYPTFFEDIRSLK 428

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>ref|ZP_01627121.1| response regulator receiver domain protein (CheY-like) [marine
      gamma proteobacterium HTCC2080]
gb|EAW40126.1| response regulator receiver domain protein (CheY-like) [marine
      gamma proteobacterium HTCC2080]
      Length = 432

```

Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 126/444 (28%), Positives = 216/444 (48%), Gaps = 29/444 (6%)

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Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      V+QP +++G ++PG KS+S+R ++L +L+EG T V L ED + A R +G+
Sbjct: 2 RFVVQPQGQLTGEHRVPGDKSMHSRVMGLSLAEGVTEVAGFLEGEDALRTIAAFRQMGV 61

Query: 66 SVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      ++E +A + VG G ++A + LGNAG MR + AG N L
Sbjct: 62 TIEGPEAGSLKISGVLHGLMAPQEAI-----LGNAGTGMRLFAGIL--AGQNFDESELI 114

Query: 125 GVPRMRERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G + +RP+G ++ L ++GA +D L PP+ ++G L G L + S+Q S
Sbjct: 115 GDASLMQRPMGRVINPLSRMGARIDS-LSQGRPELLISGGQSLQGIHYDLPIA-SAQVKS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      +L+A A G + P + T R++ FG + ++ + GG +
Sbjct: 173 CVLLAGLYAKGRTSVT-----EPAPTRDHTERMLIGFGYDVDSTNGV--IGLDGGGRLMG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      + + D SSA++ L GA+I G+ V ++ G + V +L +MGA ++
Sbjct: 226 -TSIDIPADVSSAAFLLVGASIAAGSDVLLKHVGMNPTR--VGVLNLTLMGADISVLNP 282

Query: 304 SVTVTGPPREPFGGRKH--LKVIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
      + G P ++ L ID+ +++P D L + A A G T +R + RV
Sbjct: 283 R-EIGGEPVADLQVRYAPLHGIDIPEDVPLAIDFPAIFIAACASGTTTLRGASELRV 341

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
      KE++R+ A+ L LG E PD +I KL +++T+ DHR+AMAF++A A
Sbjct: 342 KESDRIAAMAEGDLTLGIKNEPTPDGIVIE-GGKLGGSVNTFHDHRIAMAFIAIAGLRAS 400

Query: 418 VPVTIRDPGCTRKTFPDYFDVLST 441
      + + D +FP + +++S+
Sbjct: 401 AAIEVLDCDHVATSFPGFAELISS 424

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>ref|ZP_03729562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dethiobacter
      alkaliphilus AHT 1]
gb|EEG77697.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dethiobacter
      alkaliphilus AHT 1]
      Length = 432

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Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 129/447 (28%), Positives = 209/447 (46%), Gaps = 51/447 (11%)

Query: 15 ISGTVKLPKSGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R +LL +L+ G T + L ED + ++ LG+ V+ + +
Sbjct: 11 LTGEITVPGDKSVSHRAVLLGSLANGETRISGFLTGEDCLSTVSCMQKLGVPVQVNGSDV 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG G ED L GN+G R L + AG V+ G +R+RP+
Sbjct: 71 TVNGVGLGLELREPEDI-----LDCGNSGTTARLLLGVL--AGQPFYSVMTGDSLLRKRPM 123

Query: 135 GDLVVGLKQLGADVDCFLGTD-----CPPVRVNGIGGLPGGKVKLSGSISSQ 181
G + LKQ+GA++ LG D P+ N S S+Q
Sbjct: 124 GRVTKPLKQMGAEI---LGRDDGKLLPLSVLHGRLRPIHYN-----SPVASAQ 168

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
SA+L+A A G + +K + + R++ FG + E + R + G+
Sbjct: 169 VKSAVLLAGLADGVTAVTEPEK-----SRDHSERMLAAGAEVEVDGNTVRVH---GKP 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ V GD SSA++FL A+I G+ + V+ G + V EVL+ MGA +
Sbjct: 221 KLQGGTVRVPGDISAFAFLVAASIVPGSDDLKVNKGVPNPTRTGV--LEVLDKMGADLEL 278

Query: 301 TETSVTVTGPPREPFGK-KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASW 356
V P + R K L+ +++ + +P D LAV A+FA G T +RD A
Sbjct: 279 VNERVESGEPVADIRVRAKELQGEIGGDIVRLIDELPVLAVAAMFAKGTVVRDAAEL 338

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-C 415
+VKET+R+ A+ E KLGA+V D ++ L+ + DHR+AM+ +AA
Sbjct: 339 KVKETDRIA+VVEEFDKLGA+VATATEDGFVVEGGRPLSGAIAHSGDHRIAMSLCVAALA 398

Query: 416 AEVPVTIRDPGCTRKTFFDYFDVLSTF 442
A+ VT+ +P ++P+++D L
Sbjct: 399 AQGAVTVEEPESVAISYPNFWDTLQEL 425

>sp|Q2JLV2.2|AROA_SYNJB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 444

Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 135/450 (30%), Positives = 209/450 (46%), Gaps = 31/450 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ L P K + G V +PG KS+S+R L+L +L+EG T + LL ED R LG
Sbjct: 11 LTLSPAKGLRGQVSIPGDKSISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGAD 70

Query: 67 V-EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ E + R VG G D L GN+G +R L + A + + G
Sbjct: 71 ISELNSECVRIRGVGLGQLQEPADV----LDAGNSGTTLR-LMLGILAGQAGRFFAVTG 124

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R RP+G +V L+Q+GA + G P+ V G G L G + S S+Q S
Sbjct: 125 DRSLRSRPMGRVVEPLRQMGASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSC 182

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A LA ++ + +S + E R++ FG + + GG +
Sbjct: 183 LLLAGLLAE--GTTQVTEPALSRDHSE---RMLRAFGANIQVDPETKTAVVVGGSRLVG- 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA+++L +I + + + G + VL+ MGA + E
Sbjct: 237 QRQVQPGDISAFAFLVAVSIVPESELLLRDVLNPTN--TGALRVLQEMGADIQ-IENL 293

Query: 305 VTVTGPPEPFG-----RKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASW 356
+ G EP G L+ + + +P D LAV A FA+G T IRD A
Sbjct: 294 REMAG---EPLGDLRVRARLRGCTIAGDLIPTLIDEIPVLAVAAFAEGITVIRDAAEL 350

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC- 415
RVKE++R+ A+ EL+++GA V E PD I L+ +D+++DHR+AM+ +AA

Sbjct: 351 RVKESDRLSAMAQELSRMGAQVAEYPDGLEIKGGIPLHGAEVDSHEDHRIAMSLMVAALG 410

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445

A+ +R C R ++PD+ L +

Sbjct: 411 AQGSTLLRGADCARISYPDFIPTLQRLTAS 440

>ref|YP_328180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
A/HAR-13]
ref|YP_002887985.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
B/Jali20/OT]
ref|YP_002888867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
B/TZ1A828/OT]
sp|Q3KLZ0.1|AROACHLTA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AA50632.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
A/HAR-13]
emb|CAX09925.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
B/TZ1A828/OT]
emb|CAX10818.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
B/Jali20/OT]
Length = 440

Score = 138 bits (348), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 122/431 (28%), Positives = 196/431 (45%), Gaps = 44/431 (10%)

Query: 17 GTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV EADKAAKRA 76

G + +P SKS S R +L A+LS+GT++++N L S D ML A +G V +

Sbjct: 17 GBIAVPPSKSHSLRAILFASLSKGTSLIENCLFSPDSQAMLTACEKMGAVHVR--RIGDSL 74

Query: 77 VVVGCGKGFVVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136

+ G P +GN+GIA+R LTA T + ++ G ++ RPI

Sbjct: 75 HIQGN----PDPHHCHPRYFHMGNISGIALRFLTALSTLSP--TPTLTGSHTLKRRPIAP 128

Query: 137 LVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196

L+ LKQLGA + + P G L G V +SG SQY SAL + A LA

Sbjct: 129 LLSSSLKQLGAHIRQKTSSSIP---FTIHGPLSPGHVTISGQ-DSQYASALAITAALAPYP 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256

+ I+ L P+ ++TL + + D GGQ +S + V GD SS

Sbjct: 185 LSFS-IENLKERPFWFDLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314

A++ + ++ + + QGD +L+ +GA +

Sbjct: 241 AAFSLASGGLSSSSKPTILRNLSQDSQGDKLLFSLKQLGAHIL----- 285

Query: 315 FGRKHLKAI-----DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367

G+ H++ +++M+ D LAV+ FA P+ + + + KE+ R+ AI

Sbjct: 286 IGHKHIEHMPSSFSGGEIDMDPFIDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEAI 345

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425

EL K+G SV D I P +L+ +D+++DHR+AMA ++A + + +

Sbjct: 346 AHQLQMGGSVHPTRDGLYIK-PSRLHGAVVDSHNDHRIAMALAVAGVHASSGQTLLCNT 404

Query: 426 GCTRKTFPDYF 436

C K+FP YF

Sbjct: 405 QCINKSFP-YF 414

>ref|NP_219875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
D/UW-3/CX]
ref|ZP_05353743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
6276]
ref|ZP_05382589.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
D(s)2923]
sp|O84371.1|AROACHLTR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC67962.1| Phosphoshikimate 1-carboxyl vinyltransferase [Chlamydia trachomatis
D/UW-3/CX]

gb|ADH18061.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis G/9768]
gb|ADH18983.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis G/11222]
gb|ADH19908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis G/11074]
gb|ADH97004.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis G/9301]
gb|ADI51042.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis D-EC]
gb|ADI52054.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis D-LC]
Length = 440

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 122/431 (28%), Positives = 196/431 (45%), Gaps = 44/431 (10%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + P SKS S R +L A+LS+GT+++N L S D ML A +G V +
Sbjct: 17 GEIAVPPSKSHSLRAILFASLSKGTIIENCLFSPDSQAMLTACEKMGAVR--RIGDSL 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA T + ++ G ++ RPI
Sbjct: 75 HIQGN----PDPHHCHPRYFHMGN SGIALRFLTALSTLSP--TPTLITGSHTLKRRIAP 128

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ LKQLGA + + P G L G V +SG SQY SAL + A LA
Sbjct: 129 LLSSLKQLGAHIRQKTSSSIP---FTIHGPLSPGHVTISGQ--DSQYASALAITAALAPYP 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSDWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + D GGQ +S + V GD SS
Sbjct: 185 LSFS-IENLKERPWFDLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREP 314
A++ + ++ + + QGD +L+ +GA +
Sbjct: 241 AAFLASFGLLSSSSKPTILRNLSQDQGDKLLFSLKQLGAHIL----- 285

Query: 315 FGRKHLKAI-----DVMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G+ H++ +++M+ D LAV+ FA P+ + + + KE+ R+ AI
Sbjct: 286 IGKHHIEMHPPSSFSGGEIDMDPFIDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEAI 345

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
EL K+G SV D I P +L+ +D+++DHR+AMA ++A + + +
Sbjct: 346 AHELQKMGGSVHPTRDGLYIE-PSRLHGAVVDSHNDHRIAMALAVAGVHASSGQTLLCNT 404

Query: 426 GCTRKTFFDYF 436
C K+FP YF
Sbjct: 405 QCINKSFYF-YF 414

>ref|ZP_07638919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis NCTC 12261]
gb|EFN95913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis NCTC 12261]
Length = 427

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 123/443 (27%), Positives = 211/443 (47%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 ISHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 EVITIQQVGMDGLKAPQNA-----LDMNGSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVTIPLKKMGVSISGQTERDLPPLHLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V
Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLIVPNSRVVLKNVGINETRTGI--IDVIRAMGGKLEVTEIDPVAKSA 288

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II LN ++T+ DHR+ M ++AA AE V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKKSALNSARVNTFGDHRIGMMTAIAALLVAEGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L +
Sbjct: 403 ELDRAEAINTSYPSFFDDLENLI 425

>ref|YP_003723243.1| 3-phosphoshikimate 1-carboxyvinyltransferase ['Nostoc azollae'
0708]
gb|ADI66120.1| 3-phosphoshikimate 1-carboxyvinyltransferase ['Nostoc azollae'
0708]
Length = 449

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 127/436 (29%), Positives = 202/436 (46%), Gaps = 31/436 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G +++PG KS+S+R L+LAA++EG T + LL ED R LG + E +
Sbjct: 29 LQGRIRVPGDKSISHRALMLAAIAEGETQIQGLLLGEDPRSTANCFRVLGAIEISELNTEF 88

Query: 74 KRAVVVGCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
R +G G F V +A GN+G +R L + A+ + + G +R
Sbjct: 89 VRVKIGLGNFQEPFNVLNA-----GNSGTTIR-LMLGLLASHPGRFFTVTGDDSLR 139

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ +V L+Q+ A++ G P+ + G P + I+S + + ++ A
Sbjct: 140 ARPMSRVVKPLQQMAAEIWGRKGNLAPLAIQGGALKP---IHYHSPIASAQVKSCILLA 196

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
L + + + +S + E R++ FG + + + G K K V
Sbjct: 197 GLNT-EGQTTTFTEPALSRDHSE---RMLRAFGAELSIDPETNSVTVTGNAKLYGQK-VIV 251

Query: 251 EGDASSASYFL-AGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA+++L AGA + G + VE G + V E L MMGA + E V G
Sbjct: 252 PGDISSAAFVLVAGAIVPGSDLVVENGVNPNRTGV--LEALSMMGADIEL-ENQREVAG 308

Query: 310 PPREFPG--RKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P LK+ + + +P D LAV A FA G T IRD A RVKE++R+
Sbjct: 309 EPVADLRVCSSQLKSCSTIAGDIIPRLIDEIPILAVAAFAQGTTIIRDAAELRVKESDRI 368

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIR 423
+ +L ++GA V + PD IT L +D+Y DHR+AM+ ++AA A TI
Sbjct: 369 TVMAQQNLNQMGAQKVTQLPDGMEITGGTPLMGAEVDSYTDHRIAMSLAIAALNASGTTTIH 428

Query: 424 DPGCTRKTFPDYFDVL 439
++P++ + L
Sbjct: 429 RAEAAAISSYPNFTNTL 444

>ref|YP_754026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophomonas wolfei
subsp. wolfei str. Goettingen]
sp|Q0AX99.1|AROASYNWW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI68655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophomonas wolfei
subsp. wolfei str. Goettingen]
Length = 428

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 220/441 (49%), Gaps = 32/441 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + G V + KS+S+R ++ +AL+ G +++ N L + D LR LG+ + A
Sbjct: 8 LKPLKGDVSDADKSIHRAVIFSALAPGKSIKNFLQANDTLSSCSCLRQLGIKIAAMD 67

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + G G ++ L GN+G MR + ++A +L+G + +
Sbjct: 68 SEMQVYGRGLSGF-----SEPHTVLDCGNSGTTMRLMAGLLSAQ--PFLSILNGDESLNQ 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L +GA++ + PP+ + G L G +L + S+Q SAL++AA
Sbjct: 121 RPMKRIIEPLGIMGANIQARQNGNYPPLVIRG-NRLSGLSYQLPVA-SAQVKSALMLAAL 178

Query: 192 LALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A D E L+S P + + R++ G A+ + + +K G++ ++ +
Sbjct: 179 NA--DSE-----TLLSEPQKTRDHSEMLTAMG--ADIAVNGLEIRLKPGEKELQATE-FL 228

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A+I G+ + + G + + E+L MGA++ E T++
Sbjct: 229 VPGDISAFAFMVAASIIPGSELLIRHVGVNPSRAGI--IEILNEMGARIKL-ENERTIS 285

Query: 309 GPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P H L+AID++ +P D LAV A+G + +R A RVKET+R
Sbjct: 286 GEPVADLIVSHSRLQAIDIDGAVIPRLIDEIPILAVAMALAEGESTVRGAELRVKETDR 345

Query: 364 MVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
+ AI TEL K+GA + E D + I P+ L + + DHR+AM+ ++AA A+
Sbjct: 346 IAAISTELAKMGADIRERSDGFVIKGPDSLKGGRVASKGDHRIAMSLAVALAAKGESV 405

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
I D +FP ++D+L+T
Sbjct: 406 IEDSEVVNISFPRFWDLLNTL 426

>gb|EGD32898.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis SK115]
Length = 427

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 120/439 (27%), Positives = 218/439 (49%), Gaps = 35/439 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++ + G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 7 VRGLKGRIRVPGDKSISHRSIIFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVQIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ VG G ++ +L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 NLVKIHGVGFEGELQAPKN-----KLDMGNSGTSIRLISGVL--AGQDFEAMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G ++ D PP+++ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVITPLRQMGEIAGRTERDLPLKMKGSRELKSIHYQLPVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K I+ + E ++ +FG + E R I+G Q++ + + V
Sbjct: 179 QAQG--ESIIIEKEITRNHTE---DMAIQFGGQIEVKGEIR--IQGSQEF-TAQEVTVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + + +E G + + EV+E MG ++T ++ S
Sbjct: 231 GDISAFAFWLAVGLIVPDSKIVLENGINETRTGI--LEVIEAMGGQMTLSVDVPAKSA 288

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E LK ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITVETSE-----LKGTEIGGEIIPRLIDELPIIALLATQAQGRTVIRDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA++ D II L+ ++T DHR+ M ++AA V
Sbjct: 343 RIQVVADALNSMGAAITPTEDGMIIIEGKTPHGAQVNTLGDHRIGMMAIAALLAQSGQV 402

Query: 421 TIRDPGCTRKTFPDYFDVL 439
+ + ++P +F+ L
Sbjct: 403 ELERSEAIKTSYPSFFNDL 421

>ref|YP_003476808.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter italicus Ab9]
gb|ADD02246.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter italicus Ab9]
Length = 423

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 127/445 (28%), Positives = 214/445 (48%), Gaps = 34/445 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I ++ K + G + +PG KS+S+R +++ ++EG T + N L ED + +R LG+
Sbjct: 2 DIEVKKKKFLKGVISVPGDKSISHRAVMIGSIAEGITEIGNFLLGEDCISTINCMRNLGV 61

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
VE + V GK + E++ L +GN+G +R L ++ AT + G
Sbjct: 62 DVEL-----KGTNVKVYKGLYLNKSEKI-LDVGNSTTIRLLMGILSGQKFAT--VTG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ RP+G ++ L +GA ++ G + P+ V G L G K+ I+S + +
Sbjct: 114 DESIKRRPMGRVITPLSMMGAKIEAREG-NFAPLTVFG-NKLKGIYYKMP--IASAQVKS 169

Query: 186 LLMAAPLALGDVEIEIIDKLISIPY--VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+M A L D I I PY T + FG K + + + Y G K +
Sbjct: 170 SIMLASLYADDKTI-----IEEPYPSRNHTELMFSSFGAKVDVNGTKITCY--PGYKLQ 221

Query: 244 SPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT- 301
K V GD SSA+YF+ A + VT++ + + +V+E MG + T
Sbjct: 222 GQK-IVVPGDISAAYFIVAATLVPNSEVTIKNVNPNTRTGI--IDVIEKMGGDIVLTN 278

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
E ++ LK I++ + +P D +AV A+FA+G T I+D +V
Sbjct: 279 ERTINNEKVADITVKTSLRGIEIGGSLIPRLIDEIPVIAVAAVFAEGKTVIKDAEELKV 338

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
KE+ R+ I +EL K+GA + E D II L +++Y+DHR+AM+ +A AE
Sbjct: 339 KESNRINTITSELKMGAKIFEREDGMIEGTGFLRGNTVESYNDHRIAMSLWVAGLMAE 398

Query: 418 VPVTIRDPGCTRKTFPDY---FDVL 439
I++ C ++PD+ FD+L
Sbjct: 399 GETKIKNAECVNISYPDFYKTFDIL 423

>ref|YP_906373.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium ulcerans Agy99]
sp|A0PRD3.1|ARO_A_MYCUA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABL04902.1| 3-phosphoshikimate 1-carboxyvinyltransferase AroA [Mycobacterium ulcerans Agy99]
Length = 431

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 134/437 (30%), Positives = 215/437 (49%), Gaps = 32/437 (7%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEG---TTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL+ ++ + L S D M+ AL+TLGL V D
Sbjct: 16 VHATVTVPGSKSQTNRTLVLAAALAAQGGSSITITGALRSRDTLMI EALQTLGLRV--D 73

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G P E ++ G AG +R + T+ DG + R
Sbjct: 74 GTGSELTVSGRIRPCP-----EARVDCGLAGTVLRFAPPLAALSAAPITF--DGDEQAR 125

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA- 189
RPI L+ L+ LG VD G P RV G G + GG V + S SSQ++S LL++
Sbjct: 126 ARPIAPLLDALRGLGVPVD---GAGLP-FRVQGTGSGVAGGTVAIDASASSQFVSGLLLSG 181

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G +L S P++ MT++++ + GV + S +R+ ++ G P++
Sbjct: 182 ASFTDGLTVQHTGSELPSAPHIAMTVQMLRQAGVDVDD SIP-NRWLVRPGALR--PRHWD 238

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
E D ++A FLA A +TGGTVT+ G S+Q ++L+ + + V ++ + V G
Sbjct: 239 AEPDLTNAVAFLAAAVTVGGTVTITGWPADSVQPAKNILDILQTLNSTVRHIDSCLQVQG 298

Query: 310 PPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIR--DVASWRVKETERMVAI 367
P + + DV++ + ++ ++A +A A + R +A R ET+R+ A+
Sbjct: 299 P-----QSYRGFDVLDLVDVGLTPSVAALAAALASPGSVSRLAGIAHLRGHETDRLAAL 351

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
TE+ +LG + E+ D +IT L + Y DHRMAMA ++ V + D G
Sbjct: 352 STEINRLGGNCEQTS DGLVIT-ATPLRPGSWRAYADHRMAMAGAI VGLRVAGVEVDDIGA 410

Query: 428 TRKTFPDYFDVLSTFVK 444
T KT P++ + + V+
Sbjct: 411 TSKTLPEFPQLWTEMVE 427

>ref|ZP_05503074.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T3]
gb|EEU23440.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T3]
Length = 428

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 127/435 (29%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPKSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRAGDASIAK 121

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTTFPPISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E D + + G Q+ +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVDDK--KIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + +E G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVDPDEILLENVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 290

Query: 310 PPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRD AEELVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEA VSVSYPAFFDDL 423

>ref|ZP_07929811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerostipes sp.
3_2_56FAA]
gb|EFV24027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerostipes sp.
3_2_56FAA]
Length = 426

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.

Identities = 120/433 (27%), Positives = 204/433 (47%), Gaps = 35/433 (8%)

Query: 18 TVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T+ +PG KS+S+R ++ +L++GTT + N L+ D + R +G+ +E +
Sbjct: 12 TISIPGDKSISHRAVMFGSLAKGTTHTITNFLSGADCLATIDCFRAMGVRIE-----QEGT 66

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
VV G K E QL +GN+G R ++ ++ G + L G + +RP+G +
Sbjct: 67 VVTVHGNGLRGLKKPEKQLDVGNSGTTTRLISGILS--GQDFEVTLSGDASLNKRPMGRI 124

Query: 138 VVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGD 196
+ L +GA+++ G C P+++ G P V+ ++S Q SA+L+A A D
Sbjct: 125 MKPLSMMGAEIESVNGDGCAPLKITG---KPLKAVRYESPVASAQVKSALLAGLYA--D 179

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ + +S + E+ L+ FGV+ + K + + V GD SS
Sbjct: 180 GRTSVTEPALSRNHTELMLK---SFGVQVLSEGTTASVM---PPKEMTATDIAVPGDISS 233

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPF 315
A++F+A +T +T++ G + + +V E MGA +T + V G EP
Sbjct: 234 AAFFIAAGLVTPDSCITLKQVGINPTRNGI--IKVCEAMGADLTMSN---VKGDNGEPT 287

Query: 316 G-----RKHLKAIDVNMNKMMPDVAMTLAVVAL---FADGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + + V+AL FA+G T I++ A +VKE+ R+
Sbjct: 288 ADITVTKSRLKGTEIGGELIPTLIDEIPVIALMAAFAEGETVIKNAELVKESNRIDLT 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
L K+GA E D II L AI DHR+AM FS+A A+ I D
Sbjct: 348 VDNLVKMGADAEATDDGMIIRGGNPLRGAAIHCKYDHRIAMTFSVAGINAQGTTVIEDAE 407

Query: 427 CTRKTFPDYFDVL 439
C ++P++++ L
Sbjct: 408 CVDVSYPNFYEQ 420

>ref|ZP_06850660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
parascrofulaceum ATCC BAA-614]
gb|EFG75992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium
parascrofulaceum ATCC BAA-614]
Length = 427

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 139/442 (31%), Positives = 213/442 (48%), Gaps = 33/442 (7%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLALLAAL----SEGTTVDNLLNSEDVHYMLGALRTLGL 65
QP++ TV +PGSKS +NR L+LAAL GT + L S D M+GALRTLGL
Sbjct: 11 QPVRA---TTVTPGSKSQTNRALVLAALAAAQGRGTPTIGGALRSRDTLDMIGALRTLGL 67

Query: 66 SVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D A V GG+ P A+ + L AG +R + AA A D
Sbjct: 68 RV--DGAGSELTV---GGRIAPGPGARVDCGL---AGTVLRFVPP--LAALAEAVVEFD 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + R RPI L+ L+ LG ++ G P RV+G G + GG V + S SSQ++S
Sbjct: 117 GDEQARARPIAPLLDALRGLGVPIE---GAGLP-FRVHGGGSVAGGTVDIDASASSQFVS 172

Query: 185 ALLMAAP-LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
LL+ AP A G L S P++ MT+ ++ + GV + S + + + ++ G
Sbjct: 173 GLLLCAPSFAEGLTVRHTGATLPSAPHIAMTVVMLRQAGVDVDSVA-NVWRVRPGPV-- 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
+ ++ VE D ++A FLA A ++GGTV + G S+Q VL + A VT ++
Sbjct: 230 AARHWQVEPDLTNAVPLAAAVVSGGTVRITGWPAASVQPADHILSVLGLKNAVVTQGDS 289

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V G P L+A+ + +A ++ + + + R ET+R
Sbjct: 290 FLEVQGSADYPGFVLDLRAVGELTPAVAALAAALAKPGSV-----SHLSGIGHLRGHETDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTIR 423
+ A+ E+ +LG E PD +IT L Y DHRMAMA ++ V +
Sbjct: 345 LAALSAEINRLGGDCTETPDGLVIT-ATPLRAGVWRAYADHRMAMAGAIVGLRVAGVEVD 403

Query: 424 DPGCTRKTFPDYFDVLSTFVK 445
D G T K T P++ ++ + +++
Sbjct: 404 DIGSTSKTLPEFPPELWARMLES 425

>ref|YP_002832573.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
L.S.2.15]
ref|YP_002838088.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
Y.G.57.14]
ref|YP_002840044.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
Y.N.15.51]
ref|YP_003420075.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
L.D.8.5]
sp|C3MRB5.1|AROA_SULIL RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
sp|C3NG04.1|AROA_SULIN RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
sp|C3N7H2.1|AROA_SULIY RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACP35928.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
L.S.2.15]
gb|ACP46166.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
Y.G.57.14]
gb|ACP48122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
Y.N.15.51]
gb|ADB87705.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
L.D.8.5]
Length = 414

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 202/440 (45%), Gaps = 47/440 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
EISGT+K P SKSL+ R++ L+ + + NL+ SEDV + ++R LG+ V+ +
Sbjct: 9 EISGTIKAPQSKSLAIRLIFLSLFTR--IHLHNLVLSERVEDIDAINSVRALGVEVKNNSEF 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERP 133
+ KF + L +G +R L V A GG T +D +R RP
Sbjct: 67 IPPEKLEIKKF-----IKLKGSGTTLRMLIPIVAAIGGEVT--IDAEESLRRRP 114

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L G + P+ + G L +K+SG SSQY+S L+ A +
Sbjct: 115 LKRIVEALSNGYIS----FSSSLPLTITG--KLSSYNIKISGDESSQYISGLIYALHIL 168

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-----A 248
G IEI+ + S Y+ +T+ L RFG +FY G + + +P N
Sbjct: 169 NGG-SIEILPPISSKSYILLTVDLFNRFSGSNV-----KFY--GNKIHINPNNLVEFQG 218

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD AS++ A ++GG T+ GD ++L+ MGA + + V
Sbjct: 219 EVAGDYGSLASFYALSALVSGGRTTIVNLWEPKEYFGDHSIVKILKEMGATSEYLDGKWYV 278

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ +I VN++ PD+AMT+A +A A+G + I + R+KE++R+ +I
Sbjct: 279 EA-----KDKYSSIKVNIDDAPDLAMTIAGLAAIAEGTSEITGIERLRIKESDRIESI 331

Query: 368 RTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
R L G E + +I K L+ D +DHR+AM S A V I
Sbjct: 332 RKVLGLYGVGSEVKSNSILIFGINKRMLSSPITDCLNDRVAMMSSALALVNGGV-ITSA 390

Query: 426 GCTRKTFPDYF-DVLSTFVK 444
C K+ P+Y+ D+LS K
Sbjct: 391 ECVSKSNPNYWQDLSLNAK 410

>ref|ZP_06945970.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Finergoldia magna ATCC 53516]
gb|EFH94025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Finergoldia magna ATCC 53516]
Length = 398

Score = 138 bits (347), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 116/425 (27%), Positives = 204/425 (48%), Gaps = 46/425 (10%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GTV SKS ++R L+LA++++ TT++ N S D+ + LR LG+ +E +
Sbjct: 7 KLQGTVDIAISSKSFAHRFLILASVADTDTTIIINEF-SNDIMTTIDCLRNLGVEIEINGN 65

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V F +D + + + ++G +R L V+ G R+++R
Sbjct: 66 E-----VTVHPSFFQKDVSD---INVNDSGSTLRFLPLVLSFSLQKTNIKCSG--RLQDR 115

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +L+ LK G + P V+G + G +SSQY+SA++M APL
Sbjct: 116 PIKELMDQLKLSGLT---FSKEKLPFTVDG--TFHKIDFEFPGDVSSQYISAIMMIAPL 169

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+G EI++ +L S Y+++T ++ FGV++E D+ +K G KSP VEG
Sbjct: 170 -IGGCEIKLTSQLESTGYIKITQECLKLFGVESEILP--DKVIVKPGA-LKSPGQIIVEG 225

Query: 253 DASSASYFLAGAAITGGTVTVVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S+A++FL + G + V S+Q D K E+LE + + E
Sbjct: 226 DWSNAAFFLCANEL-GADIKVLNLNKKSVQADRKIVELLEKIDNNEDYCE----- 274

Query: 313 EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
++++ PD+ + LAVV + +++ R+KE++R+ + L
Sbjct: 275 -----IDISQTPDLFVILAVVLSQKCEKSVLKNKRLRLKESDRIQSTFDMLQ 322

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIIRDPGCTRKT 432
G + + D II E + I++ DDHR+ MA ++A+ V I+D +K++
Sbjct: 323 SFGVNCKIDGDDLIIYKSE-MKPAVINSCDDHRIVMAATIASIITKEVEIKDWQAVKKS 381

Query: 433 PDYFD 437
P +FD
Sbjct: 382 PSFFD 386

>gb|ACN18367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18478.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18481.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18589.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18697.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
Length = 428

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 121/437 (27%), Positives = 220/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GAITVPDGKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGKQADGGLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMPN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195

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      +++ L+Q+GA +      G++ P+ + G  L  +  +  + S+Q  SA++ AA  A G
Sbjct: 124 RVMLPLQMQGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
      + I  +K      + T  ++ +FG + E      R  +KGGQK+ + +  V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
      SA++F+      IT G  + +  G  + +  +V+E MG  +  ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVKDSSRS-TGKLAGT 291

Query: 315 FGRK--HLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
      K  LK  ++  + +P +  + V+AL A  +G T I+D A  +VKET R+ A+ T
Sbjct: 292 VVVKTSSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAT 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
      EL K+GA +  D  II      L+  + +Y DHR+ M  +AA  E V +  P
Sbjct: 352 ELNKMGAIDITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELEERPEA 411

Query: 428 TRKTFPDYFDVLSTFVK 444
      ++P +F+ + + +K
Sbjct: 412 VSVSYPTFFEDIRSLK 428

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>ref|YP_477562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
      JA-2-3B'a(2-13)]
gb|ABD02299.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
      JA-2-3B'a(2-13)]
      Length = 434

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Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 137/455 (30%), Positives = 211/455 (46%), Gaps = 41/455 (9%)

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Query: 7  IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
      + L P K + G V +PG KS+S+R L+L +L+EG T +  LL  ED      R LG
Sbjct: 1  MTLSPAKGLRGQVSIPGDKSISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGAD 60

Query: 67  V-EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      + E +  R  VG G  D      L  GN+G +R L  + A      + + G
Sbjct: 61  ISELNSECVRIRGVGLGQLQEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      +R RP+G +V  L+Q+GA +  G  P+ V G G L G  + S  S+Q  S
Sbjct: 115 DRSLRSRPMGRVVEPLRQMGASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSC 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      LL+A  LA      ++ +  +S + E  R++  FG  +      + GG +
Sbjct: 173 LLLAGLLAE--GTTQVTEPALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRLVG- 226

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
      +  V GD SSA+++L  +I  +  V +  T +L+      VL+  MGA +
Sbjct: 227 QRVQVPGDISAASFVWVAVSIVPESELLLRDVGLNPTRTGALR-----VLQEMGADIQ 279

Query: 300 WTETSVTVTGPPREPFG-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIR 351
      E  + G  EP G      L+  +  + +P  D  LAV A  FA+G T IR
Sbjct: 280 -IENLREMAG---EPLGDLRVRSARLRGCTIAGDLIPTLIDEIPVLAVAAFAEGITVIR 335

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
      D A  RVKE++R+ A+  EL+++GA V E PD  I      L+  +D+++DHR+AM+
Sbjct: 336 DAAELRVKESDRLSAMAQELSRMGAQVAEYPDGLEIKGGIPLHGAEVDSHEDHRIAMSLM 395

Query: 412 LAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
      +AA  A+      +R  C R ++PD+  L      +
Sbjct: 396 VAALGAQGSTLLRGADCARISYPDFIPTLQRLTAS 430

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>ref|YP_171991.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus
      elongatus PCC 6301]
      ref|YP_399251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus
      elongatus PCC 7942]
      sp|Q5N2J9.1|ARO_A_SYNP6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

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AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q31RQ5.1|AROA_SYNE7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAD79471.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus
elongatus PCC 6301]
gb|ABB56264.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus
elongatus PCC 7942]
Length = 448

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 122/437 (27%), Positives = 215/437 (49%), Gaps = 25/437 (5%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+L A++ G T ++ LL ED R +G + ++ ++
Sbjct: 28 LRGRIRVPGDKSISHRALMLGAIASGETTIEGLLLGEDPLSTAACFRAMGAEI-SELNSE 86

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G +++ +E + L GN+G +R L + A + + + G +R RP
Sbjct: 87 LVRVKGIG---LQNLQEPLDVLNAGNSGTTIR-LMMGLLAGQRDRFFCVTGDESLRSRP 141

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L Q+GA++ G P+ ++G P V S S+Q S++L+A
Sbjct: 142 MARVIQPLSQMGAEIRGRQGNTRAPLAISGRSLQPIRYV--SPIASAQVKSSILLAGLTC 199

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + +++ +S + E R+ FG K + ++G + + V GD
Sbjct: 200 EG--QTTVVEPALSRDHSE---RMFRAFGAKLTVNPEEISVTVEGPAELTG-QPVVVPD 253

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L AAI + + +E G + + E L+ M A++T E V G P
Sbjct: 254 ISSAAFWLVAAAIVPDSLLIENVGVNPTRTGI--LEALQQMEAQITL-ENERIVAGEPV 310

Query: 313 EPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ +L+AI++ + +P D LAV A FA G T IRD RVKE++R+ +
Sbjct: 311 ADLRVRSSNLQAIEIGGSLIPRLIDEVPILAVAAFAKGTIIIRDAEELRVKESDRIAVM 370

Query: 368 RTELTGLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
+EL ++GA++ E PD IT L +D+Y DHR+AM+ ++AA A+ I+
Sbjct: 371 ASELGRMGATISERPDGLEITGGAALTGATVDSYTDHRIAMSLAIALQAKGQTQIQQAE 430

Query: 427 CTRKTFPDYFDVLSTFV 443
++PD+ L +
Sbjct: 431 AAASYPDFVPTLQQL 447

>ref|ZP_07794480.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE prephenate
dehydrogenase [Pseudomonas aeruginosa 39016]
gb|EFQ39576.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE prephenate
dehydrogenase [Pseudomonas aeruginosa 39016]
Length = 746

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 212/436 (48%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQAFRDMGVVIEG 377

Query: 70 DKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGDA 429

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA ++ L PP+ + G L G + + S+Q S LL
Sbjct: 430 SLSKRPMNRVAKPLREMGAVIETGL-EGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSCLL 487

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G+ + P + T R++ FG E S + ++ G K S +
Sbjct: 488 LAGLYAAGETSVT-----EPAPTRDHTERMLRGFGYPVEVEGSTAK--VESGHKL-SATH 539

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
Sbjct: 540 IEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VGVEILRLMGDLNL-ENQRE 596

Query: 307 VTGPPREPFGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P + LK ID+ + +P D L V A A+G T +R RVKE+
Sbjct: 597 VGGEVPADIRVRSARLKGIDIPEDLVLPLAIDEFPVLFVAAACAEGRTVLRGAELRVKES 656

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPV 420
+R+ + L LG E PD +I + + DHR+AM+FS+A+ A P+
Sbjct: 657 DRIQVMADGLKALGVKAEPDTPDGIVIEGG-AFGGGEVWAHGDHRIAMSFSVASLRASGPI 715

Query: 421 TIRDPGCTRKTFPDYF 436
I D +FP++
Sbjct: 716 RIHDCANVATSPFNFL 731

>ref|ZP_03824672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter sp.
ATCC 27244]
gb|EEH67423.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter sp.
ATCC 27244]
Length = 749

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 133/448 (29%), Positives = 210/448 (46%), Gaps = 41/448 (9%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KTFTGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHHVGMHGLKVPAS-----ALYMGNSGTSMRLLSGMLSQAQKFDSD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+++GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLREMGAIQTTGEKGTTPVVSITGNQALKGIQYDLMA-SAQVKSGILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G + + P + T R++ FG VK E + + GG K N
Sbjct: 485 LWAEGVTSVTEPE-----PTRDHTEMLRAFGYDVKTE----GNNISLVGGGKLVG-TNI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISSAAFFMVGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIIHKGSRITLKGIMHPEDQVPLAIDEFPALFIAAACAEGQTTLTGAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDITYDDHRMAMAFSLAA 414
+R+ + L +G D II K N I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSAIFNGGEIESHHDHRIAMSFSIAG 711

Query: 415 CAEV-PVTIRDPGCTRKTFPDYFDVLST 441
+TI +FP + ++ +T
Sbjct: 712 LRTAGAITIHGTETVATSFPTFTELANT 739

>emb|CBJ14884.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
Sweden2]
gb|ADH17139.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
E/150]
gb|ADH20834.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
E/11023]
Length = 440

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 119/423 (28%), Positives = 194/423 (45%), Gaps = 29/423 (6%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +P SKS S R +L A+LS+GT++++N L S D ML A +G V +
Sbjct: 17 GEIAVPPSKSHSLRAILFASLSKGTSTIENCLFSPDSQAMLTACEKMGAVR--RIGDSL 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA T + ++ G ++ RPI
Sbjct: 75 HIQGN----PDPHHCHPRYFHMGNSGIALRFLTALSTLSP--TPTLITGSHTLKRRPIAP 128

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ LKQLGA + + P G L G V +SG SQY SAL + A LA
Sbjct: 129 LLSSLKQLGAHIRQKTSSSIP---FTIHGPLSPGHVTISGQ-DSQYASALAITAALAPYP 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + D GGQ +S + V GD SS
Sbjct: 185 LSFS-IENLKERPFWDLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A++ + ++ + + + QGD +L+ +GA + + + + P
Sbjct: 241 AAFASFGLSSSSSKPTILRNLPQSQGDKLLFSLKQLGAHILIEKHHIEM----HP 295

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+++M+ D LAV+ FA P+ + + + KE+ R+ AI EL K+
Sbjct: 296 ---SSFSGGEIDMPFIDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEAIHAELQKM 352

Query: 375 GASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTF 432
G SV D I P +L+ +D+++DHR+AMA ++A + + + C K+F
Sbjct: 353 GGSVHPTRDGLYIE-PSRLHGAVVDSDHNDHRIAMALAVAGVHASSGQTLNCNTQCINKSF 411

Query: 433 PDY 435
P +
Sbjct: 412 PHF 414

>ref|YP_002843827.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
M.16.27]
sp|C3MZFO.1|AROASULIA RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACP55782.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
M.16.27]
Length = 414

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 202/440 (45%), Gaps = 47/440 (10%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
EISGT+K P SKSL+ R++ L+ + + NL+ SEDV + ++R LG+ V+ +
Sbjct: 9 EISGTIKAPQSKSLAIRLIFLSLFT--IHLHNLVLSERVEDIDAINSVRALGVEVKNNSEF 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ KF + L +G +R L V A GG T +D +R RP
Sbjct: 67 IPPEKLEIKKKF-----IKLKGSGTTLRLIPIVAAIGGEVT--IDAEESLRRRP 114

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L G + P+ + G L +K+SG SSQY+S L+ A +
Sbjct: 115 LKRIVEALTNYGIS----FSSSSLPLTITG--KLSSYNIKISGDESSQYISGLIYALHIL 168

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-----A 248
G IEI+ + S Y+ +T+ L RFG +FY G + + +P N
Sbjct: 169 NGG-SIEILPPISSKSYILLTVDLFNRFSGSNV-----KFY--GNKIHINPNNLVEFQG 218

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD AS++ A ++GG T+ GD ++L+ MGA + + V
Sbjct: 219 EVAGDYGLASFYALSALVSGGRTTIVNLWEPKEYFGDHSIVKILKEMGATSEYLDGKWYV 278

Query: 308 TGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ +I VN++ PD+AMT+A +A A+G + I + R+KE++R+ +I
Sbjct: 279 EA-----KDKYSSIKVNIDDAPDLAMTIAGLAAIAEGTSEITGIERLRRIKESDRIESI 331

Query: 368 RTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDP 425

R L G E + +I K L+ D +DHR+AM S A V I
Sbjct: 332 R K V L G L Y G V G S E V K S N I L I F G I N K R M L S S P I T D C L N D H R V A M M S S A L A L V N G G V - I T S A 390

Query: 426 G C T R K T F P D Y F - D V L S T F V K 444
C K+ P+Y+ D+LS K

Sbjct: 391 E C V S K S N P N Y W Q D L L S L N A K 410

>ref|ZP_03917251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
glucuronolyticum ATCC 51867]
gb|EEI28321.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
glucuronolyticum ATCC 51867]
Length = 400

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 132/428 (30%), Positives = 204/428 (47%), Gaps = 41/428 (9%)

Query: 27 L S N R I L L L A A L S E G T T V V D N L L N S E D V H Y M L G A L R T L G L S V E A D K A A K - - R A V V V G C G G K 84
++NR L++AA + +V+ L S D M A L R T L G V+ D + R V G G+
Sbjct: 1 M T N R A L I I A A G A T S P S V I R G A L A S R D S D L M A D A L R T L G C E V D V D G S T V T V R P G P V T G G G R 60

Query: 85 F P V E D A K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P I G D L V V G L K Q L 144
+ G A G M R V A T ++ G R R P+ + L Q L
Sbjct: 61 - - - - - V D C G L A G T V M R - F V P P V A A L S A T P T - L I S G D Q A A R R R P M S T M T D A L V Q L 107

Query: 145 G A D V D C F L G T D C P P V R V N G I G G L P G G K V K L S G S I S S Q Y L S A L L M A - A P L A L G D V E I E I I D 203
G A V+ + P+ V+G + G G ++ S S Q ++ S L L ++ A G I D
Sbjct: 108 G A H V E G - - - - E T L P M T V S G P - - I T G G T A R I D A S A S S Q F V S G L L L S G A R F P A G V T V I H T G D 161

Query: 204 K L I S I P Y V E M T L R L M E R F G V K A - E H S D S W D R F Y I K G G Q K Y K S P K N A Y - - - - - V E G D A S S 256
+ S+P++EMTL ++ G V++ +H D Y + P Y +E D S+
Sbjct: 162 S V P S L P H I E M T L D M L H T A G V E S T Q H H D E E T G T Y - - - - - S W T V P H Q E Y A G G E V T I E P D L S N 216

Query: 257 A S Y F L A G A A I T G G T V T V E G C G T T S L Q G D V K F A E V L E M M G A K V T W T - E T S V T V T G P P R E P F 315
A+ F L A A A + T G G V + V G T+ Q + + M G + + + + T V + G P
Sbjct: 217 A A A F L A A A A V T G G H V S V P G W P A T T T Q P G D D I R H I F D A M G C T H E L S S D G T L T V S G P T D - - - 273

Query: 316 G R K H L K A I D V N M N K M P D V A M T L A V V A L F A D G P T A I R D V A S W R V K E T E R M V A I R T E L T K L G 375
L I D + + + + + T + A V F A D P + + + A R E T + R + A + E L T L G
Sbjct: 274 - - G V L H G I D A D L S A V G E L T P T V A A V C A F A D S P S R L T G I A H L R G H E T D R L Q A L T A E L T N L G 331

Query: 376 A S V E E G P D Y C I I T P P E K L N V T A I D T Y D D H R M A M A F S L A A C A E V P V T I R D P G C T R K T F P D Y 435
E E D I T P + + Y + D H R M A A + + + + T K T P D +
Sbjct: 332 C G C E E L A D G L A I T - P A P M T G G L W R S Y E D H R M A T A G A I V G L K V K D T F V E N I E T T S K T M P D F 390

Query: 436 F D V L S T F V 443
+L +
Sbjct: 391 A R M L E A L L 398

>ref|ZP_05358720.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia trachomatis
6276s]
Length = 440

Score = 137 bits (346), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 122/431 (28%), Positives = 196/431 (45%), Gaps = 44/431 (10%)

Query: 17 G T V K L P G S K S L S N R I L L L A A L S E G T T V V D N L L N S E D V H Y M L G A L R T L G L S V E A D K A A K R A 76
G + + P S K S S R + L A + L S + G T + + + + N L S D M L A + G V +
Sbjct: 17 G E I A V P P S K S H S L R A I L F A S L S K G T S I I E N C L F S P D S Q A M L T A C E K M G A H V R - - R I G D S L 74

Query: 77 V V V G C G G K F P V E D A K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P I G D 136
+ G P + G N + G I A + R L T A T + + + G + + R P I
Sbjct: 75 H I Q G N - - - - P D P H H C H P R Y F H M G N S G I A L R F L T A L S T L S P - - T P T L I T G S H I L K R R P I A P 128

Query: 137 L V V G L K Q L G A D V D C F L G T D C P P V R V N G I G G L P G G K V K L S G S I S S Q Y L S A L L M A A P L A L G D 196
L+ L K Q L G A + + P G L G V + S G S Q Y S A L + A L A
Sbjct: 129 L L S S L K Q L G A H I R Q K T S S S I P - - - F T I H G P L S P G H V T I S G Q - D S Q Y A S A L A I T A A L A P Y P 184

Query: 197 V E I E I I D K L I S I P Y V E M T L R L M E R F G V K A E H S D S W D R F Y I K G G Q K Y K S P K N A Y V E G D A S S 256
+ I+ L P+ ++TL + + D G G Q +S + V G D S S

Sbjct: 185 LSFS-IENLKERPWFDLTLDWLHSLNISFLRDQ--DSLTFPGGQSLESFSYS-VPGDYSS 240

Query: 257 ASYFLAGAAITGGT--VTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A++ + ++ + + QGD +L+ +GA +

Sbjct: 241 AAFSLASGGLSSSSKPTILRNLSQSQGDKLLFSLKQLGAHIL----- 285

Query: 315 FGRKHLKAI-----DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G+ H++ +++M+ D LAV+ FA P+ + + + KE+ R+ AI

Sbjct: 286 IGHKHIEHMPSSFSGGEIDMPFIDALPILAVLCCFAKNPSRLYNALGAKDKESNRIEAI 345

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
EL K+G SV D I P +L+ +D+++DHR+AMA ++A + + +

Sbjct: 346 AHELQKMGGSVHPTDRGLYIE-PSRLHGAVVDSHNDHRIAMALAVAGVHASSGQTLLCNT 404

Query: 426 GCTRKTFFPDYF 436
C K+FP YF

Sbjct: 405 QCINKSFP-YF 414

>ref|ZP_06695533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1636]
gb|EFF23161.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
E1636]
Length = 431

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 211/441 (47%), Gaps = 24/441 (5%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +
Sbjct: 3 LLQQIHGLRGTVRIPADKSIHSRISIMFGAIAEGTTTTIQNFLRAEDCLSTLHAFQQLGVEI 62

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E ++ + + G G V+ + +GN+G R L + AG T L G
Sbjct: 63 EEEEEVIK--IHGRGSHSFVQPT---APIDMGNSGTTSRLLMGIL--AGQPFTTTTLVGDA 115

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 116 SLSKRPMPGRVMEPLREMGADLQGNENDQYLPITVTGTRSLSTIRYNPVA-SAQVKSALL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA A G I ++K S + E +R +FG + D + G QK + +
Sbjct: 175 FAALQAEGTSVI--VEKERSRNHTEEMIR---QFGGRITVEDKT--IMVTGPQKL-TGQQ 226

Query: 248 AYVEGDASSASYFLA-GAAITGGTTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++F+A G + + ++ G + + +VLE MGA +T T +
Sbjct: 227 ITVPGDISAAFFIAAGLLVPESQLLLKNVGVNPTRTGI--LDVLEEMGAAITQTNHNEH 284

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK + +P D LA+VA A+G T I D +VKET R
Sbjct: 285 NQSADLS-VKTSHLKKATIGGEIIPRLIDELPILALVATQAEGVTIIEDAEELKVKETNR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ EL K+GA ++ D II P L+ + + DHR+ M +AA A+ P +
Sbjct: 344 IDAVAEEELQKMGAKIKATADGLIIHGPTPLHGAKVSSRGDHRIGMMLQVAALIADGPCEL 403

Query: 423 RDPGCTRKTFFPDYFDVLSTFV 443
++P +FD L+ V
Sbjct: 404 EGAEAVSISYPAFFDDLAEIV 424

>ref|ZP_04150599.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
pseudomycoides DSM 12442]
gb|EEM17758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
pseudomycoides DSM 12442]
Length = 415

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 122/438 (27%), Positives = 213/438 (48%), Gaps = 33/438 (7%)

Query: 15 ISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

++GT+ +PG KS+S+R ++ A++EGTT + N L ED + R LG+ +E D
Sbjct: 1 MNGTIAVPGDKSISHRAVMFGAIAEGTTKISNFFLLGEDCLSTIACFRKLGIMIEQDG--- 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+V G +++ KE L +GN+G +R + + A + T + D + +RP+

Sbjct: 58 NDVIVYGKGLAGLQEPKE--VLDVGNSGTTIRLMLGILANAPFHCTIIGD--ESIGKRPM 113

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+++ A ++ P+ + G G + G S S+Q SA+L+A

Sbjct: 114 KRVTAFLREMDAQIEGREDDGQYTPLSIRG-GNIKGIHYH-SPVASAQVKSAILLAG--LQ 169

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ + + L S + E R++ FG E + ++GGQ + V GD

Sbjct: 170 GEGVTSVTEPLQSRDHTE---RMLRAFG--CEVNVEGRTVSLQGGQSLVGTE-IEVPGDV 223

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++FL AGA + + ++ G + + +VL MGA ++ V E

Sbjct: 224 SSAAFFLVAGAIVPNSKLVKLVNVLNPTRTGI--LDVLSEMGALISIR---NVRNEEFE 277

Query: 314 PFG-----RKHLKAIDVNMNMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMV 365
P G LK I++ + +P + + ++AL A G T I+D +VKET R+

Sbjct: 278 PCGDITITETSELKGIIEGGLIPRLIDEIPIIALLATQATGTTIKDAEELKVKETNRIN 337

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRD 424
+ EL KLG +E PD II +KL +++++ DHR+ M ++A+C AE + I +

Sbjct: 338 TVVDELRLKLGVEIEATPDGMIINGNQLQGNIVNSHGDHRIGMMLAIASCI AE GEMQIEN 397

Query: 425 PGCTRKTFFPDYFDVLSTF 442
++P++F+ L +

Sbjct: 398 GDAVAVSYPNFFEQLESL 415

>ref|YP_958304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter
aquaeolei VT8]
gb|ABM18117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Marinobacter
aquaeolei VT8]
Length = 742

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 128/438 (29%), Positives = 206/438 (47%), Gaps = 28/438 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+QP + G +++PG KS+S+R ++L AL+EGTT V L ED L A R +G+++E

Sbjct: 311 MQPGGTVRGDIRVPGDKSMSHRSIMLGALAEAGTTEVKGFLGEDSLATLQAFRDMGVITIE 370

Query: 69 A-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D R VG G L+LGN+G AMR + A ++ L G

Sbjct: 371 GPDDGFVRIHVGVMKGL-----QAPRGPLYLGNSTAMRLFAGLLAAQPFDSSE--LTGDA 423

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G + L+ +GA +D G PP+++ G L G ++ + S+Q S LL

Sbjct: 424 SLSKRPMGRVADPLRAMGAVIDTGEGR-PPLKIRGGHALTGIHYEMPVA-SAQVKSCLL 481

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++E FG H D GG+ +

Sbjct: 482 LAGLYAEG-----VTSVTEPAPTRDHTERMLEGFGYHV-HRDGATASVTGGGKLSACAI 535

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I + +T+ G + V +L+ MGA + V

Sbjct: 536 --VPADISSAAFFLVAAASIAEDSDLTLRHVGMNPTR--VGVINILKQMGANIEVFNEKV- 590

Query: 307 VTGPPREFF--GRKHLKAIDVNMNMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ G P LK ID+ ++P D L + A A+G T +R RVKE+

Sbjct: 591 IGGEFVADLRVQSARLKGIDIPQVLAIDEFPVLFIAACAEGRTVLRGAEEELRVKES 650

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPV 420
+R+ + L LG PD II +++ +++++ DHR++M+F++A+ A P+

Sbjct: 651 DRIQVMADGLAALGVETVTPDGIIDGGQIEGGTVESHGDHRISMSFAVASLRATGPI 710

Query: 421 TIRDPGCTRKTFFPDYFDV 438
I D +FP + D+

Sbjct: 711 RINDCANVATSFPGFVDL 728

>ref|YP_003417278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes 08-5923]
gb|ADB71916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes 08-5923]
Length = 430

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 121/437 (27%), Positives = 220/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPGSKSLSNRILLALAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 14 GAITVPGDKSMSHRSIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 71

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMN 125

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 126 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 185 ETIIHEKEK-----TRDHTHEMIRQFGEIEMDGLTIR--VKGQKF-TGQEMTVPGDVS 236

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 237 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGSLEVKDSSRS-TGKLAGT 293

Query: 315 FGRK--HLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 294 VVVKTSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAT 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 ELNKMGAADITPTEDGLIIRGKTPHAAANVTSYGDHRIGMMLQIAALLVEEGDVLELERPEA 413

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSVSYPTFFEDIRSLK 430

>ref|ZP_06163678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 848 str. F0332]
gb|EEZ77069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces sp. oral
taxon 848 str. F0332]
Length = 425

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 132/422 (31%), Positives = 191/422 (45%), Gaps = 63/422 (14%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
M AL +G VE D AA +VV G P+ A +V L AG MR + A
Sbjct: 1 MAQALAAMGAGVEGDGAA---IVVTPG---PLRGAHVVDVGL---AGTVMRFVPPIALFA 50

Query: 116 GGNATYVLDGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKV 172
G+ V DG R RPI LV L+QLG + G P+ V G G + GG V
Sbjct: 51 RGD--VVFDDGEAARTRPIAPLVRALQLGGQIAHSTSASGQAALPMTVKKGKGTVTGGTV 108

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFGVKAHSDSW 231
++ S SSQ++SALL+AAP ++I + I S P++ MT+ ++ G+ D
Sbjct: 109 EIDASASSQFVSALLAAPRMERGLDIRHTGRRIPSAPHIAMTVDLREAGIAVRAIDRS 168

Query: 232 DRFYIKGGQKYKSPKNAY-----VEGDASSAS 258
R SP N VE D S+A
Sbjct: 169 GRSGLSPSVEPSPCNGSDARGGLGAEPADPPGQPTRWTVPEGPRIQDVTVEPDLSNAG 228

Query: 259 YFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRK 318

```

      FLA A TGG  ++      S Q      + E+ E MGA+      + + + GP
Sbjct: 229 PFLAAMATGGETILDW--PDSRQPGAAYRELFEAMGARTRAADGRLALRGP-----A 279

Query: 319 HLKVIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
      + +D +M+ + ++ T+A VA FA+GP+A+R++ R ET+R+ A+ ELTK+GA+
Sbjct: 280 TIAPLDADMHDVGVLPVTAVAFAFANGPSALRNIGQLRGHETDRLAALVAELTKVGATA 339

Query: 379 E-EGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVP-VTIRDPGCTRKTFPDYF 436
      + EG D I P K      I+TY DHRMA F      +P + + + T KTFP +
Sbjct: 340 QIEGDDLLIEPGPPK--PATIETYADHRMAT-FGAILGLRIPGLRVANVETAKTFPQFV 396

Query: 437 DV 438
      D+
Sbjct: 397 DM 398

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>ref|YP_141056.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
      thermophilus CNRZ1066]
sp|Q5M0L5.1|AROA_STRT1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|AAV62241.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
      thermophilus CNRZ1066]
      Length = 427

```

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/434 (27%), Positives = 217/434 (50%), Gaps = 37/434 (8%)

```

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G++++PG KS+S+R ++ +L++G T V ++L EDV + R LG+++E D
Sbjct: 10 LRGSRLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVTIEDDGDVV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      R VG G K P      + +L +GN+G ++R ++ + AG + + G + +RP
Sbjct: 70 RIHGVSFVDFGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFDVEMFGDDSLSKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      + + + L+Q+G +V      D PP++++G L      +L + S+Q SAL+ AA A
Sbjct: 122 MDRVVTIPLRQMGEVSGQTDRLDPLPKMHGSKSLKPIYYELPVA-SAQVKSALIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      D E II+K + + E      ++++FG + +      R I GGQ + + + V GD
Sbjct: 181 --DGESVIEIEKTRNHE---DMIQQFGGQLQVEGKEIR--ISGGQTF-TAQEVVVPD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
      SSA+++L AG + + ++ G + +V++ MG K+ ++ S T+
Sbjct: 233 ISSAAFVLVAGLVVPSKIVLKNVGINETR--TGIIDVIKDMGGKIKLSIDIDQVAKSATI 290

Query: 308 TGPPREPFGKHLKVIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERM 364
      T E      LK ++ + +P + L ++ L A G T IRD +VKET+R+
Sbjct: 291 TVETSE-----LKGTEIGGDIIPRLIDELPIITLLATQAQKTVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTI 422
      + L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +
Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTPHGAENVTFGDHRIGMMAIAALLVQDGEVDL 404

Query: 423 RDPGCTRKTFPDYF 436
      +      ++P +F
Sbjct: 405 QRAEAINTSYPSFF 418

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>gb|ACN18616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
      monocytogenes]
      Length = 428

```

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/435 (27%), Positives = 216/435 (49%), Gaps = 25/435 (5%)

```

Query: 17 GTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
      G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

```

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSATIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVLNPTRTGI-FDVKQMGGSLVVKDSSRSTRKLAGTVV 293

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLKGTEDGLIIPRLIDEIPVIALLATQAEGTTIKDAAELKVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAITPTEDGLIIGHKTPHAAANVTSYGDHRIGMMLQIAALLVEEGDVLELERPEAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTTFEDIRSLK 428

>ref|YP_001010994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9515]
sp|A2BVS6.1|ARO_A_PROM5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM71887.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9515]
Length = 438

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 123/447 (27%), Positives = 210/447 (46%), Gaps = 38/447 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GT+K+PG KS+S+R L++ +++EG T ++ L SED LR LG+ + K
Sbjct: 13 KSLQGTIKVPGDKSISHRSLIIGSIAEGETNIEGFLYSEDPLSTADCLRKLGVHPIEIKK 72

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + G G ++ +E ++ GN+G MR L + A + ++L G + E
Sbjct: 73 DQPFITIRGLG----IDGFREPKEILNCGNSGTTMR--LLMGLLAGQTDNRNFIITGDKSLNE 127

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSA 185
RP+G + L +G + P+ + G KL G + S+Q SA
Sbjct: 128 RPMGRVSKPLSLMGGKIYGRENKTAISITG-----NKLKGCVIGTPVASAQVKA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKS 244
+L+A A G + I+ S + E R+++ FG + R IK G +
Sbjct: 180 ILLAGLNASGTTTSV--IEPASSRDHTE---RMLKAFGADIKIRGELGRNIVIKSGNNL-T 233

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
+N + GD SSA++++ A+I + V+ G + + V++ MG E
Sbjct: 234 GQNILIPGDISAFAFMIAASIVPESEILVKNVGLNPTRTGI--LHVMDMGCDYKIIK 291

Query: 304 SVTVTGPPREPFGFRKH---LKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
S T+ G P K+ LK V + +P D L V A F +G + I+D R
Sbjct: 292 S-TIAGEPIGSIKVKYVSNLKPFKVQGDILPKLIDEIPILTVAACFCNGVSEIKDAKELR 350

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CA 416
VKET+R+ + +L K GA++ E D IIT K + +D+ DHR++M+ ++A+ A
Sbjct: 351 VKETDRLKVMARQLKKFGANITEKGLIITGESKFHSAEVDSETDHRVMSLAIASLLA 410

Query: 417 EVPVTIRDPGCTRKTTFPDYFDVLSTFV 443

+ I G + ++P ++D L +
Sbjct: 411 KGSTRIARAGASNVSYPTFWDDLEKLI 437

>ref|ZP_06194827.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia muridarum
Nigg]
ref|ZP_06195747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia muridarum
Weiss]
Length = 438

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/433 (27%), Positives = 200/433 (46%), Gaps = 28/433 (6%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVLEADKAAKRA 76
G +P SKS S R +L A+LS+GT+++N L+S D ML A + G + +
Sbjct: 14 GEFSIIPPSKSHSLRAILFASLSKGTSLIINNSLSSPDTDTMLSACKKFGARI-----TRVG 68

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA + + + ++ G ++ RPI
Sbjct: 69 ETLHIQGNPPPYQYSSHHFHMGNNGIALRFLTALSSLSP--SPILITGAHTLKRRPIEP 126

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L+QLG+++ + P V G + G V +SG SQY SAL + A +A
Sbjct: 127 LLSSLEQLGSEIRQKKSSSIPFVIR---GPISSGHVTISGQ-DSQYASALAITAAVAPHP 182

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + S D + G Q KS + V GD SS
Sbjct: 183 LSFS-IENLKERPWFDLTLDWLHSLNISF--SREQDSLFFPGAQSIKSFSYS-VPGDYSS 238

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A++ A ++ + + + QGD + +L+ +GA + + + + P
Sbjct: 239 AAFLAALGLLSSSNPTVLYNLPSKDPQGDQLFSLKSLGADIVIEKDHIEIR--PSSF 296

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G ++M+ D LAV+ FA P+ + + R KE+ R+ AI EL K+
Sbjct: 297 SGGV-----IDMDPFIDALPILAVLCCFAKNPShLYNALGARDKESNRIEAIAHELKRM 350

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTF 432
G SV D I P +L+ + +++DHR+AMA ++A + + + C K+F
Sbjct: 351 GGSVHPTQDGLYIE-PSRLHGAVVHSHNDHRIAMALAVAGVHASSGQTLLCNTQC VNKSF 409

Query: 433 PDYFDVLSTFVKN 445
P + T N
Sbjct: 410 PHFVIAAQT LHAN 422

>gb|ADY01630.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vulcanisaeta
moutnovskia 768-28]
Length = 433

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 126/438 (28%), Positives = 211/438 (48%), Gaps = 31/438 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL- 64
++++ + G V+ P SK+L+ R +L +ALS ++ L +D M+ ++ +
Sbjct: 3 KLIINGFRAREGVVEAPPSKALTLYILASALSRTWVLLRKLNWGDDTWSMIRGIKPISE 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V+ D R V +F V D G +G +R+LT + G V
Sbjct: 63 VEVKNDSVIRIRREV--TLERFRVIDT-----GESGFTLRTLTVYSGIDGTTLLVPR 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ +L+ LK L A VD LG+ +RV G L GG V +SGSISSQY+S
Sbjct: 113 G--SLIGRPMDELLNALKNLNAKVDR-LGS---VIRVIG-SKLVGGYVTISGSISSQYVS 165

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL APL G +EI I + S PY++ T+ +++ F + E ++ D Y+ G Q++K+
Sbjct: 166 ALLYLAPLTEGGIEISIKPPVKS RPYIDATINVLKDFNINVEGNN--DMIYVSGSQEFKA 223

Query: 245 PKNAYV-EGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTE 302
+V GD S A+Y+ + +TG + + +++ + F +G ++ E

Sbjct: 224 VNEEFVIPGDYSLAAYTTLSVLTGVDIRITNLHRDRAIESEYAFIRYAREVGVIEEKE 283

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SV V G LK +++++ PD+ M LA++ A G + I + KE+

Sbjct: 284 GSVIVKGS-----SVGDLKPLNIDLSDSPDIVMPLALLLARAHGKSRIVGINHLVYKESN 338

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPP---EKLNVTAIDTYDDHRMAMAFSLAA-CAEV 418
R+ + + L LGA V II E ID +DHR+ M + A A+

Sbjct: 339 RLRGVASVLKCLGAGVNIDEVNGIIEIEGVHEMRGGCEIDAVNDHRIVMMSVIGALSAKE 398

Query: 419 PVTIRDPGCTRKTFPDYF 436
P+TI + K++P +

Sbjct: 399 PITIINWEGISKSWPAFI 416

>ref|ZP_03971954.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
glucuronolyticum ATCC 51866]
gb|EEI63320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
glucuronolyticum ATCC 51866]
Length = 400

Score = 137 bits (346), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 131/427 (30%), Positives = 203/427 (47%), Gaps = 55/427 (12%)

Query: 27 LSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA--KRAVVVGCGG 83
++NR L+AA + +V+ L S D M ALRTL G V+ D + + V G G

Sbjct: 1 MTNRLIIAAGATSPSVIRGALASRDSLDLADALRTLGCVEVDVGSTVTVRPGPVTGGG- 59

Query: 84 KFPVEDAKEEVQLFLGNAGIAMR-----SLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
++ G AG MR +L+A T GG+ R RP+ +

Sbjct: 60 -----RVDCGLAGTVMRFPVPAALSATPTLIGGDQAA-----RRRPMSTM 100

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLALGD 196
L QLGA V+ + P+ V+G + GG ++ S SSQ++S LL++ A G

Sbjct: 101 TDALVQLGAHVEG---ETLPMTVSGP--ITGGTARIDASASSQFVSGLLSGARFPAGV 154

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKA-EHSDSWDRFYIKGGQKYKSPKNAY----- 249
I D + S+P++EMTL ++ GV++ +H D Y + P Y

Sbjct: 155 TVIHTGDSVPSLPHIEMTLDMRLTAGVESTQHHEETGTY-----SWTVPHQEYAGGEVT 209

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWT-ETSVTVT 308
+E D S+A+ FLA AA+TGG V+V G T+ Q + + MG + + ++TV+

Sbjct: 210 IEPDLSNAAFLAAAVTGHHVSVGPWATTTPQPGDDIRHIFDAMGCTHELSSDGTLTVS 269

Query: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
GP L ID +++ + ++ T+A V FAD P+ + +A R ET+R+ A+

Sbjct: 270 GP-----ADGVLHGIDADLSAVGELTPTVAAVCAFADSPSRLTGIAHLRGHETDRLQALT 324

Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAAAEVPTIRDPGCT 428
ELT LG EE D IT P + +Y+DHRMA A ++ + + T

Sbjct: 325 AELTNLGCDCCELADGLAIT-PAPMTGGLWRSYEDHRMATAGAIIVGLKVKDTFVENIETT 383

Query: 429 RKTFPDY 435
KT PD+

Sbjct: 384 SKTMPDF 390

>emb|CBK63796.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alistipes shahii WAL
8301]
Length = 414

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 134/430 (31%), Positives = 202/430 (46%), Gaps = 33/430 (7%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + GT+ P SKS + R L A LSE +V+ N+ +D L + TLG V

Sbjct: 6 PPGRVKGTLTPPCSKSYAQRALAAALLSEEVSVLRNIEFCDDTRSAQCIEITLGARVRRV 65

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
++ G K V L +G +G++ R T + T ++G +

Sbjct: 66 DPTSLSIEGGLSPKGCV-----LNVGESGLSTRLFTPVASLCPTPVT--IEGRGSL 115

Query: 131 ERPIGDLVVGLKQLGA---DVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RP+ + L++LG D FL P+ V G + GG+ ++ GS+SSQ+++ LL
Sbjct: 116 RRPMQMMFEPLRRLGVRVRDNGGFL-----PIEV--CGPIQGGEAEVDGSVSSQFITGLL 168

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A PLA D + + +S PY++MTL RFG++ D ++ FYI G Q+Y+S
Sbjct: 169 LALPLARRDTSLHV-RGAVSTPYLDMTLDTAARFGIEISQRD-YEEFYIPGRQRYRSTYF 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ +EGD S+A+ L A T G VTV S Q D L GA V E SVT
Sbjct: 227 S-IEGDWSAAAMLLVAGA-TAGEVTVRVNSMLSKQADTAICTALVRAGAAVINEEDSVTA 284

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
P L+A + + PD+ LA +A ADG + IR + KE R AI
Sbjct: 285 LHRP-----LRAFEFDATNCPDLFPALAAALAAADGVSVIRGTSRLEYKECNRSEAI 336

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
R E KLG V+ + + K+ ++ DHRMAM+ ++AA ++ V I
Sbjct: 337 REEYAKLGIEVDTSEEDLMKIRGGKVRARTQSHGDHRMAMSLAVAALRSDEAVEIEGAE 396

Query: 427 CTRKTFPDYF 436
K++P +F
Sbjct: 397 SVAKSYPGFF 406

>gb|ACN18406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
Length = 428

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/435 (27%), Positives = 216/435 (49%), Gaps = 25/435 (5%)

Query: 17 GTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVLEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GAITVPKDKSMHSRSMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGAG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMPN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMMEYHMPVA-SAQVKSIIIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLAIR--VKGQKQF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI-FDVVKQMGGSLLVVKDSSRSTGKLAGTVV 293

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLGKTEIDGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAADITPTEDGLIIHGKTPHAAANVTSYGDHRIGMMLQIAALLVEEGDVLELERPEAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTFFEDIRSLK 428

>ref|YP_002829836.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus M.14.25]
ref|YP_002915112.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus M.16.4]
sp|C4KIN0.1|AROASULIK RecName: Full=Probable 3-phosphoshikimate

1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
sp|C3MXK4.1|AROASULIM RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ACP38538.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
M.14.25]
gb|ACR42444.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
M.16.4]
gb|ADX85753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
REY15A]
gb|ADX83117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus islandicus
HVE10/4]
Length = 414

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 202/440 (45%), Gaps = 47/440 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
EISGT+K P SKSL+ R++ L+ + + NL+ SEDV + ++R LG+ V+ +
Sbjct: 9 EISGTIKAPQSKSLAIRLIFLSLFTTR--IHLHNLVLSERVEDIDAINSVRALGVEVKNNSEF 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ KF + L +G +R L V A GG T +D +R RP
Sbjct: 67 IPPEKLEIKKKF-----IKLKGSGTTLRMLIPIVAAIGGEVT--IDAEESLRRRP 114

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L G + P+ + G L +K+SG SSQY+S L+ A +
Sbjct: 115 LKRIVEALSNGYIS----FSSSSLPLTITG--KLSSYNIKISGDESSQYISGLIYALHIL 168

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-----A 248
G IEI+ + S Y+ +T+ L RFG +FY G + + +P N
Sbjct: 169 NGG-SIEILPPISSKSYILLTVDLFNRFSGSNV-----KFY--GNKIHINPNNLVEFQG 218

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD AS++ A ++GG T+ GD ++L+ MGA + + V
Sbjct: 219 EVAGDYGLASFYALSALLSGGRTTIVNLWEPKEYFGDHSIVKILKEMGATSEYLDGKWYV 278

Query: 308 TGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ +I VN++ PD+AMT+A +A A+G + I + R+KE++R+ +I
Sbjct: 279 EA-----KDKYSSIKVNIDDAPDLAMTIAGLAAIAEGTSEITGIERLRKESDRIESI 331

Query: 368 RTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
R L G E + +I K L+ D +DHR+AM S A V I
Sbjct: 332 RKVLGLYGVGSEVKSNSILIFGINKRMLSSPITDCLNDHRVAMMSSALALVNGGV-ITSA 390

Query: 426 GCTRKTFPDYF-DVLSTFVK 444
C K+ P+Y+ D+LS K
Sbjct: 391 ECVSKSNPNYWQDLLSLNAK 410

>ref|YP_001680496.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Heliobacterium
modesticaldum Icel]
gb|ABZ84485.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Heliobacterium
modesticaldum Icel]
Length = 424

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 130/438 (29%), Positives = 207/438 (47%), Gaps = 22/438 (5%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G ++PG KS+S+R ++ AL+ G T V L +D + R LG+ +E ++
Sbjct: 1 MRGETEVPGDKSISHRAVMFGALARGVTRVHRFLPGQDCLSTIDCFRKLGVRIEQPNPSE 60

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VVV G +++ E L +GN+G +R +T ++ G ++ G +R RP+
Sbjct: 61 --VVVYGQGPGLKEPSE--VLDVGNSGTTIRLMTGILS--GLPFFSIVTGDTSIRRRPM 114

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194


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      G +   L ++GA +           P+ +NG           S   S+Q   SA+L+A   A
Sbjct: 115 GRVTRPLLEMGASIWGRENATKAPLAINGASMALEAIHYNSPVASAQVKSAVLLAGLFAE 174

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G   +   + L+S + E   R++ FG K   S+           ++G + ++ +   V GD
Sbjct: 175 GCTSVR--EPLVSRDHTE---RMLAAGAKIGRSEDRLTASVEGFPELRA-QEVEVPGDI 228

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPRE 313
      SSA++ L A+I G+ + +   G   + +   EVL MG V   E +   V G
Sbjct: 229 SSAAFLVAASIVPGSELVLYNIGVNPTRDGI--IEVLRAMGGDV-QVENAREVAGELVA 285

Query: 314 PF--GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      LK   +   +P   D   +AV ALFA+G T IRD A   RVKET+R+   +
Sbjct: 286 DLIVRSASLKGTTIGGAIIPRLIDELPIIAVAALFAEGTTEIRDAEMRVKETDRIAVMI 345

Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGC 427
      EL KLGA +EE PD   II           L   A +++ DHR+AMA ++A   AE   I D G
Sbjct: 346 RELRKLGADIERPDGMIIRGGAALRGAATESHGDHRVAMALAVAGLLAEGETVINDAGS 405

Query: 428 TRKTFPDYFDVLSTFVKN 445
      +FP + ++L   +
Sbjct: 406 IDVSFPGFAELLERLRRR 423

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>ref|ZP_05236131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes 10403S]
gb|ACN18352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18358.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18394.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18397.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18418.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18421.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18565.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18631.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
Length = 428

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/435 (27%), Positives = 216/435 (49%), Gaps = 25/435 (5%)

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Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
      G + +PG KS+S+R ++   A++EG TV+ + L ++D   + A + LG+ +E   + +
Sbjct: 12 GAITVPGDKSMHSRIMFGAIAEGKTIVRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

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Query: 77 VVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMM 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQMQGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSIIIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQKQF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI-FDVVKQMGGSLLVVKDSSRSTGKLACTVV 293

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLGKTEIDGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAADITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVLELPEREAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTFFEDIRSLK 428

>ref|NP_297019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia muridarum
Nigg]
ref|ZP_07225032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia muridarum
MopnTet14]
sp|Q9PK28.1|ARO_A_CHLMU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAF73581.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydia muridarum
Nigg]
Length = 441

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/433 (27%), Positives = 200/433 (46%), Gaps = 28/433 (6%)

Query: 17 GTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G +P SKS S R +L A+LS+GT++++N L+S D ML A + G + +
Sbjct: 17 GEFSIPPSKSHSLRAILFASLSKGTISIINNSLSSPDTDMLSACKKFGARI-----TRVG 71

Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ G P +GN+GIA+R LTA + + + ++ G ++ RPI
Sbjct: 72 ETLHIQGNPPYSQYSSHHFHMGNSGIALRFLTALSSLSP--SPILITGAHTLKRRPIEP 129

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L+QLG+++ + P V G + G V +SG SQY SAL + A +A
Sbjct: 130 LLSSLEQLGSEIRQKKSSSIPFVIR---GPISGHVTISGQ-DSQYASALAITAAVAPHP 185

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ I+ L P+ ++TL + + S D + G Q KS + V GD SS
Sbjct: 186 LSFS-IENLKERPWFDLTLDWLHSLNISF--SREQDSLFFPGAQSIKSFSYS-VPGDYSS 241

Query: 257 ASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A++ A ++ + + + QGD + +L+ +GA + + + + P
Sbjct: 242 AAFLAALGLLSSSSNPTVLYNLPSKDPQGDQLFSLKSLGADIVIEKDHIIEIR--PSSF 299

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
G ++M+ D LAV+ FA P+ + + R KE+ R+ AI EL K+
Sbjct: 300 SGGV-----IDMPFIDALPILAVLCCFAKNPSHLYNALGARDKESNRIEAIHAELRKM 353

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTF 432
G SV D I P +L+ + +++DHR+AMA ++A + + + C K+F
Sbjct: 354 GGSVHPTQDGLYIE-PSRLHGAVVHSHNDHRIAMALAVAGVHASSGQTLLCNTQCYNKSF 412

Query: 433 PDYFDVLSTFVKN 445
P + T N
Sbjct: 413 PHFVIAAQTLAN 425

>ref|ZP_04162154.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock1-4]
gb|EEM06141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock1-4]
Length = 415

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 122/438 (27%), Positives = 214/438 (48%), Gaps = 33/438 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EGTT + N L ED + R LG+ +E D
Sbjct: 1 MNGTIAVPGDKSISHRAVMFGAIAEGTTKISNLLGEDCLSTIACFRKLGIMIEEDG--- 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+V G +++ KE L +GN+G +R + + A + T + D + +RP+
Sbjct: 58 NDVIVYGKGLAGLQEPKE--VLDVGNSGTTIRMLGILANAPFHCTIIGD--ESIGKRPM 113

Query: 135 GDLVVLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+++ A ++ P+ + G G + G S S+Q SA+L+A
Sbjct: 114 KRVTAPLREMDAQIEGREDDGQYTPLSIRG-GNIKGIHYH-SPVASAQVKSAILLAG--LQ 169

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ + + L S + E R++ FG E + ++GGQ + V GD
Sbjct: 170 GEGVTSVTEPLQSRDHTE---RMLRAFG--CEVNVEGRTVSLQGGQSLVGTE-IEVPGDV 223

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++FL AGA + + + + G + + + +VL MGA ++ V E
Sbjct: 224 SSAAFFLVAGAIVPNSKLVLKNVGLNPTRTGI--LDVLSEMGALISIR---NVRNEEFE 277

Query: 314 PFG----RKHLKAIDVNMNMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMV 365
P G LK I++ + +P + + ++AL A G T I+D +VKET R+
Sbjct: 278 PCGDITITETSELKIEIGGSLIPRLIDEIPIIALLATQATGTTIHKDAEELKVKETNRIN 337

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC-AEVPVTIRD 424
+ EL KLGA +E PD II +KL ++++ DHR+ + ++A+C AE + I +
Sbjct: 338 TVVDELRLKLGAEIATPDGMIINGNQKLQGNIVNSHGDHRIGIMLAIASCIAEGEMQIEN 397

Query: 425 PGCTRKTFPDYFDVLSTF 442
++P++F+ L +
Sbjct: 398 GDAVAVSYPNFFEQLESL 415

>ref|NP_465447.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes EGD-e]
ref|ZP_03668620.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes Finland 1988]
ref|ZP_03669585.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes FSL R2-561]
ref|ZP_05231879.1| aroE [Listeria monocytogenes FSL N3-165]
ref|ZP_05301052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes LO28]
sp|Q8Y5Y0.1|AROALISMO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD00001.1| aroE [Listeria monocytogenes EGD-e]
gb|ACN18361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18364.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18373.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18376.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18382.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria

gb|ACN18547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18550.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18556.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18568.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18571.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18574.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18577.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18586.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18598.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18601.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18622.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18637.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18676.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18679.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18685.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18703.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18721.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18724.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|EEW12900.1| aroE [Listeria monocytogenes FSL N3-165]

Length = 428

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 119/435 (27%), Positives = 216/435 (49%), Gaps = 25/435 (5%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GAITVPGDKSMHSRIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIAKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSAAIFAAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFLFIVAGLITPGSEIELTHVGLNPTRTGI-FDVVKQMGGSLVVKDSSRSTGKLAGTVV 293

Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLGTEIDGDIIPRLIDEIPVIALLATQAEGTTIIKDAELKVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAADITPTEDGLIIHGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVLELERPEAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTTFEDIRSLK 428

>ref|YP_003433377.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenobacter
thermophilus TK-6]
dbj|BAI70176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenobacter
thermophilus TK-6]
gb|ADO46096.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenobacter
thermophilus TK-6]
Length = 432

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 129/446 (28%), Positives = 211/446 (47%), Gaps = 31/446 (6%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L+ K + G +++P KS+S+R ++L+A++EG +V+ N L+SED L + LG VE
Sbjct: 4 LKAKSVKGELRVPSDKSISHRAVILSAIAEGKSVIRNWLSSDRTLATLQIAKALGTKVE 63

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 128
++ G F D + + N+G R + A V+ G
Sbjct: 64 TK--GNELMITGRDFNFCEDYVLDAR---NSGTTARLFLGV--ATQEFFSVITGDES 115

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+ +V L+Q+GA +D + P+ V G G L G + S+Q S+LL+
Sbjct: 116 LRNRPMRLRVVEPLRQMGAFLDGREKGNKLPICVRG-GKLGVSF-FNKRASQVKSSLLL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKS 244
A A G EI + PY+ + T R+++ FG + IK GGQK
Sbjct: 174 AGLKAEGITEI-----TEPYLSRDHTEMLKLFGANITQLEGSSGHIKIAGGQKLYG 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETST 304
+ D SSA++F+A A + + + + D F L MGA V +
Sbjct: 227 CE-VLCPADPSSAAFFVALATLLEDSQLILKDVLINPTRD-GFFRKLQMGAYVEYANVR 284

Query: 305 VTVTGPPEPF---GRKHLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRV 358
V+G P G + LK +++ +P + L ++AL A+G + ++ R

Sbjct: 285 -EVSGEPVADIVVEGGRKLKGLNITKEDVPSLIDELPLLALVMSLAEGSSIVKGAEELRF 343

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KE++R+ A+ L +GA++EE D I EKL I TY DHR+AM FS+A AE

Sbjct: 344 KESDRIKAVVENLRSMGANIEEYQDGFYIEGVEKLKGANIKTYS DHRIAMTFSVAGLVAE 403

Query: 418 VPVTIRDPGCTRKTTFPDYFDVLSTFV 443
TI +P C ++P++++ L+ +

Sbjct: 404 GETTIDNPECVSVSYPNFYEDLNKII 429

>ref|ZP_05623317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Treponema vincentii
ATCC 35580]
gb|EEV19546.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Treponema vincentii
ATCC 35580]
Length = 485

Score = 137 bits (345), Expect = 3e-30, Method: Compositional matrix adjust.
Identities = 131/468 (27%), Positives = 202/468 (43%), Gaps = 60/468 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV----- 67
GT+ P SKS + R L+ A+L+E + + L S D+ + ALR LG+++

Sbjct: 10 FCGTMTAPTSSKSHITIRALICASLAESPFITAPLISGDMESAIQALRQLGVTITEVSHKP 69

Query: 68 -----EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI 103
++ + + + G GGK +D EE+ L LGN+G

Sbjct: 70 LTLKVTPPARGLLSFAEGAVNTGQNSEYSEQNIPFGHGGKQSGQD--EELLLNLGNSGS 127

Query: 104 AMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLG-----ADVDCFLGTDC 156
+ L + AA L G +R RP L+ +Q G D D TD

Sbjct: 128 LLYFLGMILAAA--ETPVCLTGDESLRSRPAAPLLSIYRQAGISYSAAKPSDT-RSTDV 184

Query: 157 PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLR 216
PP+R G LP G +L G S Q ++ LL APL G I +K PY+ MT

Sbjct: 185 PPLRF--CGPLPAGNYQLDGPFS-QPVTGLLFTAPLLNGMSRI-TFNKAGERPYLRMTCD 240

Query: 217 LMERFGVKAEH---SDSWDRFYIKGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVT 272
+ G+ H +D+ F I G Q+Y+ P + GD SSA + L A I +T

Sbjct: 241 WLRIAGITLTHGGFDTDTCS-FEIAQNRYQ-PFRTTIPGDWSSALFPLTAAVICNAALT 298

Query: 273 VEGCGTTSLQGDVKAFAEVLMMGAKVWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPD 332
+ QGD + +L+ MGA + TV+ P L+ + +PD

Sbjct: 299 LTNLDPADTQGDSRALSILQAMGADIRCD AERTTVSVFPIS----GTLRGGRFDCGDIPD 354

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPP 390
LA A+F G T + + R KE +R+ A EL K GA + +G ++ I +

Sbjct: 355 AVPILAAAVFCSGQTLTLAGVCRFKECDRLAASAEELAKFGAHIVQGENFLRIDSGG 414

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAACAEVPVT-IRDPGCTRKTTFPDYFD 437
L+ + + DHR+AM ++AAC + I D C + ++P + +

Sbjct: 415 TGLHPAQVRSRGRDHRIAMMLAVAACGIAETSCIEDFCVKISYPRFIE 462

>gb|ACN18640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
Length = 428

Score = 137 bits (345), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 119/435 (27%), Positives = 216/435 (49%), Gaps = 25/435 (5%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +

Sbjct: 12 GAITVPGDKSMHSRIMFGAIAEGKTIVRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+

Sbjct: 70 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G

Sbjct: 124 RVMLPLQMQGAKMHGKDGSEFAPITITGKQSLKRMEYHPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I ++K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHEHMIRQFGGEIEMDGLAIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + F V +M G+ V + T
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI-FDVVKQMGSLVVKDSSRSTGKLAGTVV 293

Query: 315 FGRKHLKAIDVNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTEL 371
LK +++ + +P + + V+AL A +G T I+D A +VKET R+ A+ TEL
Sbjct: 294 VKTSKLKGTEIDGDIIPRLIDEIPVIALLATQAEGTTIKDAAELKVKETNRIDAVATEL 353

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTR 429
K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 NKMGAIDITPTEDGLIIGHKTPHLAANVTSYGDHRIGMMLQIAALLVEEGDVLELPERPEAVS 413

Query: 430 KTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSYPTFFEDIRSLK 428

>ref|YP_001664977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
pseudethanolicus ATCC 33223]
ref|YP_001663052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X514]
ref|ZP_05493541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
ethanolicus CCSD1]
ref|ZP_07131467.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X561]
ref|YP_003904364.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X513]
ref|YP_004185972.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
brockii subsp. finnii Ako-1]
sp|B0K0J1.1|AROA_THEPX RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B0K928.1|AROA_THEP3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABY92716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X514]
gb|ABY94641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
pseudethanolicus ATCC 33223]
gb|EEU61464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
ethanolicus CCSD1]
gb|EFK84232.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X561]
gb|ADN55073.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
sp. X513]
gb|ADV79589.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoanaerobacter
brockii subsp. finnii Ako-1]
Length = 423

Score = 137 bits (345), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 123/443 (27%), Positives = 215/443 (48%), Gaps = 30/443 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I ++ + + G + +PG KS+S+R +++ +++EG T ++N L ED + ++ LG+
Sbjct: 2 DIEVKKRFLKGVISVPGDKSISHRAVMIGSIAEGITEIENFLLGEDCISTINCMKNLG 61

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + V GK + E++ L +GN+G +R L + AG L G
Sbjct: 62 DIEL-----KGTNVKVQKGGLYLNKSEKI-LDVGNSGTTIRLLMGIL--AGQKFETTLTG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
++ RP+G ++ L +GA ++ G + P+ V G L G K+ + S+Q S+
Sbjct: 114 DDSIKRRPMGRVITPLSMMGAKIEAREG-NFAPLTVFG-NKLKGIYKMPIA-SAQVKSS 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+++A+ A IE P T + FG K E + + Y G K +

Sbjct: 171 IMLASLYADDKTTIEE-----PYPSRNHTELMFSSFGAKVEVNGTKITCY--PGYKLQGG 223

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT-ET 303
K V GD SSA+YF+ A + VT++ + + +V++ MG + T E

Sbjct: 224 K-VIVPGDISSAAYFIVAATLVPNSEVTIKNVNPNTRTGI--IDVIKEMGGDIVLTNER 280

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
++ LK I++ + +P D +AV A+FA+G T I+D +VKE

Sbjct: 281 TINNEKVADITVKTSLRGIEIGGSLIPRLIDEIPVIAVAAVFAEGKTVIKDAEELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVP 419
+ R+ I +EL K+GA + E D II L +++Y+DHR+AM+ +A AE

Sbjct: 341 SNRINTITSELKKMGAKIFETEDGMIEGTGFLKGNTVESYNDHRIAMSLWVAGLMAEGE 400

Query: 420 VTIRDPGCTRKTFPDY---FDVL 439
I++ C ++PD+ FD+L

Sbjct: 401 TKIKNAECVNISYPDFYKTFDML 423

>ref|ZP_05133085.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stenotrophomonas sp.
SKA14]
gb|EED37146.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stenotrophomonas sp.
SKA14]
Length = 435

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 130/445 (29%), Positives = 217/445 (48%), Gaps = 32/445 (7%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ A+ + + + G++ +PG KS+S+R ++ AAL++GT+ +D L ED

Sbjct: 1 MSNAQHWIARKGQPLQGSALTIPGDKSVSHRSVMFAALADGTSHIDGFLEGEDTRATARIF 60

Query: 61 RTLGLSVEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
LG+ +E ++R V VG G K P + L GNAG MR L + +

Sbjct: 61 SQLGVRIETPSPSQRIVHGVGIDGLKAP-----DAPLDCGNAGTGMRLLAGLLAGQAFD 114

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
T + D + RP+ + L Q+GA +D PP+ V+G L G + + +

Sbjct: 115 CTLIGD--ESLSGRPMRRVTGPLSQMGAKIDT-ESDGTPLHVHGGQTLHG--IDFASPV 169

Query: 179 SS-QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S Q SA+L+A A G+ ++ P + T R++ FGV E S R ++

Sbjct: 170 ASAQIKSAVLLAGLYAQGETQVTEPH-----PTRDYTERMLSAFGVDIEFSPGKAR--LR 222

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
GGQ+ ++ + V D SSA+++L A+I G+ + ++ G + + A L +MGA

Sbjct: 223 GGQRLRA-TDIVVPADFSSAAFYLVAASIIIPGSELRLKQVGLNPRRTGLLHA--LRLMGA 279

Query: 297 KVTWTETSVTVTGPPREPFGFRKH--LKAIDVNMNKMPPDVA---MTLAVVALFADGPTAIR 351
+T E G P ++ LK + + +PD+ L V A A+G T +

Sbjct: 280 DIT-EENPAEQGGEVADLVVRYAPLKGARIPESLVPDMIDEFPALFVAAAAAEGQTVVS 338

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS 411
A RVKE++R+ A+ T L LG V+E D + +L I+++ DHR+AMAF+

Sbjct: 339 GAAELRVKESDRLAAMATGLRALGMQVDEDEDGATLHGGVRLGSGTIESHGDHRIAMAF 398

Query: 412 LAA-CAEVPVTIRDPGCTRKTFPDY 435
+A ++ V I D +FPD+

Sbjct: 399 IAGQISDGEVRINDIANVATSFDPF 423

>ref|ZP_01667017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosinus
carboxydivorans Nor1]
gb|EAX47120.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosinus
carboxydivorans Nor1]
Length = 445

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 135/447 (30%), Positives = 212/447 (47%), Gaps = 28/447 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66

Sbjct: 2 IVL+ + GTV +PG KS+S+R ++L AL+EG T +D L +D + R LG++
IVLKC�HGLQGTVTVPGDKSISHRAVLMGALAEGITTIDGFLPGKDCLATIDCFRKLGVN 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ + R V G G + A +EV L++GN+G +R L + A V+ G

Sbjct: 62 IC--QTGSRVEVEGVLRG--LRAPQEV-LYVGNSGTTIRLLLGILAAQ--PFRTVITGD 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS-QYLSA 185
+ RP+G +VV L+ +GA +D + P+ V + GL G + S ++S Q SA

Sbjct: 115 ESICRRPMGRVVVPLRAMGARIDGEGDGNFAPLSVYPVNGLSG--IDYSTPVASAQVKSA 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A A + + +S + E R++ FGV + G +

Sbjct: 173 LLLAGLYA--QSATTVTEPAVSRDHTE--RMLAYFGVDIRREGLSVQVRPASGL---TG 224

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
++ V GD SSA++ +A A I G+ V + G + V +VL+ MG + E

Sbjct: 225 RHVVVPGDISAFLMAAALIVPGSEVIIRNVGVNPTRTGV--IDVLKAMGGDINI-ENL 281

Query: 305 VVTGTGPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G P +H L+ I + +P D +AV A FA+G T IRD A +VK

Sbjct: 282 RDECCEPVADVRVRSRLRGITAGPIIPRLIDEIPVIAVAAFAEGTTTIRDAELKVK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEV 418
E++R+ AI L ++G PD + L ID+ DHR+AMAF++A A

Sbjct: 342 ESDRIAAIVNGLRQMGDAVALPDGLRVQGGGRPLKGAVIDSQGDHRIAMAFIAIAGLMANG 401

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 445
I + C +FP + ++ST N

Sbjct: 402 DTVIGNAECIDVSFPGFAALISTLGAN 428

>ref|ZP_04584797.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium
yellowstonense SS-5]
gb|EFP60641.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium
yellowstonense SS-5]
Length = 431

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 131/447 (29%), Positives = 216/447 (48%), Gaps = 25/447 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E ++ +K I G+++P KS+S+R ++L++L++G ++V N L + D + A R LG+

Sbjct: 2 EKTVMKVKRIEGLRVPSDKSISHRAIILSSLDAGISIVKNFLKAGDTLTTVNAYRKLGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVL 123
+ K V G D +E FL GN+G R LT V A G N L

Sbjct: 62 EI---VEKEGVYIYHKGKL---DGLKEPDDDLDMGNSGTTTR-LTLGVLA-GFNFFTAL 112

Query: 124 DGVPMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
G +R+RP+ + L ++GA +D + P+ + G G L G + +S+Q

Sbjct: 113 TGDDSLRKRPKRVAEPLSKMGAKIDGRKDGNLLPISIRG-GKLTGIDF-FNEKMSAQVK 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+L+A A G E +I+ +IS + E L M + V E + R +K K

Sbjct: 171 SAILLAGLFAKG--ETTVIEPVISRDHTENMLNSMGAY-VSREFTKGYRVTVKKADKL- 226

Query: 244 SPKNAYVEGD-ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+P + V D +S+A + A + I G + ++ + F L+ MGAKV +

Sbjct: 227 NPIHINVADPSSAAFFAAAASVIPGSHIELKDVLVNPTRDG--FFRKLKEMGAKVEYKN 284

Query: 303 TSVTVTGPPREPFGGRKH-LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ + H LK + V ++P D LA++A A+G T I RV

Sbjct: 285 KRDEAGEIVADIYVSYHELGKVKVPKEVPSMIDEIPLLAIIATQAEGETVITGAHEL RV 344

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAE 417
KE++R+ ++ +LG EE PD II +K+ +D+Y DHR+AM F+ L +E

Sbjct: 345 KESDRIKSVIENFKRLGLEAEELPDGMIIRGKQKVKGGIVDSYKDHVRVAMGFAILGLVSE 404

Query: 418 VPTVIRDPGCTRKTFPDYFDVLSTFVK 444
+TI+D C ++P++F+ L K

Sbjct: 405 EGITIKDADCYISYPEFFNHLEKVS 431

>ref|ZP_05023338.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microcoleus
chthonoplastes PCC 7420]
gb|EDX78537.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Microcoleus
chthonoplastes PCC 7420]
Length = 453

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 122/439 (27%), Positives = 214/439 (48%), Gaps = 31/439 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+L A+++G T + LL +D + +G ++ ++ A
Sbjct: 28 LKGNIQVPGDKSISHRALMLGAIAQGETRIQGLLLGDDPRSTARCFQGMGATI-SELNAD 86

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+V G G V + +E + + GN+G +R + + + G + + G +R RP
Sbjct: 87 EVIVKGVG---VGELQEPLDILNAGNSGTTLRMLGLLASQPGRF-FTVTGDNSLSRSP 141

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
+ +V L+Q+GA + P+ + G P + I+S Q S +L+A +
Sbjct: 142 MSRVVHPLQQMGAQIWGRGNGSLAPLAIQGGQLKP---IHYSPIASAQVKSCILLAGLM 198

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G E + + +S + E R+++ FG K + G + + + V G
Sbjct: 199 AQG--ETTVTEPALSRDHSE---RMLKAFGAKITVDPDTHSATVTGPAQLQG-QTVIVPG 252

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L AGA + + +E G + + + L MM A + E V G P
Sbjct: 253 DISSAAFVWLAGAIVPDSDLLIENIGVNPTRTGI--LDALAMNADIQL-ENQRIVAGEP 309

Query: 312 ----REFPGRKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
R + R LKA +++ + +M D LAV A+FA G T IRD A RVKE++R+
Sbjct: 310 VADIRVRYSR--LKACEISGALIPRIDEIPILAVAAIFAQGTTVIRDAELRVKESDRL 367

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIR 423
+ ++L ++GA++ E PD IT L T +D++ DHR+ M+ +AA A+ TI
Sbjct: 368 AVMASQLNRMGATITELPDGLEITGNTPLTGTEVDSHTDHRITMSLAIAALNAQGITTIIH 427

Query: 424 DPGCTRKTFPDYFDVLSTF 442
++PD+ L
Sbjct: 428 GAEEATISYPDFTTTLQRL 446

>ref|YP_003786694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira
pilosicoli 95/1000]
gb|ADK32193.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira
pilosicoli 95/1000]
Length = 422

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 128/448 (28%), Positives = 218/448 (48%), Gaps = 48/448 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+V++P +I G+V + SKS ++R L+ AALS+ D+ + ++ +G
Sbjct: 3 LVIKPSYDIYGSVYI QISKSDAHRALISAALSK-----DISILKPWMKNVGN 50

Query: 67 VEADKAAKRAVVVGCGGKFP-----VEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
+E K A V P +++ ++ + + +G ++R L ++A
Sbjct: 51 IEVTKNA---VSNFADLVPELDYLRVIPKDNSINDIVVDVKESGTSRLRLIPIMSALN 106

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
N T++ G ++ RPI +Q+ F + + G L G + G
Sbjct: 107 INTTFI--GSKKLFSPRIS----VYEQIWQAQGLFFDKKEDSLTIKG--QLKSGDFTIKG 158

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+ISSQ++S LL AAPL G+ +I I +L S PYV MTL+ ++ + I
Sbjct: 159 NISSQFISGLLFAAPLLEGNSKIIIEGELESSPYVFM LKTLKEAKIEISKNMENSLIEI 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296

G Q+Y S N +E D S A++ A A GG VT+ G S+QGD + +L+ MGA
Sbjct: 219 YGSQEY-SALNYEIESDWSHAAF-FAAAGALGGEVTLYGLNKYSIQGDKEILNLIKFMGA 276

Query: 297 KVTWTET-SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
+ E S+TV + GR H A+D++++ +PD+A + +A A G T + + +
Sbjct: 277 SINCNEDGSITV-----KKMGRLH--AMDIDVSDIPDLAPIITALASTAKGTTKLYNASR 329

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC 415
R KE++R+ ++ TK+GA +E D I EKL +++DHR+AMA S+A+
Sbjct: 330 LRYKESDRINDLKDSFTKIGAKIEVTDDEIYIEGVEKLEGGNTTSHNDHRIAMALSVAST 389

Query: 416 -AEVPTVIRDPGCTRKTFPDYFDVLSTF 442
+ + I D K+ F+ L F
Sbjct: 390 ISNNDIIDAESINKS---SFNFLEQF 414

>ref|ZP_02045125.1| hypothetical protein ACTODO_02015 [Actinomyces odontolyticus ATCC 17982]
gb|EDN81537.1| hypothetical protein ACTODO_02015 [Actinomyces odontolyticus ATCC 17982]
Length = 450

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 136/442 (30%), Positives = 208/442 (47%), Gaps = 34/442 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ TV++PGSKS++ R L LAA+++ +V+ L++ D AL +G V+ + A
Sbjct: 14 VDATVEVPGSKSITARALYLAADVADSPSVIRGALDARDTRLFADALEVMGARVKDEGAGI 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRERPI 134
V P+ ++ G AG MR L AA + G + RP+
Sbjct: 74 LRVT-----PMSLPVRGGRIECLAGTVMRFLPP--LAALSPEETLFGGDEQAYARPL 124

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
G L+ L ++GA V P V G P G + + S SSQ+LSALL+ +PL
Sbjct: 125 GPLLDALVRMGATVTYHGERGHLPTVQGP IHTPLGAQAWVDSSSSSQFLSALLLVSPV 184

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIK--GGQKYKS 244
+ + + S+P+VEMTL + GV E D +W F + GG
Sbjct: 185 GDPLFVSAPGVIPSPHVEMTLASLAGAGVDLEVVDTEGRANLSTWHIFPSRPIGG----- 239

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGC-GTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ VE D S+A FLA A +TGG V + G T+ GD A +L MGA +T E
Sbjct: 240 --DITVEPDLNAGPFLAAAMVTGGRVRIPAWPGATTQAGDAWRA-LLGHMGATITLDEE 296

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+T+TGP G + I M ++ ++ T+A + +A P+ + +A R ET+R
Sbjct: 297 GLTLTGTP-----GAGNYPGIKATMAEVGELTPTMAAICAYASTPSHLSGIAHLRGHETDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ A+ E+ + G EE D IIT P L+ I +Y DHRMA ++ +T+
Sbjct: 352 LAALVAEINRAGGQAEETEDGLIIT-PRPLHAAQIRSYADHRMATFGAILGLVTPGITVD 410

Query: 424 DPGCTRKTFPDYFDVLSTFVKN 445
D CT KT P + + ++ V
Sbjct: 411 DIACTSKTLPTFEAMWASLVSE 432

>ref|YP_001200158.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis 98HAH33]
sp|A4W069.1|AROAS_STRS2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP91758.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis 98HAH33]
Length = 426

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 121/446 (27%), Positives = 222/446 (49%), Gaps = 37/446 (8%)

Query: 10 QPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEA 69

+ +++++ GT+++PG KS+S+R ++ +L++G T N+L EDV + R LG+ +E
Sbjct: 5 RSVEKLKGTIRVPGDKSISHRSIIFGSLAKGVTRFHNILRGEDVLSTMQVFRDLGVKIED 64

Query: 70 DKAARKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ VG G + P D L +GN+G ++R ++ + AG + + G
Sbjct: 65 NGDIVEVHGVGFDGLQAPKND-----LDMGNSGTSIRLISGVL--AGQDFEATMFGDDS 116

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + + L Q+G + D PP+ + G L + +L + S+Q SAL+
Sbjct: 117 LSKRPMDRVITIPLSQMGLKISGQTERDLPPLTIKGNKNLKPITYQLPVA-SAQVKSALIF 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G+ I + K ++ + E ++ +FG + + + R I+GGQ++ + +
Sbjct: 176 AALQAEGNSVI--VKKDLTRNHT---DMIVQFGGQLKFNKEIR--IQGGQEFIA-QEI 227

Query: 249 YVEGDASSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V GD SSA+++L AG I G + +E G + + +V++ MG K+T +
Sbjct: 228 TVPGDISAASFVWVAGLIIPGSKIVLENVGINETRTGI--LDVIKAMGGKMTLSNIDELA 285

Query: 303 TSVTVTGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVK 359
S T+T E LKA ++ +P + L ++ L A G T I D +VK
Sbjct: 286 KSATITVETSE-----LKATEIAGELIPRLIDELPIITLLATQAHGTTIICDAEELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAE 417
ET+ + + L +GA++E D II P L+ I+T+ DHR+ M ++AA +
Sbjct: 340 ETDCIQVVADALNSMGATIEPTEDGMIHGPALHGAEINTFGDHRIGMMAIAAALLAKD 399

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +F+ L++ +
Sbjct: 400 GEVVLERAEAINTSYPAFFEHLNSLM 425

>ref|ZP_07888310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis ATCC 49296]
gb|EFU62679.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
sanguinis ATCC 49296]
Length = 427

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 121/443 (27%), Positives = 214/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVKIEDKD 66

Query: 72 AAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQGVGMDGIKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVITIPLKKMGVSISGQTERDLPPLCLKGTKNLKPITYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++ +FG S + ++G QK K V
Sbjct: 179 QAQG--ESVIEKECTRNHT---DMLHQFG--GHLSVDGKKITVQGPQKLIGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA+++L AG + V ++ G + + +V+ MG K+ TET S
Sbjct: 231 GDISSAASFVWVAGLIVPNSRVVLQNVGINETRTGI--IDVIRAMGGKLEITETDPVAKSA 288

Query: 306 TVTGGPPREPFRGKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGETVIKDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D I+ +L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIVKGKSRLHGARVNTFGDHRIGMMAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +

Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|ZP_04084926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar huazhongensis BGSC 4BD1]
gb|EEM83366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar huazhongensis BGSC 4BD1]
Length = 429

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 127/456 (27%), Positives = 214/456 (46%), Gaps = 44/456 (9%)

Query: 5 EEIVLQPIKE-ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E +QP+ ++G + +PG KS+S+R ++ A++EG T + L D + + +
Sbjct: 2 KERTIQPVNGLNGNITIPGDKSISHRAVMFGAIAEGKTTIKGFLPGADCLSTISCFKEM 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ + + VVG G +E +E + L +GN+G +R ++ + N +
Sbjct: 62 GVDIVQN--GDEVTVVGKG---LEGLQEPKAVLDVGNSTTIRLMSGIL---ANTPFF 111

Query: 123 --LDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSG 176
+ G + +RP+ + LKQ+GA++D P+ + G G +K S
Sbjct: 112 SCVQGDASIAKRPMKRVTNPLKQMGANIDGREEGTFTPLTIRG-----GDLKAIEYTSP 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A G + + P++ + T R++E FGV +
Sbjct: 166 VASAQVKSAILLAGLRTGVTAV-----TEPHISRDHTERMLEAFGVTV--TREGKTV 216

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ GGQK + + V GD SSA++FL AGA I + ++ G + + +VLE
Sbjct: 217 KLAGGQKL-TATDVQVPDGVSSAAFFLVAGAIIPNSKLVLQNVGMNPTRTGI--IDVLEK 273

Query: 294 MGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTA 349
MGA T + + P LK I++ + +P + + V+AL A +G T
Sbjct: 274 MGATFTVEPINEGSSEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQAEGITV 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I+D +VKET R+ + ELTKLGA +E D II L +++Y DHR+ M
Sbjct: 334 IKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNIVNSYGDHRIGMM 393

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
++A C AE I D ++P +FD L K
Sbjct: 394 LAIAGCLAEGKTIIEDAEAVGVSYPPTFFDELQKLAK 429

>ref|YP_001930209.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium
sp. YO3AOP1]
sp|B2V630.1|AROA_SULSY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD65655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium
sp. YO3AOP1]
Length = 431

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 132/444 (29%), Positives = 217/444 (48%), Gaps = 19/444 (4%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E ++ +K I G++++P KS+S+R ++L++L++GT++V N L + D + A R LG+
Sbjct: 2 EKTVMKVKRIEGLRVPSPDKSISHRAIILSSLADGTSIVKNFLKAGDTLTTVNAYRKLGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + G G +D L +GN+G R LT V A G + L G
Sbjct: 62 EIVEKEGVYVHKGGLDGLKEPDDL-----LDMGNSGTTTR-LTLGVLA-GFDFFAALTG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R+RP+ + L ++GA +D + P+ + G G L G + +S+Q SA
Sbjct: 115 DDSLRKRPMKRAVEPLSKMGAKIDGRKDGNNLPISIRG-GKLTGIDF-FNEKMSAQVKSA 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A GD + I+ +IS + E L M + V E + R +K K +P

Sbjct: 173 ILLAGLFAKGDTTV--IEPVISRDHTENMLNSMGAY-VSREFTKDGVRVTVKKADKL-NP 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++F A A+I G+ +E F L+ MGAKV +

Sbjct: 229 IHINVPADPSSAAFFAAAASIISGS-HIELKDVLINPTRDGFRRKLKEMGAKVEYKNKRD 287

Query: 306 TVTGPPPREPFGRKH-LKAIDVNMNMKP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + H LK + V ++P D LA++A A+G T I RVKE+

Sbjct: 288 EAGEIVADIYISYHELGKGVKEPQEVPSMIDEIPLLAIATQAEGETVITGAHELVRKES 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFS-LAACAEVPV 420
+R+ ++ +LG EE PD II +K+ +D+Y DHR+AM F+ L +E +

Sbjct: 348 DRIKSVIENFKRLGLEAEELPDGMIIRGKQKVGKIVDSYKDHRIAMGFAILGLVSEEGI 407

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
TI+D C ++P++F+ L K

Sbjct: 408 TIKDADCVYISYPEFFNHLEKVS 431

>ref|ZP_01172026.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. NRRL B-14911]
gb|EAR65399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. NRRL B-14911]
Length = 429

Score = 137 bits (344), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 131/439 (29%), Positives = 214/439 (48%), Gaps = 33/439 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
+ G + +PG KS+S+R ++ A++EG T V N L ED + R LG+S+ E DK

Sbjct: 13 LRGEIDIPGDKSVSHRSIMFGAIAEGRTEVTNFLMGEDCLSTVSCFRKLGVSTNEGDKM 72

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
++ G G F + EV L +GN+G +R L + AG VL G + +R

Sbjct: 73 ----IIDGRG--FEGLEPNNEV-LDVGNSGTTIRLLLGIL--AGLPFAVLAGEDESIAGR 123

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + V L ++GA + G + P+ + G G + G + +L + S+Q S+LL A

Sbjct: 124 PMTRVSVPLSEMGAIQRGRKGELTPLSIQG-GEVKGIRYELPVA-SAQVKSLLFAGLQ 181

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPNAYVEG 252
A G E +I+ + + E R++ +FG E ++GGQK K+ K +V G

Sbjct: 182 ASG--ETVLIIEPAKTRDHE---RMIRQFG--GEIVSEGTEVRLQGGQKLKAAG-VHVP 233

Query: 253 DASSASYFL-AGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVT---WTETSVTVT 308
D SSA++FL AGA I G + + G + + EVL+ MGA +T + S

Sbjct: 234 DISSAAFFLSAGAIIPGSEIVLRNVGLNPTRTGI--LEVLQRMGADMTILPYNNESEAEPA 291

Query: 309 GPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMV 365
G F LK + + +P + + ++AL A +G T I+D +VKET R+

Sbjct: 292 GDITIRF--SQLKGTVEGDIIPLRLIDEIPIIALLATQAEGETVIKDAEELVKETNRID 349

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSL-AACAEVPVTIRD 424
+ EL KLGA +E D +I L + ++ DHR+ M ++ AA V++

Sbjct: 350 TVVNELKKLGADIEATADGMVINGRTPLKGGNVSSHGDHRIGMMLAIGAAICTGEVSLSG 409

Query: 425 PGCTRKTFPDYFDVLSTFV 443
++P +F+ L + +

Sbjct: 410 AEAISVSYPAFFEHLESLI 428

>ref|ZP_08065064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus peroris ATCC 700780]
gb|EFX41070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus peroris ATCC 700780]
Length = 427

Score = 137 bits (344), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 125/444 (28%), Positives = 216/444 (48%), Gaps = 37/444 (8%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV EADK 71

I ++G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IDHLNGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A VG G K P + L +GN+G ++R ++ + AG + + G +
Sbjct: 67 GAVTIQGVGLDGLKAP-----QKALDMGNSGTSIRLISGVL--AGTDFEVEFMFGDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 119 KRPMDRVTLPLKKMGVSISGQTERDLPLHLKGTKNLKPITYELPIA-SAQVKSALIFAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + II+K + + E LR +FG + S + ++G QK S + V
Sbjct: 178 LQAHG--QSIIIEKECTRNHTEDMLR---QFG--GDLSVDGKKITVQGPQL-SGQTVVV 229

Query: 251 EGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TS 304
GD SSA+++L AG + V ++ G + + +V+ MG K+ T+ S
Sbjct: 230 PGDISSAAFVWVAGLIVPNSRVVLKNVGINETRTGI--IDVIRAMGGKLEITDMDPIAKS 287

Query: 305 VVTGTGPREPFGRKHLKAIDVNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
T+T E L I++ +P + L ++AL A G T I+D +VKET
Sbjct: 288 ATLTVETSE-----LNRIEIGGALIPRLIDELPIIALLATQAQQGVIKDAEELVKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVP 419
+R+ + L +GA++ D II L+ ++T+ DHR+ M ++AA A+
Sbjct: 342 DRIQVADALNSMGATITPTADGMIKGSVLHGARVNTFGDHRIGMMTAIAALLVADGE 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +FD L T +
Sbjct: 402 VELDRAEAINTSYPSFDDLETLI 425

>gb|ACN18610.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
Length = 428

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 124/439 (28%), Positives = 222/439 (50%), Gaps = 33/439 (7%)

Query: 17 GTVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITINGKQTLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SA++F+ IT G+ +T G T ++V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTR---TGISDVVEQMGGSLLVVKDSSRS-TGKLA 289

Query: 313 EPFGRK--HLKAIDVNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 290 GTVVVKTSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAEELVKETNRIDAV 349

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
TEL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 350 ATELNMGADITPTEDGLIIRKKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERP 409

Query: 426 GCTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 410 EAVSVSYPTFFEDIRSLK 428

>ref|ZP_01822665.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP9-BS68]
gb|EDK79289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP9-BS68]
Length = 427

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 121/443 (27%), Positives = 214/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITVQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKKMGVSISGQTERDLPRLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKEYTRNHT---DMLKQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISAFAFWLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEIDPAKSS 288

Query: 306 TVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|YP_003506276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Meiothermus ruber DSM 1279]
gb|ADD27256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Meiothermus ruber DSM 1279]
Length = 426

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 133/447 (29%), Positives = 212/447 (47%), Gaps = 36/447 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 65
E ++ P + GT+++PG KS+++R L+L AL++G + + L + D +R LG
Sbjct: 2 ERLIPPTPSLKGTLRVPGDKSVTHRGLMLGALAQGESTLYYPLKAGDTLSTAQVMRQLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY-VLD 124
+ VG K P + L GNAG MR + ++ G T+ VL
Sbjct: 62 EITEQGQHFHIKGVGLRLKEPGD-----VLDCGNAGTLMRLVAGLLS---GQETFAVL 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+G + + L+Q+GA ++ P+ + G GGL G +L + S+Q S
Sbjct: 113 GDASLRRRPMGRVTLPLRQMGARIEGRENGQLAPLAIRG-GGLRGIHYELPVA-SAQVKS 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+A A D E+ + P + T R+ +G+ E R + + + +
Sbjct: 171 ALLLAGLFAEEDTEV-----VEPAPTRDHTERVFRHYGLPIEVEGLRIR--TRRAEPFAA 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
K+ V GD SSA++F+ A IT + VT+EG G + VL+ MGA ++W T
Sbjct: 224 -KDLTVPGDFSSAAFFIVAALITPDSEVTLEGVGLNPTR--TGLLTVLKEMGADLSWEVT 280

Query: 304 SVTVTGPPREPF-----RKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVAS 355
G EP G L+ + V+ +P D LA A +A G T I +
Sbjct: 281 E----GQDGEVGVWIRARSSQLRGVVDPLIPLMVDEVPIAAAAAWAAGETYIPGLEE 336

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC 415
RVKE++R+ AI L LG VE GPD+ I ++ + DHR+AMAF++
Sbjct: 337 LRVKESDRVAIAKLNQLNGVPVEAGPDWLRIRGGHVAGGGLVEPFHDHRIAMAFVCGCL 396

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
+ VT++D +FP +++ L
Sbjct: 397 PK-GVTVQDAEWASISFSPFWEDLERL 422

>ref|ZP_07864434.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
anginosus F0211]
gb|EFU21957.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
anginosus F0211]
Length = 427

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 117/444 (26%), Positives = 214/444 (48%), Gaps = 37/444 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 8 KGLAGCIRVPGDKSISHSRISIMFGSLAKGVTTVHDILRGEDVLSTMQVFRDLGVQIEDDGN 67

Query: 73 AKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G + P +L +GN+G ++R ++ + AG + + G + +
Sbjct: 68 VVTIHGVGFAGLQAPT-----KLNMGNSGTSIRLISGVL--AGQDFAVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G + D PP+ ++G L L + S+Q SAL+ AA
Sbjct: 120 RPYMDRITIPLRQMGVQIAGRTNRDLPLTIHGNKNLQPIHYTLPTV-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E I++K ++ + E ++++FG + S + I+GGQ++ + +N V
Sbjct: 179 QAQG--ESVIVEKEMTRNHT---DMIKQFG--GQISVNGKEIRIQGGQEF-TGQNVLPV 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA++++ AG I + +E G + + +V++ MG + + S
Sbjct: 231 GDISSAAFVWVAGLIIPNSKIILENVGINETRTGI--LDVVKAMGGNINLSNIDRVAKSA 288

Query: 306 TVTGPPREPFGRKHLKAIDVNMNKM---DVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E G ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITIETSELIG-----TEIGGEIIPRLIDELPIALLATQAKGQTVIRDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ + T+ DHR+ M ++AA + V
Sbjct: 343 RIQVVADALNSMGADITPTEDGMIKGTSLHGAKVHTFGDHRIGMMTAIAALLVNDGQV 402

Query: 421 TIRDPGCTRKTFFPDYFDVLSTFVK 444
+ ++P++F L +
Sbjct: 403 ELERAEAINTSYPNFFHDLEDLLH 426

>ref|YP_001929990.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Porphyromonas gingivalis ATCC 33277]
dbj|BAG34393.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Porphyromonas gingivalis ATCC 33277]
Length = 419

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 140/438 (31%), Positives = 207/438 (47%), Gaps = 68/438 (15%)

Query: 18 TVKLPKSGKSLNRILLLAALS-----EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+++LP SKS R+LLL A+S EG D + VH +L +
Sbjct: 18 SLRLPPSKSEWIRLLLLRAMSGEVLAPLEG----DAPTDVRTVHRILTS----- 62

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
D +EV + +AG AMR LTA + A + L G RM

Sbjct: 63 -----DISDEVNV--RDAGTAMRFLTAYM-ARFASRPVRLYGTERMC 101

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI LV L+ LGADV D PP+ + + GG V + +SSQ++SALL+ A

Sbjct: 102 ARPIRPLVEALRSLGADVIERVEDFPPLLIRP-AAMCGGNVCVDAGVSSQFVSALLLIA 160

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
P G + I++ ++ +S PY +MT RL+ FG++ E S+ D + G + + +P Y

Sbjct: 161 PTLRGGLSIKLENREVSAPYTDMTCRLLTAFGIEVERSE--DSITV-GERPFVAPTEWYP 217

Query: 251 EGDASSASYFLAGAAI--TGGTVTVEGC--GTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
D S+A Y A+ G+V++ S+Q D + A + +G T++ +T

Sbjct: 218 SADWSAAGYIYNMVAVGELSGSVSLPDLLPPEESMQADSRAATLFGR LGVVTEKTDSGIT 277

Query: 307 VTGPP---REPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
++ P + FG + ++ PD+ TLAV L P + V R+KE +R

Sbjct: 278 LSYSPVRCTDDFGTE-----DVRDCPDLVPTLAVCCLLRVPFCLTGVGHLRLKECDR 330

Query: 364 MVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTADTYDDHRMAMAFSLAAC-AEV 418
+ AI TE KLG V D + PE+L V I YDDHRMAMAF+ AA ++

Sbjct: 331 LAAICTEARKLGYVVRSDKDALLWDGERCTPEELPV--IRVYDDHRMAMAFAAAAVLSKK 388

Query: 419 PVTIRDPGCTRKTFPDYF 436
V I D G K+FP +F

Sbjct: 389 GVMIEDAGVVGKSFPFGFF 406

>ref|ZP_07641931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis SK597]
gb|EFO00450.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis SK597]
Length = 427

Score = 136 bits (343), Expect = 5e-30, Method: Compositional matrix adjust.
Identities = 120/443 (27%), Positives = 214/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E

Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +

Sbjct: 67 GVITIQGVGMDGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G ++ D PP+ + G L + +LS + S+Q SAL+ AA

Sbjct: 120 RPMDRVITPLKKMGVNISGQTERDLPPLHLKGTKNLRPIQYELSIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG + ++G QK K V

Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLIVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE S

Sbjct: 231 GDISSAAFVLVAGLIVPNSCLVLQNVGINETRTGI--IDVIRAMGGKLEMTIDPVAKSA 288

Query: 306 TVTGPPEPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+

Sbjct: 289 TLTVESSD-----LKGT EIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V

Sbjct: 343 RIQVVADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L +

Sbjct: 403 ELDRAEAINTSYSPFFDLENLI 425

>ref|ZP_06062931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter johnsonii SH046]

gb|EEY96710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter johnsonii SH046]
Length = 749

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 127/419 (30%), Positives = 200/419 (47%), Gaps = 40/419 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 315 KSFQGFVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIEGPKN 374

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 375 GEVTIHGVGVNGLKAPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 426

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+++GA + PPV + G L G L + S+Q S +L+A
Sbjct: 427 KRPMERIAKPLREMGAIQTTGERGTPPVSTITGNQALQGIHYDLPA-SAQVKSIGILLAG 485

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E +R ++GG K +
Sbjct: 486 LWAAGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNRISLQGGGKLVGTE-I 535

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G+ VT+E G + V E+L+ MGA +T E
Sbjct: 536 QVPSDISAAFFVMGAAITEGSDVTLEAVGINPRTGTG--IEILKQMGADIT-VENERIA 592

Query: 308 TGPPREPF---GRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 593 GGEPIADIRIQGTRTLKGIHPEDQVPLAIDFPAIFIAAACAEGQTVLTGAELRVKES 652

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLA 413
+R+ + L +G D II I+++ DHR+AM+FS+A
Sbjct: 653 DRIQVMADGLKTMGIDCTPTDDGIIIEGKGHSGEWGAIFTGGEIESHHDRIAMSFMA 711

>ref|ZP_02711877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC1087-00]
gb|EDT90298.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC1087-00]
Length = 427

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 210/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVTLPLKKMGVSISGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISSAAFVLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +

Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFFDYFDVLSTFV 443

++P +FD L + +

Sbjct: 408 EAINTSYPSFDDLES LI 425

>ref|ZP_04849461.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
1_1_6]
gb|EES66324.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacteroides sp.
1_1_6]
Length = 285

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 96/294 (32%), Positives = 150/294 (51%), Gaps = 36/294 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALASEGTTVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74

+ T++LP SKS+SNR L++ AL +G +NL + +D M+ AL

Sbjct: 12 VKATIQLPASKSISNRALIINALGKGIYPENLSDCDDTQVMIKAL----- 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

+ KE + + AG AMR LTA ++A G ++ G RM++RPI

Sbjct: 58 -----TEGKETIDIM--AAGTAMRFLTAYLSATSGER--IITGTARMQQRPI 100

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

LV L++LGA+++ PP+R+ G L G ++ L G++SSQY+SALLM P+

Sbjct: 101 QILVNALRELGAIEYTHNEGYPPLRIKG-AELKGNEITLKGNVSSQYISALLMIGPVLK 159

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254

+ + + ++IS PY+ +TL+LM+ FG KA + Q Y+S VE D

Sbjct: 160 DGLTLHLTGEIISRPIINLTQLMQDFGAKAAWTSPPS--ISVAPQPYQSVFPT-VESDW 216

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307

S+ASY+ AA++ + + G S QGD + AEV +G +T V +

Sbjct: 217 SAASYWYQIAALSPEAEIELLGLFRNSYQGDSRGAEVFSRLGITTEFTPKGVKI 270

>ref|ZP_01832802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP19-BS75]
ref|ZP_01834028.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP19-BS75]
ref|ZP_01834686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP23-BS72]
ref|YP_002511266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae ATCC 700669]
ref|YP_002736331.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae JJA]
ref|YP_002738518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae P1031]
ref|YP_002740648.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae 70585]
sp|C1C7X2.1|AROA_STRP7 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B8ZKM0.1|AROA_STRPJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|C1CEW0.1|AROA_STRZJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|C1CL80.1|AROA_STRZP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EDK69938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP19-BS75]
gb|EDK70969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP19-BS75]
gb|EDK82173.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP23-BS72]
emb|CAR69137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae ATCC 700669]

gb|AC016466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae 70585]
gb|AC018606.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae JJA]
gb|AC020656.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae P1031]
Length = 427

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 121/443 (27%), Positives = 214/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA-----LNMGNSTGSIIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKMGVSISSQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEIDPVAKSS 288

Query: 306 TVTGPPREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMAIAAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|YP_003879090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae 670-6B]
gb|ADM90990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae 670-6B]
Length = 427

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 210/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA-----LNMGNSTGSIIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKMGVSISSQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSVDSKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE V

Sbjct: 231 GDISSAAFVLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
L K ++ +P + L ++AL A G T I+D +VKET+R+ +

Sbjct: 288 STLTVESSDLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +

Sbjct: 348 ADALNSMGADITPTADGMIKKSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443

++P +FD L + +

Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|ZP_05563156.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis DS5]
ref|ZP_05569291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis HIP11704]
ref|ZP_05573377.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis JH1]
ref|ZP_07552296.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX4248]
ref|ZP_07554466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0855]
ref|ZP_07760062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0470]
gb|EEU66113.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis DS5]
gb|EEU72248.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis HIP11704]
gb|EEU74348.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis JH1]
gb|EFM79229.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0855]
gb|EFM81160.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX4248]
gb|EFQ70802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0470]
gb|EFT45906.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0017]
gb|EFT48915.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis TX0027]
Length = 428

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71

+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

+ V G ++ AK ++ GN+G +R + + AG L G ++
Sbjct: 69 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191

RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAECCQGVQQTFFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251

A G + ++K + + E +R +FG E D + + G Q+ + +N V
Sbjct: 181 QAKGTSVV--VEKEKTRDHEMIR---QFGGTLEVDDK--KIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309

GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISSAAFVLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKNMGGSVTILNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366

L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQTLATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAHSVSYPAFFDDL 423

>ref|YP_001055788.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum
calidifontis JCM 11548]
gb|AB008322.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum
calidifontis JCM 11548]
Length = 403

Score = 136 bits (343), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 133/432 (30%), Positives = 205/432 (47%), Gaps = 47/432 (10%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
SGT K P SK +S R+LL AL+EG TVV + S+DV ML A++ L
Sbjct: 9 FSGTFKAPPSKPIISQRLLAGALAEGETTVVKGVELSDDVVAMLRAIQPL----- 57

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLG--NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A + GG VE + +V +G +R+ A G +R R
Sbjct: 58 -ARISYGGDVHVERREPVDYRAFNMESGFTLRATAVAVYAGVPGLTAVYYGGT--LRGR 114

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +L+ L+ L DV G V + G L +V++ ISSQ++S L+ A
Sbjct: 115 PIDEIQLALRSL-TDVAKAPGA---VFIRG-KRLSRFEVEMRADISSQFISGLMFLAAA 168

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G V + + S +VE T ++++FG + E D + ++GG + P V G
Sbjct: 169 GEGGV-VRPVGGRKSWSFVEATASVLKQFGARVEVGDVIE---VEGG--LRGPGEVAVPG 222

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S A++ +A ITGG V VEG + D + ++ MGA V + T G P
Sbjct: 223 DYSLAFLIAAGLITGRVEVEGQASDV---DKQVLDIFAAMGAHVAYDGRRATAWGTPS 279

Query: 313 EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
+ +DV++ PD+ M +A+VA F + T IR V R KE++R+ ++ L
Sbjct: 280 -----RGVDVLDGSLNPDVMPVALVAAFVEDWTVIRGVEHLRYKESDRVASVLDVLQ 331

Query: 373 KLG--ASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
+LG A+ ++G + I PP + NV + ++ DHR+ + +LAA V + D K
Sbjct: 332 RLGVETATYKDGALH-IRGPPRRRNQVFL-SHGDHRIGL-MALAASKAVGGCLDDVSPISK 388

Query: 431 TFPD---YFDVL 439
++P YF VL
Sbjct: 389 SWPTAPLYFIVL 400

>ref|ZP_07871245.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria marthii FSL
S4-120]
gb|EFR87250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria marthii FSL
S4-120]
Length = 430

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 120/437 (27%), Positives = 222/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + ++
Sbjct: 14 GAITVPGDKSMHSRIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEKI 71

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMM 125

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G

Sbjct: 126 RVMLPLQQMGAKMHGKDGSEFAPITIVGKQTLKRM EYHMPVA-SAQVKS AIIFAALQAEG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKA EHSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S

Sbjct: 185 ETIIHEKEK-----TRDHT EHMIRQFGGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 236

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG

Sbjct: 237 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVKDSSRS-TGKLAGT 293

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T

Sbjct: 294 VVVKTSELKGTEIGDIIIPRLIDEIPVIALLATQAEGTTIIKDAELKVKETNRIDAVAT 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA + V + P

Sbjct: 354 ELNKMGA DITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEDGDVELERPEA 413

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ +++ +K

Sbjct: 414 VSVSYPTFFEDINSLK 430

>ref|ZP_05627896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D12]

ref|ZP_07925544.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D12]

gb|EFS23570.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
D12]

Length = 408

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 100/424 (23%), Positives = 200/424 (47%), Gaps = 36/424 (8%)

Query: 15 ISGTVKLPGSKSLSNRIILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++P SKS +R ++ A+L++ +++ N+ S+D+ + ++ LG +E +

Sbjct: 8 LKGKQLIPASKSYCHRYIIAASLAKEMSILHNISLSDDIQSTIEIMKKLGAKIEQ---RE 64

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ ++ G + D K+ + F + +R L ++ G + RP+

Sbjct: 65 QDFLIQKGD---ICDNKKNLHFFCSESASTLRFLIPLSLIQYRKVSFY--GRNTLPNRPL 119

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L G G + +++ G L G L G+ISSQ+++ LL A PL

Sbjct: 120 SPFFFPILNSSGISFRT-EGENSLCIQLEG--QLKAGNYSLEGNISSQFITGLLFALPLLD 176

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ ++ I+ L S YV+M+L ++E+F ++ + F+I G Q+Y++ +EGD

Sbjct: 177 GNSQLHLILGNLESKAYVMSLDLVLEKFKIQIFREK--NHFFIPGKQEYQAYSTT-IEGDY 233

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPPREP 314
S A++FL ++ G + + G S Q D + + +++ + K P+E

Sbjct: 234 SQA AFFLVANSM-GNEIEIAGLT KDSKQADFQISSMIQALEKA-----PQE- 279

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+ ++ ++ PD+ L+V A G T I+++ R+KE +R+ A L KL

Sbjct: 280 -----TLILDGSGCPDIIPILSVKAALTQGKTVIQNIKRLRMKECDRLHATADI LNKL 332

Query: 375 GASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFP 433
GA V E ++ ++ DHRMAM ++A+ + + + + C K++P

Sbjct: 333 GAKVVENSSSLEFEGVSHFKGNSVSSFGDHRMAMMIAVASTRCQGEILLDNATCVSKSYP 392

Query: 434 DYFD 437
+++

Sbjct: 393 TFEW 396

>ref|ZP_07837595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium
cellulosolvens 6]

gb|EFR66341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium
cellulosolvens 6]

Length = 428

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 130/444 (29%), Positives = 214/444 (48%), Gaps = 36/444 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G + +PG KS+S+R ++ ++++G T + N L D + R +G+S++ D+
Sbjct: 8 KPLKGRNLNIPGDKSISHRAVMFGSIAQGDTEITNFLPGADCISTINCFRQMGVSIIDEE 67

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VVV G ++ + E L GN+G R L + AG + VL G +++R
Sbjct: 68 NNSHVHVHGNGLHGLK--RPEDVLDGNSGTTTLLAGIL--AGQDFACVLGTDESQKR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNG--IGGLPGGKVKLSGSISSQYLSALLMAA 190
P+ ++ L +G D++ DC P+ +NG + G+ S + S L A L A+
Sbjct: 124 PMRRIITPLTMDGDIESVRENDCAPLLINGTRLQGIHYNPVASAQVKSCILLAGLYAS 183

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP--KNA 248
+ + + IS + E+ LR FG + R Q +P K
Sbjct: 184 SMT-----SVTEPAISRNHTEMLR---NFGAEV-----RCEAFSTQIQPNPVLKGC 227

Query: 249 YVE--GDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
VE GD SSA+YF+A AA I +VT+ GT + + VL+ MG V + S
Sbjct: 228 KVEVPGDISAAYFIAAAAMIPDSSVTLRKVGTPNPTDGI--LRVLQNMGGSV EYKHL- 284

Query: 306 TVTGPPREPFPGRKH--LK AIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
T G P ++ L + + +P D +AV+A A+G T IRD RVKE
Sbjct: 285 TSGGEPFADLKIRYAPLHGTITIEGSLIPTLIDEIPIIAVMAATAEGDTIIRDAQELRVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVP 419
+ R+ + L+K+G VE D II +KL+ ID++ DHR+AM+F++A+ AE
Sbjct: 345 SNRLDIMVESLSKMGVDVEATS DGMIIHGKKLHGAVIDSHKDHRIAMSFAIASLVAEGE 404

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
I D C ++P++++ L + +
Sbjct: 405 TEIIDADCVDISYPNFYEDLES LI 428

>ref|YP_820149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
thermophilus LMD-9]
sp|Q03LG9.1|ARO A_STRTD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ65953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
thermophilus LMD-9]
gb|ADQ62706.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
thermophilus ND03]
Length = 427

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 118/434 (27%), Positives = 217/434 (50%), Gaps = 37/434 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++++PG KS+S+R ++ +L+G T V ++L EDV + R LG+++E D
Sbjct: 10 LRGLSLRIPGDKSISHRSIMFGSLAKGVTTVRDILRGEDVLSTMQVFRDLGVITIEDDGDVV 69

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G K P + +L +GN+G ++R ++ + AG + + G + +RP
Sbjct: 70 RIHGVGFDGLKAP-----QNKLDMGNSGTSIRLISGVL--AGQDFDVEFMFGDSDLKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L+Q+G +V D PP++++G L +L + S+Q SAL+ AA A
Sbjct: 122 MDRVTTIPLRQMGEVVSQGTDRDLPLKMHGSKSLKPIYYELPVA-SAQVKSA LIFAALQA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D E II+K + + E ++++FG + + R I GGQ + + + V GD
Sbjct: 181 --DGESVIEIEKTRNHT---DMIQQFGGQLQVEGKEIR--ISGGQTF-TAQEVVVP GD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++L AG + + ++ G + + +V++ MG K+ ++ S T+
Sbjct: 233 ISSAAFVWLAVGLVVPNSKIVLKNVGINETRTGI--IDVIKNMGGKIKLSIDIDQVAKSATI 290

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERM 364
T E L ++ + +P + L ++ L A G T IRD +VKET+R+
Sbjct: 291 TVETSE-----LNGTEIGGDIIPRLIDELPIITLLATQAQKTVIRDAEELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D IIT L+ ++T+ DHR+ M ++AA + V +
Sbjct: 345 QVVADALNAMGADIVPTEDGMIITGKTPHGAEVNTFGDHRIGMMTAIAALLVQDGEVDL 404

Query: 423 RDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 405 QRAEAINTSYPSFF 418

>ref|ZP_06746991.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
PC1.1]
gb|EFG19675.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
PC1.1]
Length = 429

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 10 VKHLQGTLMVPSDKSISHSRSMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 69

Query: 72 AAKRAVVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 70 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 122

Query: 132 RPIGDLVVLGLKQLGADVDCFLGTDCCPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 123 RPMNRVMLPLNQMGAEQGVQQTTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 181

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E D + + G Q+ + +N V
Sbjct: 182 QAKGTSVV--VEKEKTRDHEEMIR---QFGGTLEVDDK--KIMLTGPQQQL-TGQNVVVP 233

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVITVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 234 GDISAFAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 291

Query: 310 PPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 292 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELKVKETNRIDA 349

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 350 VAKELTILGADITPTDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 409

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 410 AEAVSVSYPAFFDDL 424

>ref|YP_001717324.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Desulforudis audaxviator MP104C]
sp|B1I3Z0.1|ARO_A_DESAP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACA59692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Desulforudis audaxviator MP104C]
Length = 429

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 130/454 (28%), Positives = 211/454 (46%), Gaps = 52/454 (11%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + + G +PG KS+S+R+++L +L+ G T N L ED + R LG+ +E
Sbjct: 5 ITPARGLRGEAWVPGDKSISHRVVMGLSLARGETAATNFLPGEDCLATVRCFRALGVEIE 64

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ G+ P + L GN+G MR + + AG V+ G
Sbjct: 65 GPDGD-----TIRIRGRGPEALTEAPDVLDAAGSGTTMRLMLGIL--AGQPFFSVITGDAS 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+G + L+++GA + + P+ V G G L G + +L + S+Q SALL+
Sbjct: 119 LRRRPMGRVTGPLQEMGATILGRRNANLAPIAVAG-GRLSGIRYRLPVA-SAQLKSALLL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP--- 245
A A D E+ + + + + E R++ FG +G +P
Sbjct: 177 AGLFA--DSPTEVTEPVATRDHTE---RMLAAFALVAR-----RGSSVTVAPSPE 222

Query: 246 ---KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + GD SSA++F+ A IT + + ++ G + + L MGA+++ +
Sbjct: 223 LCGREIRIPGDISAAFFIVAALITPESDLVLKDVGNPTR--TGILDALANMGARISVS 280

Query: 302 ETSVTVTGPPREPFGFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTA 349
PRE G L+ + +P D LAV A +ADG T
Sbjct: 281 R-----PRESGGEVPADIRVRSSALRGTVIEGALIPRLVDEIPVLAVAAAYADGETV 332

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMA 409
IRD A RVKE++R+ A R EL+ LGA + E PD +I P +L + +++ DHR+AMA
Sbjct: 333 IRDAAELRVKESDRLAATRKELSTLGADIRETPDGLVIRGPRRLTGGSNCNSHGDHRIAMA 392

Query: 410 FSLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTF 442
++A A VT IRD C +FP + L++
Sbjct: 393 AAVAGLAASDVTIIRDNSCIDVSFPGFAHALNSL 426

>ref|YP_001269252.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas putida F1]
gb|ABQ80068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida
F1]
Length = 746

Score = 136 bits (342), Expect = 7e-30, Method: Compositional matrix adjust.
Identities = 131/436 (30%), Positives = 209/436 (47%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 QPGGRLNGRIRVPKDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAAKRAVV-VGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P L++GN+G +MR L+ + AG + + G
Sbjct: 377 PNHGRVTIHGVLHGLKPPPG-----PLYVGNSGTSMRLLSGLL--AGQSFVDVTMTGDAS 429

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA V+ G D PP+ + G L G L + S+Q S LL
Sbjct: 430 LSKRPMNRVANPLREMGAVVET--GPDGRPPLTIRGGHKLKGLTYTLPMA-SAQVKSCLL 486

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG + + ++ G K + +
Sbjct: 487 LAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYSVDSNGPV--ASLQSGGKLTATR- 538

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + +E G + V ++L +MG +T E
Sbjct: 539 IEVPADISSAAFFLVAAASIAEGSELVLEHVGINPRTTGV--IDILRLMGGDITL-ENQRE 595

Query: 307 VTGPPREPFGFRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P + LK ID+ +P D L V A A+G T +R RVKE+
Sbjct: 596 VGGEVPADLVRVGAKLKGIDIPALVLAIDFPPVLFVAAACAEGRTVLRGAEEELRVKES 655

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ + LT LG E PD II + L + + DHR+AMAFS+A+ A P+
Sbjct: 656 DRIQVMADGLTTLGIKCEPTDGIIDGGQ-LGGGEVHGHGDHRIAMAFSVASLRASAPI 714

Query: 421 TIRDPGCTRKTFPDYF 436
I D +FP++
Sbjct: 715 RIHDCANVATSFNPNFL 730

>ref|YP_001347346.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas aeruginosa PA7]
gb|ABR81204.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas aeruginosa PA7]
Length = 746

Score = 136 bits (342), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 131/437 (29%), Positives = 212/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQAFRDMGVVIEG 377

Query: 70 DKAACKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGDA 429

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L
Sbjct: 430 SLKSRPMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSCL 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G+ + P + T R++ FG E S R ++ G K S
Sbjct: 487 LLAGLYAAGETSVT----EPAPTRDHTERMLRGFGYPVEVEGSTAR--VESGHKL-SAT 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VGVEIILRLMGGDLNL-ENQR 595

Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNKMP--DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V G P + LK ID+ + +P D L V A A+G T +R RVKE
Sbjct: 596 EVGGEPVADIRVRSARLKGIDIPEDLVPLAIDFPPVLFVAAACAEGRTVLRGAEEELRVKE 655

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG E PD +I + DHR+AM+FS+A+ A P
Sbjct: 656 SDRIQVMADGLKTLGVKAEPTPDGIVIEGGPIGGGEVW-AHGDHRIAMSFSVASLRASAP 714

Query: 420 VTIRDPGCTRKTFPDYF 436
+ I D +FP++
Sbjct: 715 IRIHDCANVATSFNPNFL 731

>gb|ADX80168.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
62]
Length = 426

Score = 136 bits (342), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED + L A R+LG+++E D
Sbjct: 7 VKHLQGTLMVPKSKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 67 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMGLIL--AGCPFETRLAGDASIAG 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 120 RPMNRVMLPLNQMGAECCQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E D + + G Q+ + +N V
Sbjct: 179 QAKGTSVV--VEKEKTRDHTTEEMIR---QFGGTLEVDK--KIMLTGPQQL-TGQNVVVP 230

Query: 252 GDASSASYFL-AGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 231 GDISSAAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 288

Query: 310 PPREFPGRKHLKAIDVNMNKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366

Sbjct: 289 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRD AEELKVKETNRIDA 346
Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 347 VAKELTILGADITPTDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 406
Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 407 AEA VSVSYPAFFDDL 421

>ref|YP_261402.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas fluorescens Pf-5]
gb|AA93565.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas fluorescens Pf-5]
Length = 741

Score = 135 bits (341), Expect = 8e-30, Method: Compositional matrix adjust.
Identities = 131/440 (29%), Positives = 213/440 (48%), Gaps = 39/440 (8%)

Query: 10 QPIKEISGTVKLP GSKSLSNRILL AALSEGTTVDNLLNSE DVHYMLGALRTLGLSVEA 69
P +SG +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 312 NPGGR LSGRIRVPGDKSISHRSIMLGS LAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 371
Query: 70 DKA AKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P ++LGN+G +MR L+ + A ++T L G P
Sbjct: 372 PHHGRVTIHGVGLHGLKPAPGP-----IYLGNSGTS MRLLSGLLAAQSFDST--LTGDPS 424
Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTD C P PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + L+++GA ++ PP+ + G L G L + S+Q S LL+
Sbjct: 425 LSKRPMNRVANPLREMGAVIET-AAEGRPPMVIRGGHRLKGLTYTLPMA-SAQVKSCLLL 482
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHS DSWD--RFYIKGGQKYKSPK 246
A A G + P + T R++ FG +S S D ++ G K K+
Sbjct: 483 AGLYAEKTKTTVT-----EPAPTRDHTERMLRGFG----YSVSVDGATASVESGGKKA-T 532
Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL A+I G+ + +E G + V ++L +MGA + E
Sbjct: 533 HIEVPADISSAAFFLVAASIAEGSELVLEHVGINPRTGTG--IDILRLMGADIRL-ENQR 589
Query: 306 TVTGPPREPFG RKHLKAIDVNMNMKMPDVAMTLA-----VVALFADGPTAIRDVASWR 357
V G EP H++A + ++P+ + LA V A A+G T +R R
Sbjct: 590 EVGG---EPVADLHVRAAKLK GIEIPEELVPLAID EFPVLFVAAACAEGRTVLRGAEE LR 646
Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-A 416
VKE++R+ + L LG E PD II ++ + + DHR+AMAFS+A+ A
Sbjct: 647 VKESDRIQVMADGLLT LGVKCEPTPDGIIIE-GGQIGGGEVHGHGDHRIAMAFSVASLRA 705
Query: 417 EVPVTIRDPGCTRKTFPDYF 436
P+ I D +FP++
Sbjct: 706 NAPIRIHDCANVATSF PNFL 725

>ref|YP_724293.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Trichodesmium
erythraeum IMS101]
gb|ABG53820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Trichodesmium
erythraeum IMS101]
Length = 462

Score = 135 bits (341), Expect = 9e-30, Method: Compositional matrix adjust.
Identities = 126/446 (28%), Positives = 213/446 (47%), Gaps = 28/446 (6%)

Query: 5 EEIVLQPIK---EISGTVKLP GSKSLSNRILL AALSEGTTVDNLLNSE DVHYMLGALR 61
E +++Q K + G + +PG KS+S+R L+L A+++G T + LL D + G
Sbjct: 25 ETLLIQNP KLGSLCGNISIPGDKSISHRALMLGAIAQGQTNIQGLLLGADPYSTAGCFS 84
Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG A+ + + V G + + L GN+G MR L + A+ +
Sbjct: 85 LLG----ANISQLNSEFVQVDGVGLLNLTEPSCVLD CGNSGTTMR-LMLGILASHPEHFF 139

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS- 180
+ G + +RP+ ++ L ++GA + G P+ + G P + I+S
Sbjct: 140 TVTGDSSLVQRPMRVIQPLTEMGAIWGRKGNLAPLAIQGGKLRP---IHYYSPIASA 196

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q S +L+A +A G + I + +S + E R+++ FG + + + + G
Sbjct: 197 QVKSCILLAGLMAEG--KTTITEPALSRDHSE--RMLKAFGAIEIQVDPETNSVTVTGPA 251

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ K ++ V GD SSA+++L AAI G+ + +E G S + + EVLE M +
Sbjct: 252 QLKG-QDVVVPGDISSAAFVLAIAIVPGSELVIENVGVNSTRGTI--LEVLERMEVDIR 308

Query: 300 WTETSVTVTGPPREPFP--GRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
E V G P LKA +++ + +P D LAV A+FA+G T IRD A
Sbjct: 309 Q-ENHRVVGAGEPVADLRVCYSSSLKACEISGSIIPRLIDEIPILAVAAMFAEGTTVIRDAA 367

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
RVKE++R+ + T+L KLGA + E PD IT + T +++ DHR+AM+ +AA
Sbjct: 368 ELRVKESDR LAVMATQLQKLGAIIELPDGLEITGGVSITGTDVESNGDHRVAMSLAIAA 427

Query: 415 CAEVPVT-IRDPGCTRKTFPDYFDVL 439
+T I ++P + L
Sbjct: 428 LNATGITNIHHAETVNISYPSFVQTL 453

>ref|ZP_08013228.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
anginosus 1_2_62CV]
gb|EFW08180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
anginosus 1_2_62CV]
Length = 427

Score = 135 bits (341), Expect = 9e-30, Method: Compositional matrix adjust.
Identities = 115/444 (25%), Positives = 215/444 (48%), Gaps = 37/444 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E D
Sbjct: 8 KGLAGCIRVPGDKSISHRSIMFGSLAKGVTTVHDILRGEDVLSTMQVFRDLGVQIEDDGN 67

Query: 73 AKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G + P +L +GN+G ++R ++ + AG + + G ++
Sbjct: 68 VVTIHGVGFAGLQAPTN-----KLNMGNSGTSIRLISGVL--AGQDFVAEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + L+Q+G + D PP+ ++G L L + S+Q SAL+ AA
Sbjct: 120 RPYMDRITPLRQMGVQIAGRTERDLPPLTIHGNKNLQSIHYTLPLVA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E I++K ++ + E ++++FG + S + ++GGQ++ + +N V
Sbjct: 179 QAQG--ESVIVEKEMTRNHT---DMIKQFG--QGISVNGKEIRVQGGQEF-TGQNVLP 230

Query: 252 GDASSASYFL-AGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SV 305
GD SSA++++ AG + + +E G + + +V++ MG + + S
Sbjct: 231 GDISSAAFVIVAGLIVPNSKIILENVGINETRTGI--LDVVKAMGGNINLSNVDNIAKSA 288

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T E G ++ +P + L ++AL A G T IRD +VKET+
Sbjct: 289 TITITSELVG-----TEIGGEIIPRLIDELPIIALLATQAKGQTVIRDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D +I L+ + T+ DHR+ M ++AA + V
Sbjct: 343 RIQVVADALNSMGADITPTEDGMLIKGKTSLHGAKVHTFGDHRIGMMAIAALLVKDGQV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
+ ++P++FD L +
Sbjct: 403 ELERAFAINTSYPNFFDDLEDLLH 426

>gb|ACZ32941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae LPCoLN]
Length = 445

Score = 135 bits (341), Expect = 9e-30, Method: Compositional matrix adjust.
Identities = 116/429 (27%), Positives = 205/429 (47%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +P SKS + R +L A+++EG +++ N L+S D M+ A + +G S++ K +
Sbjct: 11 VYGNAPFPSSKSHTLRAILWASVAEGKSIIYNYLSDSPTEAMICACKQMGASIK--KFPQ 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VG P+ + + GN+GI +R +TA T + G +++ RP+
Sbjct: 69 ILEIVGN----PLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEIT--VTGSSQLQRRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L+ GA +D + G L + GS SQ+ SAL +A LA
Sbjct: 123 APLLQALRNFGASFH--FSSDKSVLPFTMSGPLRSAYSDEGS-DSQFASALAVACSLAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G II+ P+ +++L +E+ + SD+ F G + + +V GD
Sbjct: 180 GPCSFTIIEPK-ERPWFDSLWLEKLHLPYSCSDTTYF---PGSSHPQGSYHVVTGDF 235

Query: 255 SSASYFLAGAAITGGT--VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++ A A ++ + + +QGD F +++ +GA + + + V
Sbjct: 236 SSAAFIAAAALSKSLQPIRLRNLDILDIDQDKIFFSLMQSLGASIQYDNEEILVFP--- 292

Query: 313 EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
++M+ D L V+ FAD P+ + + S + KE++R++AI EL
Sbjct: 293 -----SSFSGSIDMDGCIDALPILTVLCCFADSPSHLYNARSADKESDRILAITTELQ 347

Query: 373 KLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
K+GA ++ D ++ P L +D++DDHR+AMA ++AA A I + C RKT
Sbjct: 348 KMGACIQPTHGLLVN-PSPLYGAVLDSHDDHRIAMALTIAALYASGDSRIHNTACVRKT 406

Query: 432 FPDYFDVLS 440
FP++ L+
Sbjct: 407 FPNFVQTLN 415

>ref|ZP_01366612.1| hypothetical protein PaerPA_01003760 [Pseudomonas aeruginosa PACS2]
Length = 746

Score = 135 bits (341), Expect = 9e-30, Method: Compositional matrix adjust.
Identities = 130/437 (29%), Positives = 213/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMGLSLAEGTTEVEGFLEGEDALATIQAFRDMGVVIEG 377

Query: 70 DKAARAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGDA 429

Query: 128 RMRERPIGDLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L
Sbjct: 430 SLSKRPMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSC 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G+ + P + T R++ FG E S + ++ G K S
Sbjct: 487 LLAGLYAAGETSVT-----EPAPTRDHTERMLRGFGYPVELEGSTAK--VESGHKL-SAT 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VGVEIILRLMGDLDSL-ENQR 595

Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V G P + LK ID+ + +P D L V A A+G T +R RVKE
Sbjct: 596 EVGGEPPVADIRVRSARLKGIDIPEDLVPLAIDEFPVLFVAACAEGRTVLRGAEEELRVKE 655

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG E PD +I + + DHR+AM+FS+A+ A P
Sbjct: 656 SDRIQVMADGLKALGVKAEPDPGIVIE--GGAFGGGEVWAHGDHRIAMSFSVASLRASGP 714

Query: 420 VTIRDPGCTRKTFFPDYF 436

+ I D +FP++
Sbjct: 715 IRIHDCANVATSFNPL 731

>ref|YP_515210.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomophila felis
Fe/C-56]
sp|Q255H3.1|AROA_CHLFF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE81065.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomophila felis
Fe/C-56]
Length = 445

Score = 135 bits (341), Expect = 9e-30, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 210/435 (48%), Gaps = 29/435 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISG+V +P SKS + R + LA++++GT+ + N L S D M+ A LG ++ K
Sbjct: 11 ISGSVCVPPSKSHTLRAIFLASIAQGTSTIYNALTSPDSEAMIQACEQLGAKIQ-----K 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ + G P + G++GI R TA AA + + G +++ RPI
Sbjct: 66 KSSFLEITGT-PHLSLPPNTIINAGSSGIVFRFFTA--LAAIFSEKVTITGSSQLQRRPI 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSISSQYLSALLMAAPLA 193
L+ L+ GA F P + G + G ++SG SQY SAL MA LA
Sbjct: 123 APLIHALENFGA--TFSYEGAPYTLSTFTVSGPISSGYTEVSGD-DSQYASALAMACSLA 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G I++ P+ ++TL +E+ + +S S D + G + ++ + V GD
Sbjct: 179 EGPFSFTIVNPK-ERPWFDLTLWWLEQLAMP--YSQSGDTYSFLGKSRPRT-FSYTVGGD 234

Query: 254 ASSASYFLAGAAI--TGGTIVTEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
SSA++ A A + + + QGD + +L+ +GA +T+ SV V
Sbjct: 235 FSSAAFLAAALSKSPHPTYLNDLNSNDAQGDKELFYLLQLKGADITFENDSVIVFS-- 292

Query: 312 REPFGKHLKKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
+++M+ D LAV+ FA P+ + + + KE++R++AI EL
Sbjct: 293 -----STFSGGNIDMPFIDALPILAVLCCFATSPSHLYNARGAKDKESDRIIAITEEL 346

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
K+GA ++ + +I P L ++ +++DHR+AMA S+AA A I D C +K
Sbjct: 347 QKMGACIQPCHNGLLIN-PSPLYGASMHSNDHRIAMALSVAAMNASGDSIIHDETCVKK 405

Query: 431 TFPDYFDVLSTFVKN 445
TFP++ L++ N
Sbjct: 406 TFPNFIQALNSLHAN 420

>ref|YP_002439508.1| still frameshift 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
prephenate dehydrogenase [Pseudomonas aeruginosa LESB58]
emb|CAW26632.1| still frameshift 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE
prephenate dehydrogenase [Pseudomonas aeruginosa LESB58]
Length = 746

Score = 135 bits (341), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 130/437 (29%), Positives = 213/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLSLAEGTTEVEGFLEGEDALATIQAFRDMGVVIEG 377

Query: 70 DKAARKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGDA 429

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L
Sbjct: 430 SLSKRPMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSCL 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

L+A A G+ + P + T R++ FG E S + ++ G K S
 Sbjct: 487 LLAGLYAAGETSVT-----EPAPTRDHTERMLRGFGYPVEVEGSTAK--VESGHKL-SAT 538
 Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
 + V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
 Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VGVIEILRLMGGDLNL-ENQR 595
 Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
 V G P + LK ID+ + +P D L V A A+G T +R RVKE
 Sbjct: 596 EVGGEPVADIRVRSARLKGIDIPEDLVPLAIDEFPVLFVAAACAEGRTVLRGAEELRVKE 655
 Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
 ++R+ + L LG E PD +I + + DHR+AM+FS+A+ A P
 Sbjct: 656 SDRIQVMADGLKALGVKAEPTPDGIVIE-GGAFGGGEVWAHGDHRIAMSFSVASLRASGP 714
 Query: 420 VTIRDPGCTRKTFPDYF 436
 + I D +FP++
 Sbjct: 715 IRIHDCANVATSFNPL 731

>gb|ACN18619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
 monocytogenes]
 Length = 428

Score = 135 bits (341), Expect = 1e-29, Method: Compositional matrix adjust.
 Identities = 124/439 (28%), Positives = 220/439 (50%), Gaps = 33/439 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV EADKAAKRA 76
 G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
 Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTIVIRHFLRADDCLGTIKAFKALG--VKIEETEEIEI 69
 Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
 +V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
 Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRP MN 123
 Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
 +++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
 Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITINGKQTLKRMEYHMPVA-SAQVKSALIFAALQAEG 182
 Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
 + I +K P ++ +FG + E R +KGGQK+ + + V GD S
 Sbjct: 183 ETIIHEKEKTRDHPE-----HMIRQFGGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234
 Query: 256 SASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
 SA++F+ IT G+ +T G T +V+E MG + ++S + TG
 Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTR----TGIFDVVEQMGSLVVKDSSRS-TGKLA 289
 Query: 313 EPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
 K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
 Sbjct: 290 GTVVVKTSELKGTIEIGDIIPRLIDEIPVIALLATQAEGTTIIKDAEELKVKETNRIDAV 349
 Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
 TEL K+GA + D II L+ + +Y DHR+ M +AA E V + P
 Sbjct: 350 ATELNMKGADITPTEDGLIIRGKTPHAAVNTSYGDHRIGMMLQIAALLVEEGDVELERP 409
 Query: 426 GCTRKTFPDYFDVLSTFVK 444
 ++P +F+ + + +K
 Sbjct: 410 EAVSVSYPTFFEDIRSLK 428

>ref|YP_004200006.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. M18]
 gb|ADW14730.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter sp. M18]
 Length = 429

Score = 135 bits (341), Expect = 1e-29, Method: Compositional matrix adjust.
 Identities = 127/452 (28%), Positives = 220/452 (48%), Gaps = 35/452 (7%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 64
 + +Q K + G +++PG KS+S+R ++ ++++G T V L ED L A R +G
 Sbjct: 2 QSYTVQTAKGLRGEIRVPGDKSISHRSIMFGSIKGVTKVSGFLRGEDALATLEAFRAMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVL 123
+ ++ D + +VG G + +E + GN+G +MR LT + AG N VL
Sbjct: 62 VQIDDD--GETVTIVGKG----LHGLEPTDVLDCNGSGTSMRLLTGLL--AGQNFFSVL 113

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QY 182
G +R RP+ +V L ++GA + G + P+ + G L G ++ +SS Q
Sbjct: 114 SGDKYLRARPMKRVVGPLGRMGARIGGRAGGEKAPLAIQG-SKLKG--IEYDSPVSSAQV 170

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
SA+++A A G+ ++ P++ + + R++ FG E ++GG
Sbjct: 171 KSAIMLAGLYAEGET-----VREPHLSRDHSERMLRAFGANVETFPGG--VKVRGGA 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + ++ V GD SSA++F+ A I G + + G G + + ++L+ MGA +
Sbjct: 222 EL-TGRDIVVPGDISSAAFFMVAALIIPGADLLIRGVGNPTRTGI--IDILKGMGADLE 278

Query: 300 WTETSVTVTGPPREPFGGRKH--LKAI DVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
TG P +H LKA++++ +P D + V A A G T +R +
Sbjct: 279 LVNER-DETGEPVADIRVRHSQKAMEISGELVPRAIDFPAICVAASLAQGTTVVRGAS 337

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA 414
RVKET+R+ A+ L + G +V E PD IT L A D++ DHR+AM+ +A
Sbjct: 338 ELRVKETDRIAMADNLKRAGVTVLETPDGMEITGSAALKACAADSF GDHRIAMSMVAG 397

Query: 415 -CAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 445
A+ T+ D C +FP + ++L V+
Sbjct: 398 LAAKGETTVSDVDCIATSFPFGFRELLEGVVQR 429

>ref|YP_060391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10394]
ref|YP_596876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS9429]
ref|YP_600759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS2096]
ref|YP_001128322.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes str. Manfredo]
sp|Q5XBK5.1|ARO_A_STRP6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q1JB43.1|ARO_A_STRPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q1JL87.1|ARO_A_STRPC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A2RE13.1|ARO_A_STRPG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAT87208.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10394]
gb|ABF32332.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS9429]
gb|ABF36215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS2096]
emb|CAM30088.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes str. Manfredo]
Length = 430

Score = 135 bits (341), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 124/444 (27%), Positives = 214/444 (48%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 13 LQGTIQVPKDKSISHRAVILGAVAKGETRVKGLLKGEDVLTSTIQAFRN LGVRIE--EKDD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 71 QLVIEGQGFQGLTAPCQT---LNMGNSGTSMRLIAGLL--AGQPFSVKMIGDESLSKRPM 125

Query: 135 GDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

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      +V LKQ+G ++      PP+++ G   L       L S S+Q SA+L+AA A
Sbjct: 126 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLQPITYTLPIS-SAQVKSAILLAALQAK 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G ++ ++K I+ + E      ++++FG      R + G Q+ + + V GD
Sbjct: 185 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 236

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
      SSA+++L AG I G + ++ G   + + EV+E MGA++ + + TS+
Sbjct: 237 SSAAFWLAVAGLIIPGSELLKNVGVNPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 294

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
      V          HLK ++ +P + L ++AL A   G T I+D   RVKET+R
Sbjct: 295 VV-----YSHLKGTTIISGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
      + + L +GA+++ D II P L      TY DHR+ M ++AA + V
Sbjct: 347 IQVVTDTLNSMGANIKATADGMIKGPVTVLYGANTSTYGDHRIGMMTAIAALLVKQGQVH 406

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVKN 445
      +          ++P +F L   +
Sbjct: 407 LDKEEAIMTSYPTFFKDLERLCHD 430

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>ref|ZP_06060710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
2_1_36FAA]
gb|EEY79894.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
2_1_36FAA]
Length = 427

```

Score = 135 bits (341), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 127/447 (28%), Positives = 221/447 (49%), Gaps = 41/447 (9%)

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Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K + G++++PG KS+S+R ++ +L++G T V ++L EDV + R +G+ +E DK
Sbjct: 8 KGLRGSRLRVPKDKSISHRSIIFGSLAKGVTKVHDILRGEDVLSTMQVFREMGVQIE-DKG 66

Query: 73 AKRAVVVGCGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      + GCG F D +E Q L +GN+G +MR L A V A G N + + G +
Sbjct: 67 -DLVEIHGCG--F---DGLQEPQRPLDMGNSGTSMR-LIAGVLA-GQNFSAQMVGDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      +RP+ + + L+Q+G ++ D PP+ ++G L + +L + S+Q SAL+ AA
Sbjct: 119 KRPMDRISLPLRQMGVEIAGQTERDLPLTIHGNPSLKPIQYQLPIA-SAQVKSALIFAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVE-MTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
      A G E II+K ++ + E M L+ + V + + G Q+ ++ +
Sbjct: 178 LQAQG--ESLIIKDLTRNHTEDMLLQFGGQLKVDGKE-----IRVAGKQELQA-QEVV 228

Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----- 303
      V GD SSA++ L AG + +T+ G + + +V++ MG K++ +E
Sbjct: 229 VPGDISSAAFCLVAGLVVPNSKITLTNVGINETRTGI--LDVIQAMGGKLSVSEVDEVA 286

Query: 304 SVTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
      S T+T E L ++ +P + L ++AL A +G T IRD +VKE
Sbjct: 287 SATITVESSE-----LHGTEIGGELIPRLIDELPIIALLATQAEGQTLIRDAEELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEV 418
      T+R+ + L +GA++ D II L ++ TY DHR+ M ++AA +
Sbjct: 341 TDRIQVVADALNSMGADIQPTADGMIQKTPKLGASVHTYGDHRIGMMTAIAALLVKDG 400

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVKN 445
      V + ++PD+F L + +
Sbjct: 401 NVELERAEAINTSYPDFFAHLEGLSD 427

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>ref|ZP_07643638.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis
SK321]
gb|EFN96940.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis
SK321]
Length = 427

```

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 121/443 (27%), Positives = 213/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 ISHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMDGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L + +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKKMGVSISSQTERDLPPLHLKGTKNLPIQYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK S + V
Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKL-SGQKVVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLIVPNSRVVLKNVGINETRTGI--IDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKKSALHGARVNTFGDHRIGMMTTIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L +
Sbjct: 403 ELDRAEAINTSYSPFFDDLENLI 425

>ref|YP_002250779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dictyoglomus
thermophilum H-6-12]
gb|ACI18321.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dictyoglomus
thermophilum H-6-12]
Length = 435

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 123/449 (27%), Positives = 225/449 (50%), Gaps = 31/449 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++ K + G V++PG KS+S+R L+ +++ EG +++ N L S+D + L++LG+
Sbjct: 3 KLLVKKSKVLKGEVEVPKDKSISHRALIFSSMGEGESIIRNLFQSQCISTMNCCLKSLGV 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
S+E + R V G G ++ KE E L GN+G +R LT ++ G V+
Sbjct: 63 SIEVYDSIVR--VKNG-----IKGFKEPENVLDAAGNSGTTIRLLTGLLSGLPG-VFSVIT 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+ +V L+++GA++ + PP+ + G + G+ + S+Q S
Sbjct: 116 GDSSLRRRPMKRVVDPLRKMGANIWRNNDNNPLAIKGEKLV--GESHLNVASAQVKS 173

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+A LA G E + + +S + E R+ + G+ + + + G + YK+
Sbjct: 174 ALLIAGLLAEG--ETCVTEPSLSRDHTE---RMFQYLGGLPLKREGLTLKTH--GIESYKN 226

Query: 245 PKNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV----T 299
K+ + GD SSA++ +A G + G V ++ G + ++L+ GAK T
Sbjct: 227 -KDFNIPGDFSSAAFIIAAGLLVEGSKVVIKNVGINPTR--TGMLDILKEAGAKFNIIDT 283

Query: 300 WTETSVTVTGPPREPFGKRHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASW 356
W + + E LKA ++ + +P D LA++A A G + +DV
Sbjct: 284 WEDGGELIGNLMIE---YSDLKAFEIKGDIVPTLIDEVPILAIATQAKGESIFKDVEEL 340

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACA 416

+VKE++R+ A+ + K+G + + ++ P KL I+TY DHR+AMAF++A
Sbjct: 341 KVKESDRIKAVVDGINKMGGKAKVIDNGFVVYGP TKLKGGEIETYGDHRIAMAFIAAGLI 400

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
TI + +FP + + + + N

Sbjct: 401 ADDETIVESDSINISFPTFTETIKSLG 429

>ref|ZP_06877827.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas aeruginosa PAb1]
Length = 746

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 130/437 (29%), Positives = 213/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQA FRDMGVVIEG 377

Query: 70 DKA AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPF DST--LTGDA 429

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L
Sbjct: 430 SLSKRPMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVK SCL 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHSDSWDRFYIKGGQKYKSPK 246
L+A A G+ + P + T R++ FG E S + ++ G K S
Sbjct: 487 LLAGLYAAGETSVT-----EPAPTRDHTERMLRGFGYPVEVEGSTAK--VESGHKL-SAT 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VG VIEILRLMGDLSL-ENQR 595

Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V G P + LK ID+ + +P D L V A A+G T +R RVKE
Sbjct: 596 EVGGEPVADIRVRSARLKGIDIPEDLVPLAIDFPPVLVFAAACAEGRTVLRGAEEELRVKE 655

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG E PD +I + + DHR+AM+FS+A+ A P
Sbjct: 656 SDRIQVMADGLKALGVKAEPTPDGIVIE-GGAFGGGEVWAHGDHRIAMSFVASLRASGP 714

Query: 420 VTIRDPGCTRKTFPDYF 436
+ I D +FP++
Sbjct: 715 IRIHDCANVATSFPNFL 731

>ref|NP_225233.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae CWL029]
ref|NP_301094.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae J138]
ref|NP_445352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae AR39]
ref|NP_877351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae TW-183]
sp|Q9Z6M0.1|ARO A_CHLPN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAD19176.1| Phosphoshikimate Vinyltransferase [Chlamydomonas pneumoniae CWL029]
gb|AAF73706.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae AR39]
dbj|BAA99246.1| phosphoshikimate vinyltransferase [Chlamydomonas pneumoniae J138]
gb|AAP99008.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas
pneumoniae TW-183]
Length = 445

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 116/429 (27%), Positives = 205/429 (47%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPKSKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G +P SKS + R +L A+++EG +++ N L+S D M+ A + +G S++ K +
Sbjct: 11 VYGNAPFPSSKSHLTRAILWASVAEGKSIIYNYLDSPTTEAMICACKQMGASIK--KFPQ 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VG P+ + + GN+GI +R +TA T + G +++ RP+
Sbjct: 69 ILEIVGN----PLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEIT--VTGSSQLQRRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L+ GA +D + G L + GS SQ+ SAL +A LA
Sbjct: 123 APLLQALRNFGASFH--FSSDKSVLPFTMSGPLRSAYSDEGS-DSQFASALAVACSLAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G II+ P+ +++L +E+ + SD+ F G + + +V GD
Sbjct: 180 GPCSFTIIEPK-ERPWFDSLWLEKLHLPYSCSDTTYF---PGSSHPQGFSYHVTGDF 235

Query: 255 SSASYFLAGAAITGGT--VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++ A A ++ + + +QGD F +++ +GA + + + V
Sbjct: 236 SSAAFIAAAALSKSLQPIRLRNLDILDIDQDKIFFSLMQNLGASIQYDNEEILVFP--- 292

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
++M+ D L V+ FAD P+ + + S + KE++R++AI EL
Sbjct: 293 -----SSFSGSIDMDGCIDALPILTVLCCFADSPSHLYNARSADKESDRILAITTELQ 347

Query: 373 KLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
K+GA ++ D ++ P L +D++DDHR+AMA ++AA A I + C RKT
Sbjct: 348 KMGACIQPTHDGLLVN-PSPLYGAVLSDHDDHRIAMALTIAALYASGDSRIHNTACVRKT 406

Query: 432 FPDYFDVLS 440
FP++ L+
Sbjct: 407 FPNFVQTLN 415

>ref|YP_002319974.1| hypothetical protein AB57_2630 [Acinetobacter baumannii AB0057]
ref|YP_002325075.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii AB307-0294]
ref|ZP_05826672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii ATCC 19606]
ref|ZP_06781607.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. 6013113]
ref|ZP_06795992.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. 6013150]
ref|ZP_07237203.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter baumannii
AB058]
gb|AB012699.2| hypothetical protein AIs_2276 [Acinetobacter baumannii ATCC 17978]
gb|ACJ42738.1| hypothetical protein AB57_2630 [Acinetobacter baumannii AB0057]
gb|ACJ56148.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii AB307-0294]
gb|EEX04290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii ATCC 19606]
Length = 756

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 382 GEVTIHVGVMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSQKFDSD--VMTGDASLS 433

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGEKGTTPVVSITGGQQLKGIQYDLPMASQVKSIGILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 493 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 542

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 543 QVPSDISAFAFFMVGAITEGADVLEAVGINPRTGV--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPREPF---GRKHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 600 GGEPIADIIHGKSRITLKGHPEDQVPLAIDEFPALFIAAACAEGQTVLTGAAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 660 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDRHAMSFSMAG 719

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 720 LRTSGPITIHTGTETVATSFPTFTEL 744

>ref|YP_003840078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
obsidiansis OB47]
gb|ADL42092.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
obsidiansis OB47]
Length = 433

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 127/446 (28%), Positives = 211/446 (47%), Gaps = 37/446 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ V +P KS+S+R +++ +L++G T ++N L S+D + L+ LG AD
Sbjct: 9 RKINSNVIVPPDKSISHRSIMIGSLAKGVTEIENFLFSDDCLATINCLKNLG---ADIE 64

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++ G F + K+ L N+G R L ++ + +L G +++R
Sbjct: 65 IRNDKIIVKGNDFNLSAPKQ--ILDQNSGTTTLLLGILSTQEFES--ILTDGSSSLKKR 120

Query: 133 PIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + V L Q+GA + D P++V G L + L S S+Q SAL+ A+
Sbjct: 121 PMKRVTVPLSQMGAKFEFLEKEDFLPIKVKGSKKLKPIEYTLPIIS-SAQVKSALIFASLK 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G I+ K S + E+ L+ + SW+ + ++ S
Sbjct: 180 AEGKSVIKESPK--SRDHTELMLKHA-----GANIKSWEENGIYIVEILPSQLSSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++F+ A I +V +E C + + +VL+ MGA++ V
Sbjct: 232 IPSDISAFAFFIVLALICDNSSVVIENCILNPRTGTI--IDVLKQMGAEIRIE---NVE 285

Query: 309 GPPREPFGR-----KHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +LK + V+ N +P D LAV A FA+G T I + + RVKE
Sbjct: 286 NRNGEFVGKIVAKSSNLKGVKVDKNIPRIIDEIPIILAVAAFAEGKTTIDNASSELRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADTYDDHRMAMAFSLAACA-EV 418
++R+ L GA E + II EKL +++Y DHR+AMA S+ ACA E
Sbjct: 346 SDRIKTTAQMLRSFGAECHELENGLEIIGSKEKLKSAIVNSYKDHRIAMAASIMACAVEG 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D C +FP+++D+L + K
Sbjct: 406 ESTILDADCASISFPNFYDILFSSTK 431

>ref|YP_001713131.1| bifunctional protein [Includes: putative prephenate or
cyclohexadienyl dehydrogenase; 3-phosphoshikimate
1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (AroA)] [Acinetobacter baumannii AYE]
ref|ZP_07227906.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter baumannii
AB056]
ref|ZP_07240660.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter baumannii
AB059]
emb|CAM86130.1| bifunctional protein [Includes: putative prephenate or

cyclohexadienyl dehydrogenase; 3-phosphoshikimate
1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (AroA)] [Acinetobacter baumannii AYE]
Length = 748

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KAFKKGFTVPGDKSVSHRSIMFGAIAEGTTHVTGTFLEGEDALATLQAFRDMGVSIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMLRLSGMLSAQKFDS--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRMGAQIQTTGKEGTTPPVSTITGGQQLKGIQYDLPLMA-SAQVKSIGILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISSAAFFMVGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPPREPF---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + ++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIIHKGSRITLKGIMHPEDQVLAIDEFPALFIAAACAEGQTVLGTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAG 711

Query: 415 C-AEVPVTIRDPGCTRTKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 712 LRTSGPITIHTGTETVATSFPTFTTEL 736

>gb|EFU13047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1341]
Length = 428

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGLTMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + GI L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTTEFPPIISIRGIQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAKGTSVV--VEKEKTRDHTTEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISSAAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMMGGSVTILNEDEANHS 290

Query: 310 PPREFGRKHLKAIDVNMNMKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A

Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRD A EELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +

Sbjct: 349 VAKELTILGADITPTDGLI IHGPTS LHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L

Sbjct: 409 AEA VSVSYPAFFDDL 423

>ref|YP_001085301.1| hypothetical protein AIs_2276 [Acinetobacter baumannii ATCC 17978]
Length = 714

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLP GSKLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K

Sbjct: 280 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFL EGEDALATLQAFRDMGVSI EGPKN 339

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +

Sbjct: 340 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 391

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A

Sbjct: 392 KRPMERIAKPLRLMGAQIQTTGEKGTPPV SITGGQQLKGIQYDL PMA-SAQVKS GILLAG 450

Query: 191 PLALGDVEIEI IDKLISIPYVEMTLRLMERFG--VKA EHS DSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N

Sbjct: 451 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 500

Query: 249 YVEGDASSASYFLAGAAIT-GGT VTVEGCGT TSLQGDVKFAEVLEMMGAKV TWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E

Sbjct: 501 QVPSDISSAAFFMVGA AITEGADVLEAVGINP TRTGV--IEILKQMGADLT-VENERIA 557

Query: 308 TGPPPREPF---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGP TAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+

Sbjct: 558 GGEPIADIHIKGSRTLKGIHMPEDQVPLAIDEFPALFIAAACAEGQT VLTGAAELRVKES 617

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A

Sbjct: 618 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAG 677

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++

Sbjct: 678 LRTSGPITIHGTETVATSFPTFTEL 702

>ref|ZP_00234980.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes str. 1/2a F6854]
ref|ZP_05259304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes J0161]
ref|ZP_05262493.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes J2818]
ref|ZP_05268505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes F6900]
gb|EAL05174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes str. 1/2a F6854]
gb|ACN18349.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18439.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18445.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
gb|ACN18562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria

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monocytogenes]
gb|ACN18583.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18628.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18634.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18649.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18652.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18664.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|ACN18706.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes]
gb|EEW22011.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes F6900]
gb|EFF98797.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes J2818]
Length = 428

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 122/437 (27%), Positives = 221/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIETEETEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITINGKQTLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHEHMIHQFGEIEMDGLTIR--VKGGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPRTGTI--FDVVEQMGGSLLVVKDSSRS-TGKLAGT 291

Query: 315 FGRK--HLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 292 VVVKTSSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAT 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 352 ELNKMGAIDITPTEDGLIIRGKTPHAAANVTSYGDHRIGMMLQIAALLVEEGDVLELPERPEA 411

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 412 VSVSYPTFFEDIRSLK 428

>ref|ZP_00682490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Ann-1]
gb|EA031956.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Ann-1]
Length = 442

```

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 131/432 (30%), Positives = 207/432 (47%), Gaps = 35/432 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AAL++GT+ +D L +ED L LG+ +E + +
Sbjct: 17 LHGVLSPGDKSISHRAVMFAALADGTSRIDGFLEAEDTRSTAAILARLGVRIETPSSTQ 76

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R V VG G F D + L GNAG MR L + A ++ VL G + +RP
Sbjct: 77 RIVHGVGVGDG-FQASD----IALDCGNAGTGMRLLAGLLVAQPFDS--VLVGDAASLSKRP 129

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+R+ G G L G +S S+Q SA+L+A A
Sbjct: 130 MRRVTDPLSQMGARIDTS-DDGTPPLRIYG-GQLLRGIDFISPVASAQIKSAVLLAGLYA 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + P + T R++ FGV + S R ++GGQ+ + N + D
Sbjct: 188 RNETVTVREPH-----PTRDYTERMLTAFGVDIDVSTGCAR--LRGGQRLCA-TNITIPAD 239

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + I G +T+ G + + VL +MGA + E++ G
Sbjct: 240 FSSAAFYLVAASVIPGSDITLRAVGLNPRR--IGLLTVLRLMGADI--VESNCHEQGG-- 293

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP ++ + ++P D L + A A+G T + A RVKE++R+
Sbjct: 294 EPVADLVRVYAPLQGTTRVPEDLVPDMIDEFPVLFIAAAAEGQTVVSGAAELRVKESDRL 353

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP-VTIR 423
A+ T L LG V+E D I + I+++ DHR+AMAFS+A V V I
Sbjct: 354 AAMVTGLRVLVGVQVDETDADGATIH-GGPIGHGTINSHGDHRIAMAFSIAGQLSVSTVRIE 412

Query: 424 DPGCTRKTFFDY 435
D +FP+Y
Sbjct: 413 DVANVATSFPNY 424

>ref|YP_001706723.1| bifunctional protein [Includes: putative prephenate or
cyclohexadienyl dehydrogenase; 3-phosphoshikimate
1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (AroA)] [Acinetobacter baumannii SDF]
emb|CAP00598.1| bifunctional protein [Includes: putative prephenate or
cyclohexadienyl dehydrogenase; 3-phosphoshikimate
1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (AroA)] [Acinetobacter baumannii]
Length = 748

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGTFLEGEDALATLQAFRDMGVSIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSQAQKFDSD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGKEGTTPVVSITGGQQLKGIQYDLMA-SAQVKS GILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISAAFFMVGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIHIKGSRTLKGIHMPEDQVPLAIDEFPALFIAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAG 711

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 712 LRTSGPITIHTETVATSFPTFTEL 736

>ref|YP_598767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10270]
sp|Q1JGC1.1|ARO_A_STRPD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF34223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10270]
Length = 430

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 126/444 (28%), Positives = 216/444 (48%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 13 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLLKGEDVLTSTIQAFRNLGVRIE--EKDD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G F +A + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 71 QLVIEGQG--FQGLNAPCQT-LNMGNSGTSMLRIAGLL--AGQPFSVKMIGDESLSKRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTD CPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 126 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLPITYTLPIS-SAQVKSAILLAALQAK 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 185 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 236

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA++L AG I G + ++ G + + EV+E MGA++ + + TS+
Sbjct: 237 SSAAFWLAVAGLIIPGSELLLNKVGVPNTRTGI--LEVVEKMGAQIAYEDMNKKEQVTSIR 294

Query: 307 VTGPPREPFGRKHLKAIDVNMNMKPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V HLK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 295 VV-----YSHLKGTTISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 347 IQVVTDILNSMGANIKATADGMIKGPVLYGANTSTYGDHRIGMMTAIAALLVKQGQVH 406

Query: 422 IRDPGCTRKTFPDYFDVLFVKN 445
+ ++P +F L +
Sbjct: 407 LDKEEAIMTSYPTFFKDLERLCHD 430

>ref|ZP_01086437.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH
5701]
gb|EAQ73732.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH
5701]
Length = 454

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 134/445 (30%), Positives = 212/445 (47%), Gaps = 37/445 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + GTV++PG KS+S+R LL A++EG T ++ LL +ED LR +G+S+ +A
Sbjct: 23 RSLRGTVRVPGDKSISHRALLFGAIAEGETRIEGLLPAEDPLSTAACLAMGVSIGPIQA 82

Query: 73 AKRAVVVCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ +V G G D +E L GN+G MR + + G +VL+G +R
Sbjct: 83 GEPVLVQGVG-----LDGLQEPDDVLDCGNSGTTMRLMLGLLAGRTGR-HFVLNGDASLR 136

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLS 184
RP+ + L +GA + G + P+ + G +L G++ S+Q S
Sbjct: 137 RRPMAVVGQPLAGMGALIRGRAGGNLAPLAIEG-----CQLHGAVIGTPVASAQVKS 188

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
ALL+AA A G + I+ S + E R++ FG K + R
Sbjct: 189 ALLLAALTASGSTTV--IEPARSRDHSE--RMLSAFGAKLDVGGDMGRMICLHPGASLR 243

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ V GD SSA+++L AAIT G +TVE G + EVL+ M A++
Sbjct: 244 GLSVVPGDISAFAFWLVAIAITPGAEITVENVGLNPTR--TGILEVLQQMEARLEVLNP 301

Query: 304 SVTVTGPPEPFRGRKH--LKAI DVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V G P H LKA ++ + +P D LAV A A+G + IRD RV
Sbjct: 302 R-DVAGEFVGDVVRVSHGPLKAFEIGGDLIPRLVDEIPILAVAACCAEGVSRIRDAEELRV 360

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
KET+R+ + +L +GA++EE D +I L+ +D+ DHR+AM+ +AA V
Sbjct: 361 KETDRLAVMARQLGAMGALEETSDGLVIEGGRPLHGAEVDSETDHRVAMSLGVAAQVAV 420

Query: 419 PVT-IRDPGCTRKTFPDYFDVLSTF 442
+T + ++P ++D L+
Sbjct: 421 GITRLHRCDAAAVSYPGFWDLLARL 445

>ref|ZP_06750766.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_27]
gb|EFG34554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium sp.
3_1_27]
Length = 421

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 101/430 (23%), Positives = 206/430 (47%), Gaps = 40/430 (9%)

Query: 17 GTVKLPKSGKSLNRIILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V P SKS+ +R ++ ++L++G + ++N+ S+D+ + A++ LG + K
Sbjct: 13 GEVSPPPSKSILHRYIIASSLAKGISKIENISYSDDIIATIEAMKKLGAKI---KKNNNY 69

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ F E + ++ +G +R L + G ++ +RP+
Sbjct: 70 LLIDGSKTFDKEYLNNDSEIDCNESGTLRFLFPLSIVKQNRILF--KGKGLKFRPLSP 127

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ + + + ++ G L G ++ G+ISSQ+++ LL + PL +
Sbjct: 128 YFENFDKYQIN---YSYINSEIILLD--GELKSGVYEIDGNISSQFITGLLFSPLLNEN 182

Query: 197 VEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+I I KL S Y+++T+ + +FG+K ++S F I+G Q YKS + VE D S
Sbjct: 183 SKIIIRKLESSSYIDITVDCLNFKGIKI-INNSRQEFIIENQTYKSG-DYEVEADYSQ 240

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPEPFG 316
++FL +I G + + G + SLQGD K + + + W + +
Sbjct: 241 IAFFFLVANSI-GSNIKINGLNSNSLQGDRKIVDFISQID---NWNKKEKLI----- 287

Query: 317 RKHLKAI DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
++ ++ PD+ L++ A + I ++A R+KE++R+ A ELTKLG
Sbjct: 288 -----LDGSETPDIIPIILSLKACISKKEIEIINIARLRIKESDRLKATVEELTKLGF 339

Query: 377 SVEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTR 429
+ E D +I + N + + ++ DHR+AM ++A+ + + + + C +
Sbjct: 340 DLIEKEDSILINSRKNFNEISNNSPIYLLSSHSDHRIAMMIAIASTYYDGKIILDNLDCVK 399

Query: 430 KTFPDYFDVL 439
K++P++++V
Sbjct: 400 KSYPNFWEVF 409

>gb|ABX52003.1| G6 [synthetic construct]
Length = 507

Score = 135 bits (340), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 132/446 (29%), Positives = 214/446 (47%), Gaps = 33/446 (7%)

Query: 2 AGAEEIVL--QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGA 59
+GA +++ QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A
Sbjct: 68 SGANDLIFLAQPGGRLNGRIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQA 127

Query: 60 LRTLGLSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
R +G+ +E + + VG G P L++GN+G +MR L+ + AG +
Sbjct: 128 FRDMGVVIEGPNHGRVTIHGVLHGLKPPPG-----PLYVGNSGTSMRLLSGLL--AGQS 180

Query: 119 ATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGS 177
+ G + +RP+ + L+++GA V+ G + PP+ + G L G L +
Sbjct: 181 FDTVMTGDASLSKRPMMNRVANPLREMGAVVET--GPEGRPPLTIRGGHKLKGLTYTLPMA 238

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S+Q S LL+A A G + P + T R++ FG E + ++
Sbjct: 239 -SAQVKSCLLLAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYVESNGPV--ASLQ 290

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
G K + + V D SSA++FL A+I G+ + +E G + V ++L +MG
Sbjct: 291 SGGKLTATR-IEVPADISSAAFFLVAASIAEGSELVLEHVGINPRTGTG--IDILRLMGG 347

Query: 297 KVTWTETSVTVTGPPREPFGGRK--HLKAIDVMNMKMP--DVAMTLAVVALFADGPTAIR 351
+T E V G P + LK ID+ +P D L V A A+G T +R
Sbjct: 348 DITL-ENQREVGGEPVADLRVRGAQLKGIDIPALVPLAIDFPPVLFVAAACAEGRTVLR 406

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFS 411
RVKE++R+ + L LG E PD II +L + + DHR+AMAFS
Sbjct: 407 GAEELRVKESDRIQVMADGLITLGIKCEPTDGI IID-GGQLGGGEVHGHGDHRIAMAFS 465

Query: 412 LAAC-AEVPVTIRDPGCTRKTFFPDYF 436
+A+ A P+ I D +FP++
Sbjct: 466 VASLRASAPIRIHDCANVATSFNPL 491

>ref|YP_790016.1| EPSP synthase/prephenate dehydrogenase [Pseudomonas aeruginosa
UCBPP-PA14]
gb|ABJ12389.1| EPSP synthase/prephenate dehydrogenase [Pseudomonas aeruginosa
UCBPP-PA14]
Length = 746

Score = 135 bits (339), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 130/437 (29%), Positives = 213/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQA FRDMGVVIEG 377

Query: 70 DKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGVDV 429

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L
Sbjct: 430 SLSKRPMMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSC L 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G+ + P + T R++ FG E S + ++ G K S
Sbjct: 487 LLAGLYAAGETSVT-----EPAPTRDHTERMLRGFGYPVEVEGSTAK--VESGHKL-SAT 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E
Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVQLHVGINPTR--VGVEILRLMGGDLSL-ENQR 595

Query: 306 TVTGPPREPFGGRK--HLKAIDVMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V G P + LK ID+ + +P D L V A A+G T +R RVKE
Sbjct: 596 EVGGEPVADIRVRSARLKGIDIPEDLVPLAIDFPPVLFVAAACAEGRTVLRGAEELRVKE 655

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG E PD +I + + DHR+AM+FS+A+ A P
Sbjct: 656 SDRIQVMADGLKALGVKAEPDGPVIE-GGAFGGGEVWAHGDHRIAMSFSVASLRASGP 714

Query: 420 VTIRDPGCTRKTFPDYF 436
+ I D +FP++
Sbjct: 715 IRIHDCANVATSFNPNFL 731

>ref|YP_003474269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermocrinis albus
DSM 14484]
gb|ADC90142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermocrinis albus
DSM 14484]
Length = 433

Score = 135 bits (339), Expect = 1e-29, Method: Compositional matrix adjust.
Identities = 133/442 (30%), Positives = 219/442 (49%), Gaps = 29/442 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +K++ G +++P KS+S+R ++L+A++EG +VV + L S D L A+R LG V+
Sbjct: 4 VRKVKKVRGELRVPSDKSVSHRAVILSAMAEGESVVDHDLISADTLATLRAVRALGTVQ 63

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A R + G +F Q N+G R L + +T + G
Sbjct: 64 RKGATLR--IWGRAMRFQEPSDVINAQ----NSGTTARLLMGLLATQPFST--ITGDSS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R+RP+ +V L+Q+GA +D + PV V G G G + S+Q SA+L+
Sbjct: 116 LRKRPMRLRVVEPLRQMGAWLDGRERGNKLPVSVRG--GTLKGISFFNVKASQVKSAILL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKSPK 246
A A G ++E + ++S + E L+L FGV+ D+ +K GGQ KS +
Sbjct: 174 AGLGAEGYQTQE--EPVLSRDHTERMMLKL---FGVEVLTLDTEKGRMVKIEGGQIPKSAE 228

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ D SSA++F+A A + + + + D F +V +M G + E
Sbjct: 229 -VFCPADPSSAAFFVALALLVDDSEVLLKDVMMVNPTRDGFFRKVRQMGE--IYYENLRE 285

Query: 307 VTGPP----REPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
++G P R GRK LK ++V ++P D L+V+ A+G + ++ + RVK
Sbjct: 286 ISGEPIADIRVVGGRK-LKGVEVKGEVPSLIDEIPVLSVLMALAEGRSRVKGASELRVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEV 418
E++R+ A+ L +GA VEE D I L I TY DHR+AMAF++A AE
Sbjct: 345 ESDRIRAVVENLRSMGAKVEELEDGFEIEGVSSSLKGAFIKTYGDHRIAMAFTVAGLVAEG 404

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
I +P C ++PD++ L+
Sbjct: 405 ETVIDNPHCAVSYPDFYRDLA 426

>ref|ZP_05825120.1| 5-enolpyruvylshikimate-3-phosphate synthase [Acinetobacter sp.
RUH2624]
gb|EEW99527.1| 5-enolpyruvylshikimate-3-phosphate synthase [Acinetobacter sp.
RUH2624]
Length = 756

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 129/443 (29%), Positives = 209/443 (47%), Gaps = 37/443 (8%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KTFKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLEGEDALATLQAFRDMGVSIEGPKN 381

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 132
+ V++ G + ++ L++GN+G +MR L+ ++A ++ V+ G + +R
Sbjct: 382 GE--VIIHGVMYGLKAPAS--ALYMGNSGTSMRLSSGMLSAQKFDS--VMTGDASLSKR 435

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+ +GA + PPV + G L G + L + S+Q S +L+A

Sbjct: 436 PMERIAKPLRLMGAQIQTTGEKGTTPVSITGGQQLKGIQYDLPMA-SAQVKSGILLAGLW 494

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G+ + + P + T R++ FG VK E ++ + GG K N V

Sbjct: 495 AEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNIQV 544

Query: 251 EGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E G

Sbjct: 545 PSDISSAAFFMVGAAITEGADVLEAVGINPTRTG--IEILKQMGADLT-VENERIAGG 601

Query: 310 PPREF--GRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P G + LK I + +++P D L + A A+G T + A RVKE++R

Sbjct: 602 EPIADIIHIKSRITLKGIMHPEDQVPLAIDFPAFIAAACAEGQTVLTGAELRVKESDR 661

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAAC- 415
+ + L +G D II K I+++ DHR+AM+FS+A

Sbjct: 662 IQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAGLR 721

Query: 416 AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++

Sbjct: 722 TSGPITIHTGTETVATSFPTFTTEL 744

>gb|ADR61430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida
BIRD-1]
Length = 746

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 131/436 (30%), Positives = 208/436 (47%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E

Sbjct: 317 QPGGRLNGRIRVPGDKSISHRSIMLSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P L++GN+G +MR L+ + AG + G

Sbjct: 377 PNHGRVTIHVGLHGLKPPPG-----PLYVGNSGTSMRLLSGLL--AGQPFVMTMTGDAS 429

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA V+ G D PP+ + G L G L + S+Q S LL

Sbjct: 430 LSKRPMNRVANPLREMGAVVET--GPDGRPPLTIRGGHKLKGLTYTLPMA-SAQVKSCLL 486

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG + + ++ G K + +

Sbjct: 487 LAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYSVDSNGPV--ASLQSGGKLTATR- 538

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + +E G + V ++L +MG +T E

Sbjct: 539 IEVPADISSAAFFLVAASIAEGSELVLEHVGINPTRTG--IDILRLMGDITL-ENQRE 595

Query: 307 VTGPPREFPGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P + LK ID+ +P D L V A A+G T +R RVKE+

Sbjct: 596 VGGEPAVADLRVGRGAKLKGIDPEALVPLAIDFVLFVAAACAEGRTVLRGAELRVKES 655

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPV 420
+R+ + LT LG E PD II + L + + DHR+AMAFS+A+ A P+

Sbjct: 656 DRIQVMADGLTTLGIKCEPTPDGIIIDGGQ-LGGGEVHGHGDHRIAMAFSVASLRASAPI 714

Query: 421 TIRDPGCTRKTFPDYF 436
I D +FP++

Sbjct: 715 RIHDCANVATSFNPL 730

>ref|ZP_07737605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
lactoaceticus 6A]
gb|EFR11967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
lactoaceticus 6A]
Length = 433

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 127/446 (28%), Positives = 213/446 (47%), Gaps = 37/446 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ V +P KS+S+R +++ +L++G T ++N L S+D + + LG +E
Sbjct: 9 RKINSNVTVPSDKSISHRSIMIGSLAKGVTEIENFLSDDCLATINCFKNLGTDie---- 64

Query: 73 AKRAVVVCGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++ G F + K+ L N+G R L ++ + +L G +++R
Sbjct: 65 IRNDKIIVKGNDFNLFAPKQ--ILDQNSGTTTTRLLLGILSTQEFES--ILTGDSSLKKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSGSISSQYLSALLMAAPL 192
P+ + + L Q+GA+ + D P++V G L + L S+Q SAL+ A+
Sbjct: 121 PMKRVTLPPLSQMGAEEFLEKEDFLPIKVKGSKKLPIEYTLPIP-SAQVKSALIFASLK 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G I+ K S + E+ L+ G + SW++ + ++ S
Sbjct: 180 AEGKSIIVKESPK--SRDHTEMLK---HAGASIK---SWEKDGVTVEILPSQVSSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVT 308
+ D SSA++F+ A I G +V +E C + + +VL+ MGA + + V
Sbjct: 232 IPSDISAFAFFIVLALICEGSSVVIENCILNPRTGI--IDVLKQMGADIRIED----VE 285

Query: 309 GPPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +LK I V+ N +P D LAV A FA+G T I + + RVKE
Sbjct: 286 NRNGELVGKIIARSSNLKGIKVDKNDIPRIIDEIPI LAVAAFAEGKTTIDNASELRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTIADTYDDHRMAMAFSLAACA-EV 418
++R+ L GA E D II EKL +++Y DHR+AMA S+ ACA E
Sbjct: 346 SDRIKTTVQMLKSFADGCYELEDGLEIIGSREKLKSAVVNSYKDHRIAMAASIMACAVEG 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D C +FP+++D+L + K
Sbjct: 406 ESTILDAECASISFPNFYDILFSSTK 431

>ref|YP_001956607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured Termite
group 1 bacterium phylotype Rs-D17]
sp|B1GYQ3.1|AROAA_UNCTG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAG14146.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured Termite
group 1 bacterium phylotype Rs-D17]
Length = 430

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 126/447 (28%), Positives = 226/447 (50%), Gaps = 26/447 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EI L+ +SG +++P KS+++R ++L++L+EG ++V + L S+D + + A R +G+
Sbjct: 2 EIKLKKTNYSVSGVIEVPSDKSITHRAVMLSSLAEGNSIVRDYLPSSDCNRTIEAFRQMGV 61

Query: 66 SVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
++ D + V G G K + + ++ GN+G R L+ + AG + V+ G
Sbjct: 62 EIKIDNGS--LYVKGAGLKL-AKPQNGKYNİYAGNSGTTTTRLLSGIL--AGQDFETVITG 116

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSGSISSQYLSA 185
+ +RP+ +++ L Q+GA++ G P+ + G L + S ++Q SA
Sbjct: 117 DDSLSKRPMRRVILPLSQMGANIKSNDG--LLPLIIGRNPLKELNVE-SDKSTAQVKSA 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L A A G + + + S + E R+++ FGV + + ++ Y +K +
Sbjct: 174 ILFAGLFADGATTYK--EPVKSRDHSE---RMLKAFGVNIKVNGNFVTYV--PAEKLIA- 225

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
++ V GD SSA++F+A A I +T+ G + EVL+ MGA +T
Sbjct: 226 QDITVPGDISAFAFFIAAALIVPDSNLTIIRNVGNPTRDG--LIEVLKQMGADITLANMR 283

Query: 305 VTVTGPPEPFGR-KHLKAIDVNMN---KMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
P + + LKA D++ + +M D ++A ADG T I RVKE
Sbjct: 284 EISQEPVCDIVVKYSKLKAADIDASLVPRMVDEIPVFVLIATQADGITRISGAKELRVKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAA-CAE 417

++R+ ++ ++ KLGA +E D II K N+ T +D++DDHR+AM ++A+ AE
Sbjct: 344 SDRIESVTSQFKKLGAQIESLEDGFIINGNSKFNLAGTIVDSFDDHRIAMTLAIASLIAE 403

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVK 444
IRD C +FP ++ VL+ +

Sbjct: 404 GETIIRDSHCVDISFPGFYKVLNNICR 430

>ref|ZP_01820852.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP6-BS73]
ref|ZP_01831017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP18-BS74]
ref|ZP_02715416.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC0288-04]
gb|EDK68131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP18-BS74]
gb|EDK76117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP6-BS73]
gb|EDT94991.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC0288-04]
Length = 427

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 210/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKKMGVSISGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSVDGKKIIVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISSAAFVLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLKASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +

Sbjct: 408 EAINTSYPSFDDLES LI 425

>ref|ZP_02042497.1| hypothetical protein RUMGNA_03299 [Ruminococcus gnavus ATCC 29149]
gb|EDN76197.1| hypothetical protein RUMGNA_03299 [Ruminococcus gnavus ATCC 29149]
Length = 432

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 130/448 (29%), Positives = 203/448 (45%), Gaps = 33/448 (7%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L I + G V +PG KS+S+R ++ A+L+ G T + N LN D + R +G+ +E
Sbjct: 5 LTSITGLKGEVSIIPGDKSISHRSVMFASLANGMTEIHNFLNGADCLATIDCFRKMGIKIE 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPV 128
+ R +V G G + E +Q+ N+G R L+ + AG + L G

Sbjct: 65 EHQ--NRILVHG-KGLHGLTAPSETLQV--KNSGTTTRLLSGIL--AGQPFSTSLSGDES 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPG---GKVKLSGSISSQYLSA 185
+ RP+ ++ L Q+GA + G C P+ + PG G S S+Q S

Sbjct: 118 LNSRPMKRIIEPLTQMGAIHSLHNGCAPLVIE-----PGKLHGIHYTSPVASAQVKSC 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHE--SDSWDRFYIKGGQK 241
+L+A A G E + + ++S + E+ L+ FG ++ H + S I+ Q+

Sbjct: 173 ILLAGLYAEG--ETSVTEPILSRNHTELMLK---EFGADIRTVHQLAGSEATSVIQCQE 227

Query: 242 YKSPKNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K V GD SSA+YF+A G + + V+ G + +V E MG +T

Sbjct: 228 LHGQK-ITVPGDISAAYFIAAGLLVPDSEILVKNVGINPTRAG--LLKVCEDMGGNITL 284

Query: 301 TETSVTVTGPPREPFGRK-HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
+ R L I ++ + +P D +AV+A A+G T IRD

Sbjct: 285 LNERTEAGEKMDILVRSSQLHGSIHGDIIPTLIDEIPIIIVMAACAEGTTIIRDAQEL 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-C 415
RVKET+R+ I L +G SV D +I E L I T DHR+AMAFS+AA

Sbjct: 345 RVKETDRIETITDNLIAMGCSVLPTEDGMVIKGGEPKLGATIHLLDHRIAMAFSIAALV 404

Query: 416 AEPVVTIRDPGCTRKTFPDYFDVLSTFV 443
A+ I D C ++P ++D +

Sbjct: 405 ADGRTKILDSHCIDVSYPGFYDAFEHLL 432

>ref|ZP_06056213.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
calcoaceticus RUH2202]
gb|EEY77512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
calcoaceticus RUH2202]
Length = 756

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 130/445 (29%), Positives = 209/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPGSKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K

Sbjct: 322 KTFKGKFTVPGDKSVSHRSIMFGAIEGTTHTVTGFLGEDALATLQAFRDMGVSIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +

Sbjct: 382 GEVTIHVGVMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 433

Query: 131 ERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A

Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGEKGTPPVISITGAQQLKGIQYDLPLMA-SAQVKSGILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K +

Sbjct: 493 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TDI 542

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E

Sbjct: 543 QVPSDISAFAFMVGAATEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPREPF---GRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+

Sbjct: 600 GGEPIADIIHKGSRTLKGIHMPEDQVPLAIDEFPALFIAACAEGQTVLTGAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K +++++ DHR+AM+FS+A

Sbjct: 660 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFTGGEVESHHDRIAMSFMSAG 719

Query: 415 CAEV-PVTIRDPGCTRKTFPDYFDV 438
P+TI+ +FP + ++

Sbjct: 720 LRNSGPITIQGTETVATSFPTFTEL 744

>ref|ZP_01725453.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. B14905]
gb|EAZ83996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. B14905]

Length = 428

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 129/443 (29%), Positives = 213/443 (48%), Gaps = 34/443 (7%)

Query: 6 EIVLQPIK-EISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E VLQ K + G++ +PG KS+S+R ++ +++ GTT V+ L ED + + LG
Sbjct: 3 EKVLQYNKPSLQGSALTVPKSVSHRSVMFSGSIATGTTTVEGFLLEDCLSTIDCFQKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + V + G ++ + L+ GN+G R + + AG V+
Sbjct: 63 VHIEVEGTN---VTIESPGMNSWQEPD---VLYTGNSGTTTFLMLGIL--AGSTVHSVMT 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ ++ L+Q+GA + P+ + G L K+ + S+Q S
Sbjct: 116 GDASIGKRPMRVIDPLRQMGAHITGRADGQYTPLAIQGTK-LQAIDYKMPVA-SAQVKS 173

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+A A G + + +S + E R++ +FG E D ++GGQ S
Sbjct: 174 AILLAGLRAEGTTIVR--ETEVS RDHTE---RMLRQFGADVEVKDGV--VSLEGGQTL-S 225

Query: 245 PKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
+ V GD SSA++FL AGA +T+E G + + EVL MGA T T
Sbjct: 226 GTHVSVPGDISSAFLVAGAICNTSQTLENVGVNPTDGI--IEVLSKMGA----TMT 279

Query: 304 SVTVTGPPREPFGFRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVAS 355
+ EP ++ ++ + ++ D LA++A A G T I+D
Sbjct: 280 VIPNDDRQAEPATIIQITSTLSGTTIEGELIPRLIDEIPLALLATQAHGQTIKDAEE 339

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
+VKET+R+ A+ TEL KLGA++E D II P L ++ TY DHR+ M ++AA
Sbjct: 340 LKVKETDRITAVVTELKKGANIEATNDGMIIEGPTPLKGASLKYGDHRIGMMGAVAAL 399

Query: 415 CAEVPVTIRDPGCTRKTFPDYFD 437
E VT+ D C ++P +F+
Sbjct: 400 ITEGSVTLDDAQCIASVPSFFE 422

>ref|YP_001374559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
subsp. cytotoxis NVH 391-98]
sp|A7GN56.1|AROABACC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS21564.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cytotoxicus
NVH 391-98]
Length = 424

Score = 135 bits (339), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 123/440 (27%), Positives = 214/440 (48%), Gaps = 33/440 (7%)

Query: 13 KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+ +PG KS+S+R ++ A++EGTT V N L ED + R LG V+ D++
Sbjct: 8 KGLNGTIAIPGDKSISHRAVMFGAIAEGTTKVSNFLGEGDCLSTIACFRKLG--VKIDQS 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ G G +++ KE L +GN+G +R + + T + D + +R
Sbjct: 66 GNDVTIYG-KGLTGLQEPKE--VLDVGNSGTTIRLMLGILANVPFHCTIIGD--DSIGKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+++ A +D P+ + G G + G S S+Q SA+L+A
Sbjct: 121 PMKRVTDPLREMNAQIDGREDGQYTPLSIRG-GNIKGIHYD-SPVASAQVKSAILLAG-- 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G+ + + L S + E R++ FG E + ++GGQ + V G
Sbjct: 177 LKGEVTVTTEPLQSRDHTE---RMLRAFCTVEVTGQT--VSLRGGQSLIGTE-IEVPG 230

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPP 311
D SSA++FL AGA + + ++ G + + +VL+ MGA ++ V
Sbjct: 231 DISSAFLVAGAIVPNSKIVLKNVGLNPTRTGI--IDVLQKMGAISLVDH----VRNEE 284

Query: 312 REPFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETER 363

EP G L+ I++ + +P + + ++AL A G T I+D +VKET R
Sbjct: 285 FEPCGDITITIETSKLQGIIEIGSLIPRLIDEIPIIALLATQATGTTVIKDAEELKVKETNR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTI 422
+ + EL KLG +E D II +KL +D++ DHR+ M ++A+C A+ V I
Sbjct: 345 IDTVVQELKKLGKVKIEATSDGMIIYGNQKLQGGIVDSHGDRIGMMLAIASCIADGEVEI 404

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
+ ++P++FD L++
Sbjct: 405 QRSDAVSVSYPNFFDQLASL 424

>ref|ZP_06788118.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. 6014059]
gb|ADX93090.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter baumannii
TCDC-AB0715]
Length = 748

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHGVGMYGLKAPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGEKGTTPPV SITGGQQLKGIQYDLPMA-SAQVKS GILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISSAFFMVGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIHIKSGRTSLKGIHMPEDQVPLAIDEFPALFIAAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEK-----LNVTADITYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAG 711

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 712 LRTSGPITIHGTETVATSFPTFTEL 736

>ref|YP_001667604.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas putida GB-1]
gb|ABY97268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida
GB-1]
Length = 746

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 208/436 (47%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 QPGGRLNGRIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P L++GN+G +MR L+ + AG + + G
Sbjct: 377 PNHGRVTIHGVLHGLKPPPG-----PLYVGNSGTSMRLLSGLL--AGQSFVDTMTGDAS 429

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA V+ G + PP+ + G L G L + S+Q S LL
Sbjct: 430 LSKRPMNRVANPLREMGAUVET--GPEGRPPLTIRGGHKLKGLTYTLPMA-SAQVKSCLL 486

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG E + ++ G K + +
Sbjct: 487 LAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYSVESNGPV--ASLQSGGKLTATR- 538

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + +E G + V ++L +MG +T E
Sbjct: 539 IEVPADISSAAFFLVAASIAEGSELVLEHVGINPRTGTG--IDILRLMGGDITL-ENQRE 595

Query: 307 VTGPPREPFGRK--HLKAIDVNMNMKP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P + LK ID+ +P D L V A A+G T +R RVKE+
Sbjct: 596 VGGEPVADLRVGAQLKGIDPEALVLAIDFEPVLFVAAACAEGRTVLRGAEEELRVKES 655

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ + L LG E PD II + L + + DHR+AMAFS+A+ A P+
Sbjct: 656 DRIQVMADGLITLGIKCEPTPDGIIIDGGQ-LGGGEVHGHGDHRIAMAFSVASLRASAPI 714

Query: 421 TIRDPGCTRKTFPDYF 436
I D +FP++
Sbjct: 715 RIHDCANVATSFNPL 730

>ref|YP_003731401.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. DR1]
gb|ADI90028.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. DR1]
Length = 748

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 210/445 (47%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSDEVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSQAQKFD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGEKGTTPVSVITGSQQLKGIQYDLPA-SAQVKS GILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K +
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TDI 534

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G+ V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISAAFFMVGAAITEGSDVLEAVGINPRTGTG--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNMKP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIIHIGKSRITLKGIMHPEDQVPLAIDFEPALFIAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMIGDCTPTDDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMFSMAG 711

Query: 415 CAEV-PVTIRDPGCTRKTFPDYFDV 438
P+TI+ +FP + ++
Sbjct: 712 LRNSGPITIQGTETVATSFPTFTEL 736

>ref|YP_001847133.1| 5-enolpyruvylshikimate-3-phosphate synthase [Acinetobacter
baumannii ACICU]
gb|ACC57786.1| 5-enolpyruvylshikimate-3-phosphate synthase [Acinetobacter

baumannii ACICU]
gb|ADX02847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii 1656-2]
Length = 756

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KAFKGFVTPGDKSVSHRSIMFGAIAEGTTHVTGFLEGEDALATLQAFRDMGVSIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 382 GEVTIHGVGMYGLKAPAS-----ALYMGNSGTSMRLLSGMLSQAQKFD--VMTGDASLS 433

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGEKGTTPVVSITGGQQLKGIQYDLMA-SAQVKSIGILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 493 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE---GNKISLVGGGKLVG-TNI 542

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 543 QVPSDISAAFFVMGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPREPFP---GRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 600 GGEPIADIHIKGSRTLKGIHMPEDQVPLAIDEFPALFIAAACAEGQTVLTGAAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 660 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSPIFAGGEIESHHDRIAMSFMSAG 719

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 720 LRTSGPITIHTGTETVATSFPTFTTEL 744

>ref|YP_518495.1| hypothetical protein DSY2262 [Desulfitobacterium hafniense Y51]
ref|YP_002459846.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfitobacterium
hafniense DCB-2]
sp|Q24V91.1|ARO_A_DESHY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B8G2R0.1|ARO_A_DESHD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE84051.1| hypothetical protein [Desulfitobacterium hafniense Y51]
gb|ACL21410.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfitobacterium
hafniense DCB-2]
Length = 435

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 129/447 (28%), Positives = 212/447 (47%), Gaps = 29/447 (6%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I + P+ I G +++PG KS+S+R L +++G T + N L +D L L+TLG
Sbjct: 10 IRINPMGRIQGEIEVPGDKSISHRAALFGGMAQGETHITNFLGQDCLSTLACLKTLG-- 67

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
VE ++ + G G F +++ L +GN+G MR + AG + L G
Sbjct: 68 VEWERRDAEVDWIRGR--FENWHEPQDI-LDVGNSTGTMRLMLGV--AGCPFSATLTGD 122

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+R RP+ + + L+++GA + P+ + G GL G S +Q SA+
Sbjct: 123 SSIRSRRMARVTLPLQEMGARILGRQEGKYAPLTIQ--GLLQGIQFRSPVASAQVKSAL 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV--KAEHSDSWDRFYIKGGQKYKS 244

L+A A G E + + +S + E R++ FGV K+E + ++GG S
 Sbjct: 181 LLAGLRAGK--ETMVTEPCLSRDHTE---RMLRGFGVDLKSEGRTA---KVRGGAAL-S 230
 Query: 245 PKNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
 + V GD SSA++FL G I G + ++ G + + + L MGA + E
 Sbjct: 231 GQEVAVPGDISAFAFLVLGTLIPQGELLIKNVGMNPTRTGI--LDALWQMGAADIQVEEE 288
 Query: 304 SVTVTGPPREPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
 P R L I++ +P D LAV A A G T IRD A RVK
 Sbjct: 289 REECGEPRANLRVRPAQLHGIEIQGEMIPKLIDEVPLAVAASLAQGETVIRDAAELRVK 348
 Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEV 418
 ET+R+ + L LGA+ +E PD I + L A ++ DHR+AMA+ +A AE
 Sbjct: 349 ETDRIQTVVQGLQALGANAQELPDGLRIQGAQSLRGGAASHGDHRLAMAWVAGLLAE 408
 Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 445
 +++++ +FP++ +++ ++
 Sbjct: 409 GISLQGIEAAEVSPNPFLELIHEIAES 435

>ref|ZP_05584251.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 CH188]
 ref|ZP_07762493.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 TX0635]
 gb|EEU85222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 CH188]
 gb|EFQ16472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 TX0635]
 gb|EFT91286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 TX4244]
 gb|EFU89892.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
 TX0630]
 Length = 428

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
 Identities = 125/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
 +K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
 Sbjct: 9 VKHLQGLTMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68
 Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
 ++V G ++ AK ++ GN+G +R + + AG L G + +
 Sbjct: 69 TT---IIVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121
 Query: 132 RPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
 RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
 Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180
 Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
 A G + ++K + + E +R +FG E + + G Q+ + +N V
 Sbjct: 181 QAEGTSVV--VEKEKTRDHTTEEMIR---QFGGTLEVD--GKKIMLTGFPQQL-TGQNVVVP 232
 Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
 GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
 Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHSG 290
 Query: 310 PPREPFRGKHLKAIDVNMNMKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
 L A ++ +P + L ++AL A G T IRD +VKET R+ A
 Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRD A EELKVKETNRIDA 348
 Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
 + ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
 Sbjct: 349 VAKELTILGADITPTDDGLIIGHGPTSLHGGVRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408
 Query: 425 PGCTRKTFPDYFDVL 439
 ++P +FD L
 Sbjct: 409 ADAVSVSYPAFFDDL 423

>ref|YP_002219472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidithiobacillus

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ferrooxidans ATCC 53993]
ref|YP_002425379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidithiobacillus
ferrooxidans ATCC 23270]
sp|B7J781.1|ARO_AACIF2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B5EQ20.1|ARO_AACIF5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACH83265.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidithiobacillus
ferrooxidans ATCC 53993]
gb|ACK78170.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidithiobacillus
ferrooxidans ATCC 23270]
Length = 433

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Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 134/438 (30%), Positives = 215/438 (49%), Gaps = 35/438 (7%)

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Query: 8 VLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
+++P ++G +PG KS+S+R ++L AL+EG T V+ LL DV + A R++G+ +
Sbjct: 5 LVRPGSLAGRFVPVPGDKSISHRAVILGALAEGVTEVEGLLEGADVLATIAAFRSMGVQM 64

Query: 68 EA-DKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
E DK R G G + PV V L GN+G AMR L + +T V D
Sbjct: 65 EGPDKGHLRIHGAGLQGLRAPV-----VPLDCGNSGTAMRLLAGVLAGQPPFSTLVGDA 118

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLS 184
+++RP+G ++ L+ +GA++ G P+ ++ G P + + + S+Q S
Sbjct: 119 --SLQKRPMGRILNPLRAMGAETIAAQDGRA--PLHIH--GRPLHGIDYALPVASAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+A A G + P + + R+++ FG E R ++GG +
Sbjct: 172 AVLLAGLYADGQTCVT-----EPAPTRDHSEMLQGFQGPVER--HGPRACLRGGGRLCG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTET 303
+ V GD SSA++FL GA I G+ +T+EG G + E+L MGA++ T
Sbjct: 225 -QALQVPGDISAFAFFLLGATAPGSDLTLEGVGINPTR--TGIIEILTRMGARIDLTA 281

Query: 304 SVTVTGPPREPFGFRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V G P ++ L+ I + +P D L + A A G T I RV
Sbjct: 282 R-EVGGEFVADIRVRYAPLQGAIPPLRVPLAIDFPAFIAAACAKGQTVITGAELRV 340

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KE++R+ + L LGA+VEE D II+ L +D++ DHR+AMAF++AA A+
Sbjct: 341 KESDRIAVMAGGLRALGATVEERVVDGAIISGSALLG-GRVDSHGDHRIAMAFAMAALVAQ 399

Query: 418 VPVTIRDPGCTRKTFPDY 435
+ I D +FP +
Sbjct: 400 GDMEILDCANVATSFPSF 417

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>ref|YP_280561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS6180]
ref|ZP_07460422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes ATCC 10782]
sp|Q48SV4.1|ARO_ASTRPM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAX72206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS6180]
gb|EFM33700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes ATCC 10782]
Length = 427

```

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 212/435 (48%), Gaps = 39/435 (8%)

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Query: 15 ISGTVKLPKSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 10 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLLKGEDVLSTIQAFRNLGVRIE--EKDD 67

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Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 68 QLVIEGQGFQGLTAPCQT---LNMGNSGTSMRLIAGLL--AGQPFVSKMIGDESLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 123 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLPITYTLPIS-SAQVKSAILLAALQAK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 182 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA+++L AG I G + ++ G + + EV+E MGA++ + + TS+
Sbjct: 234 SSAAFWLAVGLIIPGSELLKNVGNPRTGTI--LEVVEKMAQIVYEDMNKKEQVTSIR 291

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V HLK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 292 VV-----YSHLKGTTISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 344 IQVVTDLNMSGANIKATADGMIKGPVLYGANTSTYGDHRIGMMTAIAALLLVKQGQVH 403

Query: 422 IRDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 404 LDKEEAIMTSYPTFF 418

>emb|CBW36848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae INV104]
Length = 427

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHSRIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQQVGVMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKMGVSISGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKEYTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISSAAFVLVAGLIAPNSRLVLQNVGINETRTGTI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYSPFFDDLES LI 425

>ref|YP_002728958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium azorense Az-Ful]

gb|ACN98673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurihydrogenibium
azorense Az-Ful]
Length = 431

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 133/446 (29%), Positives = 217/446 (48%), Gaps = 23/446 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E ++P+K I G+++P KS+S+R ++L +L+EG +V+ N L + D L R LG+
Sbjct: 2 EKTVPKPVKRIEGLRVPSDKSVSHRSIILPSLAEGESVIKNFLKAGDTLTTLNIVYRKLGV 61

Query: 66 SVEADKAAKRAVVVGGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E ++ V+ GK +E KE + L +GN+G R LT V A G N L
Sbjct: 62 DIE-----EKDNVIYVKGK-GLLEGLKEPDDVLDMGNSGTTTTR-LTLGVLA-GQNFFATLT 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R+RP+ +V L ++GA VD + P+ + G G G + +S+Q S
Sbjct: 114 GDDSLRKRPMKRVVDPLEMGAKVDGRKEANNLPISIRG--GKLGISYFNSKMSAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK- 243
A+L+A A + E+++ ++S + E L M G E D + +K + +
Sbjct: 172 AILLAGLYA--ETPTEVVEPIVSRDHTEKMLNWM---GANIEIDFMTDGYKVKISKTDRL 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWT-- 301
P + V D SSA++F A A+I + + + D F L+ MGA + +
Sbjct: 227 KPIHINVPADPSSAAFAAAASIVPKSEIILKDVMPNPTRD-GFFRKLKEMGADIEYKNK 285

Query: 302 --ETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
E V + K +K + + M D LA+VA A+G T I RVK
Sbjct: 286 RDEAGEIVADVIVKYNDLKGKVVKEEVPSPMIDELPLLAIVATQAEGETVITGAELRVK 345

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEV 418
E++R+ AI +L +EE D +I +K+ +D+Y DHR+AM F+ L +E
Sbjct: 346 ESDRIKAIVENFKRLNLEIEELEDGMVIGKQKVKGGVVDSYKDHRIAMGFAILGLVSED 405

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
+TI+D C ++PD+F L K
Sbjct: 406 GITIKDADCYIISYPDFKHLEKVK 431

>ref|ZP_06027856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
periodonticum ATCC 33693]
gb|EFE85564.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fusobacterium
periodonticum ATCC 33693]
Length = 418

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 102/438 (23%), Positives = 206/438 (47%), Gaps = 48/438 (10%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ ++ G + P SKS+ +R ++ ++L++G + ++N+ SED+ + A++ LG +E
Sbjct: 6 VDKLVGELSPPPSKSVLHRYIIASSLAKGISKIENISFSEDIATIEAMKKLGAKIE--- 62

Query: 72 AAKRAVVVGGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
++ + G ++ E +++ +G +R L + G ++ +
Sbjct: 63 --QKENYLLIDGSDTFKLNLENIEIDCNESGSTLRFLFPLSIVKENKVLF--KGRGKLFK 118

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALLM 188
RP+ ++ + N I G L G ++ G+ISSQ+++ LL
Sbjct: 119 RMPPTYFENFEKYK-----IKHSYIDENEILLEGLKAGIYEIDGNISSQFITGLLF 170

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ PL G+ +I I KL S Y++++L + +FG+K ++S+ F I+G Q Y+ N
Sbjct: 171 SLPLLDGESKIIINGKLESSNYIDISLDCLSKFGIKI-INNSYQEFIEGNQSYRVG-NY 228

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVT 308
E D S A++FL AI G + + SLQGD K +++ + W + +
Sbjct: 229 RTEADYSQAFFLVANAI-GSNIKINDLRENSLQGDKK---IIDFISEIDNWNKNTLI- 283

Query: 309 GPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
++ ++ PD+ L++ A + I ++ R+KE++R+ A

Sbjct: 284 -----LDGSETPDIIPILSLKAAVSGKKIEIVNIERLRIKESDRLKATV 327

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVT-----AIDTYDDHRMAMAFSLA-ACAEVPVT 421

EL+KL + E D +I E V ++ + DHR+AM ++A C + +

Sbjct: 328 EELSKLNFDLIEKKDSILINSRENFEVKNKIVSLSAHSDHRIAMMIAIATTCYDGEIL 387

Query: 422 IRDPGCTRKTFPDYFDVL 439

+ + C +K++P+++V

Sbjct: 388 LDNLDCIKKSYPNFWEVF 405

>ref|ZP_06612397.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus oralis
ATCC 35037]

ref|ZP_07640576.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus oralis
ATCC 35037]

gb|ACH47977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae]

gb|EFE56500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus oralis
ATCC 35037]

gb|EF002036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus oralis
ATCC 35037]

Length = 427

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 120/442 (27%), Positives = 213/442 (48%), Gaps = 35/442 (7%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71

I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E

Sbjct: 7 IRHLHGSIRVPDGKSIHSRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

VG G ++A L +GN+G ++R ++ + AG + + G ++

Sbjct: 67 GVITIKGVGMDGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVLGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191

RP+ + + LK++G + D PP+ + G+ L +L + S+Q SAL+ AA

Sbjct: 120 RPMDRVITIPLKMGVSISGQTERDLPLHLKGMKNLTPIHYELPIA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251

A G E II+K + + E ++++FG S + ++G Q+ K V

Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLKQFG--GHLSVEGKKITVQGPQRLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305

GD SSA+++L AG + V ++ G + + +V+ MG K+ TE S

Sbjct: 231 GDISSAAFVLVAGLIVPNSRVVLQNVGINETRTGI--IDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362

T+T + LK ++ +P + L ++AL A G T I+D +VKET+

Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLA--CAEVPV 420

R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V

Sbjct: 343 RIQVVADALNSMGADITPTADGMIIGKSALHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442

+ ++P +FD L +

Sbjct: 403 ELDRAEAINTSYPSFFDDLESM 424

>gb|EFT94547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0012]

Length = 428

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71

+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D

Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

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      + V  G  ++ AK  ++ GN+G  +R  +  + AG      L G  ++
Sbjct: 69  TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132  RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+  +++ L Q+GA+      T+ PP+ + G  L      +  + S+Q  SA+L AA
Sbjct: 122  RPMNRVMLPLNQMGAECCQGVQRQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192  LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G  +  ++K  +  + E  +R  +FG  E  D  +  + G Q+  + +N  V
Sbjct: 181  QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVDDK--KIMLTGFPQQL-TGQNVVVP 232

Query: 252  GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
      GD SSA++FL AG  +  +  + G  Q      +V++ MG VT  E      +G
Sbjct: 233  GDISSAAFFLVAGLVVPDSEILLVNVGLN--QTRTGILDVIKMGGSVTILNEDEANHSG 290

Query: 310  PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
      L A ++      +P  +  L ++AL A  G T IRD      +VKET R+ A
Sbjct: 291  DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELVKETNRIDA 348

Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
      +  ELT LGA  +  D  II  P  L+  + +Y DHR+ M  +AA  E  V  +
Sbjct: 349  VAKELTILGADITPTDGLIIHGPTSLHGGVRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425  PGCTRKTFFPDYFDVL 439
      ++P  +FD L
Sbjct: 409  AEAHSVSYPAFFDDL 423

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>ref|ZP_05426434.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T2]
ref|ZP_07559153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0860]
gb|EET99342.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T2]
gb|EFM74652.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0860]
Length = 428

```

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 205/435 (47%), Gaps = 27/435 (6%)

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Query: 12  IKEISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
      +K  + GT+ +P  KS+S+R ++  A+S G T  + N L  ED      L A R+LG+++E D
Sbjct: 9   VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72  AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRE 131
      ++V  G  ++ AK  ++ GN+G  +R  +  + AG      L G  ++
Sbjct: 69  TT---IIVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132  RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+  +++ L Q+GA+      T+ PP+ + G  L      +  + S+Q  SA+L AA
Sbjct: 122  RPMNRVMLPLNQMGAECCQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192  LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G  +  ++K  +  + E  +R  +FG  E      +  + G Q+  + +N  V
Sbjct: 181  QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGFPQQL-TGQNVVVP 232

Query: 252  GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
      GD SSA++FL AG  +  +  + G  Q      +V++ MG VT  E      +G
Sbjct: 233  GDISSAAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHSG 290

Query: 310  PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
      L A ++      +P  +  L ++AL A  G T IRD      +VKET R+ A
Sbjct: 291  DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELVKETNRIDA 348

Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
      +  ELT LGA  +  D  II  P  L+  + +Y DHR+ M  +AA  E  V  +
Sbjct: 349  VAKELTILGADITPTDGLIIHGPTSLHGGVRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425  PGCTRKTFFPDYFDVL 439
      ++P  +FD L

```

Sbjct: 409 AEAHSVSYPAFFDDL 423

>gb|ADY82353.1| bifunctional protein aroA [Acinetobacter calcoaceticus PHEA-2]
Length = 756

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 210/445 (47%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLLEGEDALATLQAFRDMGVSIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 382 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSAQKFDS--VMTGDASLS 433

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGKEGTTPPVSTIGSQQLKGIQYDLPLMA-SAQVKSIGILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K +
Sbjct: 493 LWAEGETSVTEPE-----PTRDHTEMLRAFGYDVKTE----GNKISLVGGGKLVG-TDI 542

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTTWTETSVTV 307
V D SSA++F+ GAAIT G+ V +E G + V E+L+ MGA +T E
Sbjct: 543 QVPSDISSAAFFMVGAAITEGSDVLEAVGINPRTGTG--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPREPF---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + ++P D L + A A+G T + A RVKE+
Sbjct: 600 GGEPIADIIHKGSRITLKGIMHPEDQVPLAIDFPAIFIAAACAEGQTVLTGAAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 660 DRIQVMADGLKIMGIDCTPTDDGIIIEGKGKSGDWSPIFAGGEIESHHDHRIAMSFSMAG 719

Query: 415 CAEV-PVTIRDPGCTRTKTFPDYFDV 438
P+TI+ +FP + ++
Sbjct: 720 LRNSGPITIQGTETVATSFPTFTEL 744

>ref|YP_003528097.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus
halophilus Nc4]
gb|ADE15710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus
halophilus Nc4]
Length = 443

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 130/442 (29%), Positives = 210/442 (47%), Gaps = 29/442 (6%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
V++P ++ +++PG KS+S+R ++ AL+EG T + L ED L A R LG++
Sbjct: 13 FVVEPGGSLAAQLRVPGDKSISHRAIIFGALAEGITEITGFLLEGEDTLATLQAFRALGVN 72

Query: 67 VEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + + + VG G E L+LGN+G +MR L AG L G
Sbjct: 73 IEGPEEGRVKIHGVGLQGL-----QAPEKPLYLGNSGTSMRLLAGLF--AGQPFDTITLVG 125

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+G + L Q+GA ++ PP+ ++G L G + + S+Q S+
Sbjct: 126 DRSLSCRPMGRVCDPLAQMGALIEA-TAQGTPLHIHGGQSLQIEYAMP-VASAQVKSS 183

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A A G + + P + T R++ FG E + + +KG +
Sbjct: 184 LLLAGLYATGSTCV-----IEPAPTRDHTEMLMGFGYPVEREGA--KVCVKGTGVLRG- 235

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTTWTETS 304
V D SSA++F+ GAAI+ G+ + +E G + V E+L MGA++ ET
Sbjct: 236 TAVEVPADISSAAFFMVGAAISQGSIDILLEHVGINPRTGTG--IEILGRMGAQIEIEETG 293

Query: 305 VVTGPPREPFGGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V V G P + L+ I++ +P D L V A A+G T + RVK
Sbjct: 294 V-VGGEFVAAIRVRASRLQGINIPEELVPLAIDEFPALFVAAACAEGETVLTGAELRVK 352

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEV 418
E++R+ + L +LG S + PD II L + ++ DHR AMAF++A A+
Sbjct: 353 ESDRIQVMADGLQRLGISAQPTPDGIIIQ-GGALQGGEVHSHGDHRCAMAFAMAGLAAKD 411

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
VT+ D +FP + ++ S
Sbjct: 412 TVTVHDCANVATSFPGFLELAS 433

>gb|ACN18355.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes]
Length = 428

Score = 134 bits (338), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 222/439 (50%), Gaps = 33/439 (7%)

Query: 17 GTVKLPGSKSLSNRILLALAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIETEEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGQDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQMGAKMHGKDGSEFAPITINGKQTLKRMEYHMPVA-SAQVKSATIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHEHMRQFGEIEMDGLTIR--VKGQKF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SA++F+ IT G+ +T G T +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTR---TGIFDVVEQMGGSLLVKDSSRS-TGKLA 289

Query: 313 EPFGRK--HLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 290 GTVVVKTSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAELKVKETNRIDAV 349

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
TEL K+GA + D II L+ + +Y DHR+ M +AA + V + P
Sbjct: 350 ATELNKMGAIDITPTEDGLIIRKKTPLHAANVTSYGDHRIGMMLQIAALLVEDGDVELERP 409

Query: 426 GCTRKTFPDYFDVLSFVK 444
++P +F+ +++ +K
Sbjct: 410 EAVSVSYPTFFEDINSLK 428

>ref|ZP_07029961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium sp. MP5ACTX8]
gb|EFI57448.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium sp. MP5ACTX8]
Length = 437

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 129/449 (28%), Positives = 206/449 (45%), Gaps = 48/449 (10%)

Query: 8 VLQPIKEISGTVKLPGSKSLSNRILLALAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+++P + + G++ LPG KS+S+R +LA + GT+ + N D H LG ++ +G V
Sbjct: 14 IVRPARSLRGSRLTLPDGKSI SHRYAMLAGFAAGTSRLTNFSTGADPHSSLGCMKAMGAQV 73

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D + V G GG + + L GN+G MR L V G T+V D
Sbjct: 74 ALD--GRTISVTGTGGNLH---QPKHNLDCGNSGSTMRLAGLVAPOQGVYTFVGD--E 125

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSAL 186


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      + RP+ + L+ +GA ++ G P+ V+G P + I+S Q +A+
Sbjct: 126 SLTVRPMERIRKPLEAMGARIELTEGH--APMTVHGA---PLKAIDFDAPIASQVKTAV 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      L A A G + + + + E LR FGV+ E D +R YI+GGQK ++
Sbjct: 181 LFAGLQAQGVTSFA--ESVRTRDHTHEHALRA---FGVELERRD--ERLYIQGGQKLQA-I 232

Query: 247 NAYVEGDASSASYFLAGAAI-TGGTVTVEGCGT-----TSLQGDVKFAEVLEMM 294
      +A V GD SSA++FL A + + ++ G T+L G +K +V E
Sbjct: 233 DATVPGDMSSAAFFLCAALLFEDSNLVLDDLGMNPTRAALLDVITALGGTIKVLDVQEY 292

Query: 295 GAKVTWTETSVTVTGPPREPFRGRKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIR 351
      G + + + R LK ID+ ++ D +A +A + IR
Sbjct: 293 GEMAGTIQVNRS-----RGGLKGIDIAGALSAQLIDELPVIAAIAPYTQDGIRIR 342

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS 411
      D RVKE++R+ + L +GA V E D + ++L +D+ DHR+AMAFS
Sbjct: 343 DAKELRVKESDRIALVVKNLRAMGAEVTEHEDGMDVPGGQRLRGGIVDSGMDHRIAMAFS 402

Query: 412 LAAC-AEVPVTIRDPGCTRKTFFDYFDVL 439
      +AA AE I +FP++F L
Sbjct: 403 IAALRAEGETEIHGAEAASISFPEFFTYL 431

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>ref|NP_358822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
      pneumoniae R6]
gb|AAL00033.1| 3-Enolpyruvylshikimate-5-phosphate synthetase [Streptococcus
      pneumoniae R6]
Length = 431

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Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 120/443 (27%), Positives = 212/443 (47%), Gaps = 35/443 (7%)

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Query: 12 IKEISGTVKLPKSKSLSNRILLALLSEGTTVVDNLNSEDVHYMLGALRTLGLSVEADK 71
      I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 11 IRHLHGSIRVPDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 70

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 71 GVITIQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 123

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
      RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 124 RPMDRVTLPLKKMGVSISGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G E II+K + + E +++++FG S + ++G QK K V
Sbjct: 183 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 234

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
      GD SSA+++L I + ++ G + + +V+ MG K+ TE S
Sbjct: 235 GDISSAAFVLVAGLINPNSHLVLQNVGINETRTGI--IDVIRAMGGKLEVTEIDPVAKSS 292

Query: 306 TVTGPPREPFRGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
      T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 293 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPV 420
      R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 347 RIQVVADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEV 406

Query: 421 TIRDPGCTRKTFFDYFDVLSTFV 443
      + ++P +FD L + +
Sbjct: 407 ELDRAEAINTSYPSFFDDLES LI 429

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>ref|ZP_07107141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
      TUSoD Ef11]
gb|EFK77843.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
      TUSoD Ef11]
Length = 429

```

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 10 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 69

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 70 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 123 RPMNRVMLPLNQMGAEQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 181

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + KN V
Sbjct: 182 QAKGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGFPQL-TGKNVVVP 233

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 234 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVKNMGGSVTILNEDEANHS 291

Query: 310 PPREFPGRKHLKAIDVNMNMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 292 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRD AEELVKETNRIDA 349

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 350 VAKELTILGADITPTDDGLIIHGPTSLHGGRRVTSYGDHRIGMMLQIAALLVKEGTVELDK 409

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 410 AEAVSVSYPAFFDDL 424

>ref|YP_004026961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
kristjanssonii 177R1B]
gb|ADQ41348.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
kristjanssonii 177R1B]
Length = 433

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 126/446 (28%), Positives = 213/446 (47%), Gaps = 37/446 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ V +P KS+S+R +++ +L++G T ++N L S+D + + LG +E
Sbjct: 9 RKINSNVTVPSPDKSISHRSIMISGLAKGVTEIENFLSDDCLATINCFKNLGTDIE---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++ G F + K+ L N+G R L ++ + +L G ++R
Sbjct: 65 IRNDKIIIVKGNDFNLFAPKQ--ILDQNSGTTTRLLLGILSTQEFES--ILTDSSSLKKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + + L Q+GA+ + D P++V G L + L S+Q SAL+ A+
Sbjct: 121 PMKRVTLPLSQMGAEFEFLEKEDFLPIKVKGSKKLPIEYTLPIP-SAQVKSALIFASLK 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G I+ K S + E+ L+ G + SW++ + ++ S
Sbjct: 180 AEGKSVIKESPK--SRDHTELMLK---HAGASIK---SWEKDGVTVEILPSQVSSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++F+ A I G +V +E C + + +VL+ MGA + + V
Sbjct: 232 IPSDISAFAFIVLALICEGSSVVIENCILNPRTGI--IDVLKQMGADIRIED----VE 285

Query: 309 GPPREFPGR-----KHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +LK + V+ N +P D LAV A FA+G T I + + RVKE
Sbjct: 286 NRNGELVGKIIARSSNLKGVKVDKNDIPRIIDEIPI LAVAAFAEGKTTIDNASEL RVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA-EV 418

++R+ L GA E D II EKL +++Y DHR+AMA S+ ACA E
Sbjct: 346 SDRIKTTVQMLKSFADCYELEDGLEIIGSREKLKSAVVNSYKDHRIAMAASIMACAVEG 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D C +FP+++D+L + K

Sbjct: 406 ESTILDAECASISFPNFYDILFSSTK 431

>ref|ZP_07458332.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
oral taxon 071 str. 73H25AP]
gb|EFM35789.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
oral taxon 071 str. 73H25AP]
Length = 427

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 119/443 (26%), Positives = 213/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVKIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 GVITIQGVGMDALKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVTIPLKMGVSISSGQTERDLPPLYLKGTKNLTPIHYELPIA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E I++K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAQG--ESVILEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLIAGLIVPNSRVVLQNVGINETRTGI--IDVIRAMGGKLEITEIDPIAKSA 288

Query: 306 TVTGPPREPFGFRKHLKVIDNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGETVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II +L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKKGSRHLHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|ZP_01825180.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP11-BS70]
ref|ZP_02721747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae MLV-016]
ref|YP_002038019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae G54]
sp|B5E5M9.1|ARO_A_STRP4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EDK63671.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP11-BS70]
gb|EDT98889.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae MLV-016]
gb|ACF55539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae G54]
emb|CBW32859.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae OXC141]
Length = 427

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPDGSISHSRIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 GVITVQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKMGVSISSQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKEYTRNTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISSAFLPLKMGVSISSQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIKIGKSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|YP_003759471.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus watsoni
C-113]
gb|ADJ27150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus watsoni
C-113]
Length = 444

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 131/442 (29%), Positives = 215/442 (48%), Gaps = 33/442 (7%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
V++P +SG +++PG KS+S+R ++L AL+EG T + L ED L A R LG+S
Sbjct: 14 FVVEPGGALSGRRLVPDGSISHRVILGALAEGVTRITGFLEGEDTLATLRAFRDLGVS 73

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E + R + G G A EE L+LGN+G + R L AG + +L G
Sbjct: 74 IEGPEGG-RVEIHVG--MQGLQAPEE-PLYLGNSGTSARLLAGLF--AGQSFDVILRGD 127

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + L ++GA ++ PP+ ++G L G + + + S+Q S+L
Sbjct: 128 ELSRRPMRRVCDPLARMGAFIET-TAQGTPPLHIHGRQPLYGIEYAMPMA-SAQVKSSL 185

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G + + P + T R++ FG E + + I+GG
Sbjct: 186 LLAGLYASGRTCV-----IEPAPTRDHTERMLAGFGYPVEREGA--KVCIQGGGSLYG-T 237

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSV 305
+ D SSA++F+ GAAI G+ + +E G + + ++L MGA + ET V
Sbjct: 238 VVEIPADISSAAFFMVGAAGIGKSDILLEHVGINPRTGTI--VDILRRMGADIEIKETGV 295

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAV---VALF-----ADGPTAIRDVASWR 357
V G EP ++A ++ +P+ + LA+ ALF A+G T + R
Sbjct: 296 -VGG---EPVAAIRVRASRLHGINIPEDLVPLAIDEFPALFVAAACAEGETVLGAGAGELR 351

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CA 416
VKE++R+ + L LG S + D II KL + ++ DHR AMAF++ + A
Sbjct: 352 VKESDRIQVMADGLQALGISAQPTADGIIIQ-GGKLQGGEVHSHGDHRCAMAFAMTSLVA 410

Query: 417 EVPVTIRDPGCTRKTFPDYFDV 438
+ P+ IRD +FP + ++
Sbjct: 411 KGFIIIRDCANVATSFPGFLEL 432

>ref|ZP_07957165.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 5_1_63FAA]
gb|EFV16004.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 5_1_63FAA]
Length = 424

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 122/442 (27%), Positives = 204/442 (46%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ +L++GTT + N L+ D + R +G+ +E +
Sbjct: 9 LRGLSIPGDKSISHRAVMFGSLAKGTTHISNFLSGADCLSTIDCFRKMGLVIEQNGTNV 68

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
G G K P E L +GN+G R ++ + AG + VL G + +RP
Sbjct: 69 TVHGNGLHLGLKAPSE-----TLDVGNSGTTTRLISGIL--AGQDFETVLSGDASLNKRP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS-----ISSQYLSALL 187
+G ++ L+Q+GA + G C P+++ G KL+ + S+Q S +L
Sbjct: 121 MGRIIKPLEQMGAKITSVNGNGCAPLKIEG-----TKLNATHYDSPVASAQVKSCVL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A D + + + +S + E+ LR FGVK E D+ + +
Sbjct: 173 LAGLYA--DGKTSVTEPALSRNHTELMLR---SFGVKVESHDTTATIT---PPEEMIATD 224

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++F+ IT + ++ G + + V + MGA VT E +
Sbjct: 225 IIVPGDISSATFFIVAGLITPNSCIRLKNVGINPTRDGI--LRVCKDMGADVTL-ENVID 281

Query: 307 VTGPPREPFGGR--HLKAIDVNMKNMPDVAMTLAVVAL---FADGPTAIRDVASWRVKET 361
G P K LK + +P + + V+AL FA+G T I+D A +VKE+
Sbjct: 282 NGGEPTADIVKTSKLKGTVIGGEVIPTLIDEIPVIALLAFAEGETVIKDAAEKVKES 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIDTYDDHRMAMAFSLAAC-AEVPV 420
+R+ L K+G D II L+ +I+ DHR+AM FS+A AE
Sbjct: 342 DRIALTVDNLVKMGVDATATDDGMIKGGNPLHGASINCKYDHRIAMTFSIAGINAEGET 401

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I D C ++P +++ L++
Sbjct: 402 VIEDSECVDVSYPTFYEQNLNSL 423

>ref|YP_002352953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dictyoglomus turgidum
DSM 6724]
gb|ACK42339.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dictyoglomus turgidum
DSM 6724]
Length = 433

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 123/453 (27%), Positives = 219/453 (48%), Gaps = 39/453 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++ + + G +K+PG KS+S+R L+ +++ EG +++ N L S+D + LR LG
Sbjct: 3 KLMIKKSRSLMGEIKIPGDKSISHRALIFSSMGEGESIIKNFLFSQDCISTMNCRLALGT 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
S+E + + G G E+ L GN+G +R T ++ G V+ G
Sbjct: 63 SIEICENVIKVKGNGINGFREPENV-----LDAGNSGTTIRLFTGLLSGLPG-IFSVITG 116

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R RP+ +V L +GA + G + PP+ + G L G LS + S+Q SA
Sbjct: 117 DDSLRRRPMKRVEPLLGMGAKIWGRNGGNNPPLAIG-EKLGRDHTLSVA-SAQVKA 174

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A LA D E + + +S + E R+ + G+ + + G + +K+
Sbjct: 175 LLIAGLLA--DGETSVTEPSLSRDHTE---RIFQYLGPLIRNGLTLKTH--GIEGFKN- 226

Query: 246 KNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT---W 300
K+ + GD SSA++ +A G + G + ++ G + + VL+ GAK+ W
Sbjct: 227 KDFNIPGDFSSAAFIIAAGLLVEGSKIVIKNVGINPTR--IGMLSVLKEAGAKIQILNQW 284

Query: 301 TETSVTVTGPPREPFGFR-----KHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRD 352
E EP G L++ +V + K+ D LA++A A G + +D
Sbjct: 285 EEGG-----EPIGDLIVEFSILESFEVRGEIVPKLIDEVPILAIATQAKGKSVFKD 336

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
V +VKE++R+ A+ + K+G E + + P KLN I+TY+DHR+AM+F++
Sbjct: 337 VGELKVKESDRKAVVDGINKMGGKAEIIDEGFVAVYGPTKLNENEIETYNDRHRIAMSFAI 396

Query: 413 AACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
A TI + +FP++ + + N
Sbjct: 397 AGLLADGETIVESNSISISFPNFGETIKKLGN 429

>ref|YP_004002066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
owensensis OL]
gb|ADQ04266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
owensensis OL]
Length = 433

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 123/446 (27%), Positives = 210/446 (47%), Gaps = 37/446 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ + +P KS+S+R +++ +L++G T ++N L S+D + + LG+ +E
Sbjct: 9 RKINSNIIIPDKSISHRSIMIGSLAKGVTEIENFLFSDCLATINCFKNLGIDIEIRN- 67

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +V G F + + Q N+G R L ++ + +L G +++R
Sbjct: 68 -DKIIVKGNNFNFVAPEKSLDCQ---NSGTTARLLLGILSTQEFES--ILTGDNSLKKR 120

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + + L Q+GA + D P+RV G L + L S+Q SAL+ A+
Sbjct: 121 PMKRVTLPLSQMGAKFEFLEKEDFLPIRVKGKNLKPITYTLPIP-SAQVKSALIFASLR 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G ++ K S + E+ L+ + SW+ + ++ S
Sbjct: 180 AEGKSILKESPK--SRDHTELMLKHA-----GANIKSWEEDGVYTVTEILPSQLSSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++F+ A I +V +E C + + +VL+ MGA +T + V
Sbjct: 232 IPSDISAAFFIVLALICENSSVVIENCILNPTRTGI--IDVLKQMGADITIED----VE 285

Query: 309 GPPREPFGFR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +LK + V+ N +P D LAV A FA+G T I + + RVKE
Sbjct: 286 NRNGELVGKIVARSSNLKGVKVDKNDIPRIIDEIPILAVAAFAEGKTIIDNASELRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV 418
++R+ L GA E + II EKL +++Y DHR+AMA S+ ACA E
Sbjct: 346 SDRIKTTAQMLRSFGAECHELENLEIGSREKLKSAIVNSYKDHRIAMAASIMACAVEG 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D C +FP+++D+L + K
Sbjct: 406 ESTILDADCASISFPNFYDILFSSTK 431

>ref|ZP_06691868.1| conserved hypothetical protein [Acinetobacter sp. SH024]
gb|EFF86381.1| conserved hypothetical protein [Acinetobacter sp. SH024]
Length = 756

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 209/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLEGEDALATLQAFRDMGVSIIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 382 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSQAQKFD--VMTGDASLS 433

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGEKGTTPVVSITGSQQQLKGIQYDLMA-SAQVKS GILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K +
Sbjct: 493 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TDI 542

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G+ V +E G + V E+L+ MGA +T E
Sbjct: 543 QVPSDISSAAFFVMGAAITEGSDVILEAVGINPRTGTV--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPPREPF---GRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 600 GGEPIADIHIKSGRTLKGIHMPEDQVPLAIDEFPALFIAACAEGQTVLTGAAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A
Sbjct: 660 DRIQVMADGLKIMGIDCTPTDDGIIIEGKGKSGDWSPIFAGGEIESHHDRIAMSFMSAG 719

Query: 415 CAEV-PVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++
Sbjct: 720 LRNSGPITIHGTETVATSFPTFTEL 744

>ref|YP_003622471.1| 5-enolpyruvoylshikimate-3-phosphate synthase [Leuconostoc kimchii
IMSNU 11154]
gb|ADG41502.1| 5-enolpyruvoylshikimate-3-phosphate synthase [Leuconostoc kimchii
IMSNU 11154]
Length = 432

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 133/449 (29%), Positives = 217/449 (48%), Gaps = 55/449 (12%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+ +PG KS+S+R L+ A+++G T ++N L S+DV + + R LG+++ D+ K
Sbjct: 12 LRGTMTVPKDKSISHRALMFGAIAQGVTEIENFLVSDDLHTMAVFRELGVTI--DQHGK 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+G G + + K L +GN+G + R L ++ N V D + RP+
Sbjct: 70 HVRVIGRGSEHFTQPQKA---LDMGNSGTSTRLLMGLLSRQPFNIHIVGD--ESLSRRPM 124

Query: 135 GDLVVGLKQLGADV-----DCFLGTDCCPPVRVNGIG-GLPGGKVKLSGSISSQYLSALLM 188
++ L +GAD+ D G +V GI +P S+Q SA+L+
Sbjct: 125 KRVLTPLALMGADIRLSENDTLPGVIYANSQVTGITYEMPVA-----SAQVKSAILL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G II+K IP + T R++ +FG D R + Q + + ++
Sbjct: 177 AGIQAEQVT--TIEK---IPSRDHTERMLRQFGGTITVKDG--RVSVTKHQ-HLTGQHV 228

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ IT +T++ G + V ++L+ MGA + +++ V
Sbjct: 229 IVPSDISSAAFFIVAGLITPNKSLTIKKVGINKTRDGV--LQLLKRGMANIVM--SNINV 284

Query: 308 TGPPPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
G EPF + LK ID+ +P L ++AL A G T I RVK
Sbjct: 285 NG---EPFADITIEAQLKGIDITEKDIPSSVDELPIIALAATQAQGDTTITGAGELRVK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTADIT-YDDHRMAMAFSLAAC 415
ET+R+ + +ELTKLGA++E D II TP N +A+ T + DHR+ M ++AA
Sbjct: 342 ETDRIATVISELTKLGANIEALEDGMIHGGTPLHVTNESALLTSHGDHRI GMMNAIAAL 401

Query: 416 ----AEVPVTIRDPGCTRKTFPDYFDVLS 440
+V +T D ++P + + LS
Sbjct: 402 ITTGGDVVLGTGED--AISVSYPGFLENLS 428

>ref|YP_816672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae D39]
sp|Q8CWQ7.2|ARO_A_STRR6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q04JX6.1|ARO_A_STRP2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ54185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae D39]
Length = 427

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 120/443 (27%), Positives = 212/443 (47%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPDGKSIHSRRIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGVMAGLKAPQNA-----LNMGNSTGSIIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RMDRVTLPKLMGVSISGQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSDVGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L I + ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLINPNSHLVLQNVGINETRTGI--IDVIRAMGGKLEVTEIDPVAKSS 288

Query: 306 TVTGPPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTIEIGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|YP_003239117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ammonifex degensii KC4]
gb|ACX52267.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ammonifex degensii KC4]
Length = 434

Score = 134 bits (337), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 148/451 (32%), Positives = 215/451 (47%), Gaps = 47/451 (10%)

Query: 13 KEISGTVKLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GT+ +PG KS+S+R LLL +L+ G TV++N L +D L LR LG+ +E ++
Sbjct: 9 KRLEGTTIVPGDKSISRALLLGS LAHGETV IENFLQ GKDC LATL RCLRQLGVKIE-EEG 67

Query: 73 AKRAVVVCGG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R V G G G EEV L GN+G MR L + AG VL G +R
Sbjct: 68 EGRLRVEGRGLGNL---QEPEEV-LDAGNSGTTMRLLLGV L--AGNPIFAVLTGDASLRR 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKL-----SGSISSQYLSA 185
RP+ + + LK +GA++ P+ + G + KL S S+Q SA
Sbjct: 122 RMDRVTLPKLMGAEIWGRQEGKLAPLAIRG-----QRKLRPLEYTSPPVASAQVKS A 174

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G E + + +S + E R++ FGV + R G+

Sbjct: 175 VLLAGLYAEG--ETSVTEPALSRDHTE---RMLGYFGVPVKREGLTVRLK---GRALLQG 226

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

+ V GD S+A++FLA AAI G VTV G + F EVLE MGA++ S
Sbjct: 227 RPVRVPGDFSAAAFLLAAAILPEGRVTVREVGLNPTR--TGFLEVLEAMGARL-----S 279

Query: 305 VVTGTGP-PREPFGFR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVAS 355
V VTG EP G L+ +++ +P D L VVA A G T IR

Sbjct: 280 VEVGTGEWAGEPVGNTVESSALRGVEIGGEIIPRLIDEIPVLTVVAACAAGKTVIRGAEE 339

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA- 414
R KE++R+ + EL +LGA VE PD II L + + ++ DHR+AMA ++A

Sbjct: 340 LRYKESDRLATMAQELGRLGAKVEVLDPGLIHHGGYPLQGSRVQSHGDHRVAMAMAVAGL 399

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445

AE I +FP++ +L+T +
Sbjct: 400 VAEGETIIEGAEIDVSFPNFPPTLLATLTEE 430

>ref|NP_345829.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae TIGR4]
ref|ZP_01407871.1| hypothetical protein SpneT_02001692 [Streptococcus pneumoniae TIGR4]
sp|Q9S400.2|ARO_A_STRPN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK75469.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae TIGR4]
Length = 427

Score = 134 bits (336), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E

Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G ++

Sbjct: 67 GVITIQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA

Sbjct: 120 RPMDRVTLPLKKMGVSISGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V

Sbjct: 179 QAKG--ESVIEKEYTRNHTE---DMLKQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS SVVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V

Sbjct: 231 GDISSAAFVLVAGLIAPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +

Sbjct: 288 ATLIVESSDLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +

Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +

Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|YP_001694807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae Hungary19A-6]
sp|B1ICH2.1|ARO_A_STRPI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS

gb|ACA36348.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae Hungary19A-6]
Length = 427

Score = 134 bits (336), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RMDRVTLPKMGVSISSQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ASVIIIEKECTRNTHT---DMLKQFG--GHLSVDSKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISAFAFWLVLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 STLTVESSDLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKKETDRIQVV 347

Query: 368 RTELTKLGSVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIIGKSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|YP_001181460.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor saccharolyticus DSM 8903]
sp|A4XMY4.1|ARO_A_CALS8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP68269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor saccharolyticus DSM 8903]
Length = 433

Score = 134 bits (336), Expect = 3e-29, Method: Compositional matrix adjust.
Identities = 127/445 (28%), Positives = 210/445 (47%), Gaps = 45/445 (10%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I V +P KS+S+R +++ +L+ GTT ++N L +ED + + LG +E
Sbjct: 9 RKIRAKVAIPSDKSISHRSIMIGSLARGTTEIENFLFAEDCLSTINCFKKLGAEIE---- 64

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+ G + + ++ L GN+G R L ++ A VLDG +R+R
Sbjct: 65 IKNDKVIVKGKNYSLSVPQQ--VLDCGNSGTTTRLLLGILSTQEFEA--VLDGDSLSLRK 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L Q+GA + DC P++V G L L S S+Q SAL+ AA
Sbjct: 121 PMKRVTQPLSQMGASFEFLEKEDCLPIKVGKKNLKPIDYTLVPS-SAQVKSALIFAALK 179

Query: 193 ALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYK 243
A G +I +L +S + E+ L+ A+ + ++ + K K K
Sbjct: 180 AEGK---SVIKELPMSRDHTEMLK-----SAGADIATCFENGFKYIEVMPNLEALKIK 231

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
P D SSA++F+ A I + V +E C + + ++L+ MGA +
Sbjct: 232 VP-----SDISSAFAFIVLALICEDSEVIIENCILNPTRTGI--IDILKQMGADIEIGN 283

Query: 303 TSVTVTGPPREPFGFR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ R +LK + V+ N +P D LAV A FADG T I + + RV
Sbjct: 284 VEIQNGELVGTIVARSSNLKGVVDKNDIPRIIDEIPILAVAAAFADGKTIIDNASELRV 343

Query: 359 KETERMVAIRTELTKLGA---SVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC 415
KE++R+ L GA +E G + I+ + L +++Y+DHR+AMA S+ AC
Sbjct: 344 KESDRIKTTLEMLRNFGAECYELENGLE--IVGSRDNLKAGIVNSYNDRHRIAMAASILAC 401

Query: 416 A-EVPVTIRDPGCTRKTFPDYFDVL 439
A E TI + C +FP+++++L
Sbjct: 402 AVEGESTILNAECASISFPNPFYEIL 426

>ref|YP_003414233.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes 08-5578]
gb|ADB68871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes 08-5578]
Length = 430

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 120/437 (27%), Positives = 219/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 14 GAITVPGDKSMHSRISIMFGAIAEGKTIVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 71

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIAKRPMN 125

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 126 RVMLPLQQMGAKMHGKDGSEFAPITITGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +K GQK+ + + V GD S
Sbjct: 185 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKVGQKF-TGQEMTVPGDVS 236

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 237 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLEVKDSSRS-TGKLAGT 293

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 294 VVVKTSELKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAELKVKETNRIDAVAT 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 354 ELNKMGAIDITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERPEA 413

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSVSYPTFFEDIRSLK 430

>ref|NP_743926.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas putida KT2440]
gb|AAN67390.1|AE016365_5 prephenate dehydrogenase, putative/3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas putida KT2440]
Length = 746

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 207/436 (47%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 QPGGRLNGRIRVPGDKSISHRSIMLSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P L++GN+G +MR L+ + AG + G

Sbjct: 377 PNHGRVTIHGVLHGLKPPPG-----PLYVGNSTSMRLLSGLL--AGQPFVDVMTGDAS 429

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA V+ G D PP+ + G L G L + S+Q S LL

Sbjct: 430 LSKRPMNRVANPLREMGAVVET--GPDGRPPLTIRGGHKLKGLTYTLPMA-SAQVKSCLL 486

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG + ++ G K + +

Sbjct: 487 LAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYSVDSHGPV--ASLQSGGKLTATR- 538

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + +E G + V ++L +MG +T E

Sbjct: 539 IEVPADISSAAFFLVAASIAEGSELVLEHVGINPRTGTG--IDILRLMGDITL-ENQRE 595

Query: 307 VTGPPREPFGGRK--HLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V G P + LK ID+ +P D L V A A+G T +R RVKE+

Sbjct: 596 VGGEPAVDLRVGAKLKGIDIPALVLAIDFPPVLFVAAACAEGRTVLRGAEEELRVKES 655

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPV 420
+R+ + LT LG E PD II + + + + DHR+AMAFS+A+ A P+

Sbjct: 656 DRIQVMADGLTTLGIKCEPTDGIIDGGQ-MGGGEVHGHGDHRIAMAFSVASLRASAPI 714

Query: 421 TIRDPGCTRKTFFPDYF 436
I D +FP++

Sbjct: 715 RIHDCANVATSFNPL 730

>ref|ZP_02437933.1| hypothetical protein CLOSS21_00371 [Clostridium sp. SS2/1]
gb|EDS22957.1| hypothetical protein CLOSS21_00371 [Clostridium sp. SS2/1]
emb|CBL38582.1| 3-phosphoshikimate 1-carboxyvinyltransferase [butyrate-producing
bacterium SSC/2]
Length = 424

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 122/442 (27%), Positives = 204/442 (46%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ +L++GTT + N L+ D + R +G+ +E +

Sbjct: 9 LRGELSIPGDKSISHRAVMFGSLAKGTTHISNFLSGADCLSTIDCFRKMGLIEQNGTNV 68

Query: 75 RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
G G K P E L +GN+G R ++ + AG + VL G + +RP

Sbjct: 69 TVHGNLHGLKAPSE-----TLDVGNSTTTRLISGIL--AGQDFETVLSGDASLNKRP 120

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS-----ISSQYLSALL 187
+G ++ L+Q+GA + G C P+++ G KL+ + S+Q S +L

Sbjct: 121 MGRIIKPLEQMGAKITSVNGNGCAPLKIEG-----TKLNATHYDSPVASAQVKSCVL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A D + + +S + E+ LR FGK E D+ + +

Sbjct: 173 LAGLYA--DGKTSVTEPALSRNHTELMLR---SFGVKVESHTTATIT---PPEEMIATD 224

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++F+ IT + ++ G + + V + MGA VT E +

Sbjct: 225 IVVPGDISSATFFIVAGLITPNSCIRLKNVGINPTRDGI--LRVCKDMGADVTL-ENVID 281

Query: 307 VTGPPREPFGGRK--HLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRVKET 361
G P K LK + +P + + V+AL FA+G T I+D A +VKE+

Sbjct: 282 NGGEPTADIVVKTSLKKTIVIGGEVIPTLIDEIPVIALLAFAEGETVIKDAAEELVKES 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPV 420
+R+ L K+G D II L+ +I+ DHR+AM FS+A AE

Sbjct: 342 DRIALTVDNLVKGVDATATDDGMIKGGNPLHGASINCKYDHRIAMTFSIAGINAEGET 401

Query: 421 TIRDPGCTRKTFFPDYFDVLSTF 442
I D C ++P +++ L++

Sbjct: 402 VIEDSECVDVSYPTFYEQNLNSL 423

>ref|YP_001681737.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter sp. K31]
sp|B0T270.1|ARO_A_CAUOK RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABZ69239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter sp. K31]
Length = 439

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 140/443 (31%), Positives = 209/443 (47%), Gaps = 37/443 (8%)

Query: 11 PIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + GTV+ PG KS+S+R ++L AL+ GTT V+ LL DV A+R+ G VE
Sbjct: 10 PGGPLRGTVRAPGDKSISHRSMILGALASGTTTVEGLLEGADVLATAQAMRSFGARVE-Q 68

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ R + G GG D + GNAG +R + A AT+ DG +R
Sbjct: 69 EGVGRWRIEGQGGFLEPSDVVD-----CGNAGTGVRLIMGAAAGFPLCATFTGDG--SLR 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+ ++ L ++GA +LG D P+ + G G L G + L S+Q SA+L+
Sbjct: 122 SRPMSRVLDPLARMGA---TWLGRDKGRLPLTLKG-GNLRGLQYTLP-MASAQVKSALL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKSPK 246
A A G V E+I+ + + E R++ FG + D +I+ GQK
Sbjct: 177 AGLHAEGGV--EVIEPEATRDHTE---RMLRAFGAEVIVEDQGGVRHRLPAGQKLTG-T 230

Query: 247 NAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT---E 302
+ V GD SSA++ +AG + G VTVEG L+ L MGA + + E
Sbjct: 231 HVAVPGDPSSAAFPVLVAGLIVPGSEVTVEGVMLNELR--TGLFTTLREMGADLVISNVRE 288

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+S G + R H + V + P D LAV A FA G T +R V RVK
Sbjct: 289 SSGEEVGDITARYSRMH--GVVVPPEAPAMIDEYPILAVAAAFATGDTVMRGVGMERVK 346

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMA-FSLAACA 416
E++R+ L G VEE P+ I+ T ++T+ DHR+AM+ L A
Sbjct: 347 ESDRIALTAAGLEACGVDVEEPEGEFVHGTGQAPRGAMVETHGDHRIAMSHLILGLAA 406

Query: 417 EVPVTIRDPGCTRKTFPDYFDVL 439
+ V+I +PG +FP + +++
Sbjct: 407 QSAVSIIDEPGMIATSFPGFAEMM 429

>ref|ZP_07645382.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis
SK564]
gb|EFN99374.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mitis
SK564]
Length = 427

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 211/438 (48%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTIQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
VG G ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 GVITIQVGMDGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ + G L +L + S+Q S+L+ AA
Sbjct: 120 RPYMDRVTIPLKMGVSISGQTERDLPLHLKGTKNLRPIHYELPIA-SAQVKSSLMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAQG--ESVIIKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE + V
Sbjct: 231 GDISAASFVWLVAGLIVPNSRLVLKNVGINETRTGI--IDVIRAMGGKLEITEIN-PVAKS 287

Query: 311 PREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367

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      +LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLTVESSNLKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
      L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTVDGMIKKSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
      ++P +FD L + +
Sbjct: 408 EAINTSYSPFFDDLES LI 425

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>ref|YP_002028921.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stenotrophomonas
      maltophilia R551-3]
gb|ACF52238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stenotrophomonas
      maltophilia R551-3]
Length = 435

```

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 127/445 (28%), Positives = 215/445 (48%), Gaps = 32/445 (7%)

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Query: 1  MAGAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      M+ A+ + + + G++ +PG KS+S+R ++ AAL++GT+ ++ L ED
Sbjct: 1  MSNAQHWIARKQPLQGSLTIPGDKSVSHRSVMFAALADGTSHIEGFLEGEDTRATARIF 60

Query: 61  RTLGLSVEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
      LG+ +E ++R V VG G K P + L GNAG MR L + +
Sbjct: 61  GQLGVRIETPSPSQRIVHGVGIDGLKAP-----DAPLDCGNAGTGMRLLAGLLAGQAFD 114

Query: 119  ATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      T + D + RP+ + L Q+GA +D PP+ V+G L G + + +
Sbjct: 115  CTLIGD--ESLSGRPMRRVTGPLSQMGAKIDT-ESDGTPLHVHGGQSLHG--IDFASPV 169

Query: 179  SS-QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      +S Q SA+L+A A G+ + + P + T R++ FGV+ E S R ++
Sbjct: 170  ASAQIKSAVLLAGLYAQGETSV-----VEPHPTRDYTERMLSAFGVEIEFSPGKAR--LR 222

Query: 238  GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
      GGQ+ ++ + V D SSA+++L A+I G+ + ++ G + L +MGA
Sbjct: 223  GGQRLRA-TDIVVPADFSAAFYLVAAIIIPGSELRLKQVGLNPRR--TGLLHALRLMGA 279

Query: 297  KVTWTETSVTVTGPPREPFGGRKH--LKAIDVNMNMKMPDVA---MTLAVVALFADGPFAIR 351
      ++ E G P ++ LK + +PD+ L V A A+G T +
Sbjct: 280  DIS-EENPAEQGEPVADLVVRYAPLKGARIPPELVPMIDEFPALEFVAAAAAEGQTVVS 338

Query: 352  DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
      A RVKE++R+ A+ T L LG V+E D + +L I+++ DHR+AMAF+
Sbjct: 339  GAAELRVKESDRLAAMATGLRALGMQVDETEDGATLHGGVRLGSGTIESHGDHRIAMAF 398

Query: 412  LAA-CAEVPVTIRDPGCTRKTFPDY 435
      +A ++ V I D +FPD+
Sbjct: 399  IAGQISDGEVRINDIANVATSFPDF 423

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>ref|YP_003876989.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus
      pneumoniae AP200]
gb|ADM84987.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus
      pneumoniae AP200]
Length = 431

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Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 119/438 (27%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

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Query: 12  IKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
      I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 11  IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 70

Query: 72  AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRE 131
      VG G ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 71  GVITVQGVGMAGLKAPQNA-----LNMNGSGTSIRLISGVL--AGADFEVEMFGDDSLSK 123

```

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 124 RPMDRVTLPLKKMGVSISSGQTERDLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V
Sbjct: 183 QAKG--ESVIEKEYTRNHT---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 234

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 235 GDISSAAFVLVAGLIAPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 291

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 292 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 351

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 352 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 411

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 412 EAINTSYPSFFDDLESLI 429

>ref|ZP_04438735.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
ATCC 29200]
ref|ZP_05423378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T1]
ref|ZP_05599604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
X98]
ref|ZP_07569067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0109]
ref|ZP_07770395.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0102]
gb|EEN70919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
ATCC 29200]
gb|EET96286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T1]
gb|EEU94398.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
X98]
gb|EFM69181.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0109]
gb|EFQ13748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0102]
gb|EFT96494.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0031]
gb|EFT99772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0043]
gb|EFU02095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0312]
gb|EFU08037.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1302]
Length = 428

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK ++ GN+G +R + + AG L G ++
Sbjct: 69 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASISK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAECCQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251

A G + ++K + + E +R +FG E + + G Q+ + +N V
 Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232
 Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
 GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
 Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 290
 Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
 L A ++ +P + L ++AL A G T IRD +VKET R+ A
 Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAAELVKETNRIDA 348
 Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
 + ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
 Sbjct: 349 VAKELTILGADITPTDGLIIGHGTSLSHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408
 Query: 425 PGCTRKTFFPDYFDVL 439
 ++P +FD L
 Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|YP_001450649.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
 gordonii str. Challis substr. CH1]
 sp|A8AXY9.1|AROAA_STRGC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABV10421.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
 gordonii str. Challis substr. CH1]
 Length = 427

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
 Identities = 123/438 (28%), Positives = 221/438 (50%), Gaps = 41/438 (9%)

Query: 13 KEISGTVKLPGSKSLNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
 K + G++++PG KS+S+R ++ +L++G T V ++L EDV + R +G+ +E DK
 Sbjct: 8 KGLRGSRLVPGDKSISRHSIIFGSLAKGVTKVHDILRGEDVLSTMQVFRMGVQIE-DKG 66
 Query: 73 AKRAVVVGCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
 + GCG F D +E Q L +GN+G +MR L A V A G N + + G +
 Sbjct: 67 -DLVEIHGCG--F---DGLQEPQRPLDMGNSGTSMR-LIAGVLA-GQNFSAQVMGDDSL 118
 Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
 +RP+ + + L+++G ++ D PP+ ++G L + +L + S+Q SAL+ AA
 Sbjct: 119 KRPMDRISLPLRRMGVEIAGQTERDLPLTIHGNPNLKPIQYQLPIA-SAQVKSALIFAA 177
 Query: 191 PLALGDVEIEIIDKLISIPYVE-MTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
 A G E II+K ++ + E M L+ + V + + G Q+ ++ +
 Sbjct: 178 LQAQG--ESLIEKDLTRNHTEDMLLQFGGQLKVDGKE-----IRVAGKQELQA-QEVV 228
 Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----- 303
 V GD SSA+++L AG + +T+ G + + +V++ MG K++ +E
 Sbjct: 229 VPGDISAFAFLVAGLIVPSSKITLTNVGINETRTGI--LDVIQAMGGKLSVSEVDEVVK 286
 Query: 304 SVTVTGPPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
 S T+T + +G +++ +P + L ++AL A +G T I+D +VKE
 Sbjct: 287 SATITVESSDLYG-----TEISGELIPRLIDELPIIALLATQAEGQTLIQDAEELKVKE 340
 Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEV 418
 T+R+ + L +GA ++ D II L ++ TY DHR+ M ++AA +
 Sbjct: 341 TDRIQVVADALNSMGADIQPTADGMIIQKKTSLKGASVHTYGDHRIGMMLTAIALLVKDG 400
 Query: 419 PVTIRDPGCTRKTFFDYF 436
 V + ++PD+F
 Sbjct: 401 SVELSRAEAINSYDPDF 418

>ref|YP_360747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Carboxydothermus
 hydrogenoformans Z-2901]
 sp|Q3AAT7.1|AROAA_CARHZ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABB15286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Carboxydothermus

hydrogenoformans Z-2901]
Length = 428

Score = 134 bits (336), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 134/442 (30%), Positives = 208/442 (47%), Gaps = 34/442 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G V +PG KS+S+R L+L AL+EG T ++N L ++D L L G+ +E
Sbjct: 9 KGLKGQVTPGDKSISHRALILGALAEGITEIENFLVAQDTLATLNCLEKYGVRIERRDT 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R V G F + Q N+G +R L+ AA V G +R R
Sbjct: 69 FVR--VFQTAQNFSEPQDVLDQAQ---NSGTTLRLLSG--VAATFPFVSVFTGDASLRRR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L Q+GA V D P + G G L G L + S+Q SALL+A
Sbjct: 121 PMKRVLEPLTQMGARVLARGQGDYAPFAIKG-GKLRGQDFILKKA-SAQVKSALLLAGLR 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ + + +S + E R++ FG K + R I GGQK K V G
Sbjct: 179 AEGNTSV--TEPQLSRDHTE---RMLVGFGAKIKREGL--RVEISGGQKLLGQK-VIVPG 230

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKV---TWTETSVTVT 308
D S+AS+F+ A I + + ++ G + VL+ MGA + + E S
Sbjct: 231 DFSTASFFIVAALIVPDSHLIKNVGLNPTR--TGLLTVLKEMGANIQILNFHENS---- 284

Query: 309 GPPREPFGGRKH--LKAIIDVNMKNMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P K+ LKA++V +P D LAV A G + +R RVKE++R
Sbjct: 285 GEPVGDLEVKYSPKAVEVPPEIVPAMIDEFPILAVAMALAYGESKVRGAELRVKESDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFS-LAACAEVPVTI 422
+ +I +E +K+G +V+E PD II+ K+ T +D++ DHR+AM+ + L A I
Sbjct: 345 IKSIVSEFSKMGVAVKELPDGFIISGNGKILGTTVDSHDHRIAMSLAVLGLTAAGTTEI 404

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ ++P++F L+ +
Sbjct: 405 LNADAVAISYPEFFQQLTKLTE 426

>ref|YP_381441.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9605]
sp|Q3AKJ6.1|AROASYNRC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB34886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
CC9605]
Length = 441

Score = 133 bits (335), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 129/441 (29%), Positives = 204/441 (46%), Gaps = 33/441 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+PG KS+S+R LL A++EGTT +D LL +ED LR +G+S+
Sbjct: 19 LQGRVKVPGDKSISHRSLFGAIAEGTTTIDGLLPAEDPLSTAACLRAMGVSISPITDGG 78

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G V+ +E ++ GN+G MR + + G +VLDG +R RP
Sbjct: 79 IVTVEGVG----VDGLQEPAEVLDGNSGTTMRLMLGLLAGRDGR-HFVLDGDASLRRRP 133

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L +GA+V G + P+ V G +L G++ +++ + + L
Sbjct: 134 MRRVGQPLASMGAEVRGRDGNLAPLAVQG-----RQLKGTVIGTPVASAQVKSALL 185

Query: 194 LGDVEIE----IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNA 248
L + E +I+ S + E R+++ FG R ++ G + KN
Sbjct: 186 LAALTAESPTTVIEPAQSRDHSE---RMLKAFGADLTVGGEIGRHISVRPGATLQG-KNV 241

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA+++L AGA I G +T+E G + EVLE MGA + V
Sbjct: 242 VVPGDISSAAFVWAGALIPGADLTIEENVGLNPTR--TGILEVLEQMGALIEVLNPR-DV 298

Query: 308 TGPPEPFGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P H LK + MP D L+V A F +G + I + RVKET+
Sbjct: 299 AGEVGDRLRVTHGGLKPFNFGEIIMPSLVDEVPILSVAACFCEGESRISGASELRVKETD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ + +L +GA ++E D I L A+D+ DHR+AM+ +AA A+ +
Sbjct: 359 RLAVMARQLKAMGADIDEHEDGMTIRGGRPLKGAALDSETDHRVAMSLGVAAMLADGNSS 418

Query: 422 IRDPGCTRKTFPDYFDVLS 442
+ ++P ++D L
Sbjct: 419 LARSEAAVSYPSFWDELERL 439

>ref|ZP_06483994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. vasculorum NCPPB702]
Length = 474

Score = 133 bits (335), Expect = 4e-29, Method: Compositional matrix adjust.
Identities = 131/434 (30%), Positives = 208/434 (47%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 50 LQGS LAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRIETPSASQ 109

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R V VG G P ++ L GNAG MR L + A ++ VL G + +RP
Sbjct: 110 RIVHGVGV DGLQPPTES-----LDCGNAGTGMRLLAGLLAAQRFD--VLVGDESLSKRP 162

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+RV+G+ L G +S S+Q SA+L+A A
Sbjct: 163 MRRVTGPLAQMGARIDT-QDDGTPLRVHGVQALHGIDF-VSPVASAQVKS AVLLAGLYA 220

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV + S R ++GGQ+ ++ A V D
Sbjct: 221 QGETSVTEPH-----PTRDYTERMLSAFGVDIDFSPGKAR--LRGGQRLRATDIA-VPAD 272

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I G+ V + G + L +MGA + E G P
Sbjct: 273 FSSAAFFIVAASIVPGSEVVLRAVGLNPR--TGLLAALRLMGANID-EENHAEHGGEVP 329

Query: 313 EPFGRKH--LKAIDVNMNKM PDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 330 ADLRVRYAPLRGAQIPEALVPMIDEFPALFVAAAAASGQTVVTGAELRVKESDRLAAM 389

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 390 ATGLRTLGVQVDETDPDGATIH-GGSIGSGVIESHGDRIAMAFIAAGQLSTGSGVQVNDVA 448

Query: 427 CTRKTFPDYFDVLS 440
+FP FD L+
Sbjct: 449 NVATSFPG-FDTLA 461

>ref|NP_721197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus mutans
UA159]
sp|Q8DUV8.1|AROA_STRMU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAN58503.1|AE014920_1 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus mutans
UA159]
Length = 427

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 218/437 (49%), Gaps = 37/437 (8%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+K+PG KS+S+R ++ +L++G T + +L EDV + A R LG+ + K
Sbjct: 10 LSGTLKIPGDKSISHRSIMFGSLAKGITKIYGILRGEDVLSTMQAFRDLGVEI---KDKD 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G ++ K+ L +GN+G ++R ++ + AG + T + G + +RP+

Sbjct: 67 DFVEIHGRGFDGLKSPKK--ALDMGNSGTSIRLISGVL--AGQDFTVEMFGDDSLSKRPM 122

Query: 135 GDLVVLGKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ V L+Q+G + D PP+ + G L + +L + S+Q SAL+ AA A

Sbjct: 123 DRVTVPLRQMGVQILGRTERDLPPLTMKSGKRLKPIRYELPVA-SAQVKSALIFAALQAS 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKNAYVEGD 253
G E II+K + + E ++++FG H D I GGQ++ + +N V GD

Sbjct: 182 G--ESVIEKEKTRNHT--DMIKQFG--GHLDVDGKEIRISGGQEF-TAQNVIIVPGD 232

Query: 254 ASSASYFLA-GAAITGGTVTVGCGTTSLSQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++LA G ++ +T++ G + + EV+E MG KV ++ + T+

Sbjct: 233 ISSAAFVLAAGLIVSNSKLTKNVGINETRTGI--LEVIEAMGGKVELSDRDDLAKAATL 290

Query: 308 TGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
T +LK ++ + +P + L ++AL A +G T I D +VKET+R+

Sbjct: 291 T-----VESSLKGTIEGGDIIPRLIDELPIALLATQANGRTVIYDAQELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D II L+ ++T+ DHR+ M ++AA E V +

Sbjct: 345 QVVADALNAMGAKITPTDDGMIEGKTNLHGAKVNTFGDHRIGMMTAIAALLVKEGEVEL 404

Query: 423 RDPGCTRKTFPDYFDVL 439
++P +F L

Sbjct: 405 ERAEAINTSYPTFFSDL 421

>ref|YP_002513612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thioalkalivibrio sp.
HL-EbGR7]
gb|ACL72625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thioalkalivibrio sp.
HL-EbGR7]
Length = 441

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 131/456 (28%), Positives = 221/456 (48%), Gaps = 47/456 (10%)

Query: 1 MAGAEEIVL--QPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLG 58
M+ A+E+ Q ++G +++PG KS+S+R ++L +L+EGTT V LN ED L

Sbjct: 1 MSQAQELAFEVQSGGTLTGRIVRPGDKSISHSIMLGSLAEGTTEVTGFLNGEDCMATLA 60

Query: 59 ALRTLGLSVEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
A R +G+ ++ + + + VG G K P L LGN+G +MR ++ +

Sbjct: 61 AFRAMGVQIDGPREGRVTIQGVGLHLKAPAGP-----LDLGNSGTSMRLMSGLLAGQA 114

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSG 176
+ T V D + +RP+ + L +GA +D T PP+ V+G L G ++

Sbjct: 115 FDTTLVGDA--SLTKRPMKRVTEPLAAMGARIDTS-ATGTPPLHVHGQTTLRGIDYQMPM 171

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+ S+Q S LL+A A G + P + T R++ FG S +R +

Sbjct: 172 A-SAQVKSCLLLAGLYAEGSTCVT-----EPAPTRDHTERMLTGFGYPV--SREGNRACV 223

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMG 295
+GG + K+ + V D SSA++FL GA+I G+ +T+E G + V ++L +MG

Sbjct: 224 QGGGRLKATR-IDVPADISSAAFFLVGASIAKGEITLHVGMNPNTR--VGVIDILRLMG 280

Query: 296 AKVTWTETSVTVTGPPREPFGR--KHLKAIDVNMN--KMPDVAMTLAV---VALF----- 343
A++ PRE G L+ + + ++P+ + LA+ ALF

Sbjct: 281 AEIHVEN-----PREAGGEPVADLRVVSAPLRGVRIPEELVPLAIDFPAIFIAAAC 332

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDD 403
A+G T + RVKE++R+ + L G E PD I +L +D++ D

Sbjct: 333 AGETLLTGAEELRVKESDRIQVMADGLLACGIEAEPDPGIRIR-GGQLRGATVDSHGD 391

Query: 404 HRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDV 438
HR+AM+F++ A AE + IR+ +FP + ++

Sbjct: 392 HRIAMSFAMGALRAEGAMHIRNCANVNTSFPGFVEL 427

>gb|AAM16078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16082.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]

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gb|AAM16083.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 61

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 61/61 (100%), Positives = 61/61 (100%)

Query: 385 CIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFDVLSTFVK 444
          CIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFDVLSTFVK
Sbjct: 1    CIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFDVLSTFVK 60

Query: 445 N 445
          N
Sbjct: 61  N 61

>ref|ZP_04935174.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [Pseudomonas aeruginosa 2192]
gb|EAZ59293.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [Pseudomonas aeruginosa 2192]
Length = 746

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 129/437 (29%), Positives = 213/437 (48%), Gaps = 33/437 (7%)

Query: 10  QPIKEISGTVKLP GSKSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
          QP  +SGT+++PG KS+S+R ++L +L+EGTT V+  L  ED    + A R +G+ +E
Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQAFRDMGVVIEG 377

Query: 70  DKA AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
          +  + V  VG  G K P          ++LGN+G +MR L+  + A  ++T  L G
Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPFDDST--LTGDA 429

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
          + +RP+  +  L+++GA ++  G +  PP+ +  G  L G  +  + S+Q  S L
Sbjct: 430 SLSKRP MNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSC L 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
          L+A  A+G+  +          P  + T R++ FG          S  +  ++ G K S
Sbjct: 487 LLAGLYAVGETSVT-----EPAPTRDHTERMLRGFGYPVVVEGSTAK--VESGHKL-SAT 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
          +  V  D SSA++FL  A+I  G+ + ++ G  +  V  E+L +MG ++  E
Sbjct: 539 HIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VGVI EILRLMGGDL SL-ENQR 595

Query: 306 TVTGGPPREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
          V G P          +  LK ID+  + +P  D  L V A  A+G T +R          RVKE
Sbjct: 596 EVGGEPVADIRVRSARLKGIDIPEDLVPLAIDFPPVLFVAAACAEGRTVLRGAEEELRVKE 655

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVP 419
          ++R+  +  L  LG  E PD +I          +  + DHR+AM+FS+A+  A P
Sbjct: 656 SDRIQVMADGLKALGVKAEPTPDGIVIE-GGAFGGGEVWAHGDHRIAMSFSVASLRASGP 714

Query: 420 VTIRDPGCTRKTFFPDYF 436
          + I D          +FP++
Sbjct: 715 IRIHDCANVATSFNPNFL 731

>ref|ZP_05593092.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
AR01/DG]
gb|EEU87886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
AR01/DG]
Length = 428

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12  IKEISGTVKLP GSKSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
          +K + GT+ +P KS+S+R ++  A+S G T + N L  ED    L A R +LG+++E D
Sbjct: 9    VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72  AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131

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      + V  G  ++ AK  + +  GN+G  +R  +  +  AG      L G  + +
Sbjct: 69  TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121
Query: 132  RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+  +++ L Q+GA+      T+ PP+ + G  L      + + S+Q  SA+L AA
Sbjct: 122  RPMNRVMLPLNQMAECQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180
Query: 192  LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G  +  ++K  +  + E  +R  +FG  E      +  + G Q+  + +N  V
Sbjct: 181  QAQGTSVV--VEKEKTRDHTEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232
Query: 252  GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
      GD SSA++FL AG  +  + ++  G  Q      +V++ MG  VT  E      +G
Sbjct: 233  GDISSAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 290
Query: 310  PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
      L A ++  +P  +  L ++AL A  G T  IRD      +VKET R+ A
Sbjct: 291  DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELVKETNRIDA 348
Query: 367  IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
      +  ELT LGA  +  D  II  P  L+  + +Y DHR+ M  +AA  E  V  +
Sbjct: 349  VAKELTILGADITPTDGLIIGHGPTSLHGGVRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408
Query: 425  PGCTRKTFFPDYFDVL 439
      ++P  +FD  L
Sbjct: 409  AEAHSVSYPAFFDDL 423

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>gb|EDZ73120.1| YDR127Wp-like protein [Saccharomyces cerevisiae AWRI1631]
Length = 217

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 84/187 (44%), Positives = 117/187 (62%), Gaps = 8/187 (4%)

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Query: 158  PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID-KLISIPYVEMTLR 216
      P++V      GG+++L+  ++SSQY+S++LM AP A  V  + ++  K IS  YV+MT++
Sbjct: 20  PIKVYTDSVFKGGRIELAATVSSQYVSSILMCAPYAEPPVTALVGGKPISKLYVDMTIK 79
Query: 217  LMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
      +ME+FG+  E S  +  +YI  G  Y  +P  +E DASSA+Y LA AA+TG TVTV
Sbjct: 80  MMEKFGINVESTTEPTYTYIIPKGH-YINPSEYVIESDASSATYPLAFAAMTGTTTVTPN 138
Query: 276  CGTTSLQGDVKFA-EVLEMMGAKVTWTETSVTVTGPPREFPGRKHLKAIDVNMNKMMPDVA 334
      G  SLQGD +FA +VL+ MG K+T T TS TV+GPP      K LK +D  M  M  D
Sbjct: 139  IGFESLQGDARFARDVLKPMGCKITQTATSTTVSGPPVGTGTL--KPLKHVD--MEPMTDAF 194
Query: 335  MTLAVVA 341
      +T  VVA
Sbjct: 195  LTACVVA 201

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>ref|ZP_02929027.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Verrucomicrobium spinosum DSM 4136]
Length = 459

Score = 133 bits (335), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 134/452 (29%), Positives = 224/452 (49%), Gaps = 34/452 (7%)

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Query: 6  EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      ++ ++ +K  +  + +PG KS+S+R ++ A L EGTT+++N L+S+D  L A++ +G
Sbjct: 3  QLKVRSLKHVPPELIVPGDKSISHRAVMFAGLCEGTTLIENFLSSDDCLCSLNAKAMGA 62
Query: 66  SVE---ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
      E  D  K  +  G  ++  E  +  GN+G  MR ++  + A  AT
Sbjct: 63  EYEVLTQDSRGKPVKLTVTGHGMQLKAPAETIDC--GNSGTTMRMSGILAAQSFTAT-- 118
Query: 123  LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      + G P  + +RP+  +  L Q+GA ++      P+ ++G G L      L  + S+Q
Sbjct: 119  MAGDPSLSKRPMKRVADPLSQMGARLEGQGEKISAPITIHG-GELEAITYTLPMMA-SAQV 176
Query: 183  LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242

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Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
 LK ++ +P + L ++AL A G T I+D +VKET+R+ +
 Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
 L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
 Sbjct: 348 ADALNSMGADITPTADGMIKKSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFFPDYFDVLSTFV 443
 ++P +FD L + +
 Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|YP_527618.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
 1-carboxyvinyltransferase [Saccharophagus degradans
 2-40]
 gb|ABD81406.1| prephenate dehydrogenase / 3-phosphoshikimate
 1-carboxyvinyltransferase [Saccharophagus degradans
 2-40]
 Length = 745

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
 Identities = 125/434 (28%), Positives = 210/434 (48%), Gaps = 31/434 (7%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
 P + GT+++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+ +E
 Sbjct: 318 PGGTVQGTIRVPKDKSISHRSIMLGSLAEGVTHVEGFLEGEDALATLQAFRDMGVVIEGP 377

Query: 71 KAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
 + + V VG G + P L++GN+G +MR L + AG L G
 Sbjct: 378 EDGRVTVHGVGLHGLQAP-----SGPLYVGNSGTSMRLLAGIL--AGQKFESELTGDES 429

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 + +RP+ + + L ++GA + PP++++G L G + + S+Q S LL+
 Sbjct: 430 LTKRPMNRVALPLAEMGASI-ATANEGRPPLKIHGGAALKGINYDMPMA-SAQVKSCLLL 487

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
 A A G + P + T R++ FG + + D ++ G K + +
 Sbjct: 488 AGLYAEKTSVT-----EPAPTRDHTERMLRGFGYDVQR--TGDTITVESGGKL-TATDI 539

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
 + D SSA++FL AAIT G+ +T+ G + + +L +MGA + + V
 Sbjct: 540 DIPADISSATFFLVAAAITPGSDITLTHVGINPTR--IGVINILNLMGANIELSNER-EV 596

Query: 308 TGPPREPFPGRKH--LKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
 G P ++ LK I+V +++P D L V A A+G T I RVKET+
 Sbjct: 597 GGEPVADIRLRYAPLKGIEVPESQVPLAIDEFPALMVAAACAEGTTVITGAEEELRVKETD 656

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVT 421
 R+ A+ LT LG D II + L +++++ DHR+AM+F++AA A +T
 Sbjct: 657 RIQAMIDGLTTLGIKCHATEDGAIIEGGQ-LGGGEVESFHDHRIAMSFTIAALRASGEIT 715

Query: 422 IRDPGCTRKTFFDY 435
 + + +FP++
 Sbjct: 716 VNNCANVSTSPNF 729

>emb|CBL19339.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus sp.
 SR1/5]
 Length = 424

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
 Identities = 115/454 (25%), Positives = 213/454 (46%), Gaps = 50/454 (11%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
 ++ K++SG++ +PG KS+S+R ++ +L+EGTT + N L D + R +G+++E
 Sbjct: 3 IKKAKKLSGSLAIPGDKSISHRAVMFGSLAEGTTKITNFLEGADCLSTISCFRKMGINIE 62

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
 + ++V G + E L +GN+G R ++ + AG + L G
 Sbjct: 63 NTEGE---ILVHGKGLHGLSAPSE--TLDIGNSGTTTRLISGIL--AGQDFVSELTGDAS 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+++RP+ ++ L Q+GAD+ G C P++++G + L A+
Sbjct: 116 IQKRPMPKRIMTPLSQMGADIISLNGNGCAPLKISG-----KKLHAIHY 158

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-----IKGGQKYK 243
+P+A V+ + L++ Y + R+ E + H++ ++ +G
Sbjct: 159 NSPVASAQVKSCV---LLAGMYSDGITRVTEPV-LSRNHTEIMLNIFYGANVTAEGTTASI 214

Query: 244 SP-----KNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
P + V GD SSA+YF+A G + + ++ G + + V MGA
Sbjct: 215 KPDPPLYGREILVPGDISAAYFIAAGLLVNPSEILKKNVGINPTRDGI--LRVCRAMGA 272

Query: 297 KVTWTETSVTVTGPPREPFP--GRKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIR 351
+T T G P L + +P D +AV+A FA+G T IR
Sbjct: 273 DITLLNE--TTEGEPTADLLIRSSALHGTTEGAIIPTLIDELPMIAVMAAFAEGTTVIR 330

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
D RVKE++R+ + L K+GA ++E D II + L+ ID++ DHR+AM+F+
Sbjct: 331 DAQELRVKESDRIQVMTENLRKMGDIQETEDGMIHGGKALHGAIEDSHLDHRVAMSFA 390

Query: 412 LAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+A E ++I++ C ++P+++ L + +
Sbjct: 391 VAGLLCEGTLSIKNGECVNIISYPEFYSDLYSLAE 424

>ref|YP_436095.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Hahella chejuensis KCTC 2396]
gb|ABC31670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hahella chejuensis
KCTC 2396]
Length = 738

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 125/430 (29%), Positives = 213/430 (49%), Gaps = 31/430 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+ G +++PG KS+S+R ++L +L+EG T ++ L ED L A R +G+ +E D+ +
Sbjct: 314 VCGDIRVPGDKSMSHRSIMLGS LAEGVTEIEGFLEGEDALATLQAFRDMGVVIEGPDGRS 373

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VG G K P L+LGN+G +MR L ++ G + L G + +R
Sbjct: 374 VTINGVGMHGLKQP-----PGPLYLGNSGTSMRLLAGLLS--GQSFDELVTGDESLSKR 425

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+++GA++ G PPV++ G L G + + S+Q S+L++A
Sbjct: 426 PMERVAKPLREMGAEISTSEGGR-PPVKIKGGSRLHGIHYDMPVA-SAQVKSSLVLAGLY 483

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ + P + + R++ FG + + S + IKGG K + K V
Sbjct: 484 AEGETSVT-----EPAPTRDHSERMLRGFGYPVDVNGS--KVTIKGGHKLSATK-IDVPS 535

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL A+IT G+ +T+ G + V +L+MMGA + + V G P
Sbjct: 536 DISSAAFFLVAASITPGSDLTLRHVGVPNPTR--VGVISILKMMGADIELS NHK-EVGGE 592

Query: 312 REPFGRKH--LK AIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
++ LK I + ++P D L + A+ A+G T + RVKE++R+
Sbjct: 593 VADIRVRYAPLKGIRIPEEQVPLAIDEFPVLFIAAVCAEGETVLSGAEELRVKESDRIQT 652

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ L LG S E D ++ E + +D++ DHR+AMAF++A+ A + I+D
Sbjct: 653 MADGLAALGVSSEVKEDGIVLRSAL-IGGGTVDSHGDRHRIAMAFASLRATGAIVIKDC 711

Query: 426 GCTRKTFPDY 435
+FP +
Sbjct: 712 ANVATSFPGF 721

>ref|ZP_05576906.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
ElSol]
gb|EEU77877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis


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ElSol]
gb|EFT88428.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX2141]
gb|EFU04457.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0645]
Length = 428

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKKAKNTIDV--GNSGTTIRMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAECCGVQQTFFPISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ +N V
Sbjct: 181 QAKGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFFLVAGLVDPSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAAELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAHSVSYPAFFDDL 423

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>ref|YP_002720995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira
hyodysenteriae WA1]
sp|C0QZK3.1|AROABRAHW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACN83291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brachyspira
hyodysenteriae WA1]
Length = 420

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Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 118/428 (27%), Positives = 221/428 (51%), Gaps = 31/428 (7%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLN--SEDEVHYMLGALRTLGLSVEADK 71
EI G++ + SKS ++R L+ ++L++ +++ ++ S DV A+
Sbjct: 9 EIFGSIYIQMSKSDAHRALIASLAKTPSIKRWIDNVSDVEVTKNAVSNF----- 60

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
A ++ FP ++ K+E+ + + +G ++R L ++A G T+ G ++
Sbjct: 61 -ADLEIIDNLKVFPPKKEYKKELVIDVKESGSSLRFLIPIMSAFGITCTFT--GSKKLFS 117

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI K+ G + F+ ++ ++++G L K+ G++SSQ+LS LL A P
Sbjct: 118 RPIDVYKKIWKEEGLE---FIHSE-DSIKISG--QLKASNFKVLGNLSSQFLSGLLFALP 171

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
L G+ I I +L S PYV MTL+ ++ ++ D+ + + G Q+Y S + VE
Sbjct: 172 LLDGNSNIIIDGELESEFPYVMMTLKTLKAANIETLRHDN-NIEVYGNQY-SEGIDYEVE 229

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Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-TSVTVTGP 310
D S A++F A A+ G T T+ G S+QGD + +L+ MGA V++ + S+T+
Sbjct: 230 SDWSHAFFAAAGALGGET-TLYGLNKYSIQGDKEILNLFKMGASVSYNDDNSITIKKT 288

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
R L A+D++M+ +PD+ + +A A G T + + R KE++RM +
Sbjct: 289 NR-----LNALDIDMSDIPDLGPIITTLAATAKGRTRLNAGRLRYKESDRMNDLMDS 341

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLA-ACAEVPVTIRDPGCTR 429
+++GA++E D +I E+L +++DHR+AMA ++A A ++ + I D
Sbjct: 342 FSRIGANIEVSEDEILIEGVERLKGNGNTTSHNDHRIAMALAVASAVSNDNDIIDAESIN 401

Query: 430 KTFPDYFD 437
K+ ++ +
Sbjct: 402 KSSFNFI 409

>ref|ZP_08050752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
M334]
gb|EFX59073.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus sp.
M334]
Length = 427

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 119/443 (26%), Positives = 213/443 (48%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 ISHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 GVITIQGVGMDGLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + + PP+ + G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVITPLKMGVSISGETERNLPLNLKGTKNLAPIHYELPIA-SAQVKSALIFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E L +GN+G ++R ++ + AG + + G ++
Sbjct: 179 QAQG--ESVIEKECTRNHTE---DMLQQFG--GHLSVEGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISSAAFVLVAGLIVPNSRLVLQNVGVNETRTGI--IDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLA--CAEVPV 420
R+ + L +GA++ D II L+ ++T+ DHR+ M ++AA A+ V
Sbjct: 343 RIQVVADALNSMGANITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L + +
Sbjct: 403 ELDRAEAINTSYPSFFDDLES LI 425

>ref|ZP_05475914.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
ATCC 4200]
ref|ZP_05579539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
Fly1]
gb|EEU17771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
ATCC 4200]
gb|EEU80510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
Fly1]
Length = 428

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPKSDKSIHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK ++ GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVAMFLNQMGAECCQGVQQTEFPPIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGPPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKNMGGSVTILNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQTLTATEIGGAIIPRLIDELPIALLATQATGTIIRDAEELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDDGLIHHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|ZP_02210434.1| hypothetical protein CLOBAR_02842 [Clostridium bartlettii DSM
16795]
gb|EDQ95471.1| hypothetical protein CLOBAR_02842 [Clostridium bartlettii DSM
16795]
Length = 419

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 124/445 (27%), Positives = 212/445 (47%), Gaps = 42/445 (9%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT +L G KS+S+R ++ +A+S+G V N L +D + R +G+ +E A K
Sbjct: 2 LRGTFFELIGDKSISHRSIMFSAISKGNKVSNFLMQDCLSTVSCFRKMGVDIEI--AGK 59

Query: 75 RAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ G G G P D L +GN+G +R + + AG + L G + +R
Sbjct: 60 DVFIKNGIRGLKPPTDI-----LDVGNSTTIRLIMGIL--AGNDFESTLIGDESIGKR 112

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+ +G D+ + P+ V G G L K+ + S+Q SA+++A+
Sbjct: 113 PMKRVTDPLRMGCDITGKDDANFTPTVIRG-GHLHSIDYKMPVA-SAQVKSAILLASLY 170

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
A G I +K+ S + E+ L+ FG + + + D + +
Sbjct: 171 ADGQSIIR--EKVKS RNHTEIMLK---AFGADIKENGLDIIVNPVDELFI-----NQ 216

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ YV GD SSA++ + GA I+ G+ V ++ G + + +V++ M + + V
Sbjct: 217 DIYVPGDISAFAFIIVGALISEGSEVLKVNGLNETRTGI--IDVIKNMNGNIEIIDERV 274

Query: 306 TVTGPPREPFGFR--KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ R K L A ++ +P D +AV+A A+G T I+D +VKE
Sbjct: 275 VGGEKVGDLLVRYSKDLTATTIDKTIIPRLIDEIPVIAVLATQAEGTTI IKDAQELKVKE 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLA-ACAEVP 419
+ R+ + L K+GA +EE D II KL+ I+T+ DHR+AM+FS+A ++
Sbjct: 335 SNRIKTVVDNLKMGADIEELEDGMIKGTKLHGATITETFDHRIAMSFSIADLISDSR 394

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 444
V + D C +FP YF++L K
Sbjct: 395 VMLDDTNCINISFPGYFNLLKDLTK 419

>ref|ZP_02709501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC1873-00]
gb|EDT50279.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC1873-00]
Length = 427

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 208/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPYMDRVTLPKKMGVSISGQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGTP 310
GD SSA+++L I + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISAFAFWLVAGLINPNSHLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIIGKSALHGAVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|NP_607461.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pyogenes MGAS8232]
sp|Q8P0H1.1|ARO_A_STRP8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAL97960.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Streptococcus pyogenes MGAS8232]
Length = 427

Score = 133 bits (334), Expect = 6e-29, Method: Compositional matrix adjust.
Identities = 122/435 (28%), Positives = 211/435 (48%), Gaps = 39/435 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 10 LQGTIQVPGDKSISHRAVILGAVAKGETRVKLLKGEDVLSTIQAFRN LGVRIE--EKDD 67

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 68 QLVIEGQGFQGLTAPCQT---LNMGNSGTSMRLIAGLL--AQQPFVSKMIGDESLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 123 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLPITYTLPIS-SAQVKSAILLAALQAK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E +++FG R + G Q+ + + V GD
Sbjct: 182 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA+++L AG I G + ++ G + + EV+E MGA++ + + TS+
Sbjct: 234 SSAAFWLIVAGLIIPGSELLLNKVGVPNPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 291

Query: 307 VTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V HLK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 292 VV-----YSHLKGTTISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++ A + V
Sbjct: 344 IQVVTDLNLSMGANIKATADGMIIGKPTVLYGANTSTYGDHRIGMMTAITALLVKQGQVH 403

Query: 422 IRDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 404 LDKEEAIMTSYPTFF 418

>sp|Q9ANY6.2|AROA_ENTFA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 426

Score = 133 bits (334), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 7 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 66

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 67 TT---ITVEGRGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 120 RPMNRVMLPLNQMGAEQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 179 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVITVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 231 GDISSAAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHSG 288

Query: 310 PPREFPGRKHLKAIDVNMNMKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 289 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELVKKETNRIDA 346

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 347 VAKELTILGADITPTDDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 406

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 407 AEAHSVSYPAFFDDL 421

>ref|YP_002562501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus uberis
0140J]
sp|B9DSK8.1|AROA_STRU0 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAR42616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus uberis
0140J]
Length = 427

Score = 133 bits (334), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 113/434 (26%), Positives = 216/434 (49%), Gaps = 25/434 (5%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V +PG KS+S+R L+ +++EG T + LL S+DV L ALR LG+++E ++ +
Sbjct: 10 LKGNVTVPGDKSISHRALIFGSIAEGKTEIKGLLKSQDVQRTLVALRHLGVITIE--ESDQ 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ ++ G G F A + L +GN+G ++R L ++ G + G + +RP+
Sbjct: 68 KVIIQKGK--FSGLTAPDS-PLDMGNSGTSRLLAGLLS--GQDFPVQFFGDASLSQRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V+ L+++GA V+ PP+ V G L ++ + S+Q SA+L+AA
Sbjct: 123 DRIVIPLEMGARVEGQGPKHLPPITVLGSSQLTAINYQMPLA-SAQVKSAILLAALQTK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + ++ +K ++ + E+ ++++FG E S I G Q K ++ + GD
Sbjct: 182 G--QTQVFEKAVTRNHTEV---MIKQFG--GEIFQSGKEIRIIGPQTLKG-QSLTIPGDI 233

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++++ A I G ++++ G + + ++++ MG + T+ +
Sbjct: 234 SSAAFWIVAALIIPGSAISIKNVGINPRTGTI--IDLVKMGGAIELTDRD-DINQSATI 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTE 370
LK + +P + L ++AL A +G T ++D RVKET+R+ + +
Sbjct: 291 HVSYSKLGKTRIAGEMIPRLIDELPIALLATQAEGTTVVQDAQELRVKETDRIQVVTSL 350

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCT 428
L K+GA +EE D +I +L+ D + DHR+ M ++AA + +
Sbjct: 351 LRKMGADIEEKTDFVIKGTTELHSCQADAFDHRIGMMVAIAALLVKTGEMILNGEEAI 410

Query: 429 RKTFFPDYFDVLSTF 442
+ ++P +F L +
Sbjct: 411 QTSYPQFFKDLESL 424

>ref|ZP_04261280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST196]
gb|EEL07113.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
BDRD-ST196]
Length = 424

Score = 133 bits (334), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 122/442 (27%), Positives = 212/442 (47%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A++EGTT V N L ED + + LG+ +E
Sbjct: 10 LNGTIVVPGDKSISHRSVMFGAIAEGTTKVSNFLLEDCLSTIACFQKLGVIQIEQ---FG 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G +++ KE L +GN+G +R + + ++T + D + +RP+
Sbjct: 67 NDVTIYGKGLHNLQEPKE--VLDVGNSGTTIRLMLGILANTPFHSTIIGDA--SIGKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVK----LSGSISSQYLSALLMAA 190
+ L ++ A +D P+ + G GVKV S S+Q SA+L+A
Sbjct: 123 KRVTDP LSKMNAQIDGRENGQYTPLSIRG-----GKVKGMHYHSPVASAQVKSAVLLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G+ + + + S + E R++ FG + + ++GGQ+ K + V
Sbjct: 177 --LQEGEGITTVTEPMQSRDHTE---RMLRAFCTVDVNGRT--VSLQGGQQLKGA-DIEV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + + +E G + V EVL MGA ++ +
Sbjct: 229 PGDISSAAFFLVAGAIVPNSKLVLENVGLNPRTGTG--LEVLTGMGALISIDH---IRN 282

Query: 310 PPREFPG-----RKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
EP G LK I++ +P + + V+AL A +G T I++ +VKET
Sbjct: 283 EEFEPGCDITIETSKLKGIEGGTILPRLIDEIPVIALLATQAEGITVIKNAEELKVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
R+ + EL KLGA +E PD II + L ++++ DHR+ M ++A+C + V

Sbjct: 343 NRIDTVDELGKLGAKIEATPDGMIIYGKQSLKGNTVNSHGDHRIGMMLAIASCIIDGEV 402

Query: 421 TIRDPGCTRKTFFPDYFDVLSTF 442

I + ++P++F+ L+

Sbjct: 403 KIENSDAVAVSYPEFFEQLAAL 424

>ref|YP_693467.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Alcanivorax borkumensis SK2]
emb|CAL17195.1| prephenate dehydrogenase/3-phosphoshikimate 1-carboxyvinyltr
[Alcanivorax borkumensis SK2]
Length = 760

Score = 133 bits (334), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 132/439 (30%), Positives = 210/439 (47%), Gaps = 33/439 (7%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66

V+ P ++ G +++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+

Sbjct: 331 FVVAPGGQLQGRLRVPGDKSMHSRIMLGSLAEGVTQVEGFLEGEDALATLQAFRDMGVV 390

Query: 67 VEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+E + + VG G K P E L++GN+G +MR LT + AG + L

Sbjct: 391 IEGPHNGQVTIIGHVGLHGLKAP-----EKALYMGNSGTSMRLLTGLL--AGQSFDVELT 442

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYL 183

G + +RP+ + L+++GA + GTD PPVR+ G L G L + S+Q

Sbjct: 443 GDASLSKRPMEVAKPLREMGAIQITT--GTDGRPPVIRGGQSLKGFHYDLPMA-SAQVK 499

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

SA+L+ A G+ + P + T R++ FG + + + GG K

Sbjct: 500 SAVLLGGLYADGETSVT-----EPAPTRDHTERMLGGFGYEVRRDGATS--ALSGGGKLT 552

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302

+ K V D SSA++FL GA+I + VT+ G + V ++L++MGA + E

Sbjct: 553 AGK-LEVPADISSAAFLVGASIAANSEVTLPHVGINPRTTGV--IDILKLMGADIRL-E 608

Query: 303 TSVTVTGPPPEPF--GRKHLKAIDVNMMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357

G P LK I++ +P D + + A A G T +R R

Sbjct: 609 NQRDAGGEPVADLVVNAAPLKIEIPEALVPLAIDEFPAIFIAACAQGDITLRGAEEELR 668

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-A 416

VKE++R+ + L LG S + D IT E + ++ DHR+AM+F++AA A

Sbjct: 669 VKESDRIQVMADGLAALGVSHQVFDGIRITGGE-FGGGEVQSHGDHRIAMSFAMAALRA 727

Query: 417 EVPVTIRDPGCTRKTFFDY 435

P+TI D +FP +

Sbjct: 728 TGPITIHDCANVATSFPGF 746

>ref|YP_014545.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes str. 4b F2365]
ref|ZP_00231812.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes str. 4b H7858]
ref|YP_002758634.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
Clp81459]
ref|ZP_05230583.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
FSL J1-194]
ref|ZP_05242174.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
FSL R2-503]
ref|ZP_05265265.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
HPB2262]
ref|ZP_07073764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes FSL N1-017]
sp|Q71Y92.1|AROALISM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|C1KWM3.1|AROALISM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAT04722.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes serotype 4b str. F2365]

gb|EAL08346.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes str. 4b H7858]
emb|CAS05698.1| Putative 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes serotype 4b str. CLIP 80459]
gb|EEW18763.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes FSL R2-503]
gb|EFF95490.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes HPB2262]
gb|EFG02586.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes FSL J1-194]
gb|EFK42553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes FSL N1-017]
Length = 428

Score = 133 bits (334), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 220/439 (50%), Gaps = 33/439 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G + PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMPN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQQMGAKMHGKDGSEFAPITINGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQ + + + V GD S
Sbjct: 183 ETIIHKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAITGGT---VTVEGCGTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPR 312
SA++F+ IT G+ +T G T +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTR---TGIFDVVEQMGGSLLVVKDSSRS-TGKLA 289

Query: 313 EPFGRK--HLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
K LK ++ + P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 290 GTVVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAALVKVKTNRIDAV 349

Query: 368 RTELTKLASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
TEL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 350 ATELNKMADITPTEDGLIIRKTPPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERP 409

Query: 426 GCTRKTFFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 410 EAVSVSYPTFFEDIRSLK 428

>ref|ZP_05790178.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 8109]
gb|EEX07378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 8109]
Length = 441

Score = 132 bits (333), Expect = 7e-29, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 204/441 (46%), Gaps = 33/441 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ G VK+PG KS+S+R LL A++EGTT +D LL +ED LR +G+S+
Sbjct: 19 LQGRVKVPGDKSISHSRLLFGAIAEGTTTIDGLLPAEDPLSTANCLRAMGVSIISPITDGG 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G ++ +E ++ GN+G MR + + G +VLDG +R RP
Sbjct: 79 IVTVEGVG---LDGLQEPAEVLDGSGTMTMLMLGLLAGRDGR-HFVLDGDASLRRRP 133

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L +GADV G + P+ V G +L G++ +++ + + L
Sbjct: 134 MRRVVGQPLASMGADVGRDGGNLAFLAVQG-----RQLKGTVIGSPVASAQVKSALL 185

Query: 194 LGDVEIE----IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNA 248
L + E +I+ S + E R+++ FG R ++ G + +N
Sbjct: 186 LAALTAESPTTVIEPAQSRDHSE---RMLKAFGADLTVGEMGRHISVRPGATLQG-QNV 241

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA+++L AGA I G +T+E G + EVL+ MGA++ V
Sbjct: 242 VVPGDISAFAFLVAGALIPGADLTIENTVGLNPNTR--TGILEVLKQMGARIEVLNPR-DV 298

Query: 308 TGPPREPFGGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P H LK + MP D L+V A F +G + I + RVKET+
Sbjct: 299 AGEFVGNLRVTHGLKPFNFGEQIMPRLVDEVPILSVAACFCEGESRISGASELRVKETD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ + +L +GA ++E D I L +D+ DHR+AM+ +AA A+ +
Sbjct: 359 RLAVMARQLKAMGADIDEHEDGMTIRGGRPLKGAVLDSETHRVAMSLGVAAMLADGNSS 418

Query: 422 IRDPGCTRKTFFPDYFDVLSTF 442
+ ++P ++D L
Sbjct: 419 LARSEAAVSYSPFWDELERL 439

>ref|NP_815283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
V583]
ref|ZP_03948806.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0104]
ref|ZP_05596295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T11]
gb|AAG53678.1|AF318277_6 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
OG1RF]
gb|AA081353.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
V583]
gb|EEI11715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0104]
gb|EEU91089.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T11]
gb|EFU13750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1342]
gb|EFU16323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1346]
gb|EFU88053.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0309B]
gb|EFU92705.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0309A]
Length = 428

Score = 132 bits (333), Expect = 8e-29, Method: Compositional matrix adjust.
Identities = 125/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK ++ GN+G +R + + AG L G ++
Sbjct: 69 TT---ITVEGRGFAGLKKAKNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTFFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKNMGGSVTILNEDEANHS 290

Query: 310 PPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQTLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|ZP_03393211.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
amycolatum SK46]
gb|EEB63931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Corynebacterium
amycolatum SK46]
Length = 464

Score = 132 bits (333), Expect = 8e-29, Method: Compositional matrix adjust.
Identities = 132/447 (29%), Positives = 212/447 (47%), Gaps = 50/447 (11%)

Query: 19 VKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+++ GSKS++NR L++AALS +V+ L S D M+ AL+ LG + AD A
Sbjct: 1 MQIAGSKSITNRALVIAALSSTPSVIHGALRSRDTLDMIRALQALGTDISADSTYSGA-- 58

Query: 79 VCGCGKFPVEDAKEEVQLFLGN-----AGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
P + ++ G AG MR + A G+ + +G + R
Sbjct: 59 -----PNHTLRVTPRMLRGVVECGLAGTVMRFVPPIAALAQGSVFF--EGDVEAKAR 109

Query: 133 PIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIG-----GLP--GGKVKLSGSISS 180
P+ ++ L+ LG ++ F P + N +G LP GG+V++ S SS
Sbjct: 110 PMSAVLDALRSLGVNIAGNGLPFTVNPQGNQGNRLGDSVQEQLDLPDIGGEVEIDASASS 169

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDS-----WDRF 234
Q++S LL++AP + + ++ S P+++MTL ++ GV+ E + + F
Sbjct: 170 QFVSGLLLSAPRYGRGLVLRPTGEIPSRPHIDMTLDMLEAGVQIEETTADTPEGPRRTTF 229

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
I + + VE D S+A+ FLA AA+TGG+VTV + Q + E+ M
Sbjct: 230 SIHPTMIG--RTWQVEPDLNAAAFLLAAAVTGGSVTPVDWPEHTTQPGDRIREIFTAM 287

Query: 295 GAKVTWT-----ETSVTVTGP-PREPFGKRHLKAIDVNMNMPDVMATLAVVALFADGPT 348
GA VT+ TS+TV GP P E L+ I ++M+++ ++ T+A +A A T
Sbjct: 288 GATVTFNRHEGRTSLTVVGPKPSE-----LRGITMDMSEIGELTPTVAIAALATRTT 341

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
+ +A R ET R+ A+ TE+ LG E D I P L+ +Y DHRMA
Sbjct: 342 ELTGIAHLRGHTNRLAALTTEINGLGGRATELDDGIAID-PVPLHGGLWHSYADHRMAT 400

Query: 409 AFSLAACAEVPVTIRDPGCTRKTFPDY 435
A ++ V + + G T KT P +
Sbjct: 401 AGAIVGLRTEGVEVENIGTTAKTMPGF 427

>ref|ZP_04434543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1322]
ref|ZP_05558500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T8]
ref|ZP_07571860.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0411]
gb|EEN75117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX1322]
gb|EEU26627.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
T8]
gb|EFM66537.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX0411]
gb|EFT41312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX4000]
Length = 428

Score = 132 bits (333), Expect = 8e-29, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ A+ ++ GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKKARNTIDV---GNSGTTIRLMLGIL--AGCPFETRLAGDASISK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAKGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGFPQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVKNMGGSVTILNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIALLATQATGTTIIRDAAELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|YP_001814262.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Exiguobacterium
sibiricum 255-15]
gb|ACB61245.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Exiguobacterium
sibiricum 255-15]
Length = 417

Score = 132 bits (333), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 126/451 (27%), Positives = 207/451 (45%), Gaps = 58/451 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV++PG KS+++R L+ ++EGTTV+ N L D L A+ LG V+ +
Sbjct: 3 LRGTVRVPGDKSMTHRAFLMGGAIEGTTVISNALLGADCLASLAAVEALGAHVQQTEQEI 62

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + G A + + GN+G +R L+ + AG TY L G ++ RP+
Sbjct: 63 R--ITGT-----TALKAAATIDCGNSGTTIRLLSGIL--AGSQETYTLTGDESLQRRPM 111

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLA 193
+ V L LGAD++ GT P I G P G S+Q SA+L+A A
Sbjct: 112 DRVTVPPLATLGADIE---GTYAPLT----IHGQPLVGTTYTLPVASQVKSALLAGLFA 164

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKS-----PK 246
G E +++ ++S + E R++ +FG + + + + ++G + ++ P
Sbjct: 165 TG--ETTVEPIILSRDHE---RMLPKFGTDLTIQEQGRKIRLQGPVRLQATEIDIPG 219

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ +A+ A + IT V + T F +VL MGA V T
Sbjct: 220 DPSSAAFVWAAAILGADSRITTEHVLNMPTRT-----GFLQVLRQMGAQVEITNR--- 269

Query: 307 VTGPPREFPGRK-----HLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
RE G + L+A+ + ++P D LA++A A+G T IRD A
Sbjct: 270 -----RETAGEETADVTLMTTSLQAVAEIEGQIPSLIDEIPLALLATQAEGRTVIRDA 324

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
RVKET+R+ + + L K+GA +E D II P L +D+ DHR+AM ++AA
Sbjct: 325 ELRVKETDRIETVSTLRKIGAQIEATEDGMIIDGPTPLVGATVDSAGDHLAMMLTIAA 384

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445

+ + + ++P ++D L T +
Sbjct: 385 TLQPEIEVLGNVEVVSYPYTFYDDLKTLQQT 415

>ref|ZP_05034721.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevundimonas sp.
BAL3]
gb|EDX82150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevundimonas sp.
BAL3]
Length = 436

Score = 132 bits (333), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 198/445 (44%), Gaps = 47/445 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV+ PG KS+S+R ++L ++ G T V+ LL +DV A+ G V+ K
Sbjct: 13 LAGTVRAPGDKSMHRSMILGGMASGVTEVEGLLEGDDVLATARAVEAFGAKVQRTGDGK 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G + P+ + GNAG +R L A AAG T DG +R+RP+
Sbjct: 73 WRIEGAGGFRTPL-----TVIDCGNAGTGVRLLMGA--AAGFPLTATFDGDASLRKRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L +GA D D PV + GG + S+Q SA+L+A A
Sbjct: 125 KRVGTPLADMGARFDWQAEDRLPVALT--GGTLTAIDYVQTVASAQVKSAILLAGLNAQ 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKA---EHSWDRFYIKGGQKYKSPKNAYVE 251
G + +K + T R++ FG + E + W +KGGQ A V
Sbjct: 183 GVTSTVTEPEK-----SRDHTEMLRAFGAEVGVEMGEGWT-VTLKGGQPLTGTFFVA-VP 235

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA++ L AG + G VTVEG L+ G TW E +T
Sbjct: 236 GDPSSAAFPLAAGLIVPGSVTVVEGVMLNPLR-----TGLFDTWLEMGADLTIS 284

Query: 311 PREPFGKRHLKAIDVNMNKMMPDVAM-----TLAVVALFADGPTAIRDVASWR 357
R G + + I + + V + LA A FADG T +R V R
Sbjct: 285 NRRQAGGEDVDGITARHSALKGVVVPEARAASMIDEYPILAATAAFADGVTVMRGVGEMR 344

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEKLNVTATIDTYDDHRMAMA-FSLAAC 415
VKE++R+ + L G VEE P+ I+T P L + T DHR+AM+ L
Sbjct: 345 VKESDRISLMVEGLRACGVQVEEPEGFIVTGAPRVLGGAVVHTAHDHRIAMSHLVLGLA 404

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLS 440
A+ PV++ +PG +FP + +++
Sbjct: 405 ADQPVSVDEPGMIATSFPGFVEMMN 429

>ref|ZP_04662200.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
baumannii AB900]
Length = 756

Score = 132 bits (332), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 207/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 322 KAFKKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIIEGPKN 381

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 382 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLSQAQKFD--VMTGDASLS 433

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G + L + S+Q S +L+A
Sbjct: 434 KRPMERIAKPLRLMGAQIQTTGKEGTTPVVSITGGQQLKGIQYDLMA-SAQVKSIGILLAG 492

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K N
Sbjct: 493 LWAEGETSVTEPE-----PTRDHTEMLRAFGYDVKTE----GNKISLVGGGKLVG-TNI 542

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT V +E G + V E+L+ MGA +T E

Sbjct: 543 QVPSDISSAAFFMVGAATEDADVLEAVGINPRTGTG--IEILKQMGADLT-VENERIA 599

Query: 308 TGPPREPFP---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+

Sbjct: 600 GGEPIADIHIKGSRTLKGIHMPEDQVPLAIDEFPALFIAAACAEGQTVLTGAAELRVKES 659

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K I+++ DHR+AM+FS+A

Sbjct: 660 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGSGDWSPIFAGGEIESHHDHRIAMSFSMAG 719

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
P+TI +FP + ++

Sbjct: 720 LRTSGPITIHTETVATSFPTFTEL 744

>ref|ZP_04168122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides DSM 2048]
gb|EEM00156.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides DSM 2048]
Length = 424

Score = 132 bits (332), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 211/442 (47%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EGTT V N L ED + + LG+ +E

Sbjct: 10 LNGKIVVPGDKSISHRSVMFGAIAEGTTKVSNFLLEDCLSTIACFQKLGVIQEQ---FG 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G +++ KE L +GN+G +R + + ++T + D + +RP+

Sbjct: 67 NDVTIYGKGLHNLQEPKE--VLDVGNSGTTIRLMLGILANTPFHSTIIGDA--SIGKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALLMAA 190
+ L Q+ A +D P+ + G GKVK S S+Q SA+L+A

Sbjct: 123 KRVTDPLSQMNAQIDGRENGQYTPLSIRG-----GKVKGMYHSPVASAQVKSAVLLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G+ + + S + E R++ FG + + ++GGQ+ K + V

Sbjct: 177 --LQEGEITTVTEPMQSRDHTE---RMLRAFCTVDVNGRT--VSLQGGQQLKGA-DIEV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + + +E G + V +VL MGA ++ +

Sbjct: 229 PGDISSAAFFLVAGAIQNSKLVLNVLNPNRTGTG--LDVLTGMGALISIDH----IRN 282

Query: 310 PPREFPG-----RKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
EP G LK I++ +P + + V+AL A +G T I++ +VKET

Sbjct: 283 EEFEPCGDITIETSKLKGIEGGTLIPRLIDEIPVIALLATQAEGSTVIKNAEELVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPV 420
R+ + EL KLGA +E PD II + L ++++ DHR+ M ++A+C + V

Sbjct: 343 NRIDTVDELGLGAKIEATPDGMIIYGKQSLKGNTVNSHGDHRIGMMLAIASCIIDGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I + ++P++F+ L+

Sbjct: 403 KIENSDAVAVSYPEFFEQLAAL 424

>gb|EGD18578.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas gardneri ATCC 19865]
Length = 438

Score = 132 bits (332), Expect = 9e-29, Method: Compositional matrix adjust.
Identities = 133/447 (29%), Positives = 208/447 (46%), Gaps = 36/447 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + Q + G++ +PG KS+S+R ++ AAL++G + +D L ED LG

Sbjct: 6 QHWIAQQGSALQGSALIPGDKSVSHRAVMFAALADGISQIDGFLEGEDTRSTAAIFAKLG 65

Query: 65 LSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E A++R V VG G P +A L GNAG MR L + A VL

Sbjct: 66 VRIETPSASQRIVHGVGDGLQPPSEA-----LDCGNAGTGMRLLAGLLAAQ--RFDSVL 118

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + +RP+ + L Q+GA +D PP+RV+G L G +S S+Q
Sbjct: 119 VGDDSLSKRPMRRVTGFLAQMGARIDTEE-DGTPPLRVHGGQALHGIDF-VSPVASAQVK 176

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+L+A A GD + P + T R++ FGV+ + S R ++GGQ+
Sbjct: 177 SAVLLAGLYAQGDTSVTEPH-----PTRDYTERMLSAFGVEIDFSPGKAR--LRGGQRLG 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ A V D SSA++F+ A+I G+ V + G + L +MGA + E
Sbjct: 230 ATDIA-VPADFSSAAFFIVAASIIPGSDVVLRAVGLNPRR--TGLLAALRLMGANIV-EE 285

Query: 303 TSVTVTGPPREPFGGRHLKAIDVNMNKMPPDVAM-----TLAVVALFADGPTAIRDVA 354
G EP ++ + ++P+ + L V A A+G T + A
Sbjct: 286 NHAHEGG---EPVADLRVRYAPLQGGQIPEALVPDMIDEFPALFVAAAAAANGQTIVTGAA 342

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLAA 414
RVKE++R+ A+ T L LG V+E PD I + I+++ DHR+AMAF++A
Sbjct: 343 ELRVKESDRLAAMATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDRIAMAFIAIG 401

Query: 415 CAEVP-VTIRDPGCTRTKTFPDYFDVLS 440
V + D +FP FD L+
Sbjct: 402 QLSTGIVQVNDVANVATSFPG-FDSL 427

>ref|YP_002742356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae Taiwan19F-14]
ref|ZP_06964225.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae str. Canada MDR_19F]
ref|ZP_06977803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae str. Canada MDR_19A]
ref|YP_003724619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae TCH8431/19A]
sp|C1CQY4.1|AROA_STRZT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ACO24195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae Taiwan19F-14]
gb|ADI69405.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae TCH8431/19A]
Length = 427

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 209/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G ++
Sbjct: 67 GVITIQVGVMAGLKAPQNA-----LNMNGSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKMGVSISGQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ASVIEKECTRNHTE---DMLKQFG--GHLSVDGKKIIVQPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISSAAFVWLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWVRKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTICGALIPRLIDELPIALLATQAQGVTVIKDAEELKVKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425

L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407
Query: 426 GCTRKTFPDYFDVLFSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYSPFFDDLES LI 425

>ref|YP_003179683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium parvulum
DSM 20469]
gb|ACV51092.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Atopobium parvulum
DSM 20469]
Length = 426

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 126/437 (28%), Positives = 211/437 (48%), Gaps = 31/437 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I + P ++ GTV+ SKS ++R L+ A+L+ GTT + SED+ + L+ LG
Sbjct: 2 DISITP-HDLFGTVEAIISSKSYAHRALICASLANGTNTITCPYISEDIQVTVDCALKALGT 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAK--EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
++ K R V P ++A + +QL +G R + + A +AT
Sbjct: 61 TIARTKQGFVRV-----PAKEANRPQNIQLNCKESGTTFRFILPLLGA LNISATISA 112

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+G R+ RP+ L+ L G F D + V+G L GG ++ G+ISSQ++
Sbjct: 113 EG--RLFSRPLEPLISELSSHGMS---FTWLDEKFLEVSG--QLDGGSFEMPGNISSQFI 165

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYK 243
S LL++ PL I+I + S Y+ +T +M F + + + I+ Q Y
Sbjct: 166 SGLLLSLPLLNNKPSITQITGPIQSKDYLAITEHVMTDFDITPFEVNSATYITIEA-QHYV 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTET 303
P +EGD S+A+ +L AI G V V G S QGD L ++GA+V+ +
Sbjct: 225 CPGVYSIEGDSNAAPWLVAIGAIGQG-VEVTGLSMQSTQGDKAILAALSLVGARVSRQOK 283

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HL+ +++++ D+A LA +A F G + + D+ R+KE+ R
Sbjct: 284 GAASM-----MDHLRPFISISISEVCDLAPVLAALAAFIPGTSKLTDIQRLRLKESNR 335

Query: 364 MVAIRTELTKLGASVEEGPDYD--IITPPEKLNVTADITYDDHRMAMAFS-LAACAEVPV 420
+ +I T L G +VE D +IT ++ +D+Y+DHR+ M + LA+ A PV
Sbjct: 336 VQSICITTLKAFGVTVELSEDQTELVTITGGKQPTSCIVDSYNDRHIVMMSAILASYATGPV 395

Query: 421 TIRDPGCTRKTFPDYFD 437
I K++P +F+
Sbjct: 396 VITHAEAINKSYPLFFE 412

>ref|YP_003713717.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xenorhabdus
nematophila ATCC 19061]
emb|CBJ91611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xenorhabdus
nematophila ATCC 19061]
Length = 449

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 111/448 (24%), Positives = 219/448 (48%), Gaps = 32/448 (7%)

Query: 1 MAGAEIEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ + + + P + + +P SK + R +L A+L++G +++N L + + M A
Sbjct: 1 MSLLKYLAVNPSNYLLHSAYIPSSKPETQRAILAASLADGKSIINNDLRCLTNTMKEAC 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R++G + + +R ++ G GKG E ++V LG +G+ R+TA + A
Sbjct: 61 RSIGAQIIIE--PERLIYGTGGKIRPE---KKVIDALG-SGLVFRVITALTCHSETPA- 113

Query: 121 YVLGDVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
V+ G +R R + L+ L +LG ++ P +N GG GG+ ++ G+ISS
Sbjct: 114 -VISGDATLRTRVMEPLLNALVELGGINISIIHMNGKAPF-INW-GGYIGGECEIEGNIS 170

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q+++A+L APLA ++I ++S+ Y++ TL ++ G+K +H++++ + + G
Sbjct: 171 QFITAILFTAPLAKKSTTVKIKGDILSLSYIQQTLEILTIAGIKFQHNNFSQLTVFPG- 229

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
KY + + + GD +S SY +A A + +T+ + SLQG+ +E MG ++
Sbjct: 230 KYNAAEYT-ITGDYTSYLVAAATLFPDCLTLRNINSKSLQGEQAILTFVEKMGLEIIR 288

Query: 301 TE--TSVTVTGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ + + + G + N++ P++ TLA + ++ DG I + R+
Sbjct: 289 NDQRNEIRLINKKQQLTGN-----YEFNVSNCPNIVPTLASIGIYIDGCFRITGGSITRL 343

Query: 359 KETERMVAIRTELTKLGASV-----EEGPDYCIITPPEKLNVTADITYDDHRMAMAFSL 412
++ R+ A+ EL KLG + + + I + ++ DHR+ M+ +
Sbjct: 344 HKSPRIKAMVNELLLKLGVRIRPLIINDVYDGEIHDSSYSGNCTLSSWGDHRIFMSLFV 403

Query: 413 AA--CAEVPVT--IRDPGCTRKTFPDYF 436
A+ C + D C +FPD+F
Sbjct: 404 ASLRRCQANYIDGYEDVHC---SFPDFF 428

>ref|NP_147332.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeropyrum pernix K1]
sp|Q9YEK9.1|AROA_AERPE RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
dbj|BAA79537.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeropyrum pernix K1]
Length = 427

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 140/443 (31%), Positives = 218/443 (49%), Gaps = 40/443 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ +V+ P + G V+ P SKS ++R+L LA L+ G +VV L S D L A+ LG
Sbjct: 8 DRVVVHP-STVEGRVEAPPSKSYTHRMFLALLARGRSVVRPLVSNDTLATLNAVAL 66

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
R V GG + + ++ +G +R + V A AT +L
Sbjct: 67 ----GKPRLGGRVAAVEEGG-----EVGGAVVYAAGSGTTIR-IAMGVAHSAEAT-LLY 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ L L+ +GA V C G + PPV+V+G L V++ +ISSQ+ +
Sbjct: 116 GDES LNRRPVHPLSEALRSMGARV-CDTGGN-PPVKVSGP--LRRASVEVDAAISSQFAT 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+LL+A LG+ E+ +L S YV++TL + FGV+ E + + F ++G K
Sbjct: 172 SLLIAGS-RLGEFELSAA-RLSSRGYVDITLESLSMFGVVRVER-EGYRLFRLRGTPK--- 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P +A V GD SSAS+ LA AI G V VEG Q D + E+L MGA+V
Sbjct: 226 PVDAAVPGDYSSASFMLAAGAIAAG-RVEVEGLRPVDPQPDRIVELLRSMGARVRVEGGV 284

Query: 305 VTV--TGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
V V TGP L+ +DV+++ PD+A AV+A +A G + +R + + KE++
Sbjct: 285 VAVESTGP-----LEPVDVLDLGGSPDLAPVAAVLAAYARGVSRRLRGLERLKYKESD 335

Query: 363 RMVAIRTELTKLG--ASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
R+ AI L +LG A V G + + ++ DHR+AMA ++A A P
Sbjct: 336 RLSAIAWNLARLGVEARVRGG---ILEIRGGGVEGGVARSWGDHRIAMAMAVAGLGARRP 392

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
V + ++P + + L+
Sbjct: 393 VAVEGFSRVPDYPGFLEDLARL 415

>ref|YP_003445878.1| 3-enolpyruvylshikimate-5-phosphate synthetase, 3-phosphoshikimate
1-carboxyvinyltransferase [Streptococcus mitis B6]
emb|CBJ22011.1| 3-enolpyruvylshikimate-5-phosphate synthetase, 3-phosphoshikimate
1-carboxyvinyltransferase [Streptococcus mitis B6]
Length = 427

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 120/443 (27%), Positives = 210/443 (47%), Gaps = 35/443 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPKDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMGDLKAPQNA-----LDMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+ V G L +L + S+Q SAL+ AA
Sbjct: 120 RMDRVTIPLKMGVSISSQTERDLPPLHVKGTKKLPPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAQG--KSVIIEKECTRNHTE---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSV 305
GD SSA+++L AG + V ++ G + + +V+ MG K+ TE S
Sbjct: 231 GDISAFAFWLAVGLIVPNSRVVLKNVGINETRTGI--IDVIRAMGGKLEITEIDPVAKSA 288

Query: 306 TVTGPPREPFGKRLKKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
T+T + LK ++ +P + L ++AL A G T I+D +VKET+
Sbjct: 289 TLTVESSD-----LKGTEIGGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETD 342

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPV 420
R+ + L +GA + D II L+ ++T+ DHR+ M +AA + V
Sbjct: 343 RIQVADALNSMGADITPTADGMIKGSALHGAVNTFGDHRIGMMTVIAALLVSNGEV 402

Query: 421 TIRDPGCTRKTFPDYFDVLSTFV 443
+ ++P +FD L +
Sbjct: 403 DLDRAEAINTSYPSFFDDLENLI 425

>ref|YP_003485141.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus mutans
NN2025]
dbj|BAH88249.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus mutans
NN2025]
Length = 427

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 123/437 (28%), Positives = 217/437 (49%), Gaps = 37/437 (8%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+K+PG KS+S+R ++ +L++G T + +L EDV + R LG+ + K
Sbjct: 10 LSGTLKIPGDKSISHRSIMFGSLAKGITKIYGILRGEDVLSTMQTFRDLGVEI---KDKD 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G ++ K+ L +GN+G ++R ++ + AG + T + G + +RP+
Sbjct: 67 DFVEIHGRGFDGLKSPKK--ALDMGNSGTSIRLISGVL--AQQDFTVEMFGDDSLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ V L+Q+G + D PP+ + G L + +L + S+Q SAL+ AA A
Sbjct: 123 DRVTVPLRQMGVQILGRTERDLPPLTMKGSKRLKPIRYQLPVA-SAQVKSALIFAALQAS 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-SWDRFYIKGGQKYKSPKNAYVEGD 253
G E II+K + + E ++++FG H D I GGQ++ + +N V GD
Sbjct: 182 G--ESVIEIEKEKTRNHTE---DMIKQFG---GHLDVDGKEIRISGGQEF-TAQNVIVPGD 232

Query: 254 ASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVTV 307
SSA+++LA G ++ +T++ G + + EV+E MG KV ++ + T+
Sbjct: 233 ISSAAFVLAAGLIVSNSKLTNLKNVGINETRTGI--LEVIEAMGGKVELSDRDDLAKAATL 290

Query: 308 TGPPREPFGKRLKKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERM 364
T +LK ++ + +P + L ++AL A +G T I D +VKET+R+
Sbjct: 291 T-----VESSNLKGTEIGGDIIPRLIDELPIIALLATQANGRTVIYDAQELKVKETDRI 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L +GA + D II L+ ++T+ DHR+ M +AA E V +

Sbjct: 345 QVVADALNAMGAKITPTDDGMIIEGKTNLHGAKVNTFGDHRIGMMTAIAALLVKEGEVEL 404

Query: 423 RDPGCTRKTFPDYFDVL 439

++P +F L

Sbjct: 405 ERAEAINTSYPTFFSDL 421

>emb|CBY17222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas reinhardtii RD1]
gb|ADZ18366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas reinhardtii 6BC]
Length = 445

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 121/434 (27%), Positives = 207/434 (47%), Gaps = 27/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAK 74

ISG V +P SKS + R + A+++GT+++ N L S D M+ A LG + K+

Sbjct: 11 ISGRVSVPPSKSHTLRAIFWASVAQGTSHHNLASPDSEAMIQACEQLGAKI-LRKSTH 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

+ P + + G++GI R TA AA + + G +++ RPI

Sbjct: 70 LEITGTSQTLTP-----RDTISINAGSSGIVFRFFTA--LAAIFSEKITITGSSQLQRRPI 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

L+ L+ GA P V +G + G ++ G SQY SAL +A LA

Sbjct: 123 APLIRALENFAGATFSYEGDPYSLPFSV--LGPISSGYTEVLGD-DSQYASALAIACSLAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254

G II+ P+ +TL ++ + SD D + +G + ++ + V GD

Sbjct: 180 GPFSFTIINPK-ERPWFALTLLWLDLFAIPYVQSD--DTYSFEGNARPQA-FSYTVGGDF 235

Query: 255 SSASYFLAGAAITGG--TVTVEGCGTTSQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPR 312

S+A++ A A ++ +E +QGD + +L+ +GA +T+ E + + P

Sbjct: 236 STAAFLAAAALLSQSPHPTYLENLNIDDIQGDKEFLFLKKLGANITF-ENNTMIIFPST 294

Query: 313 EPFGRKHLKADVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372

G +++M+ D LAV+ FA + + + + KE++R++AI EL

Sbjct: 295 FSGG-----NIDMDLFIDALPILAVLCCFATSSSYLYNARGAKDKESDRIIAITQELQ 347

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431

K+GA ++ D +I P L ++ +++DHR+AMA S+AA A I D GC KT

Sbjct: 348 KMGACIQPCHDGLLIN-PSPLYGASMHSHNDHRIAMALSIAAMHASGESIIYDTGCVKEK 406

Query: 432 FPDYFDVLSTFVKN 445

FP++ +L++ N

Sbjct: 407 FPNFIQILNSLHAN 420

>ref|ZP_01963432.1| hypothetical protein RUMOB_01148 [Ruminococcus obeum ATCC 29174]
gb|EDM88242.1| hypothetical protein RUMOB_01148 [Ruminococcus obeum ATCC 29174]
Length = 425

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 120/439 (27%), Positives = 207/439 (47%), Gaps = 34/439 (7%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73

+ GT+ +PG KS+S+R ++ +L++GTT + + L D + R +G+S+E K+

Sbjct: 8 NLRGTLTVPGDKSISRVMFGLAKGTCISHFLEGADCLSTISCFRKMGISIECKRSE 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

G G + E L +GN+G R ++ + AG LDG +R RP

Sbjct: 68 ILVHGKGLHGL-----SAPEALLDVNGSGTTTRLISGIL--AGQKFISELDGDSIRTRP 120

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192

+ ++ L +GAD+ G C P+ ++G V ++S Q S +L+A

Sbjct: 121 MKRIMTPLASMGADITSKRNGCVPLLIHG---KELHAVHYDSPVASAQVKSCVLLAGMY 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKSPKNAY 249

A D + + +S + E+ ++ FG + + G+ K P

Sbjct: 178 A--DGVTSVTEPFLSRNHTEI---MLNYFGANVTSEGTASILPEPVLEGRAVKVP---- 228

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SSA+YF+A +T G+ + ++ G + + +V MGA +T S T
Sbjct: 229 --GDISAAYFIAAGLLTPGSEILLKNGVINPTRAGM--LKVCMMDGADITLLNQS-TEG 283

Query: 309 GPPREPFGFR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + R +LK V +P D +AV+A FADG T IRD +VKE++R+
Sbjct: 284 EPTADLLIRTSNLKGTVEGAVIPTLIDEIPMIAVMAAFADGTTVIRDAQELKVKESDRI 343

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAAC-AEVPVTIR 423
+ L ++GA +E D II + L+ ID++ DHR+AM+F++A + P+ I
Sbjct: 344 TVMVENLKRMGADIEGDDGMIHGGKPLHGATIDSHLDHRVAMSFVAGTICDDPMEIL 403

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
C + ++P+++ L +
Sbjct: 404 HGDCVKISYPNFYQDLYSL 422

>ref|YP_602694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10750]
sp|Q1J633.1|AROA_STRPF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF38150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS10750]
Length = 427

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 124/444 (27%), Positives = 215/444 (48%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 10 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLKGEDVLSTIQAFRN LGVRIE--EKDD 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 68 QLVIEGQGFQGLTAPCQT---LNMGNSGTSMRLIAGLL--AQQPFVSKMIGDESLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 123 DRIVYPLKQMGVEISGETDRQFPPLQLQGNHNLQPITYTLPIS-SAQVKSAILLAALQAK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 182 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SA+++L AG I G + ++ G + + EV+E MGA++ + + TS+
Sbjct: 234 SSAAFWLVLGLIIPGSELLKNGVINPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 291

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V + R LK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 292 VV-----YSR--LKGTTISGLIPRLIDELPIIALLATQAQGTTCCKDAQELRVKETDR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 344 IQVVTDTLNSMGANIKATADGMIKGPVTVLYGANTSTYGDHRIGMMAIAALLVKQGQVH 403

Query: 422 IRDPGCTRKTFFPDYFDVLSTFVK 445
+ ++P +F L +
Sbjct: 404 LDKEEAIMTSYPTFFKDLERLCHD 427

>ref|NP_664831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS315]
ref|NP_802095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes SSI-1]
sp|Q8K719.1|AROA_STRP3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM79634.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase

[Streptococcus pyogenes MGAS315]
dbj|BAC63928.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Streptococcus pyogenes SSI-1]
Length = 430

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 124/444 (27%), Positives = 215/444 (48%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 13 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLLKGEDVLSTIQAFRNLGVRIE--EKDD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 71 QLVIEQGQFQGLTAPCQT---LNMGNSGTSMRLIAGLL--AGQPFVSKMIGDESLSKRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 126 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLPITYTLPIS-SAQVKSAILLAALQAK 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 185 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 236

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA+++L AG I G + ++ G + + EV+E MGA++ + + TS+
Sbjct: 237 SSAAFWLAVGLIIPGSELLKNVGVNPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 294

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V + R LK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 295 VV-----YSR--LKGTTISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 347 IQVVTDTLNSMGANIKATADGMIIGKPTVLYGANTSTYGDHRIGMMTAIAALLVKQGVH 406

Query: 422 IRDPGCTRKTFPDYFDVLSTFVKN 445
+ ++P +F L +
Sbjct: 407 LDKEEAIMTSYPTFFKDLERLCHD 430

>ref|ZP_02037297.1| hypothetical protein BACCAP_02911 [Bacteroides capillosus ATCC 29799]
gb|EDM98985.1| hypothetical protein BACCAP_02911 [Bacteroides capillosus ATCC 29799]
Length = 411

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 127/427 (29%), Positives = 197/427 (46%), Gaps = 42/427 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V P SKS ++R+LL AAL++GT+ + N+ S+D+ + L LG +V +
Sbjct: 10 LHGSVTPPPSKSQAHRLLLAALADGTSALANVAFSQDIQATVRCLEALGA AVRQE--GD 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V G G+ KE +L G +G +R L A G + G R+ ERP
Sbjct: 68 RLAVTGLAGQ--TVSGKELPELDCGESGSLRFLIPVALAVRGGGVFTGHG--RLMERPQ 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ G + GT + G L G L G++SSQ+++ LL A PL
Sbjct: 124 EPYFDIFREKGISYEQQDGT-----LTVKGQLTSGVYTLPGNVSSQFVTGLLYALPLLP 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD EI + L S YV MT+ + +FGV E+ +R + G + P VE D
Sbjct: 178 GDSEIHLTTPLESADYVYMTMDALAQFGVAVEYDG--ERIFRVPGNQTGHPAAMTVEADW 235

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+A+++ A AA + + G S QGD ++ WT P E
Sbjct: 236 SNAAFWYA-AAYLDSKLDIRGLNYQSAQGDACI-----GRLYWT-----LAKPGE- 279

Query: 315 FGRKHLKAIDVNMNMPDVAMTLAVVALF--ADGPTAIRDVASWRVKETERMVAIRTELT 372

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+++++ PD+ LA +A T + + A R+KE++R+ + LT
Sbjct: 280 -----AEIDVSGCPDLVPPLAAMAALRGVQVTRLVNARLRIKESDRLATVTEVLT 331

Query: 373 KLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHR-MAMAFSLAACAEVPVTIRDPGCTRK 430
          LGA VEE D+ +IT + L + ++DHR MA A PVTI C RK
Sbjct: 332 ALGAEVEEHADHLVITGKDSLPGGVTVSGHNDHRIAMMAAIAATNCAAPVITITGAECVRK 391

Query: 431 TFPDYFD 437
          ++P ++D
Sbjct: 392 SYPSFWD 398

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>ref|YP_003226559.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
      subsp. mobilis NCIB 11163]
gb|ACV75975.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
      subsp. mobilis NCIMB 11163]
Length = 453

```

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 131/439 (29%), Positives = 215/439 (48%), Gaps = 38/439 (8%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD-KAA 73
          +SG V +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R++G + D K
Sbjct: 18 LSGKVHVPBGDKSISHRALMLSALAVGESFVEGLLEGEDVLATAEAMRSMGADIRKDEKGC 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
          VG G ++A L +GN+G + R L V + AT++ D + +RP
Sbjct: 78 WHIHGVGVGSLLPQNA-----LDMGNSGTSTRLLMGVVASHPITATFIGDA--SLSKRP 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
          +G + L +GA G P+ V G+ P ++ + S+Q SA+L+A
Sbjct: 131 MGRISTPLSLMGARFSAAEGNRL-PMTVTGL--YPAIPYIEYRLPVASAQVKSAILLAGLN 187

Query: 193 ALGDVEIEIIDLKIS-IPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
          G I ++I +P + + R+++ +G + E +D I G + K P++
Sbjct: 188 TPG-----ITRVIEPVPTRDHSERMLKGYGANLSVEENDGVRIISIHGEAELK-PQHII 240

Query: 250 VEGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
          V GD SSA++ +AG + G + VE G + + +L+ MG ++ + V
Sbjct: 241 VPGDPSSAFLVAVGLIVPGSDLIVENVGLNPTRSGLY--TMLKAMGGQIEYLNPR-EVG 297

Query: 309 GPPREPFGFRK--HLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          G P K HLKAIDV + +P D L + A A+G + ++ +A RVKE++R
Sbjct: 298 GEPVADLSVKYSHLKAIDVPPSIVPSMIDFPIILFIAAAMAEKGKSTLQGLAELRVKESDR 357

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPP-----EKLNVTAIDTYDDHRMAMAFSLAA-CA 416
          + + L LG S+EE D II +K + +I + DHR+AM+F++A +
Sbjct: 358 IAVMAEGLKALGVSLLEEKEDGLIIEGSAGEGLGQKGKMSIAAHLDHRIAMSAFAVAGLVS 417

Query: 417 EVPVTIRDPGCTRKTTFPDY 435
          E VTI D +FP +
Sbjct: 418 EGAVTIDRRPIMTSFPVF 436

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>ref|YP_001972835.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stenotrophomonas
      maltophilia K279a]
emb|CAQ46544.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
      [Stenotrophomonas maltophilia K279a]
Length = 435

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Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 126/444 (28%), Positives = 211/444 (47%), Gaps = 30/444 (6%)

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Query: 1 MAGAEIEVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
          M+ A+ + + + G++ +PG KS+S+R ++ AAL++GT+ ++ L ED
Sbjct: 1 MSNAQHWIARKGQPLQGSALTIPGDKSVSHRSVMFAALADGTSHIEGFLEGEDTRATARIF 60

Query: 61 RTLGLSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
          LG+ +E ++R V VG G L GNAG MR L + +
Sbjct: 61 SQLGVRIETSPSPQRIVHGVGIDGL-----QAPSAPLDCGNAGTGMRLLAGLLAGQAFDC 115

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Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSIS 179
T + D + RP+ + L Q+GA +D PP+ V+G L G + + ++
Sbjct: 116 TLIGD--ESLSGRPMRRVTGPLSQMGAKIDT-QDDGTPPLHVHGGQTLHG--IDFASPVA 170

Query: 180 S-QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S Q SA+L+A A G+ + + P + T R++ FGV E S R ++G
Sbjct: 171 SAQIKSAVLLAGLYAQGETSV-----VEPHPTRDYTERMLSAFGVDIEFSPGKAR--LRG 223

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQ+ ++ + V D SSA+++L A+I G+ + ++ G + L +MGA
Sbjct: 224 GQRLRA-TDIVVPADFSSAAFYLVAASIIPGSELRLKQVGLNPRR--TGLLHALRLMGAD 280

Query: 298 VTWTETSVTVTGPPREPFGGRKH--LKAIDVNMNKMVDVA---MTLAVVALFADGPTAIR 352
+T E G P ++ LK + +PD+ L V A A+G T +
Sbjct: 281 IT-EENPAEQGGEFVADLVVRYAPLKARIPALVPMIDFEPALFVAAAAAEGQTVVSG 339

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
A RVKE++R+ A+ T L LG V+E D + +L I+++ DHR+AMAF++
Sbjct: 340 AAELRVKESDRLAAMATGLRALGMQVDETDGATLHGGVRLGSGTIESHGDHRIAMAFAI 399

Query: 413 AA-CAEVPVTIRDPGCTRKTFPDY 435
A ++ V I D +FPD+
Sbjct: 400 AGQISDGEVRINDIANVATSFPDF 423

>ref|YP_003190309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
acetoxidans DSM 771]
gb|ACV61686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfotomaculum
acetoxidans DSM 771]
Length = 429

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 129/452 (28%), Positives = 210/452 (46%), Gaps = 43/452 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
++ + P K + G + +PG KS+S+R ++L ++ G T ++N L +D + +R LG+
Sbjct: 2 DLTVLPKKAVQGIISIPGDKSVSHRSVMLGGIARGVTEIENFLPGQDCLSTVRCMRQLGV 61

Query: 66 SVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
S+E + V GC G ED L +GN+G +R ++ + AG VL+
Sbjct: 62 SIEQISQTRLKVEGKGCGLSEPEDI-----LDVGNSGTTIRLISGLL--AGQKFFSVLN 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+ ++ L+++GA + P+ + G L G + S+Q S
Sbjct: 115 GDESIRRRPMARVIKPLQEMGARIQGRDANRLAPLAIQG-AALKGIHCH-TPVASAQVKS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+A A D E + + S + E ++++ FG R I+ G+ +
Sbjct: 173 AVLLAGLYA--DGETAVTEPSQSRDHTE---KMLKSGAHIVTEGLTTR--IRPGEL--T 223

Query: 245 PKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ V GD SSA++FL AGA I +TV+ G + + +VLE MGA + +
Sbjct: 224 GRKVIVPGDISAFAFLVAGAVIPDARITVKNVGLNPTRTGI--LDVLEEMGADIALSNV 281

Query: 304 -----SVTVTGPPREPFGGRKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIR 351
+TVTG LK I + + +M D LAV A A G T I+
Sbjct: 282 YENSIGELIGDITVTG-----SSLKGIVIGGALIPRMVDEIPVLAVAAAVASGQTIIK 333

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
D A +VKE+ R+ A+ E + G ++E D II K ++Y DHR+AMA +
Sbjct: 334 DAAELVKYKESNRLQAVAGEFARFGVDLQETRDGLIINGGRKFGGAVTESYHDHRIAMACA 393

Query: 412 LAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
L A +R C +FP + VL +
Sbjct: 394 LMGLVASGKTVVRGAECIDISFSPFQTVLES 425

>ref|YP_046840.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Acinetobacter sp. ADP1]
emb|CAG69018.1| bifunctional protein [Includes: putative prephenate or
cyclohexadienyl dehydrogenase; 3-phosphoshikimate

1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (AroA) [Acinetobacter sp. ADP1]
Length = 748

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 126/419 (30%), Positives = 200/419 (47%), Gaps = 40/419 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KAFKGFKTIPGDKSVSHRSIMFGAIAEGTTHVTGFLEGEDALATLQAFRDMGVSIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K PV L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHVGVMNGLKAPVG-----ALYMGNSGTSMLRLSGMLSQAQKFD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV ++G L G + L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGEKGTTPVVISGSQLKGIQYDLPMA-SAQVKSIGILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ ++GG K +
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE---GNKITLQGGGKLVG-THI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT V +E G + V E+L+ MGA + E
Sbjct: 535 QVPSDISAFAFMVGAAITENADVLEAVGINPTRTGV--IEILKQMGADIA-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D +L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIHIKSGRTLKGIIHIPEDQVPLAIDEFPSLFIAAACAEGQTVLTGAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLA 413
+R+ + L +G D II K N I ++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTSDGIIIEGKGKSGDWSVPFNGGQIQSHHDHRIAMSFSA 710

>ref|ZP_05581100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
D6]
gb|EEU82071.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
D6]
gb|EFT39193.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX2137]
Length = 428

Score = 132 bits (332), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 204/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAIISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ V G ++ A+ ++ GN+G +R + + AG L G ++
Sbjct: 69 TT---ITVEGQGFAGLKKARNTIDV--GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNVRMLPLNQMGAECQGVQQTTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGFPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKMGGSVTILNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIALLATQATGTTIIRDAAELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTTLGADITPTDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|ZP_08094921.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planococcus
donghaensis MPALU2]
gb|EGA89644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Planococcus
donghaensis MPALU2]
Length = 427

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 119/431 (27%), Positives = 212/431 (49%), Gaps = 24/431 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++++PG KS+S+R ++ +++ GTT V+ L +D + R LG+ ++
Sbjct: 12 LKGSIQVPGDKSISHRAIMFGSIATGTTTVEGFLMGDDCLSTISCFRKLGVKIDV---TD 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G+ ++ E L GN+G R + + + ++ V+ G + +RP+
Sbjct: 69 DLVTIQSEGEASWKEPSE--VLDGTGSGTTTTRMLGLLASTSFHS--VMAGDESIARPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L+++GAD+ P+ V G L L + S+Q SA+L+AA A
Sbjct: 125 KRIINPLREMGADIRGRQDQFTPLAVQGTQ-LKAIDYTL PVA-SAQVKSAILLAALKAD 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G I + + S + E+ ++E FG + ++GGQK + + V GD
Sbjct: 183 GQTVIH--EPIASRDHTEI---MLEHFGATVNRENHV--IKLEGGQKL-TAAHVQVPGDI 234

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLOQDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++ + A IT + VT+ G + + +V+E MGA + E
Sbjct: 235 SSAAFMIGAALITEDSKVTLTNVGINPRTGTI--LDVVEKMGAVIEIEEKETAGERSADL 292

Query: 314 PFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
LK +++ + +P D +A++A A+G T I+D RVKET+R+ A+ TE
Sbjct: 293 TISSSTLKGTEISGDLIPRLIDEIPLIALIATQAEGTTVIKDAEELRVKETDRIA AVVTE 352

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV-PVTIRDPGCTR 429
L+K+GA++E D II P L+ + +Y DHR+ M ++AA V I DP C
Sbjct: 353 LSKMGANIEATEDGMIIHGPTVLSGAEMTSYGDHRLGMMAVAALVASDEVAIDDPECIS 412

Query: 430 KTFPDYFDVLS 440
++P++F+ L+
Sbjct: 413 ISYPNFFEQLN 423

>ref|ZP_03925314.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
coleocanis DSM 15436]
gb|EEH63833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
coleocanis DSM 15436]
Length = 462

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 131/470 (27%), Positives = 206/470 (43%), Gaps = 57/470 (12%)

Query: 1 MAGAEEIVL---QPIK--EISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHY 55
M+ A + VL P++ ++G +++PGSKS +NR LLLAA + + L S D
Sbjct: 1 MSSASQQVLWWPAPLRVGLPLNGVLEVPGSKSQTNRFLLLAATGQSKCRLRGCLWSRDTLL 60

Query: 56 MLGALRTLGLS-----VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS 107
M L LG S +E R + +E V + G AG MR
Sbjct: 61 MRAGLEKLGASFLALPDGTIEVSPITTRVL-----REPVTIECLAGTVMRF 107

Query: 108 LTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNG-IGG 166
L A T+ D + RP+ + LK+ GA V F G + P V G +

Sbjct: 108 LPLLAVAFNPITFTADV--QANARPMQPIFEVLKRFGAKVT-FSGGESFPFTVTGPLTT 164

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPL---ALGDVEIEIIDKLISIPYVEMTLRLMERFGV 223
LP ++++ S+SSQ+ SA+L+A P + G IE + S P+V MT+ ++ FG

Sbjct: 165 LPE-RIEVDCLSSQFFSAVLLALPFLAESPGTFFIETVAS-PSHPHVAMTVATLKTFGH 222

Query: 224 KAEHSDSWDRFYIKGGQKYKSPKN-----AYVEGDASSASYFLAGAAITGGTVTVEGC 276
+ + +K S VE D SSA+ F+A A GG++ +

Sbjct: 223 EVSLVSDSELKSLKATATITSQPTFNQRLPELIVEPDLSSAAPFIAAVAFAGGSLQLPAV 282

Query: 277 GTTSLQGDVKFAEVLEMMG---AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPD 332
TS Q ++F E++ +G +K T+ F L ++N+ + +

Sbjct: 283 PKTSTQVGIRFLEIVSELGLLTVSKTEDTQNCYYRVASLSTDFSTSPL---EMNLTALGE 339

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-- 390
+ L +A T + R ET+R+ A+ EL KLG E GPD + PP

Sbjct: 340 LTPILVALATLLPHETFTTGIGHLRGHETDRLTALEKELGKLIECETGPDCLRHHPPAA 399

Query: 391 -----EKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDY 435
E+ ++TY+DHR+AM +L + PV + + G T KT P++

Sbjct: 400 PAVTRERSQPVKLNLYNDHRLAMFAALMGLRQ-PVLVENIGTTCKTMPNF 448

>ref|YP_002315470.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anoxybacillus
flavithermus WK1]
gb|ACJ33485.1| 5-enolpyruvylshikimate-3-phosphate synthase [Anoxybacillus
flavithermus WK1]
Length = 428

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 127/443 (28%), Positives = 210/443 (47%), Gaps = 41/443 (9%)

Query: 12 IKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I + G + +PG KS+S+R ++ AL+ GTT + N L ED + R +G+ + +

Sbjct: 7 IHALRGEIAVPGDKSISHRAVMFGALANGTTRITNFLTGEDCLSTIDCFRKMGVVIT--Q 64

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+V G G VE KE + +GN+G R L + A +A + D +

Sbjct: 65 QGNEVIVEGKG---VEGLKEPTHILNVGNSGTTTTRLLLGILAACPFHACLIGDD--SIA 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK----LSGSISSQYLSAL 186
+RP+ + LKQ+GA +D P+ + G G+++ S S+Q SA+

Sbjct: 119 KRPMDRVTKPLKQMGAHIDGREDGRYPLAIRG-----GQLQPITYHSPVASAQVKSAT 172

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSP 245
L+A A G + I+ S + E R++ FG D + G++

Sbjct: 173 LLAGLHAEGTTTV--IEPHQSRDHTE---RMLRAFGADV---VDGLSVSVAGRQTLQA 223

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA++FL AGA + +T+ G + + +VL+ MGA ++

Sbjct: 224 IDIEVPGDISSAAFFLVAGAIVPNSEITLTHVGINPRTGI--IDVLKNMGANISIENVR 281

Query: 305 VVTGPPREPFGRKH-LKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
+ P + R LKA + + +P + + ++AL A +G T I D + +VKE

Sbjct: 282 HEESEPVAIDTVRTSTLKATHIGGDIIPRLIDEIPIIALLATQAEGTTIITDASELKVKE 341

Query: 361 TERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMAFSLAAC-A 416
T+R+ + +EL KLGA +E D II TP N T +D+Y DHR+ M ++AA

Sbjct: 342 TDRIATVVSELRLKLGADIEATEDGMIHKGTPLYAEN-TTVDSYGDHRIGMMLAIAASIT 400

Query: 417 EVPVTIRDPGCTRKTFFPDYFDVL 439
+ VT++ P ++P +FD L

Sbjct: 401 KGSVTLQHPEAIAVSYPTFFDHL 423

>ref|ZP_03167189.1| hypothetical protein RUMLAC_00856 [Ruminococcus lactaris ATCC
29176]
gb|EDY33356.1| hypothetical protein RUMLAC_00856 [Ruminococcus lactaris ATCC
29176]
Length = 427

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 129/449 (28%), Positives = 205/449 (45%), Gaps = 45/449 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V +PG KS+S+R ++ +++ GTT + N L+ D + TLG+ +E D +
Sbjct: 4 LKGKVTIPGDKSISHRCVMFGSIANGTTEIHNFLSGADCLATIRCFSTLGIKIETDLSQS 63

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ +V G G +A + L +GN+G R ++ + AG L G + RP+
Sbjct: 64 KVIVHGKG--LHGLNAPSSI-LDVGNSGTTTTRLISGIL--AGQPFNSELSGDESLNSRPM 118

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L +GA++ L C P+ + L G S S+Q S LL+A A
Sbjct: 119 KRIIIEPLTSMGANIASVLQNGCAPLYITP-AQLHGIHYD-SPVASAQVKSCLLLAGLYA- 175

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY----- 249
D E + + +S + E+ LR FG A+ +++ K + + Y
Sbjct: 176 -DGETSVTEPLSRNHTELMLR---EFG--ADIRSTYEIGSTKATASIRPCTDLYGQKIT 229

Query: 250 VEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
V GD SSA+YF+A G + + +E G + + +V E MG +T
Sbjct: 230 VPGDISAAYFIAAGLIVPDSEILIENTGINPTRAGI--LKVCEDMGGDITLLN----- 281

Query: 309 GPPREPFGKHLKAIDVNMNKM-----DVAMTL-----AVVALFADGPTAIRDVAS 355
R G K + I V +K+ D+ TL AV+A A+G T I+D A
Sbjct: 282 --ERTEGGEK-IADILVRTSKLHGTTIEGDIIPTLIDEIPVIAVMAVAEGTTVIKDAAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA- 414
+VKET+R+ + L +GA V D II L+ T+I T DHR+AMAFS+AA
Sbjct: 339 LKVKETDRIETVTDNLKAMGADVTPPTDDGMIHGGNPLHGTSIHTLLDHRMAMAFSIAAL 398

Query: 415 CAEVPVTIRDPGCTRKTTFPDYFDVLSTFV 443
AE I D C ++P ++D +
Sbjct: 399 VAEGNTKILDSKCVDVSYPTFYDTFEALL 427

>ref|YP_004024475.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
kronotskyensis 2002]
gb|ADQ46656.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
kronotskyensis 2002]
Length = 433

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 127/448 (28%), Positives = 213/448 (47%), Gaps = 41/448 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ V +P KS+S+R +++ +L+ G T ++N L S+D + + LG +E
Sbjct: 9 RKINSNVIVPPDKSISHRSIMIGSLANGVTEIENFLFSDDCLATINCKNLGTDIEIRN- 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +V G G F + K+ L N+G R L ++ + +L G +++R
Sbjct: 68 -DKIIVRGNG--FALSAPKQ--ILDCQNSGTTTLLLLGILSTQEFES--ILTGDSSELKRR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + V L Q+GA+ + D P++V G L + L S+Q SAL+ A+
Sbjct: 121 PMKRVTVPLSQMGAEFEFLEKEDFLPIKVGSKKLKPIEYTLPIP-SAQVKSALIFASLK 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G I+ K S + E+ L+ + SW++ + ++ S
Sbjct: 180 AEGKSVIKESPK--SRDHTELMLKHA-----GANIKSWEKDGVTVEILPSQISSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
+ D SSA++F+ A I G +V +E C + + +VL+ MGA++ + V
Sbjct: 232 IPSDISAFAFFIVLALICEGSSVVIENCILNPTRTGI--IDVLKQMGAEIKIED---VE 285

Query: 309 GPPREPFG-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +L+ + V N +P D LAV A FA+G T I + RVKE
Sbjct: 286 NRNGELVGKIVARSSNLRGVKEKNIPRIIDEIPILAVAAFAEGKTTIDHASLVRVKE 345

Query: 361 TERMVAIRTELTKLGA---SVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACA- 416
++R+ L GA +E G + II EKL +++Y DHR+AMA S+ ACA

Sbjct: 346 SDRIKTTVEMLKSFGEACYELENGLE--IIGSREKLKSAVVNSYKDHRIAMAASIMACAV 403

Query: 417 EVPVTIIRDPGCTRKTFPDYFDVLSTFVK 444
E TI D C +FP+++D+L + K

Sbjct: 404 EGESTILDADCVSISFPNFYDILFSLTK 431

>ref|YP_342240.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus oceanus
ATCC 19707]
ref|ZP_05048972.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus oceanus
AFC27]
sp|Q3JEN6.1|AROANITOC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABA56710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus oceanus
ATCC 19707]
gb|EDZ65848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrosococcus oceanus
AFC27]
Length = 444

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 131/457 (28%), Positives = 219/457 (47%), Gaps = 52/457 (11%)

Query: 9 LQPIKEIS-----GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDV 53
+QPI+E+S G +++PG KS+S+R ++L AL+EG T + L ED
Sbjct: 1 MQPIEEVSQDTMAFVVAPGGALRGRLRVPGDKSISHRAIILGALAEGITQITGFLEGEDT 60

Query: 54 HYMLGALRTLGLSVEADKAAKRAV--VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA 111
L A R LG+S+E + + + V G + P E L+LGN+G ++R L
Sbjct: 61 LATLQAFRDGLVSIIEGPEGGRVKIHGVSLLQGLRAP-----EKPLYLGNSTSVRLLAGL 114

Query: 112 VTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGK 171
AG + +L G + RP+ + L ++GA ++ PP+ ++G L G +
Sbjct: 115 F--AGQSFVDVILRGDESLRRRPMRRVCDPLARMGAFIET-TAQGTPPLHIHGGQSLYGIE 171

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
+ + S+Q S+LL+A A G + + P + + R++ FG E +
Sbjct: 172 YAMPMA-SAQVKSSLLLAGLYASGRTCV-----VEPAPTRDHSERMLAGFGYPVEREGA- 224

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEV 290
+ I+GG + D SSA++F+ GAAI G+ + +E G + ++
Sbjct: 225 -KVCIQGGGTLHG-TVVEIPADISSAAFFMVGAAIGKGSDDILLEHVGINPTR--TGIIDI 280

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAV---VALF---- 343
L MGA++ ET V V G EP ++A ++ +P+ + LA+ ALF
Sbjct: 281 LRRMGAEIEIRETG-VGG---EPVAAIRVRASRLHGINIPEDLVPLAIDEFPALFIAAA 336

Query: 344 -ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
A+G T + RVKE++R+ + L LG S + D II E L + ++
Sbjct: 337 CAEGETVLGAGELRVKESDRIQVMADGLQALGISAQPTADGIIIQGGE-LQGGEVHSHG 395

Query: 403 DHRMAMAFSLAA-CAEVPVTIIRDPGCTRKTFPDYFDV 438
DHR AMAF++A+ A+ P+ IRD +FP + ++
Sbjct: 396 DHRMAMAFSLAA-CAEVPVTIIRDPGCTRKTFPDYFDV 438

>ref|YP_444812.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinibacter ruber
DSM 13855]
ref|YP_003570723.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinibacter ruber
M8]
sp|Q2S4R9.1|AROASALRD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABC44832.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinibacter ruber
DSM 13855]
emb|CBH23771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salinibacter ruber
M8]
Length = 430

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 136/442 (30%), Positives = 208/442 (47%), Gaps = 43/442 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV LP KS+S+R LL+AL G + V N +S D L +RTLG +EA + +
Sbjct: 11 LRGTVSLPADKSIHSRSALLSALGTGRSRVYNFPDSADPQSTLDCVRTLG--IEAGRND 68

Query: 75 RAVVV---GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + G GG P + L GN+G MR L+ + AG VL G +++
Sbjct: 69 GVLAIHGRGLGGLHPPSEP-----LDCGNSGTTMRLLSGMM--AGQEFSGVLTGDESLQQ 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + L+ +GA +D G +R GL + +L + S+Q S +L+A
Sbjct: 122 RPMERIADPLQAMGARIDLRSGHAPIRIRPQRSDGLRPLEYRLPVA-SAQVKSCVLLAGL 180

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-V 250
A G + + + P + T R++ G++ + ++ + + P + V
Sbjct: 181 YASGRTVV-----IETTPSRDHTERM---GLEVQEVGGERHIIVE--EDHTVPAVDWSV 230

Query: 251 EGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDKFAEVLEMMGAKVTWTETSVTVTG 309
GD S A++FL AG + + ++ G + +VL+ MGA +T V +
Sbjct: 231 PGDFSGAAFFLVAGTLVPDSELHLDVGLNPSR--TALLDVLDMGADITVENERVQGS- 287

Query: 310 PPREFPG-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
EP G L ID+ +P D +AV A A+G T IRD RVKET
Sbjct: 288 ---EPVGDITVRSASLSGIDIGRRLIPNLIDEIPVIAVAAACAEGRTEIRDAEELRVKET 344

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEV 418
+R+ A+ L LGA V+E D II P L A+ ++DDHR+AMA +A A
Sbjct: 345 DRLHAMAQNLEALGAKVQEREDGLIIDGNGPNLLG-AAVTSHDDHRIAMAMGVAGLVAHG 403

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
TI D C R +FP ++D LS
Sbjct: 404 TTTISDAECARVSFPFGWDELS 425

>ref|NP_779554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Temecula1]
sp|Q87BU2.1|AROAXYLFT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAO29203.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Temecula1]
Length = 454

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 131/432 (30%), Positives = 205/432 (47%), Gaps = 35/432 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AAL++GT+ +D L +ED L LG+ +E +
Sbjct: 29 LHGVLSIPGDKSISHRAVMFAALADGTSRIDGFLEAEDTRSTAAILARLGVRIETPSFTQ 88

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G ++ L GNAG MR L + A ++ VL G + +RP
Sbjct: 89 RIVHGVGVLDGL-----QASDIALDCGNAGTGMRLLAGLLVAQPFFDS--VLVGDAASLSKRP 141

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+R+ G G L G +S S+Q SA+L+A A
Sbjct: 142 MRRVTDPPLSQMGARIDTS-DDGTPPLRIYG-QLLRGIDFISPVASAIKSAVLLAGLYA 199

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + P + T R++ FGV + S R ++GGQ+ + N + D
Sbjct: 200 RNETVREPH-----PTRDYTERMLTAFGVDDIDVSTGCVR--LRGGQRLCA-TNITIPAD 251

Query: 254 ASSASYFL-AGAAITGGTVTEGCGTTSLQGDKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + I G +T+ G + + VL +MGA + E++ G
Sbjct: 252 FSAAFYLVAAASVIPGSDITLRAVGLNPRR--IGLLTVLRLMGADI--VESNRHEQGG-- 305

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP ++ + ++P D L V A A+G T + A RVKE++R+
Sbjct: 306 EPVADLRVRYASLQGTTRVPEDLVPMIDFPAFVAAAAAEGQTVVSGAAELRVKESDRL 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP-VTIR 423

A+ T L LG V+E D I + I+++ DHR+AMAFS+A V V I
Sbjct: 366 AAMVTGLRVLGVQVDETADGATIH-GGPIGHGTINSHGDHRIAMAFSIAQQLSVSTVRIE 424

Query: 424 DPGCTRKTFFPDY 435
D +FPDY

Sbjct: 425 DVANVATSFPDY 436

>ref|ZP_04173803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1273]
ref|ZP_04179595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1272]
gb|EEL88709.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1272]
gb|EEL94510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH1273]
Length = 424

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 120/442 (27%), Positives = 211/442 (47%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EGTT V N L ED + + LG+ +E +
Sbjct: 10 LNKIVVPBGDKSISHRSVMFGAIAEGTTKVSNFLGEGDCLSTIACFQKLGVKIEQ---SG 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPI 134
V + G +++ KE L +GN+G +R + + +T + D + RP+
Sbjct: 67 NDVKIYKGKGLHNLQEPKE--VLDVGNSGTTIRLMLGILANTPFQSTIIGD--TSIGNRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVK----LSGSISSQYLSALLMAA 190
+ L + A +D P+ + G GKVK S S+Q SA+L+A
Sbjct: 123 KRVTEPLSMNAQIDGRENGQYTPLSIRG-----GKVKGMHYHSPVASAQVKSALLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
G+ + + S + E R++ FG + ++ ++GGQ+ K + V
Sbjct: 177 --LQEGVTTTVEPMQSRDHE---RMLRAFGCTVDVNERT--VSLQGGQQLKGA-DIEV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + + +E G + + +VL MGA ++ +
Sbjct: 229 PGDVSSAAFFLVAGAIIVQNSKLVLENVGLNPTRTGI--LDVLTGMGALISID---NMRN 282

Query: 310 PPREFPG-----RKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
EP G LK I++ + +P + + V+AL A +G T I+D +VKET
Sbjct: 283 EEFEPGCDITIETSKLKGIEIGGSLIPRLIDEIPVIALLATQAEGITVIKDAEELKVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPV 420
R+ + EL KLGA +E PD II + L ++++ DHR+ M ++A+C + V
Sbjct: 343 NRIDTVVDELKGLGAKIEATPDGMIYIGKQNLKGNVTNSHGDHRIGMMLAIASCIIDGEV 402

Query: 421 TIRDPGCTRKTFFPDYFDVLSTF 442
I + ++P++F+ L+

Sbjct: 403 KIENSDAVAVSYPNFFEQLAAL 424

>ref|ZP_00366200.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus
pyogenes M49 591]
ref|YP_002286064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes NZ131]
sp|B5XM07.1|ARO_A_STRPZ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI61369.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes NZ131]
Length = 427

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 213/435 (48%), Gaps = 39/435 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 10 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLLKGEDVLSTIQAFRLGVRIE--EKDD 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G + + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 68 QLVIEGQGFQGLTAPCQT---LNMGNSTSMRLIAGLL--AGQPFSVKMIGDESLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 123 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLQPITYTLPIS-SAQVKSAILLAALQAK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 182 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA+++L AG I G + + + G + + EV+E MGA++ + + TS+
Sbjct: 234 SSAAFWLKQGLIIPGSELLKKNVGVNPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 291

Query: 307 VTGPPREPFGFRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V + R LK ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 292 VV-----YSR--LKGTIISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 343

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 344 IQVVTDTLNSMGANIKATADGMIKGTPLVYGANTSTYGDHRIGMMTAIAALLVKQGQVH 403

Query: 422 IRDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 404 LDKEEAIMTSYPTFF 418

>ref|ZP_01471841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
RS9916]
gb|EAU73555.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp.
RS9916]
Length = 417

Score = 132 bits (331), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 134/437 (30%), Positives = 206/437 (47%), Gaps = 37/437 (8%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PG KS+S+R LL A++EGTT ++ LL +ED LR +G ++ + K V G
Sbjct: 1 MPGDKSISHRALLFGAIAEGTTTIEGLLPAEDPISTAACLAMGTTSPIEDGKLITVEG 60

Query: 81 CGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G ++ +E ++ GN+G MR + + G +VL G +R RP+ +
Sbjct: 61 VG---LDGLQEPGEVLDCGNSGTTMRLMLGLLAGRNGR-HFVLSGDASLRRRPMQRVGQ 115

Query: 140 GLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALLMAAPLA 193
L +GADV G + P+ V G KL G++ S+Q SALL+AA A
Sbjct: 116 PLALMGADVGRNGGNLAPLAVQG-----RKLRAVVGTPVASAQVKSALLLAALTA 167

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNAYVEG 252
D +I+ S + E R+++ FG + R +K G ++ V G
Sbjct: 168 --DGPTTVIEPAHSRDHSE---RMLKAFGADLDVGEMGRHVSVPKASLTG-QHVVPVG 221

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L AGA + G +T+E G + V EVLE MGA++ V G P
Sbjct: 222 DISSAAFVLVAGALVPGADLTIENVGLNPTRTG--LEVLEQMGAIEVLNRR-DVAGEP 278

Query: 312 REPFGRKH--LKADVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
H LK + MP D L+V A F +G + I RVKET+R+
Sbjct: 279 VGDLRVTHGPLKPFNFGEVMPRLVDEVPILSVAACFCEGESRITGAEELRVKETDRLAV 338

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDP 425
+ +L +GA +EE PD I L +D+ DHR+AM+ ++AA AE T+
Sbjct: 339 MARQLKAMGADIEHPDGLTIRGGRPLKGAVLDSETDHRVAMSLAIAAMMAEGDSTLARS 398

Query: 426 GCTRKTFPDYFDVLSTF 442
++P ++D L+
Sbjct: 399 EAAAVSYPTFWDLLTRL 415

>gb|ADI33303.1| 5-enolpyruvylshikimate 3-phosphate synthase [Pseudomonas fluorescens]
Length = 444

Score = 132 bits (331), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 215/441 (48%), Gaps = 41/441 (9%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
+P +SG++++PG KS+S+R ++L +L+ G T V+ L ED L A R +G+ +E
Sbjct: 15 EPGGRLSGSIRVPGDKSISHRSIMLGSLAGGVTEVEGFLEGEDALATLQAFRDMGVVIEG 74

Query: 70 DKAACKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P ++LGN+G +MR L+ + A ++ VL G
Sbjct: 75 PHHGRVTIHVGVLHGLKPAPG-----PIYLGNSGTSMRLLSGLLAAQSFDS--VLTGDAF 127

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S LL
Sbjct: 128 LSKRPMRSRVARPLREMGAVIET--GPEGRPPLTIRGGQSLKGLAYAMPMA-SAQVKSCLL 184

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G + P + T R++ FG V E + + ++ G +
Sbjct: 185 LAGLYAEGKTAVT-----EPAPTRDHTERMLRGFGYPVAVEGATAS---VESGHALTA- 234

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SS+++FL A+I G+ + +E G + V ++L +MGA +T E
Sbjct: 235 AHIEVPGDISSAFFLVAASIAEGSELLLEHVGVNPNTRTG--IDILRLMGADITL-ENQ 291

Query: 305 VTVTGPPEPFGKHLKKAIDVNMNKMPPDVAMTLA-----VVALFADGPTAIRDVASW 356
V G EP ++A+ + ++P+ + LA V A A+G T +R +
Sbjct: 292 REVGG--EPVADLRVRAVALKGIEIPEALVPLAIDEFPVLFVAAACAEGRTVLRGASEL 348

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC- 415
RVKE++R+ + L LG E PD II + + + DHR+AMAFS+A+
Sbjct: 349 RVKESDRIQVMADGLLALGVKCEPTPDGIIIE-GGPMGGGEVHAHGDHRIAMAFSVASLR 407

Query: 416 AEVPVTIRDPGCTRKTFFPDYF 436
A P+ IRD +FP++
Sbjct: 408 AAAPIRIRDCANVATSFNPNFL 428

>ref|ZP_06306238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Raphidiopsis brookii D9]
gb|EFA71683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Raphidiopsis brookii D9]
Length = 454

Score = 132 bits (331), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 204/437 (46%), Gaps = 33/437 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+L A++EG T + LL ED R+LG + +D +
Sbjct: 29 LQGRIQVPGDKSISHRALMLGAIAEGETEIQGLLLGEDPRSTASCFRSLGAEI-SDLNTQ 87

Query: 75 RAVVVGCG-GKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G G F +E V L GN+G +R L + A+ + + G +R R
Sbjct: 88 LVRVQGIGLGNF-----QEPVDVLNAGNSGTTIR-LMLGLLASHPGIFFAVTGDDSLRSR 141

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L+Q+ A + G P+ + G P + I+S + + ++ A L
Sbjct: 142 PMSRVVQLQQAQIWGRKGNLAPLAIQGSQSLKP---IHYHSPIASAQVKSCILLAGL 198

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ + + + +S + E R+++ FG + I G K K V G
Sbjct: 199 NT-EGKTTVTPEALSRDHSE---RMLKAFGADLTIDPGSNSVTITGNAKLYGQK-VIVPG 253

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 311
D SSA+++L AG+ + G + VE G + + E L +MGA + E V G
Sbjct: 254 DISSAAFVWLVAGSIVPGSDLVVENGVNPNTRTGI--LEALTVMGANIQL-ENQREVAG-- 308

Query: 312 REPFGRKHLKKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASVRVKETER 363

EP H+++ + + ++ D L+V A FA G T IRD A RVKE++R
Sbjct: 309 -EPVADLHVRSSQLQSCSTIAGDIIPRLIDEIPILSVAASFAKGTTIIRDAAELRVKESDR 367

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTI 422
+ + +L K+GA V E D IT L T +D+Y DHR+ M+ ++AA + TI
Sbjct: 368 ITVMAQQLNKMGARVTELAGMEITGGASLVGTQVDSYADHRIGMSLAIAALNAIGTTTI 427

Query: 423 RDPGCTRKTFPDYFDVL 439
++P++ L
Sbjct: 428 HRAEAAAISYPNFTSTL 444

>ref|YP_001830126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
M23]
gb|ACB92852.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
M23]
gb|ADN62199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
subsp. fastidiosa GB514]
Length = 442

Score = 132 bits (331), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 131/432 (30%), Positives = 205/432 (47%), Gaps = 35/432 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AAL++GT+ +D L +ED L LG+ +E +
Sbjct: 17 LHGVLSIPGDKSISHRAVMFAALADGTSRIDGFLEAEDTRSTAAILARLGVRIETPSFTQ 76

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G ++ L GNAG MR L + A ++ VL G + +RP
Sbjct: 77 RIVHGVGVVDGL-----QASDIALDCGNAGTGMRLLAGLLVAQPFDS--VLVDASLSKRP 129

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+R+ G G L G +S S+Q SA+L+A A
Sbjct: 130 MRRVTDPLSQMGARIDTS-DDGTPPLRIYG-QQLLRGIDFISPVASAQIKSAVLLAGLYA 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + P + T R++ FGV + S R ++GGQ+ + N + D
Sbjct: 188 RNETVVRREP-----PTRDYTERMLTAFGVDIDVSTGCVR--LRGGQRLCA-TNITIPAD 239

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + I G +T+ G + + VL +MGA + E++ G
Sbjct: 240 FSSAAFYLVAAASVIPGSDITLRAVGLNPR--IGLLTVLRLMGADI--VESNRHEQGG-- 293

Query: 313 EPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP ++ + ++P D L V A A+G T + A RVKE++R+
Sbjct: 294 EPVADLVRVYASLQGTRVPEDLVPMIDFEPALFVAAAAAEGQTVVSGAAELRVKESDRL 353

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-VTIR 423
A+ T L LG V+E D I + I+++ DHR+AMAFS+A V V I
Sbjct: 354 AAMVTGLRVLGVQVDETADGATIH-GGPIGHGTINSHGDHRIAMAFSIAGQLSVSTVRIE 412

Query: 424 DPGCTRKTFPDY 435
D +FPDY
Sbjct: 413 DVANVATSFPDY 424

>ref|YP_163531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
subsp. mobilis ZM4]
sp|Q5NLJ0.1|AROAZYMMO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAV90420.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
subsp. mobilis ZM4]
Length = 453

Score = 132 bits (331), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 131/439 (29%), Positives = 215/439 (48%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD-KAA 73
+SG V +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R++G + D K
Sbjct: 18 LSGKVHVPGDKSISHRALMLSALAVGESFVEGLLEGEDVLATAEAMRSMGADIRKDEKGC 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
VG G ++A L +GN+G + R L V + AT++ D + +RP
Sbjct: 78 WHIHGVGVGSLLPQNA-----LDMGNSGTSTRLLMGVVASHPITATFIGDA--SLSKRP 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L +GA G P+ V G+ P ++ + S+Q SA+L+A
Sbjct: 131 MGRISTPLSLMGARFSAAGNRL-PMTVTGL--YPAPIEYRLPVASAQVKSAILLAGLN 187

Query: 193 ALGDVEIEIIDKLIS-IPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G I ++I +P + + R+++ +G + E +D I G + K P++
Sbjct: 188 TPG-----ITRVIEPVPRDHSERMLKGYGANLSVEENDGVRIISIHGEALK-PQHII 240

Query: 250 VEGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++ +AG + G + VE G + + +L+ MG ++ + V
Sbjct: 241 VPGDPSSAAFLVVAGLIVPGSDLIVENGLNPTRSGLY--TMLKAMGGQIEYLNPR-EVG 297

Query: 309 GPPREPFGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P K HLKAIDV +P D L + A A+G + ++ +A RVKE++R
Sbjct: 298 GEPVADLSVKYSHLKAIDVPPSIVPSMIDFPILFIAAAMAEGKSTLQGLAELRVKESDR 357

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPP-----EKLNVTAIDTYDDHRMAMAFSLAA-CA 416
+ + L LG S+EE D II +K + +I + DHR+AM+F++A +
Sbjct: 358 IAVMAEGLKALGVSLKEEDGLIIEGSAGEGLGQKGMVSIAAHLDHRIAMSFVAVAGLVS 417

Query: 417 EVPVTIRDPGCTRKTFPDY 435
E VTI D +FP +
Sbjct: 418 EGGVTIDRRPIMTSFPVF 436

>ref|ZP_06065709.1| conserved hypothetical protein [Acinetobacter junii SH205]
gb|EEY93540.1| conserved hypothetical protein [Acinetobacter junii SH205]
Length = 749

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 208/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KTFGTGKFTVPKSKSVSHRSIMFGAIAEGTTHVTGTFLEGEDALATLQAFRDMGVSIIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ ++A ++ V+ G +
Sbjct: 374 GEVTIHGVGMQGLKAPAG-----ALYMGNSGTSMRLLSGMLSQAQKFD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV + G L G L + S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGKEGTPPV SITGSQVLKGIDYDLMA-SAQVKS GILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E ++ + GG K +
Sbjct: 485 LWAEGETSVTEPE-----PTRDHTERMLRAFGYDVKTE----GNKISLVGGGKLVG-TDI 534

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT G V +E G + V E+L+ MGA +T E
Sbjct: 535 QVPSDISAFAFFMVGAAITEGADVLEAVGINPTRTGV--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPFP---GRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L + A A+G T + A RVKE+
Sbjct: 592 GGEPIADIIHKSRTLKGIHMPEDQVPLAIDFPPALFIAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K N I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLKIMGIDCTPTEDGIIIEGKGKSGDWSAIFNGGEIESHHDHRIAMSFISIAG 711

Query: 415 CAEV-PVTIRDPGCTRKTFPDYFDV 438
+TI +FP + ++
Sbjct: 712 LRTAGAITIHGTETVATSFPTFTEL 736

>ref|ZP_07635012.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcaceae]

bacterium D16]
Length = 394

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 117/425 (27%), Positives = 191/425 (44%), Gaps = 57/425 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V P SKS ++R +L L++G + NL S+D+ V A K+ +
Sbjct: 10 LKGAVTPPSSKSQTHRAVLALMLAQGEGKLSNLAVSQDIQATQDC-----VAALKSGQ 62

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A G P+ D G +G +R L A G + G R+ ERP
Sbjct: 63 PAQADG---LPLLDG-----GESGSTLRFLIPVALAVRGGGHFT--GRGRLMERPQ 108

Query: 135 GDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
G + ++ G + + V G L G L G++SSQ+++ LL A PL
Sbjct: 109 GPYIRLFEEKG---ILWNQEGACLTG--AGQLEPGAYALPGNVSSQFITGLLYALPLLP 162

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
GD I + L S YV+MTL ++ RF +K E + D F + G Q Y++ ++ +E D
Sbjct: 163 GDSRIVLTTPLESRGYVDMTLDMLRRFDIKVEEQE--DGFLVPGNQTYQA-RDLTLEADW 219

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S A+++ A A G V ++G S+QGD + + +
Sbjct: 220 SGAAFWYA-ANFLGAQVDIQLNPDSVQGDQIGTLYWKLARPGN----- 263

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+D++++ PD+A LAV+A G T + R+KE++R+ I L L
Sbjct: 264 -----VDIDLSQCPDLAPLAVMAAVRKGTTFRVNAGRLRIKESDRLETIARTLNAL 315

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRM--AMAFSLAACAEVPTIIRDPGCTRKTF 432
GA + G D + + L +D +DHR+ A + AC E PVTI+ C +K++
Sbjct: 316 GAKAQVGEDTLTLEGVDHLKGGTVDGCNDHRIAMMAVAVAACKE-PVTIQGAECVKKSY 374

Query: 433 PDYFD 437
P +++
Sbjct: 375 PRFWE 379

>ref|YP_003072939.1| response regulator receiver domain protein [Teredinibacter turnerae
T7901]
gb|ACR12686.1| response regulator receiver domain protein [Teredinibacter turnerae
T7901]
Length = 742

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 126/439 (28%), Positives = 218/439 (49%), Gaps = 29/439 (6%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P ++GT+++PG KS+S+R ++L +L+EG T ++ L ED L A R +G+ +E
Sbjct: 315 PGGSVTGTIRVPGDKSISHRSIMLGSLAEGVTRIEGFLEGEDALATLQAFRDMGVVIEGP 374

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ AV V G ++ + L++GN+G +MR L+ + AG + T L G +
Sbjct: 375 ENG--AVTVHGVGLHGLK--QPSGPLYVGNSGTSMRLLSGIL--AGQSFTSELTGDESLS 428

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDC--PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + L+++GA V+ G + PPVRV+G L + + S+Q S +L+A
Sbjct: 429 KRPMNRVANPLREMGATVET--GEEGRPPVRVSGGSALHAIDYVMPMA-SAQVKSCVLLA 485

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G+ ++ P + T R++ FG + + S ++ G K + +
Sbjct: 486 GLYADGETKVT-----EPAPTRDHTERMLRGFGYQVNRNGST--ISLRSGGKLT-AADID 537

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++F+ AAI G+ +T+ G + + +L MGA +T + V
Sbjct: 538 IPADISSATFFMVAAAIAPGSDITLTHVGINPTR--IGVINILREMGANLTL-QNEREVG 594

Query: 309 GPPREPFGKRKH--LKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P ++ LK I + +++P D L V A A+G T + RVKET+R
Sbjct: 595 GEPVADIRVQYAPLKGIAIPEDQVPLAIDFPAALLVAAACAEGETVLTGAEEELRVKETDR 654

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAAC-AEVPVTI 422
+ A+ L LG PD I L A++++ DHR+AM+F++AA A P+T+
Sbjct: 655 IQAMADGLQALGIECSPTPD-GIRVIGGTLTGGAIVESFHDHRIAMSFTVAALRASGPITV 713

Query: 423 RDPGCTRKTFPDYFDVLST 441
+ +FP++ + T
Sbjct: 714 NNCANVTTSFPNFVALAKT 732

>ref|ZP_04669728.1| conserved hypothetical protein [Clostridiales bacterium 1_7_47_FAA]
gb|EEQ56709.1| conserved hypothetical protein [Clostridiales bacterium 1_7_47FAA]
Length = 425

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 115/438 (26%), Positives = 204/438 (46%), Gaps = 29/438 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ +++++GTT + N L D + + +G+ +E ++
Sbjct: 9 LHGEITVPDGKSIHRAVMFGSIAKGTTEIHNFLQGADCLSTIACFQKMGIDIENNR--D 66

Query: 75 RAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R +V G G G +D L GN+G R ++ + A + T L G +R+R
Sbjct: 67 RVIVRGNGLRGLRRPQDV----LDCGNSGTTTRLISGILCAQEFDVT--LTGDESIRKR 119

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L +GAD+ G C P+ + G P + + ++S + + ++ A L
Sbjct: 120 PMKRIMEPLSLMGADITSMNGNGCAPLLIKG---RPLKGIHYTSKVASAQVKSAILLAGL 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G + + +S + E+ L L FG A+ S I+ ++ + V G
Sbjct: 177 YAGS-PTSVTEPYVSRNHSEIMLDL---FG--ADIKASGTTCTIQPARELHGAQ-VMVPG 229

Query: 253 DASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVWTETSVTVTGPP 311
D SSA+YF+A G + G + + G + + V + MGA + + P
Sbjct: 230 DISSAAYFIAAGLMVPGSQLLRNVGINPTRDGI--IRVCQDMGADLELLNVTSGAGEPT 287

Query: 312 REPFGGRKH-LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ R L ++ +P D +A +A A+G T IRD A +VKE+ R+ +
Sbjct: 288 ADILVRSSSLHGTEIKGAIIPTLIDELPMIAAMACMAEGDTVIRDAELKVKESNRIAVM 347

Query: 368 RTELTCLKGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
L +GA V E D II + L+ +ID+ DHR+AM F++ A CA+ I+D
Sbjct: 348 VENLKAMGAHVAETEDGMIIHGKKPLHGASIDSRKDHRIAMTFAVTALCADGVTDIKDAD 407

Query: 427 CTRKTFPDYFDVLSTFVK 444
C ++P ++ L +K
Sbjct: 408 CVNISYPGFYHDLQELMK 425

>ref|YP_003992921.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
hydrothermalis 108]
gb|ADQ07552.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
hydrothermalis 108]
Length = 433

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 124/446 (27%), Positives = 212/446 (47%), Gaps = 37/446 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++I+ V +P KS+S+R +++ +L++G T ++N L S+D + + LG +E
Sbjct: 9 RKINSNVIVPPDKSISHRSIMIGSLAKGVTEIENFLSDDCLATINCFKNLGTDIE---- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++ G F + K+ L N+G R L ++ + +L G +++R
Sbjct: 65 IRNDKIIVKNGFALSAPKQ--ILDQNSGTTTRLLLGLSTQEFES--ILTGDSSIQKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + V L Q+GA+ + D P++V G L + L S+Q SAL+ A+
Sbjct: 121 PMKRVTVPLSQMGAEFEFLEKEDFLPIKVKGSVKLPIEYTLPIP-SAQVKSALIFASLR 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
A G ++ K S + E+ L+ + SW+ + ++ S
Sbjct: 180 AEGKSILKESPK--SRDHTEMLKHA-----GANIKSWEEDGVYTVEILPSQLSSIKIK 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D SSA++F+ A I G +V +E C + + +VL+ MGA ++ + V
Sbjct: 232 IPSDISAAFFIVLALICEGSSVVIENCILNPTRTGI--IDVLKQMGADISIED----VE 285

Query: 309 GPPREPFGFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G+ +LK + VN + +P D LAV A FA+G T I + + RVKE
Sbjct: 286 NRNGELVGKIVARSSNLKGVTVNKDDIPRIIDEIPILAVAAAFAEGKTTIDNASELRVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEV 418
++R+ L GA E D II E+L +++Y DHR+AMA S+ ACA E
Sbjct: 346 SDRIKTTAQMKSFGADCYELEDGLKIIGSRERLKSIVNSYKDHRIAMAASIMACAVEG 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
TI D C +FP+++D+L + K
Sbjct: 406 ESTILDAECASISFPNFYDILFSSTK 431

>ref|ZP_01861759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. SG-1]
gb|EDL63187.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. SG-1]
Length = 429

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 128/440 (29%), Positives = 211/440 (47%), Gaps = 33/440 (7%)

Query: 13 KEISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G + +PG KS+S+R ++ A++ GTTV+ N L ++D + R +G VE +
Sbjct: 12 KGLRGQITVPGDKSISHRSIMFGAVANGTTVIHNFLRADDCLSTMACFRKMG--VEIKEE 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
+V G G D+ +E + L GN+G R ++ ++ G V+ G +
Sbjct: 70 GSTVIVHGKGW----DSLQEPESILDVGNSTTARLMSGILS--GRPFHSVIVGDESIA 122

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L GAD+D P+ + G G L L+ + S+Q SA++ AA
Sbjct: 123 KRPMKRVGTGPLSLFGADIDGRKNGQYTPLAIRG-GELSAVDYNLTVA-SAQVKS AVIFAA 180

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G I I + +S T ++ +FG E + + +KGGQ + + V
Sbjct: 181 LQAEG---ISTITEPVSTR--NHTETMIGKFG--GEITSENNVIKVKGGQDFHGTE-VQV 232

Query: 251 EGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 309
D SS ++FLA AAI + + G G + + +VLE MGA+T E +
Sbjct: 233 PADISSGAFFLAAAAIVPDSKLVLPGLGNPRTGTI--IKVLEEMGAKIT-VEMEDSHDF 289

Query: 310 PPREFPG--RKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERM 364
PR LK ID+ + +P + + V+AL A +G T IRD +VKET R+
Sbjct: 290 EPRGTVTVETSSLKIGDIGDIIPSLIDEIPVIALLATQAEGRTVIRDAEELKVKETNRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTI 422
A+ ++L LGA +E D II L +D+ DHR+ M ++AA C E V +
Sbjct: 350 DAVVSQKILGADIESTEDGMIINGKTSLRGGTVDSLGDHRIGMTLAI AALLCNE-DVEL 408

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
++ ++P ++ L++
Sbjct: 409 KNAEAVNISYPSFYSDLASL 428

>ref|ZP_06307553.1| hypothetical protein CRC_01037 [Cylindrospermopsis raciborskii
CS-505]
gb|EFA70401.1| hypothetical protein CRC_01037 [Cylindrospermopsis raciborskii
CS-505]
Length = 454

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 123/437 (28%), Positives = 204/437 (46%), Gaps = 33/437 (7%)

Query: 15 ISGTVKLPKSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

Sbjct: 29 + G +++PG KS+S+R L+L A++EG T + LL ED R+LG + +D +
LQGRIQVPGDKSISHRALMLGAIAEGETEIQGLLLGEDPRSTASCFRSLGAEI-SDLNTQ 87

Query: 75 RAVVVGCG-GKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G G F +E + L GN+G +R L + A+ + + G +R R

Sbjct: 88 LVRVKIGLGNF-----QEPLDVLNAGNSGTIR-LMLGLLASHPGRFFAVTGDDSLRSR 141

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L+Q+ A + G P+ + G P + I+S + + ++ A L

Sbjct: 142 PMSRVVKPLQQMSAQIWGREGNTLAPLAIQGGSLKP---IHYHSPIASAQVKSCILLAGL 198

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ + + + +S + E R+++ FG + I G K K V G

Sbjct: 199 NT-EGKTTVTEPALSRDHSE---RMLKAFGADLTIDPGSNSVTITGNAKLYGQK-VIVPG 253

Query: 253 DASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L AG+ + G + VE G + + E L +MGA + E V G

Sbjct: 254 DISSAAFVLVAGSIVPGSDLVVENVGVPNTRTGI--LEALTIMGANIQL-ENQREVAG-- 308

Query: 312 REPFGKRHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
EP H+++ + + ++ D L+V A FA G T IRD A RVKE++R

Sbjct: 309 -EPVADLHVRSSQLQSCITAGDIIPRLIDEIPILSVAATFAKGTTIIRDAELRVKESDR 367

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTI 422
+ + +L K+GA V E D IT L T +D+Y DHR+ M+ ++AA + TI

Sbjct: 368 ITVMAQQLNKMGARVTELAGMEITGGTTLVGTEVDSYTDHRIGMSLAIAALNAIGTTTI 427

Query: 423 RDPGCTRKTFPDYFDVL 439
++P++ L

Sbjct: 428 HRAEAAAISYPNFTSTL 444

>ref|ZP_01766625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 305]
gb|EBA49195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 305]
Length = 451

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 120/429 (27%), Positives = 191/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++ A

Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSSSEGA- 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFGLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R

Sbjct: 79 -TVVKGV---DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVRSQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +

Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMRSTRAL-GKHEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D

Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFFVPGDRDFK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P

Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLDLDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E

Sbjct: 300 RIRIRGGTSIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIEHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-SLAACAEVPVTIIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P

Sbjct: 360 LDKLGVRSSEKLDQLIIHGNPRGYRGGAVIDGHYDHLIMALTTIGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF

Sbjct: 420 VGQTYPDYF 428

>gb|AAM16074.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16080.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16084.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16085.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 61

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 60/61 (98%), Positives = 60/61 (98%)

Query: 385 CIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVLSTFVK 444
CIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVLSTFVK
Sbjct: 1 CIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPAIRDPGCTRKTFPDYFDVLSTFVK 60

Query: 445 N 445
N
Sbjct: 61 N 61

>ref|ZP_00652443.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Dixon]
ref|ZP_00680509.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Ann-1]
ref|YP_001776041.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
M12]
gb|EAO12803.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Dixon]
gb|EAO33917.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
Ann-1]
gb|ACA12411.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
M12]
Length = 442

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 131/429 (30%), Positives = 205/429 (47%), Gaps = 29/429 (6%)

Query: 15 ISGTVKLPKSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AAL++GT+ +D L +ED L LG+ +E +
Sbjct: 17 LHGVLSIPGDKSISHRAVMFAALADGTSRIDGFLEAEDTRSTAAILARLGRIETPSFTQ 76

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G ++ L GNAG MR L + A ++ VL G + +RP
Sbjct: 77 RIVHGVGVVDGL-----QASDIALDCGNAGTGMRLLAGLLVAQPFDS--VLVGDAASLSKRP 129

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+R+ G G L G +S S+Q SA+L+A A
Sbjct: 130 MRRVTDPLSQMGARIDTS-DDGTPPLRIYG-QQLLRGIDFISPLASQAQIKSAVLLAGLYA 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + P + T R++ FGV + S R ++GGQ+ + N + D
Sbjct: 188 RNETVREPH-----PTRDYTERMLTAFGVDDIVSTGCAR--LRGGQRLCA-TNITIPAD 239

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + I G +T+ G + + VL +MGA + + G P
Sbjct: 240 FSSAAFYLVAAASVIPGSDITLRAVGLNPRR--IGLLTVLRLMGADIVESNRH-EQGGEVP 296

Query: 313 EPFGRKH--LKAIDVNMNKMMPDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ V + +PD+ L V A A+G T + A RVKE++R+ A+
Sbjct: 297 ADLRVRYAPLQGTRVPEDLVPMIDEFPALFVAAAAAEGQTVVSGAAELRVKESDRLAAM 356

Query: 368 RTELTGLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPG 426
T L LG V+E D I + I+++ DHR+AMAFS+A V V I D
Sbjct: 357 VTGLRVLGQVQVEIADGATIH-GGPIGHGTINSHGDHRIAMAFSIAGQLSVSTVRIEDVA 415

Query: 427 CTRKTFPDY 435
+FPDY
Sbjct: 416 NVATSFPDY 424

>ref|NP_242533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus halodurans
C-125]
sp|Q9KCA6.1|AROAl_BACHD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase 1;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase 1; Short=EPSP synthase 1; Short=EPSPS 1
dbj|BAB05386.1| 5-enolpyruvylshikimate-3-phosphate synthase [Bacillus halodurans
C-125]
Length = 431

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 132/439 (30%), Positives = 210/439 (47%), Gaps = 26/439 (5%)

Query: 8 VLQPIKEISGTVKLPKSKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V+ K + GT+K+PG KS+S+R ++ AL++GTT V+ L D + + LG+S+
Sbjct: 6 VIPHAKGLKGTIKVPGDKSISHRAVMFGALAKGTTTVEGFLPGADCLSTISCFQKLGVSI 65

Query: 68 EADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E +A +R V G G E + L +GN+G R + ++ ++ + D
Sbjct: 66 E--QAERTVTKGKGWDGLREPSD---ILDVGNSTTTRLILGILSTLPFHSVIIGD--E 118

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + LK +GA +D + P+ + G G L G S S+Q SA+L
Sbjct: 119 SIGKRPMKRVTEPLKSMGAQIDGRDHGNTPLSIRG-QQLKGIDFH-SPVASAQMKSAIL 176

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + K + T R++E FGV E D I+GGQ + ++
Sbjct: 177 LAGLRAEGKTSVTEPAK-----TRDHTERMLEAFGVNIE-KDGL-TVSIIEGGQML-TGQH 228

Query: 248 AYVEGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FL AGA + +T+ G + + EVL+ MGA + V
Sbjct: 229 VVVPGDISSAAFFLVAGAMVPHSRITLTNVGINPTRAGI--LEV LKQMGATLAMENERVQ 286

Query: 307 VTGPPRE-PFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
P + L+ +++ + +P D +AV+A A G T I+D +VKET
Sbjct: 287 GGEVPADLTITETSVLQVEIGDIIIPRLIDEIPIIAVLATQASGRVTIKDAEELKVKETN 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMA-MAFSLAACAEVPV 420
R+ + +ELTKLGAS+ D II P L + ++ DHR+ A AE PV
Sbjct: 347 RIDTVVSELTKLGASIHATDDGMIIEGPTPLKGGVTVSSHGDHRIGMAMAMIAALLAEKPV 406

Query: 421 TIRDPGCTRKTFPDYFDVL 439
T+ ++P +FD L
Sbjct: 407 TVEGTEAIAVSYPFFDHL 425

>ref|YP_102068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
ATCC 23344]
ref|ZP_00440254.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
GB8 horse 4]
ref|YP_994007.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
SAVP1]
ref|YP_001028329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
NCTC 10229]
ref|YP_001081973.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
NCTC 10247]
ref|ZP_02269696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
PRL-20]
ref|ZP_04883342.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
ATCC 10399]
ref|ZP_04910112.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
FMH]
ref|ZP_04915076.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
JHU]
ref|ZP_04976490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|AAU48705.1| 3-phosphoshikimate-1-carboxyvinyltransferase, putative
[Burkholderia mallei ATCC 23344]
gb|ABM52107.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
SAVP1]
gb|ABN00625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
NCTC 10229]

gb|ABO04717.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
NCTC 10247]
gb|EDK52344.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
FMH]
gb|EDK57673.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
JHU]
gb|EDK87365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|EDP87696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
ATCC 10399]
gb|EEP85861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
GB8 horse 4]
gb|EES42830.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
PRL-20]
Length = 451

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 120/429 (27%), Positives = 191/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++ A
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGAFSSEGA- 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 79 -TVVKGV----DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVSQ 132

Query: 135 GDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMRSTRAL-GKHTEVSCKKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFVPGDRDRFK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLIDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIEHIRYKESDRISDFRRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-SLAACAEVPVTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSSEKLDQLIIHGNGRGRGAVVDGHDHGLIMALTITIGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VGQTYPDYF 428

>ref|NP_269459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes M1 GAS]
ref|YP_282464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS5005]
sp|Q99Z83.1|ARO_A_STRP1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK34180.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Streptococcus pyogenes M1 GAS]
gb|AAZ51719.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pyogenes MGAS5005]
Length = 430

Score = 131 bits (330), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 214/435 (49%), Gaps = 39/435 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++L A+++G T V LL EDV + A R LG+ +E +
Sbjct: 13 LQGTIQVPGDKSISHRAVILGAVAKGETRVKGLLKGEDVLSTIQAFRNLGVRIE--EKDD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V+ G G F +A + L +GN+G +MR + + AG + + G + +RP+
Sbjct: 71 QLVEIQQG--FQGLNAPCQT-LNMGNSGTSMRLIAGLL--AGQPFSVKMIGDESLSKRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+V LKQ+G ++ PP+++ G L L S S+Q SA+L+AA A
Sbjct: 126 DRIVYPLKQMGVEISGETDRQFPPLQLQGNRNLQPITYTLPIS-SAQVKSAILLAALQAK 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++ ++K I+ + E ++++FG R + G Q+ + + V GD
Sbjct: 185 GTTQV--VEKEITRNHTE---EMIQQFG--GRLIVDGKRITLVGPQQL-TAQEITVPGDI 236

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-----TSVT 306
SSA+++L AG I G + + + G + + EV+E MGA++ + + TS+
Sbjct: 237 SSAAFWLVAGLIIPGSELLKNVGVNPTRTGI--LEVVEKMGAQIVYEDMNKKEQVTSIR 294

Query: 307 VTGPPREPFGFRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETER 363
V ++K ++ +P + L ++AL A G T I+D RVKET+R
Sbjct: 295 VV-----YSNMKGTIISGGLIPRLIDELPIIALLATQAQGTTCIKDAQELRVKETDR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA---CAEVPVT 421
+ + L +GA+++ D II P L TY DHR+ M ++AA + V
Sbjct: 347 IQVVTDLNLSMGANIKATADGMIKGTPLVYGANTSTYGDHRIGMMTAIAALLVKQGQVH 406

Query: 422 IRDPGCTRKTFPDYF 436
+ ++P +F
Sbjct: 407 LDKEEAIMTSYPTFF 421

>ref|YP_001727977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc citreum
KM20]
sp|B1MYD1.1|AROAL_EUUCK RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACA82533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc citreum
KM20]
Length = 431

Score = 131 bits (329), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 124/439 (28%), Positives = 215/439 (48%), Gaps = 36/439 (8%)

Query: 15 ISGTVKLPGSKSLSNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAK 74
+ G V +PG KS+S+R L+ A+++G TV+ N L S+DV + + R LG++++ ++ +
Sbjct: 12 LHGHVTVPGDKSISHRALMFAGIAKQGTIVITNFLASDDVLHMTTVFRNLGVAIQQNENSV 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R G G P + L +GN+G + R L ++ + + + G + +RP+
Sbjct: 72 RIQGGQFGLTTPPKP-----LDMGNSGTSTRLLMGLLSKQNFDMISII--GDESLSQRP 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L ++GA +D P + + L G + + S+Q SA+L+A A
Sbjct: 125 TRVMKPLITEMGAKIDLTANGTLPGI-IQANATLRGITYDMPVA-SAQVKSAILLAGIQAE 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G E +I+K+ S + E R++ +FG + E S + Q+ ++ V D
Sbjct: 183 G--ETCIEKIASRDHTE---RMLRQFGGQLE---SKNGVITLKKQQQLQGQHVDPADI 234

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++FL A IT + +T+ G + + ++L MGA + T + G P
Sbjct: 235 SSAAFFLVAALITPNSELITNRVGINPTDGI--LKILTRMGASIEV--TPIDTQGEPLA 290

Query: 314 PFG--RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAIR 368
+ L ID+ +P L ++AL ADG T I RVKET+R+ +
Sbjct: 291 DLTVRTQTLHGIDITAADIPSADDELPIIALAATQADGDTIISGAELRVKETDRIATVI 350

Query: 369 TELTKLGASVEEGPDYCIITPEKL----NVTADITYDDHRMAMAFSLAA---CAEVPVT 421
+EL+KLGA++EE PD II + L + +D+ DHR+AM ++AA +V +T
Sbjct: 351 SELSKLGANIEKPDGMIHGGQSLTADNDVLLDSCGDHRIAMMNAIAALITTGDVILT 410

Query: 422 IRDPGCTRKTFPDYFDVLS 440

D ++P + + LS
Sbjct: 411 GED--AMSVSYPGFLEDLS 427

>ref|ZP_04856131.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
gb|EES77762.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39BFAA]
Length = 424

Score = 131 bits (329), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 211/438 (48%), Gaps = 28/438 (6%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G + +PG KS+S+R ++ +L++GTT + + L D + R +G+ +E + A
Sbjct: 8 NLRGETVTPGDKSISRRAVMFGSLAQGTTKITHFLEGADCLSTISCRKMGIDIE--RNA 65

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V G G A E L +GN+G R ++ + AG + L+G ++ RP
Sbjct: 66 SEILVHGKG--LHGLSAPSET-LDVNGSGTTTRLISGIL--AGQSFISELNGDASIQRSP 120

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
+ ++ L +GAD+ G C P+R+ G P ++S Q S +L+A
Sbjct: 121 MKRIMTPLLSMGADIVSLRGNGCAPLRITG---KPLHAAHYQSPVASAQVKSCVLLAGMY 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D + + ++S + E+ L + S + + G++ K P G
Sbjct: 178 A--DGITSVTEPVLRSRNHTEIMLNIFYGANVTSQGTASIEPEPVLNGREIKVP-----G 229

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+YF+A +T G+ + ++ G + + V + MGA +T S T P
Sbjct: 230 DISSAAYFIAAGLLTPGSEILLKNVGINPTRDGM--LRVCKAMGADITLLNAS-TEGEPT 286

Query: 312 REPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ R L V +P D +AV+A FA+G T IRD +VKE++R+ +
Sbjct: 287 ADLLIRTSSLHGTTVEGEIIPTLIDEIPMAVMAAFAEGTTVIRDAQELKVKESDRIAVV 346

Query: 368 RTELTKLGSASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
L ++GA ++ D II + L+ I++Y DHR+AM+F++A + +TI+D
Sbjct: 347 TEGLKRMGADIQPTDDGMIHGGKPLHGAEINSYLDHRIAMSAFVAGTICDGTLTIKDGD 406

Query: 427 CTRKTFPDYFDVLSTFVK 444
C + ++P++++ L + K
Sbjct: 407 CVKISYPEFYEDLYSLGK 424

>ref|ZP_06934711.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Escherichia coli
OP50]
Length = 99

Score = 131 bits (329), Expect = 2e-28, Method: Composition-based stats.
Identities = 59/93 (63%), Positives = 72/93 (77%)

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGSASVEEGPDYCIITPPEKLNVTATIDTYDDHRMA 407
T +R++ +WRVKET+R+ A+ TEL K+GA VEEG DY ITPPEKLN I TY+DHRMA
Sbjct: 1 TTLRNIYNWRVKETDRLFAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMA 60

Query: 408 MAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
M FSL A ++ PVTI DP CT KTFPDYF+ L+
Sbjct: 61 MCFSLVALSDTPVTILDPKCTAKTFPDYFEQLA 93

>ref|YP_107312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei K96243]
sp|Q63X54.1|AROAL_BURPS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH34676.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei K96243]
Length = 451

Score = 131 bits (329), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVMKGV----DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRSLGVRSQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRLRLNVECEAVGPEARLPISMRSTRAL-GKHEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVDHITAPSMVHTTINNLAHAGVAVEYDAAFRFRFPGRDRFK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDGTGLIDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMAF-SLAACAEPVPTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSSEKLDQLIIHGNPRSYRGAVVDGHDHGLIMALTTIGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VGQTYPDYF 428

>ref|YP_001009062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. AS9601]
sp|A2BQ94.1|AROA_PROMS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM69955.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. AS9601]
Length = 436

Score = 131 bits (329), Expect = 2e-28, Method: Compositional matrix adjust.
Identities = 123/448 (27%), Positives = 208/448 (46%), Gaps = 44/448 (9%)

Query: 14 EISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G VK+PG KS+S+R L++ +++ G T ++ L+SED LR LG+++ K
Sbjct: 12 NLKGVKVPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G G ++ KE ++ GN+G MR L + A + ++L G + ER
Sbjct: 72 EPFTISGLG---LDGLKEPKEILNCGNSGTTMR-LLMGLLAGQEDKNFILTGDISLNER 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + + P+ ++G KL G + S+Q SA+
Sbjct: 127 PMGRVGKPLSLMGGKIFGREKGNKAPISIDG-----NKLKGCVIGTPVASAQVKSAL 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+A A G + I+ S + E R+++ FG R IK G K
Sbjct: 179 LLAGLKASGTTVS--IEPASSRDHTE---RMLKAFGADISVRGELGRNVVKSGLIGQ 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + GD SSAS+++ A+I V ++ G + + V++ MG + S
Sbjct: 234 R-ILIPGDISSAFWMIAASIVPNSEVLINQVGLNPTRTGI--LNVMDSMGCNYEILDKS 290

Query: 305 VTVTGPPEPFR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVAS 355
T+ G EP G +LK+ + + +P D L V A F +G + I+D
Sbjct: 291 -TIAG---EPIGSIKVKSSNNLKSFTIEGDILPKLIDEIPILTVAACFCNGVSEIKDAQE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA- 414

RVKET+R+ + +L K GA V E D II K N +D+ DHR+AM+ ++A+
Sbjct: 347 LRVKETDRLKVMARQLQKFGAEVTEKEDGLIINGQSKFNSAEVDSETHRVAMSLAIASL 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A+ I ++P +++ L+T

Sbjct: 407 LAKGTSKIMRADAASVSYPTEFWEDLATL 434

>ref|ZP_04760690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
subsp. mobilis ATCC 10988]
gb|EER62516.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zymomonas mobilis
subsp. mobilis ATCC 10988]
Length = 453

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 131/439 (29%), Positives = 213/439 (48%), Gaps = 38/439 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEAD-KAA 73
+SG V +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R++G + D K
Sbjct: 18 LSGKVHVPDGKSIHRAALMLAALVAVGESFVEGLLEGEVDLATAEAMRSMGADIRKDEKGC 77

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG G + A L +GN+G + R L V + AT++ D + +RP
Sbjct: 78 WHIHGVGVGSLLPQKA-----LDMGNSGTSTRLLMGVVASHPITATFIGDA--SLSKRP 130

Query: 134 IGDVLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L +GA G P+ V G+ P ++ + S+Q SA+L+A
Sbjct: 131 MGRISTPLSLMGARFSAAEENRL-PMTVTGL--YPAIPYRLPVASQVKSAILLAGLN 187

Query: 193 ALGDVEIEIIDLKIS-IPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G I ++I +P + + R+++ +G + E +D I G + K P++
Sbjct: 188 TPG-----ITRVIEPVPTRDHSEMLKGYGANLSVEENDGVRIISIHGEALK-PQHII 240

Query: 250 VEGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVT 308
V GD SSA++ +AG + G + VE G + +L+ MG ++ + V
Sbjct: 241 VPGDPSSAAFLVVAGLIVPGSDLIVENVGLNPNTRSG--LYTMLKAMGGQIEYLNPR-EVG 297

Query: 309 GPPREPFGFRK--HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P K HLKAIDV + +P D L + A A+G + ++ +A RVKE++R
Sbjct: 298 GEPVADLSVKYSHLKAIDVPPSIVPSMIDFPIILFIAAAMAEKGKSTLQGLAELRVKESDR 357

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPP-----EKLNVTAIDTYDDHRMAMAFSLAA-CA 416
+ + L LG S+EE D II +K + +I + DHR+AM+F++A +
Sbjct: 358 IAVMAEGLKALGVSLLEKEDGLIIEGSAGEGLGQKGKMSIAAHLDHRIAMSFVAVAGLVS 417

Query: 417 EPPVTIRDPGCTRKTFPDY 435
E VTI D +FP +
Sbjct: 418 EGGVTIDRRPIMTSFPVF 436

>ref|ZP_06116562.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium hathewayi
DSM 13479]
gb|EFC96874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium hathewayi
DSM 13479]
Length = 425

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 119/446 (26%), Positives = 211/446 (47%), Gaps = 33/446 (7%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
+ + + G +++PG KS+S+R ++ +++ GTT + + L D + + +G+++E
Sbjct: 3 FKKVTPKLGELQIPGDKSISHRSVMFGSIARGTTEISHFLQADCLSTISCFQKMGVAIE 62

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ +V+V G ++ K + L GN+G R ++ ++A N + G
Sbjct: 63 NNG---DSVIVRGNGRLGLK--KPDSILDCGNSGTTTRLISGILSAQ--NFDVTVTGDES 115

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALL 187
+++RP+ ++ L +GA ++ C P+ + G P V I S+Q SA+L
Sbjct: 116 IQKRPMKRIIEPLSMMGAQIESLRQNGCAPLHITG---KPLHSVHYHSKIPSAQVKSAIL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKYKSP 245
+A A D E + + ++S + E+ LR FG W+ I+ ++
Sbjct: 173 LAGLYA--DGETRVTEDVVSRLHSELMRLR---SFGADV---WEGTTAVIRPAEELYG- 222

Query: 246 KNAYVEGDASSASYFLA-GAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA+ FLA G + G V + G + + V MGA +T
Sbjct: 223 RQITVPGDISAAPFLAAGLLVPGSEVLIRQVGINPTRDGI--LRVCRAMGADITLMNEQ 280

Query: 305 VTVTGPPEPFGRK---HLKAID-VNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+G P K H I+ + + D +AV+A FA+G T I+D A +VK
Sbjct: 281 -DASGEPTADILVKSSSLHGTVEGAIPTLIDELPMIAVMACFAEGTTIIKDAELKVK 339

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEV 418
E+ R+ + L+ +GA V E D II + L+ ID+ DHR+AM F++A CAE
Sbjct: 340 ESNRLEVMVKNLSAMGADVTTETADGMIHGGKPLHGAVIDSLLDHRIAMTFVAVGLCAEG 399

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
I C R ++PD+++ L+ ++
Sbjct: 400 ETEILGAECVRISYPDFYEDLNRLMR 425

>ref|ZP_02401430.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei DM98]
ref|ZP_02496728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 112]
ref|YP_002895375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
gb|ACQ99133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
Length = 451

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVVKG---DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTQFVTQYRSLGVRSQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMRSTRAL-GKHTEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFFVPGDRDRFK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLDLPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIEHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAF-SLAACAEVPTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSSEKLDQLIIHGNGRGRGAVVDGHDHGLIMALTTIGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VQGTYPDYF 428

>ref|ZP_07638225.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus
mulieris FB024-16]
gb|EFN92844.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus
mulieris FB024-16]

Length = 487

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 136/488 (27%), Positives = 213/488 (43%), Gaps = 85/488 (17%)

Query: 15 ISGTVKLPKSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ +V LPSKSKSL R LLL+A+ + + V+ LL + D M+ AL+ LG + A
Sbjct: 19 VYASVHLPGSKSLSARELLLSAIGDTNSRVEGLLYARDTDLMVRLQGLGARISPWPAG 78

Query: 75 RAV-----VVGCGGKFPVE----DAKEEVQLFLGNAGIA 104
V +G G + ++ VQ+ G AG
Sbjct: 79 NPVEIQPIPLWEETKQSGVSSNSGAGLEALGSSGSLANHRNPPELEQPVQIECGLAGTV 138

Query: 105 MRSLTAAVTAAGGNATYVLVDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP-----PV 159
MR L A V A G A + D +RP+ L+ L LGA+ + +D P P
Sbjct: 139 MRFLPALVVALGVPARFTADAA--ANKRPLRGLLEALASLGANWE----SDDPLDGIFPF 192

Query: 160 RVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLM 218
+N G + + + SSQ++SALL++APL + I ++ S+P+++MTL +
Sbjct: 193 TINPRRGDVPEVITVDTAASSQFVSALLLSAPLWGKPLTIRCKTPVVPSPHIIQMTLEAL 252

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTV 273
G+ A S D + Q P + + +E D S+A FLA A I GG V+V
Sbjct: 253 SLRGINATGSIQSDGTW----QWRVEPDSVFGQDLAIEPDLSNAGPFLAAAGIIGGVVSV 308

Query: 274 EGC-GTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPD 332
G TS GD+ + +L G +V T G L+A+ ++ ++ +
Sbjct: 309 PGWPAHTSQVGDL-WRQILPQFGMQVRHRCGVFTARG-----TGVLRVSLDCSQCGE 360

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK 392
+ T+A +A A G + + ++ R ET+R+ A+ EL KLG C ITP +
Sbjct: 361 LVPTIAALAAHASGVSHLEGLSHLRGHETDRLNALYQELQKLGIR-----CAITPEDG 413

Query: 393 LNVTAID-----TYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
L + I Y+DHRMA +L + I D G T KT PD+
Sbjct: 414 LBIIGIPRTQLGARLPDQPLMMRAYEDHRMATFAALMGLYRT-IQIDDIGATTKTLPDF 472

Query: 436 FDVLSTFV 443
+ + +
Sbjct: 473 PQMWAQVI 480

>ref|ZP_06499378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. syringae FF5]
Length = 273

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 94/292 (32%), Positives = 145/292 (49%), Gaps = 33/292 (11%)

Query: 157 PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIP-YVEMTL 215
PPV + G GGL G++++ G++SSQY+SALLMA G VE+ + I Y+++TL
Sbjct: 3 PPVAIKGKGGLEAGRIEIDGNLSSQYVSALLMAGACGKGPVEVALTGSEIGARGYLDLTL 62

Query: 216 RLMEFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
M+ FG AE D + Y++ + ++E DAS+A+Y A A+T G + +
Sbjct: 63 AAMQAFG--AEVQAIGDAAWKVSASGYRA-TDFHIEPDASAATYLAQAALTEGAIDLGV 119

Query: 276 CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAM 335
Q D +++++ P P A+ ++ ++M D
Sbjct: 120 ASDAFTQPDALASQIIASF-----PNMP-----AV-IDGSQMQDAIP 155

Query: 336 TLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL--GASVEEGPDYCIITPPEKL 393
TLAV+A F P +A+ RVKE +R+ A+ L + G +VEEG D + P
Sbjct: 156 TLAVLAAFNRQPVRFGIANLRVKECDRISALSHGLCAIAPGLAVEEGDDLIVNANPALA 215

Query: 394 NVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
T IDT+ DHR+AM F+LA + I DP C KT+P Y+D L++
Sbjct: 216 GTTVDALIDTHSDHRIAMCFALAGLKIAGIRILDPDCVGKTYPGYWDALASL 267

>ref|ZP_05060593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium

HTCC5015]
gb|EDY87543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium
HTCC5015]
Length = 442

Score = 131 bits (329), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 132/450 (29%), Positives = 215/450 (47%), Gaps = 32/450 (7%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M+ + +LQ +SG +++PG KS+S+R ++ AL+EGTT V L ED L A
Sbjct: 1 MSDFSQFLLQAGGAVSGRIRVPGDKSISHRSIMFGALAEAGTTTVSGFLEGEDSLNLTALRAF 60

Query: 61 RTLGLSVEADKAAKRAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R +G+ +E A R V+ G G + L LGN+G +MR + + A + T
Sbjct: 61 RAMGVDIEG-PAGGRVVIHGVGMHGLT---APQGPLDLGNSGTSMLRMAGLLAAQPPSVT 116

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + +RP+G + L +GAD+ G PP+ + G L G L + S+
Sbjct: 117 --LTGDRSLSKRPMGRVTQPLALMGADIAAQEGGR-PPLVIPGGAALKGIDYPLMA-SA 172

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q S +L+A A G+ + + P + T R++ FG + S R + GG
Sbjct: 173 QVKSCVLLAGLYAQGETSV----VEPAPTRDHTERMLRGFGYEVLTGS--RISLSGGG 225

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
K+ + V D SSA++F+ A+I +T+E G + V ++L++MGA +
Sbjct: 226 TLKA-TDIDVPADISSAAFFMVAASIAEADLTLEHVGINPRTGTG--IDILKLMGANIA 282

Query: 300 WTETSVTVTGPPREPFGRK--HLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
E V G P + HLK ID+ N +P D L V A A+G T +
Sbjct: 283 L-ENQREVGGEVPADIRVRSTHLKGIDIPENLVPLAIDFPPALFVAAACAEGRTVLTGAE 341

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEKLNVT---IDTYDDHRMAMAF 410
RVKE++R+ + L +GA+ D +I E+L ++ +DDHR+AM+F
Sbjct: 342 ELRVKESDRIQVMADGLQAIGATATPTADGMVIEGRGEQLQCFVVGGEVEAHDHRIAMSF 401

Query: 411 SLAACAEVPTTIRDPGCTR--KTFPDYFDV 438
++A+ +IR C +FP++ ++
Sbjct: 402 AVASLRASAG-SIRVCNCENVATSFNPFVEL 430

>gb|EGD13696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas perforans
91-118]
Length = 440

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 131/434 (30%), Positives = 205/434 (47%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGSALAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRITPSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G P +A L GNAG MR L + A VL G + +RP
Sbjct: 76 RIVHGVGVLDGLQPPAEA-----LDCGNAGTGMRLLAGLLAAQ--RFDSVLVGDESLSKRP 128

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+ V+G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIDT-QDDGTPPLHVHGGQALHGIDF-VSPVASAQVKSALLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV+ + S R ++GGQ+ ++ A V D
Sbjct: 187 QGETSVTEPH-----PTRDYTERMLSAFGVEIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I G+ V + G + L +MGA + E G P
Sbjct: 239 FSSAAFFIVAASIVPGSEVVLRAVGLNPRR--TGLLAALRLMGADI-GEENHAEHGGEPPV 295

Query: 313 EPFGRKH--LKAIDVNMNKMPPDVA---MTLAVVALFADGPTAIRDVASWVRKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 296 ADLRVRYALLRGAQIPEALVPDMIDEFPALFVAAAAASGQTVVTGAAELRVKESDRLAAM 355

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 356 ATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAFIAGQLSTGQVQVNDVA 414

Query: 427 CTRKTFFPDYFDVLS 440
+FP FD L+
Sbjct: 415 NVATSFPFG-FDTLA 427

>ref|YP_201025.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae KACC10331]
ref|YP_451295.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae MAFF 311018]
ref|YP_001913309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae PX099A]
sp|Q5H081.1|AROAXANOR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q2P356.1|AROAXANOM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B2SJJ3.1|AROAXANOP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW75640.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae KACC10331]
dbj|BAE69021.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae MAFF 311018]
gb|ACD58777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzae PX099A]
Length = 440

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 132/434 (30%), Positives = 205/434 (47%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGS LAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRIETPSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G P A L GNAG MR L + A VL G + +RP
Sbjct: 76 RIVHGVGV DGLQPPTGA----LDCGNAGTGMRLLAGLLAAQ--RFDSVLVGDESLSKRP 128

Query: 134 IGD LVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+RV+G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIDT-QDDGTPPLRVHGGQALHGIDF-VSPVASAQVKSALLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G E + + + Y E R++ FGV + S R ++GGQ+ ++ A V D
Sbjct: 187 QG--ETSVTEPHPTRDYSE---RMLSAFGVDIDFSPGSAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I + V + G + L +MGA++ E G P
Sbjct: 239 FSSAAFFIVAASIVPDSEVVLRAVGLNPRR--TGLLAALRLMGADIS-EENHAHEHGGEVPV 295

Query: 313 EPFGRKH--LKAIDVNMNKMMPDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 296 ADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAATAASGQTVVTGAAELRVKESDRLAAM 355

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 356 ATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAFIAGQLSSGSRVNDVA 414

Query: 427 CTRKTFFPDYFDVLS 440
+FP FD L+
Sbjct: 415 NVATSFPFG-FDTLA 427

>ref|NP_892731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus subsp. pastoris str. CCMP1986]

sp|Q7V272.1|AROA_PROMP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE19072.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus subsp. pastoris str. CCMP1986]
Length = 438

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 122/446 (27%), Positives = 205/446 (45%), Gaps = 38/446 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R L++ +++EG T + L S+D LR LG+++ K +
Sbjct: 15 LQGILNVPKDKSISHRSIIGSIAEGETNIKGFLYSDDPLSTADCLRKLGVINIPEIKKNQ 74

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G G ++D KE E L GN+G MR L + G ++L G + ERP
Sbjct: 75 PFTIKGLG---IDDFKEPEEILDCGNSGTTMRLLMGLLAGQEGR-NFILTGDKSLNERP 129

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALL 187
+G + L +G + P+ + G KL G + S+Q SA+L
Sbjct: 130 MGRVSKPLSLMGGIIHGRKNGTKAPISITG-----NKLKGCVIGTPVASAQVKSAIL 181

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPK 246
+A A G + I+ S + E R+++ FG R IK G + +
Sbjct: 182 LAGLNAGSTTSV--IEPASSRDHTE---RMLKAFGADINIRGELGRNIVIKSGTNL-TGQ 235

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
N + GD SSA++++ A+I + ++ G + + V+ MG + S
Sbjct: 236 NILIPGDISAFAWMIAASIVPESEIIKNVGLNPTRTGI--LNVNMEMGCNYEILDKS- 292

Query: 306 TVTGPPREPFGGRKH---LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
T+ G P K+ LK V + +P D LAV A F G + I+D RVK
Sbjct: 293 TIAGEPIGSINKYVSNLKPFKVEGDILPKLIDEIPILAVAACFCSGVSEIKDAKELRVK 352

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEV 418
ET+R+ + T+L K GA++ E D II K + +D+ DHR++M+ ++A+ A+
Sbjct: 353 ETDRLKVMATQLKKFGANILEKEDGLIINGESKFHSAEVDSETDHRVSMSLAIAISLLAKG 412

Query: 419 PVTIRDPGCTRTKTFPDYFDVLSTFVK 444
I +R ++P ++D L +
Sbjct: 413 SSKIARAEEASRVSYPTFWDDLEKLIN 438

>gb|ADP97128.1| 3-phosphoshikimate 1-carboxyvinyltransferase [marine bacterium
HP15]
Length = 742

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 125/438 (28%), Positives = 205/438 (46%), Gaps = 28/438 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
LQP I+G +++PG KS+S+R ++L AL++G T V L ED L A R +G+++E
Sbjct: 311 LQPGGAITGDIRVPGDKSMSHRSIMLGALADGVTEVKGFLGEDSLATLQAFRDMGVITIE 370

Query: 69 A-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D R VG G L+LGN+G AMR + A ++ L G
Sbjct: 371 GPDDGFVRIHGVGMHGL-----QAPRGPLYLGNSTAMRLFAGLLAAQPFDSSE--LTGDA 423

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+G + L+ +GA +D G PP+++ G L G ++ + S+Q S LL
Sbjct: 424 SLSGRPMGRVADPLRAMGAVIDTAEGGR-PPLKIRGGQKLSGIHYEMPVA-SAQVKSCLL 481

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG H D + GG K + N
Sbjct: 482 LAGLYAEGSTSVT-----EPAPTRDHTERMLAGFGYHV-HRDGATA-SVSGGGKLTA-TN 533

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SS+++FL A+I G + + G + V +L MGA + +
Sbjct: 534 IDVPADISSAFLVAASIAPGSNLILRHVGMNPTR--VGVINILNQMGANIEILDER-E 590

Query: 307 VTGPPREPFGGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361

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      + G P      + L+ ID+  +++P  D    L + A  A+G T +R      RVKE+
Sbjct: 591 IGGEVPADLRVRSaelQGIDIPEDQVPLAIDEFPVLFIAAACANGRTVLRGAEEELRVKES 650

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTaidTYDDHRMAMAFSLAAC-AEVPV 420
      +R+  +  L  LG      PD  II  +  +  +++++ DHR+AM+F++A+  A  +
Sbjct: 651 DRIQVMADGLAALGVETTVTPDGIIIDGGQTIGGGTVNSHGDHRIAMSFAVASLRAAGDI 710

Query: 421 TIRDPGCTRKTFFPDYFDV 438
      T+ D      +FP + ++
Sbjct: 711 TVNDCANVATSFPGFVEL 728

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>ref|ZP_04749034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium kansasii ATCC 12478]
Length = 434

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 134/433 (30%), Positives = 204/433 (47%), Gaps = 42/433 (9%)

```

Query: 15  ISGTVKLPgSKSLsnRIllLAALSEGt----TVVDNllNSEDVHYMLGALRTlGLSVEAD 70
      +  TV +PGSKS +NR L+LAAL+      +  +  L S D  M+ AL+TLGL V+
Sbjct: 19  VRATVTVPGSKSQTNRTLVLAAALAAQQQGASTISGALRSRDtDLMIAlQTLGLRVD-- 76

Query: 71  KAAKRAVVVGCGGKFPVEDAKEE---VQLFLGNAGIAMRSLT--AAVTAAGGNATYVLDG 125
      G G + V  E      ++ G AG +R +  AA+AA      DG
Sbjct: 77  -----GTGSElTVSGRLEPGPGARVDCGLAGTVLRFVPLAALSAA----VVTFDG 123

Query: 126 VPRMRERPIGDlVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      + R RPI  L+  L+ LG +D  G  P  RV+G G + GG V +  S SSQ++S
Sbjct: 124 DEQARARPIAPllLDALRGLGVQID---GAGLP-FRVHGTGSVAGGTVAIDASASSQFVSG 179

Query: 186 LLM-AAPLALGDVEIEIIdKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      LL+ AA  A G      L S P++ MT+ ++ + GV  + S  +      G K +
Sbjct: 180 LLLSAASFAEGLTVQHSGAALPSAPHIAMTVAMLRQAGVDVDDSVPYRWRVAPGAVKAR- 238

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTtSLQGDVKFAEVLEMMGAKVTWTETS 304
      VE D ++A  FLA A ++GGTV + G  S+Q      +L  + A V+  ++
Sbjct: 239 --RWDVEPDlTNAVAFLAAAVVSGGTVRITGWPADSVQPAADILRILRQLSAVVSHNDsm 296

Query: 305 VTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIR--DVASWRVKETE 362
      + V GP      +  DV++  + ++  ++A +A A  + R  +A R ET+
Sbjct: 297 LEVRGP-----AAYRGFDVdLRDVGELTPSVAALALATPGSVSRLTGIAHLRGHETD 349

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTaidTYDDHRMAMAFSLAACAEVPVTI 422
      R+ A+  E+ +LG  E D +IT  L      Y DHRMAMA ++      V +
Sbjct: 350 RLAALSAEINRLGGDCRETSdGLVIT-ATPLRPGRWRAYADHRMAMAGAIVGLRVAGVEV 408

Query: 423 RDPGCTRKTFFPDY 435
      D G T KT P++
Sbjct: 409 DDIGATTKTLPEF 421

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>ref|ZP_04957655.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium NOR51-B]
gb|EED35239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium NOR51-B]
Length = 433

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 124/440 (28%), Positives = 215/440 (48%), Gaps = 33/440 (7%)

```

Query: 6  EIVLQPIKEISGTVKLPgSKSLsnRIllLAALSEGtTVVDNllNSEDVHYMLGALRTlGL 65
      + +++P  +SGT+++PG KS+S+R ++L AL+ GTT      L+ +D  + A R LG+
Sbjct: 2  KFIIEPGGTMSGTLRVPGDKSMShRAIMLGALATGTtRATGFLSGDDALATVAAFrdLGv 61

Query: 66 SVEA-DKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
      S+  D      VG  G  P  +      L +GN+G ++R L+  + AG  + VL
Sbjct: 62 SITGPDDGVVSIEGVGLHGLSAPANN-----LDMGNSGTsIRLLSGIL--AGQPFSSVL 113

Query: 124 DGVPMRERPIGDlVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G  +++RP+G ++  L  +GA +      +  PP+ + G  L G  L  + S+Q

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Sbjct: 114 SGDVSLLQQRPMGRIITPLSLMGAMITA-ADSGRPPLLEIAGGQKLRGIHYDLPMA-SAQVK 171

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S +L+A A G + P + T R++ FG + ++GG +

Sbjct: 172 SCVLLAGLFAEGRTSVT-----EPAPTRDHTERMLRGFGYSVHTENG--ISLEGGGSLR 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV-TWT 301
+ + + D SSA++F+ GA IT G +T+E G + V +L +MGA + +

Sbjct: 225 ATR-LDIPADISSAAFFIVGAVITAGADITLEHVGMNPTR--VGVINILRLMGADIEVFN 281

Query: 302 ETSVTVTGPPREFFGRKH--LKAIIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASW 356
E V G P +H L+ I++ + ++P D L + A A+G T +

Sbjct: 282 EQE--VGGEPAVADLRVHRSALRGIEIPVEEVPLAIDEFPVLLIAACAEGVTTLSGAEEL 339

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC- 415
RVKE++R+ ++ LT LG E D ++ E L ++ T+ DHR+AM+F++A

Sbjct: 340 RVKESDRIASMAEGLTILGIRNEVREDGIVVHGGE-LGGGSVRTFHDHRIAMSFAIAGLR 398

Query: 416 AEVPTVTRDPGCTRKTFPDY 435
A+ P+ I D +FP++

Sbjct: 399 AKEPIEILDCHVATSFNF 418

>ref|YP_148049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus
kaustophilus HTA426]
sp|Q5KXV5.1|ARO_A_GEOKA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAD76481.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) [Geobacillus kaustophilus HTA426]
Length = 427

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 124/445 (27%), Positives = 212/445 (47%), Gaps = 37/445 (8%)

Query: 12 IKEISGTVKLPGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G +++PG KS+S+R ++L AL+ G TV+D+ L D + R LG+ + D

Sbjct: 7 VSSLRGMIEVPGDKSISHRAVMLGALASGRTVIDHFLPGADCLSTIDCFRKLGVDIRQDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VV G G P + L +GN+G R L + +A V D + +

Sbjct: 67 TT--VVVEGAG---PGGLREPAAVLDVGNSTGTARLLLGILAGQPFHACLVGD--ESIAK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAA 190
RP+G + L+++GA +D G + P+ + G P ++ + + S+Q SA+L+A

Sbjct: 120 RPMGRVTKPLREMGARIDGREGNYTPLSIRGGALRP---LRYTSPVASAQVKSAILLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A D + + S + E +RL FG E + + G Q+ + + YV

Sbjct: 177 LFA--DGVTSAEPHRSRDHTERMVRL---FG--GEVNDGLTVSVAGPQRLRG-THIYV 228

Query: 251 EGDASSASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + +T++ G + +VL MGA + V

Sbjct: 229 PGDISSAAFFLVAGAIVPNSEITLKNVGLNPTR--TGIIDVLTQMGADIAIDN---VRN 282

Query: 310 PPREPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP G L+A+++ + +P + + ++AL A+G T I+D + +VKET

Sbjct: 283 EETEPVGDITVTRTSLRAVEIGGDLIPRLIDEIPIIALLATQAEGTTVIKDASELKVET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
R+ + TEL KLGA +E D +I P + +D++ DHR+ M ++AAC A+

Sbjct: 343 NRIHTVVTELKKGADIEATDDGMMIRGKTPLYADGIVVDSHGDHRIGMMLAVAACIAKG 402

Query: 419 PVTIRDPGCTRKTFPDYFDVLSFV 443
V + ++P +F L + +

Sbjct: 403 TVRLERSEAVAVSYPAFFADLRSL 427

>gb|ABE11164.1| EPSP synthase [uncultured Prochlorococcus marinus clone HF10-11H7]
Length = 436

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 122/448 (27%), Positives = 207/448 (46%), Gaps = 44/448 (9%)

Query: 14 EISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G VK+PG KS+S+R L++ ++++G T ++ L+SED LR LG+S+ K
Sbjct: 12 NLKGKVKVPGDKSISHRALIIGSIAGGETTIEGFLHSEDPLSTADCLRKLGVSIPKIKKN 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G G ++ KE ++ GN+G MR L + A G +VL G + ER
Sbjct: 72 EPFTISGLG---LDGLKEPKEILNCGNSGTTMRLMGLLAAQEGK-NFVLTGDASLNER 126

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + G + P+ ++G KL G + S+Q SA+
Sbjct: 127 PMGRVKGPLSLMGGKIYGREGNKAPISIDG-----KKLKGCVIGTPVASAQVKSAL 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+A A G + I+ S + E R+++ FG R IK G
Sbjct: 179 LLAGLNASGTTSV--IEPASSRDHTE---RMLKAFGADISIRGELGRNVVKSVCNLIGQ 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETTS 304
+ + GD SSAS+++ A+I V ++ G + + V++ MG S
Sbjct: 234 R-ILIPGDISSASFWMIAASIIPNSEVLIQNVGLNPTRTGI--LNVMSMGSCNYEILNNS 290

Query: 305 VTVTGPPEPFGR-----KHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVAS 355
T+ G EP G +L++ + + +P D L V A F +G + I+D
Sbjct: 291 -TIAG--EPIGSIKVKTSNNLRSFTIEGDILPKLIDEIPILTVAACFCNGVSEIKDAQE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA- 414
RVKET+R+ + +L K GA + E D II K + +D+ DHR+AM+ ++A+
Sbjct: 347 LRVKETDRLKVMARQLQKFGAEITEKEDGLIINGQSKFHSAEVDSETDHRVAMSLAIASL 406

Query: 415 CAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
A+ I ++P +++ L+
Sbjct: 407 LAKGTSKIMRSDAASVSYPWFWEELAKL 434

>ref|ZP_07556119.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX2134]
gb|EFM77511.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
TX2134]
Length = 428

Score = 130 bits (328), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 203/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIED-- 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 67 -VGTTITVEGQGFGAGLKKAKNTIDV--GNSGTTIRLMGLIL--AGCPFETRLAGDASISK 121

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVLMPLNQMGAEQCQGVQQTFFPISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISSAAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKNMGGSVTILNEDEANHS 290

Query: 310 PPPEPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPLRIDELPIIALLATQATGTIIRDAEELVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRD 424

+ ELT LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELTILGADITPTDGLIIHGPTSLHGGRTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L

Sbjct: 409 AEAVSVSYPAFFDDL 423

>ref|ZP_07874350.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria ivanovii FSL F6-596]
gb|EFR96413.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria ivanovii FSL F6-596]
Length = 430

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 219/438 (50%), Gaps = 31/438 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+++E + +
Sbjct: 14 GEITVPDGKSMHSRHSIMFGAIAEGKTVIRHFLRADDCLGTIQAFAKALGVITIE--ETDEEI 71

Query: 77 VVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G G P L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTGFDGLKPAAGP-----LDIGNSGTTIRLMMGIL--AGRDFDTVLGDDSIKRP 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ ++G L + + + S+Q SA++ AA A
Sbjct: 125 NRVMPLPLQEMGAKMHGKDGSEFAPITISGNKSLKQMEYHMPVA-SAQVKSALIFAALQAE 183

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K + T ++ +FG + E R +KGGQ + + + V GD
Sbjct: 184 GETIIHHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDV 235

Query: 255 SSASYFL-AGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE 313
SSA++F+ AG I + + G + + +V+E MG + ++S + TG
Sbjct: 236 SSAAFFIVAGLIIPNSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 292

Query: 314 PFGRK--HLKAIDVNMNKMPPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIR 368
K L+ ++ + +P + + V+AL A +G T I++ A +VKET R+ A+
Sbjct: 293 TVVVKTSDLRGTEIGGDIIPRLIDEIPVIALLATQAEGTTVIKNAELKVKETNRIDAVA 352

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
TEL K+GA + D II L+ + +Y DHR+ M +AA E V + P
Sbjct: 353 TELNKMGAIDITPTDGLIIRGKTPLHAAKVTSYGDHRIGMMLQIAALLVKEGEVELDRPE 412

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 413 AVSVSYPTFFEDIRSLK 430

>ref|YP_332315.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710b]
ref|ZP_04951792.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710a]
gb|ABA50742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710b]
gb|EET08811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710a]
Length = 451

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVVKGV---DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVRSQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
 ++V L++L + + P+ + L G ++S SSQ+LS LL +
 Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMRSTRAL-GKHTEVSCKKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
 D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
 Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFVPGDRFRK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
 +S + LA VT+ G F E GA + + T+T + P
 Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTGLIDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
 G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
 Sbjct: 300 RIRIRGGTSIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTAIIDYDDHRMAMAF-SLAACAEVPVTIRDPGC 427
 L KLG EE D II P +D + DH + MA ++ E PV I++P
 Sbjct: 360 LDKLGVRSSEKLDQLIIHGNPRGYRGGAVIDGHYDHLIMALTTIGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
 +T+PDYF
 Sbjct: 420 VGQTYPDYF 428

>ref|ZP_03147356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
 G11MC16]
 gb|EDY06291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
 G11MC16]
 Length = 427

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 125/445 (28%), Positives = 207/445 (46%), Gaps = 37/445 (8%)

Query: 12 IKEISGTVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
 + + GT+++PG KS+S+R ++L AL+ G TV+D+ L D + R LG+ + D
 Sbjct: 7 VSSLRGITIEVPGDKSISHRAVMLGALASGRTVIDHFLPGADCLSTIDCFRKLGVDIHQD- 65

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
 +V G G E A L +GN+G R L + +A V G + +
 Sbjct: 66 -GTNIVIEGAGSGGLEPA---AVLDVGNSGTTARLLLGILAGQPPHACLV--GDESIK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAA 190
 RP+ + L+++GA +D + P+ + G P ++ + + S+Q SA+L+A
 Sbjct: 120 RPMARVTKPLREMGAHIDGRDDGNYTPLAIRGGALRP---LRYTSPVASAQVKSAILLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
 D + + S + E +RL FG E + I G Q + + YV
 Sbjct: 177 LFT--DGVTSTVEPHRSRDHTERMIRL---FG--GEVNVGDGLTVSIAGPQSLRG-THIYV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
 GD SSA++FL AGA + +T++ G + +VLE MGA +T +
 Sbjct: 229 PGDISSAAFFLVAGAIVPNSEITLKNVGLNPTR--TGIIDVLERMGADITIDH----IRN 282

Query: 310 PPPEFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
 EP G L AI++ + +P + + ++AL A+G T I+D + +VKET
 Sbjct: 283 EETEPIDGITIRTSTLHAIEIGDIIIRLIDEIPIIALLATQAEGTTIKDASELKVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI--DTYDDHRMAMAFSLAA-CAEV 418
 R+ + EL K GA +E D II L I D++ DHR+ M ++AA CA+
 Sbjct: 343 NRIDTVVAELKFGADIEATDDGMIIRGKTALYADGIVVDVSHGDHRIGMMLAIAACCAKG 402

Query: 419 PVTIRDPGCTRKTRTFPDYFDVLSTFV 443
 + P ++P +F L + +
 Sbjct: 403 TARLERPEAVAVSYPAFFADLRSLL 427

>ref|YP_001057772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
 pseudomallei 668]
 ref|YP_001065016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
 pseudomallei 1106a]

ref|ZP_02446036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 91]
ref|ZP_02469915.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei B7210]
ref|ZP_02480323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 7894]
ref|ZP_02488611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei NCTC 13177]
ref|ZP_02504742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei BCC215]
ref|ZP_04815431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
ref|ZP_04894174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
ref|ZP_04902926.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei S13]
ref|ZP_04963684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|ABN83300.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 668]
gb|ABN90653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106a]
gb|EDO82823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|EDO91012.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
gb|EDS85938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei S13]
gb|EES26056.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
Length = 451

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVVKGV----DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVR SQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMSTRAL-GKHTEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFFVPGDRFRK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLDLDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMAF-SLAACAEPVPTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSEEKLDQLIIHGNPRGYRGGA VVDGHYDHGLIMALTITGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VGQTYPDYF 428

>ref|YP_363422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. vesicatoria str. 85-10]
sp|Q3BUZ1.1|AROA_XANC5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAJ23368.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. vesicatoria str. 85-10]
Length = 440

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 130/434 (29%), Positives = 209/434 (48%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGSLAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRITPSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G P +A L GNAG MR L + A ++ VL G + +RP
Sbjct: 76 RIVHGVVDGLQPPTA-----LDCGNAGTGMRLLAGLLAAQRFD--VLVGDESLSKRP 128

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA ++ PP+ V+G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIET-QDDGTPPLHVHGGQALHGIDF-VSPVSAQVKSAVLLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV+ + S R ++GGQ+ ++ A V D
Sbjct: 187 QGETSVTEPH-----PTRDYTERMLSFAFGVEIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I G+ V + G + L +MGA+++ E G P
Sbjct: 239 FSSAAFFIVAASIVPGSEVVLRAVGLNPRR--TGLLAALRLMGAEIS-EENHAHEHGGEVP 295

Query: 313 EPFGRKH--LKAIDVNMKNMPDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 296 ADLRVRVAPLRGAQIPEALVPDMIDEFPALFVAAAAASGQTVVTGAAELRVKESDRLAAM 355

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 356 ATGLRTLGVQVDETDPDGATIH-GGSIGSGVIESHGDRHRIAMAFIAIAGQLSTGQVQVNDVA 414

Query: 427 CTRKTFPDYFDVLS 440
+FP FD L+
Sbjct: 415 NVATSFPG-FDTLA 427

>ref|ZP_04888327.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
gb|EDU09311.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
Length = 451

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSSE--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVVKGV---DVMHVDREIVDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVR SQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMSTRAL-GKHTEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFFVPGDRDFK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLIDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIHIRYKESDRISDFRRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-SLAACAEVPVTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSSEKLDQLIIHGNPRGYRGGA VVDGHYDHLIMALTITGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VGQTYPDYF 428

>ref|YP_001904074.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. B100]
sp|B0RUW1.1|AROAXANCB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAP52030.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris]
Length = 438

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 211/445 (47%), Gaps = 32/445 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+ + Q + G++ +PG KS+S+R ++ AAL++GT+ +D L ED LG
Sbjct: 6 QHWIAQRGTALQGS LTIPGDKSVSHRAVMFAALADGTSKIDGFLEGEDTRSTAAIFAQLG 65

Query: 65 LSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E A++R V VG G P + L GNAG MR L + A ++ V
Sbjct: 66 VRIETPSASQRIVHGVGVVDGLQPPQGP-----LDCGNAGTGMRLLAGVLAQRFD SVLVG 120

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQY 182
D + +RP+ + L Q+GA ++ PP+RV+G L G + + + S+Q
Sbjct: 121 DA--SLSKRPMRRVTDPLAQMGARIET-ESDGTPLRVHGGQALQG--ITFASPVASAQV 175

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SA+L+A A G+ + P + T R++ FGV+ S R ++GGQ+
Sbjct: 176 KSAVLLAGLYATGETSVSEPH-----PTRDYTERMLSAFGVEIAFSPGQAR--LRGGQRL 228

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
++ A V D SSA++F+ A+I G+ VT+ G + L +MGA +
Sbjct: 229 RATDIA-VPADFSAAFFIVAASIIPGSDVTLRAVGLNPRR--TGLLAALRLMGADIV-E 284

Query: 302 ETSVTVTGPPPREPFGRKH--LKAIDVNMNKMMPDVA---MTLAVVALFADGPTAIRDVASW 356
+ G P ++ L+ + +PD+ L V A A G T + A
Sbjct: 285 DNHAHEGGEPVADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAAARGDTVVSGAAEL 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-C 415
RVKE++R+ A+ T L LG V+E PD I L I+++ DHR+AMAF++A
Sbjct: 345 RVKESDRLAAMATGLRALGIVVDEKPDGATIH-GGTGSGVIESHGDHRIAMAFIAGQL 403

Query: 416 AEVPVTIRDPGCTRKTTFPDYFDVLS 440
+ V + D +FP FD L+
Sbjct: 404 STGTVQVNDVANVATSFPG-FDSL A 427

>ref|YP_001126227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus
thermodenitrificans NG80-2]
sp|A4IQ78.1|AROAGEOTN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABO67482.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus
thermodenitrificans NG80-2]
Length = 432

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 125/445 (28%), Positives = 207/445 (46%), Gaps = 37/445 (8%)

Query: 12 IKEISGTVKLPKSGSKSLNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71

+ + GT+++PG KS+S+R ++L AL+ G TV+D+ L D + R LG+ + D
Sbjct: 12 VSSLRGITIEVPGDKSISHRVAMLGALASGRVIDHFLPGADCLSTIDCFRKLGVDIHQD- 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+V G G E A L +GN+G R L + +A V G + +
Sbjct: 71 -GTNVIVEGAGSGGLEPA---AVLDVGNSTGTARLLLGILAGQPPHACLV--GDESIAQ 124

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAA 190
RP+ + L+++GA +D + P+ + G P ++ + + S+Q SA+L+A
Sbjct: 125 RPMARVTKPLREMGAHIDGRDDGNYTPLAIRGGALRP--LRYTSPVASAQVKSAILLAG 181

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
D + + S + E +RL FG E + I G Q + + YV
Sbjct: 182 LFT--DGVTSVTEPHRSRDHTERMIRL---FG--GEVNV DGLTVSIAGPQSLRG-THIYV 233

Query: 251 EGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + +T++ G + +VLE MGA +T +
Sbjct: 234 PGDISSAAFFLVAGAI VNPSEITLKNVGLNPTR--TGIIDVLERMGADITIDH---IRN 287

Query: 310 PPREFPG-----RKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP G L AI++ + +P + + ++AL A+G T I+D + +VKET
Sbjct: 288 EETEPIGDITIRTSTLHAIEIGGDII PRLIDEIPIIALLATQAEGTTI IKDASELKVKET 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI--DTYDDHRMAMAFSLAA-CAEV 418
R+ + EL K GA +E D II L I D++ DHR+ M ++AA CA+
Sbjct: 348 NRIDTVVAELKKFGADIEATDDGMIIRGKTALYADGIVVDSHGDHRIGMMLAIAACCAKG 407

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFV 443
+ P ++P +F L + +
Sbjct: 408 TARLERPEAVAVSYPAFFADLRSL 432

>gb|EAY55824.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospirillum
rubarum]
Length = 454

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 132/452 (29%), Positives = 209/452 (46%), Gaps = 46/452 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+SG +++PG KS+S+R L+L ++ G TVV L S+D L A LG+ + + D
Sbjct: 26 HRVSGNIRVPGDKSISHRSLILGGMASGKTVVTGFLPSDDCLRTLSAFSRLGVQIRQQD 85

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + V G G + + L GN+G A R + + AG + V+ G +R
Sbjct: 86 ETSLELVSPGFTGL-----REPDSILDFNGSGTASRLMCGVL--AGTSFFTVMTGDDSLR 138

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ +V L +GA +D P+ V G G L+ S+Q S++L+A
Sbjct: 139 KRPMKRVVDPLSMMGAKIDGPGSGSRLPLAVRGTA--LNGISFLNAHKSQVKSILLAG 196

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +E + + T RL+ FG K Y + +V
Sbjct: 197 LNASGPTTVE-----EPVQTRDHTERLLPLFGGKVLREGLRTTVY----PSRLTGTEMHV 247

Query: 251 EGDASSASYFLAGAAIT-GGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FLA +T G ++T+EG G + F +VLE M A+ + +
Sbjct: 248 PGDFSSAAFFLALGLLTPGSSLTLEGVGLNPTR--TGFLQVLEAMKAR----SLRILPST 301

Query: 310 PP---REFPGRKH-----LKAI DVNMNKMMPDV---AMTLAVVALFADGPTAIRDVASWRV 358
PP EP+G H L+ IDV +P++ LA A A G T IR + RV
Sbjct: 302 PPSLESEPYGNIHVGFSELEGIDVPEWIPNIIDEIPILAACAACARGTTTTIRGASELRV 361

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTAI DTYDDHRMAMAFSLAAC 415
KE++R+ I + L LG +E PD I P +L ID+ +DHR+AM+ ++
Sbjct: 362 KESDRIRGIVSALQVLGVPCKEFPDGLAIDGLGPDPRLTGGTIDSLNDHRIAMSMVAVLG- 420

Query: 416 AEVP---VTIRDPGCTRKTFPDYFDVLSTFV 443
+ +P +TIR +FP + ++ + V
Sbjct: 421 SRLPESEILTIRGTDFVSTSFPGFSNLFNQVV 452

>ref|ZP_05472815.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Anaerococcus vaginalis ATCC 51170]
gb|EEU12464.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)
[Anaerococcus vaginalis ATCC 51170]
Length = 409

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 104/433 (24%), Positives = 212/433 (48%), Gaps = 43/433 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
+ I++ P K + G + SKS ++R L+LA L E T + S+D++ + +L+ LG
Sbjct: 4 DNILIHPSK-LKGEIDAISKSFAHRALILAGLCEETNIYINEFSKDINVTIESLKNLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ +E + + P + E+ + + +G ++R TA +
Sbjct: 63 VGIEKFENFVKVT-----PPKVIEKATIDMYESGSSLRFFTA VANHFAKEVKIM-- 112

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G R+ +RP +L+ L++ G ++ +D P + G L GG + + SSQY++
Sbjct: 113 GKERLSQRPNYELIKNLKKGLEI---SSDKIPYTIKG--NLFGGDFEFFENKSSQYIT 166

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+++A+ G I++ +K S+ Y++++ +++ F V + + + +I+ Q KS
Sbjct: 167 AIMLASSKLSGKTSIKLKEKPESLGYIDISREVLKDFNVVDVKEEN--NSYFIENSQ- IKS 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P N YVEGD S+A++F GA + + ++ SLQ D +
Sbjct: 224 PNNYYVEGDWSNAFFY-GANLINSQIKIKNLKEDSLQKDRE----- 264

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ + + K ++++++PD+ LA++ + D + I + R+KE++R+
Sbjct: 265 -IIDIKKIKLKCKNENKTLEIDISQIPDLCPILALLTYLDKTSYITNGKRLRLKESDRL 323

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIR 423
+ L LGA E D I+ K+ +D+++DHR+ MA S+A+ A+ + I+
Sbjct: 324 ESTSKMLNDLGAKCEIIGDNLKISG--KIIGGEVDSFNDHRIVMAASIASLMAKDIIK 381

Query: 424 DPGCTRKTFPDYF 436
+ K++P +F
Sbjct: 382 NYKAVNKSYPSPFF 394

>ref|ZP_05566093.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
Merz96]
ref|ZP_06628908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
R712]
ref|ZP_06633978.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
S613]
ref|ZP_07766530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
DAPTO 512]
ref|ZP_07769004.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
DAPTO 516]
gb|EEU69050.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
Merz96]
gb|EFE17019.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
R712]
gb|EFE18101.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
S613]
gb|EFQ09850.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
DAPTO 512]
gb|EFQ67986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
DAPTO 516]
Length = 428

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 203/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADK 71

+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGTLMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ A+ ++ GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGQGFAGLKKARNTIDV---GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAECCQGVQQTTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGPQQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFFLVAGLVVPDSEILLKNVGLN--QTRTGILDVIKNMGGSVTMLNEDEANHS 290

Query: 310 PPREFPGRKHLKAIDVNMKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPLRILDELPIIALLATQATGTIIRDAEELVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ EL LGA + D II P L+ + +Y DHR+ M +AA E V +
Sbjct: 349 VAKELAILGADITPTDGLIIHGPTSLHGGVTSYGDHRIGMMLQIAALLVKEGTVELDK 408

Query: 425 PGCTRKTFFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAVSVSYPAFFDDL 423

>gb|AAM16060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16063.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16065.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16075.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16076.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16079.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16081.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16086.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 60

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 60/60 (100%), Positives = 60/60 (100%)

Query: 386 IITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 445
IITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK
Sbjct: 1 IITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 60

>ref|ZP_03127725.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chthoniobacter flavus
Ellin428]
gb|EDY21644.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chthoniobacter flavus
Ellin428]
Length = 443

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 135/443 (30%), Positives = 214/443 (48%), Gaps = 40/443 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE-ADKAA 73
I +++PG KS+S+R ++LA++S GT V+ L SED + A+R LG+ +E AD+
Sbjct: 12 IQTELEVPGDKSISHRAVMLASMSGTCVIRGFLPSEDCLCTVAAIRALGVPIESADETT 71

Query: 74 KRAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+V G F P D + GN+G MR ++ + AG L G P + +
Sbjct: 72 --LIVQKRRVFAAPTHD-----IDCGNSGTTMRLMSGLL--AGQPFRSRLIGDPSLSK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L Q+GA + PP+ + G P V S S+Q SA+L+A
Sbjct: 122 RPMRRVMEPLTQMGAKITAEGKDGRPLVIEGGLQPIDYV--SPVASAQVKSALLAGM 179

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + + S + E R++E F ++ + +D + GG +S ++ V
Sbjct: 180 FAKG--RTSVTEPTQSRNHT---RMLFYFLIRPQKNDLT--VSLHGGLTPES-RDFQVP 231

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AA + + ++ G + V VL MGA V V
Sbjct: 232 GDISSAAFVLAQAQPRSHLLIKNVGLNETRTGV--LAVLVRMGAVREI-----VENE 284

Query: 311 PREPFG-----RKHLKAIDVNMNMKMPDVA---MTLAVVALFADGPTAIRDVASWRVKETE 362
EP G LK ++ ++P+V LAV A A+G T I+D RVKET+
Sbjct: 285 EAEPLGVIEVRGARLKGTEIGKEIPNVIDELPILAVAAALANGTTVIKDAGELRVKETD 344

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVT 421
R+ A+ T L +GA V+E D +IT L+ +D+Y DHR+AMAF++A AE
Sbjct: 345 RLAAVATNLRAMGAQVQETEDGMVITGGIPLHGARLDSYGDHRIAMAFIAGMFAEGETI 404

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + C ++P ++ L +
Sbjct: 405 ITNTDCVNTSYPGFYQTLERILH 427

>gb|AAT76791.1| 5-enolpyruvylshikimate-3-phosphate synthase [Halomonas variabilis]
Length = 449

Score = 130 bits (327), Expect = 4e-28, Method: Compositional matrix adjust.
Identities = 135/442 (30%), Positives = 211/442 (47%), Gaps = 37/442 (8%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + G +++PG KS+S+R ++L AL+EG T V L ED L A R +G+++E
Sbjct: 11 VSPGGQAQGRLRVPGDKSMSHRSIMLGALAEVTEVKGFLLEGEDSLATLQAFREMGVAIE 70

Query: 69 ADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ + VG G K P L++GN+G AMR + AG L G
Sbjct: 71 GPHQGRVTIHGVMHGLKAPAG-----PLYVGNSTAMRLFAGLL--AGQAFDSELTGD 122

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+G + L+ +GA ++ G PP+ + G L G + + S+Q S L
Sbjct: 123 ESLTKRPMGRVADPLRLMGAAIETAEGGR-PPLSIKGGAPLKGIFYDMPMA-SAQVKSC 180

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS-P 245
L+A A G+ + P + T R++ FG S D +++GG K + P
Sbjct: 181 LLAGLYAEGETRVR-----EPAPTRDHTERMLNGFGYVV--SREGDTCWLQGGGKLTAGP 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 304
+ V D SSA++FL AAIT G +T+E G + + +L +MGA + E
Sbjct: 234 ID--VPSDISSATFFLVAAAITPGADITLEHVGINPTR--IGVINILTLMGADLV-ENE 288

Query: 305 VTVTGPPEPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V G P ++ LK ID+ ++++P D L V A A G T +R RVK
Sbjct: 289 REVGGEPVADIRIRYVPLKGDIDIPVDQVPLAIDFPPALFVAAANAQGTTRLRGAEELRVK 348

Query: 360 ETERMVAIRTELTKLGAS---VEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFSLAA 414
E++R+ A+ L LG VE+G D + + ID+ DHR+AM+F++AA
Sbjct: 349 ESDRIQAMADGLAVLGVEHTVVEDGIDIVGNGNDQVASYGGGRIDSLGDHRIAMSFAIAA 408

Query: 415 C-AEVPVTIRDPGCTRKTFPDY 435
A + I D +FPD+
Sbjct: 409 LRASDTIVIDDCANVATSFPDF 430

>ref|ZP_01827678.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP14-BS69]
ref|ZP_02717416.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae CDC3059-06]
ref|ZP_04525412.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae CCRI 1974]
ref|ZP_04597090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus

pneumoniae CCRI 1974M2]
gb|EDK66040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP14-BS69]
gb|EDT97204.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae CDC3059-06]
Length = 427

Score = 130 bits (327), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 208/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA-----LNMGNSTGSIIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKKMGVSISGQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKECTRNHTE---DMLKQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISAFAFWLVAGLIVPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQDVTVIKDAEELVKVETDRIQVV 347

Query: 368 RTELTKLGSASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A V +
Sbjct: 348 ADALNSMGADITPTADGMIKKSALHGARVNTFGDHRIGMMTAIAALLVAGGEVELDRA 407

Query: 426 GCTRKTFPDYPDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|ZP_06184945.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris 28-1]
gb|EEZ90420.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris 28-1]
Length = 487

Score = 130 bits (327), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 136/488 (27%), Positives = 212/488 (43%), Gaps = 85/488 (17%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ +V LPGSKSLS R LLL+A+ + + V+ LL + D M+ AL+ LG + A
Sbjct: 19 VYASVHLPGSKSLSARELLLSAIGDTSNRVEGLLYARDTDLMVRLQQLGARISPWPAG 78

Query: 75 RAV-----VVGCGGKFPVE----DAKEEVQLFLGNAGIA 104
V +G G + ++ VQ+ G AG
Sbjct: 79 NPVEIQPIPLWEETKQSGVSSNSGAGLEALGSSGSLANHPNPPELEQPVQIECGLAGTV 138

Query: 105 MRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP-----PV 159
MR L A V A G A + D +RP+ L+ L LGA+ + +D P P
Sbjct: 139 MRFLPALVVALGVPARFTADAA--ANKRPLRGLLEALASLGANWE----SDDPLDGIFPF 192

Query: 160 RVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLM 218
+N G + + + SSQ++SALL++APL + I ++ S+P+++MTL +
Sbjct: 193 TINPRRGDVPEVITVDTAASSQFVSALLLSAPLWGKPLTIRCKTPVVPVSLPHIQMTLEAL 252

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTV 273
G+ A S D + Q P + + +E D S+A FLA A I GG V+V
Sbjct: 253 SLRGINATGSIQSDGTW---QWRVEPDSVFGQDLAIEPDLNAGPFLAAAGIIGGAVSV 308

Query: 274 EGC-GTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPD 332
G TS GD+ + ++L G +V T G L+A+ ++ ++ +
Sbjct: 309 PGWPAHTSQVGD L-WRQILPQFGMQVRHRCGVFTARG-----TGILRAVSLDCSQCGE 360

Query: 333 VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK 392
+ T+A +A A G + + ++ R ET+R+ A+ EL KLG C ITP +
Sbjct: 361 LVPTIAALAAHASGVSHLEGLSHLRGHETDRLNALYQELQKLGIR-----CAITPEDG 413

Query: 393 LNVTAID-----TYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDY 435
L + I Y DHRMA +L + I D G T KT PD+
Sbjct: 414 LEIIGIPRTQLGARLPDQPLMMRAYGDHRMATFAALMGLYRT-IQIDDIGATTKTLPDF 472

Query: 436 FDVLSTFV 443
+ + +
Sbjct: 473 PQMWAQVI 480

>ref|ZP_04196642.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH603]
gb|EEL71702.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH603]
Length = 424

Score = 130 bits (327), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 120/442 (27%), Positives = 211/442 (47%), Gaps = 41/442 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EGTT V N L ED + + LG+ +E
Sbjct: 10 LNGKIVVPGDKSISHRSVMFGAIAEGTTKVSNFLGEGDCLSTIACFQKLGIEQ---FG 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G +++ KE L +GN+G +R + + ++T + D + +RP+
Sbjct: 67 NDVTIYKGKHLNLQEPKE--VLDVGNSGTTIRLMLGILANTPFHSTIIGDA--SIGKRPM 122

Query: 135 GDLVVLGKQLGADVDCFLGTDGPPVRVNGIGLPGGKVK----LSGSISSQYLSALLMAA 190
+ L ++ A +D P+ + G GKVK S S+Q SA+L+A
Sbjct: 123 KRVTDPLSKMNAQIDGRENGQYTPLSIRG-----GKVKGMHYHSPVASAQVKSALLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G+ + + + S + E R++ FG + + ++GGQ+ K + V
Sbjct: 177 --LQEGEGITTVTEPMQSRDHTE---RMLRAFGCTVDVNGRT--VSLQGGQQLKGA-DIEV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + + +E G + V +VL MGA ++ +
Sbjct: 229 PGDISAFAFLVAGAIQNSKLVLENVGLNPTRTG--LDVLTGMGALISIDH----IRN 282

Query: 310 PPREPFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKET 361
EP G LK I++ +P + + V+AL A +G T I++ +VKET
Sbjct: 283 EEFEPGCDITIETSKLKGIEGGTLIPRLIDEIPVIALLATQAEGITVIKNAEELKVKET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPV 420
R+ + EL KLGA +E PD II + L +++++ DHR+ M ++A+C + V
Sbjct: 343 NRIDTVDELGKLGAKIEATPDGMIIYGKQSLKGNTVNSHGDHRIGMMLAIASCIIDGEV 402

Query: 421 TIRDPGCTRKTFFPDYFDVLSTF 442
I + ++P++F+ L+
Sbjct: 403 KIENSDAVAVSYPEFFEQLAAL 424

>ref|ZP_02410001.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 14]
ref|ZP_02454304.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 9]
ref|ZP_03451048.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
ref|ZP_03792360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pakistan 9]
gb|EEC36862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
gb|EEH27318.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia

pseudomallei Pakistan 9]
Length = 451

Score = 130 bits (327), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 119/429 (27%), Positives = 190/429 (44%), Gaps = 27/429 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G V E+ GN+G+ +R L V + +V + R
Sbjct: 78 TTVVKG---DVMHVDREIVFDPGNSGVVLR-LLMGVAGYLPDTRFVTQYRYSLGVR SQ 132

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 133 AEMVAALRRLNVECEAVGPEARLPISMRSTRAL-GKHTEVSCCKSSQFLSGLLYLGAIGE 191

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D+EI+++D + + V T+ + GV E+ ++ RF++ G ++K P V D
Sbjct: 192 RDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAAFRRFFVPGDRFRK-PSEFTVGADP 250

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPPRE 313
+S + LA VT+ G F E GA + + T+T + P
Sbjct: 251 ASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDTGTLIDELPGN 299

Query: 314 PF---GRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
G ++A D + + PD LA A FA+G + ++ R KE++R+ R E
Sbjct: 300 RIRIRGGASIRAQDFDGLAPDAVPALAGRAAFAEGTSTFYNIHIRYKESDRISDFRE 359

Query: 371 LTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-SLAACAEVPTIRDPGC 427
L KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 360 LDKLGVRSEEKLDQLIIHGNPRGYRGGA VVDGHDHGLIMALTITGLHCEHPVLIKEPHH 419

Query: 428 TRKTFPDYF 436
+T+PDYF
Sbjct: 420 VGQTYPDYF 428

>ref|ZP_04658748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas flueggei
ATCC 43531]
gb|EEQ48860.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas flueggei
ATCC 43531]
Length = 434

Score = 130 bits (326), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 122/437 (27%), Positives = 199/437 (45%), Gaps = 39/437 (8%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 75
G + +PG KS+S+R ++ A L ++N L++ D +G +R+LG ++E
Sbjct: 15 QGMIDIPGDKSISHRVFMFAGLNTVPVHINNFLHAADCLSTVGVMRSLGTAIEFLNE-NE 73

Query: 76 AVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G + E + + GN+G +R + + A + G + RP+
Sbjct: 74 LIVTGK---LHGLSEPMNVLDAGNSGTTTLRLMMGV L--APQSFLSAFSGDASLTRRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L ++GA + + P+ V GG G S S+Q SA+L+A A
Sbjct: 128 RRVLLPLSEMGARIYGRNANNLPLVVVPTGGKLRGIHYKSPVASAQVKSAILLAGLYA- 186

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D + + +S + E +++ FGV+ E S S F ++ G Y++P V GD
Sbjct: 187 -DAPTTVTEPYVSRDHTE---QMLAGFGVRIERSGTSVTVFPVEDG-GYRAPDEITVPGD 241

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+YFL AG+ I + + G + + +VL MGA ++ R
Sbjct: 242 ISSAAYFLVAGSIKDSRLRLNNVGINPRTGTI--LDVLRMGHAHISVQNE-----R 291

Query: 313 EPFGR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G L + MP D LAV ALFA+G T I RVKE
Sbjct: 292 ESGGECVADLFVESASLHGVSFGAEIMPRILIDEIPI LAVAALFAEGDTVITGAGELRVKE 351

Query: 361 TERMVAIRTELTKLG-ASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP 419
T+R+ A+ TE KL S++E D +I ++ + +YDDHRMAM+ ++ A
Sbjct: 352 TDR LHAVATEFQKLAPGSI DEREDGLVIHGKSEIQRARVKS YDDHRMAMSLAVLGAAGKG 411

Query: 420 VTIRDPGCTRKTFPDYF 436
V I +P ++P +F
Sbjct: 412 VLIENPESVNISYPTFF 428

>ref|ZP_03761642.1| hypothetical protein CLOSTASPAR_05676 [Clostridium asparagiforme
DSM 15981]
gb|EEG52259.1| hypothetical protein CLOSTASPAR_05676 [Clostridium asparagiforme
DSM 15981]
Length = 429

Score = 130 bits (326), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 196/435 (45%), Gaps = 39/435 (8%)

Query: 15 ISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG + +PG KS+S+R ++ ++++G T + L D + R +G+ + D
Sbjct: 13 LSGELTVPGDKSISHRAVMFGSIAKGLTEIRGFLQGADCLSTIACFRRMGVGI--DNLGD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R +V G G + K L GN+G MR ++ + A N L G +++RP
Sbjct: 71 RVLVHGNG----MRGLKRPAGLLDCGNSGTTMRLISGILAAQ--NFDVTLTGDA SIQKRP 124

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L +GAD+ C P+R+ G L G S S+Q SA+L+A A
Sbjct: 125 MKRIIDPLSMMGADIASVKNKGCAPLRIKG--RRLTGIHYN--SKVASAQVKS AVLLAGLYA 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-----DRFYIKGGQKYKSPKN 247
G + + +S + E+ LR FG + D + G K P
Sbjct: 183 QGGTSV--TEPALSRNHTELMLR---HFGAAVN SCGATATIAPADELF---GAKVAVP-- 232

Query: 248 AYVEGDASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
GD SSA+YF+AGA + G V ++G G + + +V MGA + +
Sbjct: 233 ----GDISSAAYFIAGALMVPGSQVLKIGVGINPTRAGI--LKVCRDMGADLELLNENHD 286

Query: 307 VTGPPREPFGGRKH-LKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
P + R L V +P D +A +A A G T I+D A +VKE+
Sbjct: 287 GAEPTADLLVRHSPLHGT VVEGEVIPTLIDELPMIAAMACTAQGETVIKDAAE LKVKESN 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ + L +GA V E D II L+ ID++ DHR+AM F++ A CA+ T
Sbjct: 347 RIAIMAESLNMAGADV TETEDGMIIRGGRPLHGA EIDSHLDHRIAMTFAVTALCADGLTT 406

Query: 422 IRDPGCTRKTFPDYF 436
IRD C ++P ++
Sbjct: 407 IRDAQCVNISYPGFY 421

>ref|NP_341856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus
solfataricus P2]
ref|ZP_06388466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus
solfataricus 98/2]
sp|Q980I5.1|ARO A_SULSO RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAK40646.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase)(EPSP
synthase) (aroA) [Sulfolobus solfataricus P2]
gb|ACX91520.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus
solfataricus 98/2]
Length = 414

Score = 130 bits (326), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 207/447 (46%), Gaps = 61/447 (13%)

Query: 14 EISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73

Sbjct: 9 +ISG +K P SKSL+ R++ L+ + + NL+ SEDV + ++R LG+ V+ +
KISGIIKAPQSKSLAIRLIFLSLFTF--VYLHNLVLSERVEDAIKSVRALGVKVNSEF 66

Query: 74 KRAVVVGCGGKFPVEDAK-EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
P E + +E + L + +R L + A GG T +D +R R

Sbjct: 67 -----IPPEKLEIKERFIKLGKSATTLRMLIPILAAIGGEVT--IDADESLRRR 113

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L G + P+ + G L ++K+SG SSQY+S L+ A +

Sbjct: 114 PLNRIVQALSNGYISFSSY----SLPLTITG--KLSSNEIKISGDESSQYISGLIYALHI 167

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN----- 247
G IEI+ + S Y+ +T+ L +RFG SD +FY G + + +P N

Sbjct: 168 LNGG-SIEILPPISSKSYILLTIDLFRKFG-----SDV--KFY--GSKIHVNPNNLVEFQ 217

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD AS++ A ++GG +T+ GD ++ MGA + +

Sbjct: 218 GEVAGDYGLASFYALSALVSGGITTITNLWEPKEYFGDHSIVKIFSEM GASSEYKD---- 273

Query: 307 VTGPPREPFGFRKHLKA-----IDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
GR +KA I +++ PD+AMT+A ++ A+G + I + R+KE

Sbjct: 274 -----GRWFVKAKDKYSPIKIDIDDAPDLAMTIAGLSAIAEGTSEIIGIERLRIKE 324

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEK--LNVTAIDTYDDHRMAMAFSLAACAEV 418
++R+ +IR L G E + +I K LN D +DHR+AM S A

Sbjct: 325 SDRIESIRKILGLYGVGVSEVKYNSILIFGINKGMLNSPVTDCCLNDHRVAMMSSALALVNG 384

Query: 419 PVTIRDPGCTRKTFPDYF-DVLSTFVK 444
V I C K+ P+Y+ D+LS K

Sbjct: 385 GV-ITSAECVGKSNPNYWQDL LSLNAK 410

>ref|YP_001836078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae CGSP14]
gb|ACB90613.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae CGSP14]
Length = 431

Score = 130 bits (326), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 208/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G++++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E

Sbjct: 11 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 131
VG G ++A L +GN+G ++R ++ + AG + + G + +

Sbjct: 71 GVITIQGVGMAGLKAPQNA-----LNMGNSTGTSIRLISGVL--AGADFEVEMFGDDSLSK 123

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D P+R+ G L +L + S+Q SAL+ AA

Sbjct: 124 RPMDRVTLPLKKMGVSISGQTERDLLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E +++++FG S + ++G QK K V

Sbjct: 183 QAKG--ESVIEKEYTRNHT---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 234

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V

Sbjct: 235 GDISSAAFVLVAGLIAPNSRLVLQNVGINETRTGI--IDVIRAMGGKLRKITEID-PVAKS 291

Query: 311 PREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +

Sbjct: 292 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELKVKETDRIQVV 351

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +

Sbjct: 352 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 411

Query: 426 GCTRKTFPDYFDVLSTFV 443
++P +FD L + +

Sbjct: 412 EAINTSYPSFFDDLESLI 429

>ref|YP_003251648.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
ref|YP_004132723.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
gb|ACX77166.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
gb|ADU94580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
Length = 427

Score = 130 bits (326), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 123/445 (27%), Positives = 212/445 (47%), Gaps = 37/445 (8%)

Query: 12 IKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G +++PG KS+S+R ++L AL+ G TV+D+ L D + R LG+ + D
Sbjct: 7 VSSLRGMIEVPGDKSISHRAVMLGALASGRTVIDHFLPGADCLSTIDCFRKLGVDIRQDG 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VV G G P + L +GN+G R L + +A V D + +
Sbjct: 67 TT--VVVEGAG---PGGLREPAAVLDVGNSTGTARLLLGILAGQPFHACLVGD--ESIAK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAA 190
RP+G + L+++GA +D G + P+ + G P ++ + + S+Q SA+L+A
Sbjct: 120 RPMGRVTKPLREMGARIDGREGGNYTPLSIRGGALRP--LRYTSPVASAQVKSALLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
D + + S + E +RL FG E + + G Q+ + + YV
Sbjct: 177 LFT--DGVTSVTEPHRSRDHTERMVRL--FG--GEVNVVDGLTVSVAGPQRLRG--THIYV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVGECGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + +T++ G + +VL MGA + V
Sbjct: 229 PGDISSAAFFLVAGAIVPNSEITLKNVGLNPTR--TGIIDVLTQMGADIAIDN---VRN 282

Query: 310 PPREFPG-----RKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP G L+A+++ + +P + + ++AL A+G T I+D + +VKET
Sbjct: 283 EETEPVGDITVTRTSTLRAVEIGGDLIPRLIDEIPIIALLATQAEGTTVIKDASELKVET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
+R+ + TEL KLGA +E D +I P + +D++ DHR+ M ++AAC A+
Sbjct: 343 DRIHTVVTELKKGADIEATDDGMIRGKTPLYADGIVVDSHGDHRIGMMLAVAACIAKG 402

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFV 443
V + ++P +F L + +
Sbjct: 403 TVRLERSEAVAVSYPAFFADLRSL 427

>ref|ZP_05095037.1| 3-phosphoshikimate 1-carboxyvinyltransferase [marine gamma
proteobacterium HTCC2148]
gb|EEB78587.1| 3-phosphoshikimate 1-carboxyvinyltransferase [marine gamma
proteobacterium HTCC2148]
Length = 434

Score = 130 bits (326), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 138/444 (31%), Positives = 212/444 (47%), Gaps = 32/444 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E L P ISG ++PG KS+S+R ++L AL+ GTT V L +D L R +G+
Sbjct: 2 EFKLLPGGTISGEARVPGDKSMHSRISIMLGALAAGTTRVSGFLEGDDALATLATFRAMGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
S+E + + VVV G + A + L LGNAG MR + + AG VL G
Sbjct: 62 SIE--RHGEDEVVHGVGLHGL--AAPDGPLDLGNAGTGMRLMCGLM--AGQPFDTVLTG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+G ++ L+ +GA +D G PP+++ G L G L + S+Q S
Sbjct: 116 DASLCSRPMGRVIDPLRLMGAKIDAQEGGR--PPLKITGGSQNLNGIHYDLPMASQVKS 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245

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      +L+A  A G  +      P  + T R++ FG + +      +  ++GG  K+
Sbjct: 174 VLLAGLYAQGRSVT-----EPAPTRDHTERMLRGFGYEVKR--EGEVISLQGGGSLKA- 225

Query: 246 KNAYVEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +  V D SSA++FL A+IT G+  +T G T      +  +L +MGA +T  +
Sbjct: 226 ADIDVPADISSAAFFLVAASITPGSDLLLTHVGINPTR----IGVLNILNLMGADITL-K 280

Query: 303 TSVTVTGPPPREPFGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
      V G P      ++ L +D+  +++P D      L + A A G T +R      R
Sbjct: 281 NEREVGGEVPADIQVRYAPLHGVDPEDQVPLAIDEFPALFIAAACAQGRTVLRGAEEELR 340

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-A 416
      VKE++R+ A+ L LG + E D II      +  I T+ DHR+AMAFS+AA A
Sbjct: 341 VKESDRIAAMAEGNLTLGVNNEVLEDGIIIE-GGTIGGGEIRTHMDHRIAMAFSIALRA 399

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLS 440
      E  + + D      +FP FD L+
Sbjct: 400 EQEIVVLDCDHVATSFPG-FDALA 422

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>ref|ZP_05138490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
gb|EEE40315.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
Length = 436

```

Score = 130 bits (326), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 120/445 (26%), Positives = 206/445 (46%), Gaps = 44/445 (9%)

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Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      ++ G +K+PG KS+S+R L++ ++++G T ++ L+SED      LR LG+++
Sbjct: 12 KLKGGIKVPGDKSISHRALIIGSIAGNTTIEGFLHSEDPLSTADCLRKLGVNIPKIIKN 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLGDVPRMRER 132
      +  + G G      ++ KE ++ GN+G MR L + A G ++L G + ER
Sbjct: 72 EPFTISGKG----LDGLKEPKEILNCGNSGTTMRLMLGLLAAQEGK-NFILTGDASLNER 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
      P+G + L +G +      + P+ +NG      KL G +      S+Q SA+
Sbjct: 127 PMGRVGKPLSLMGGKISGREFGNKAPISING-----EKLKGCVIGTPVASAQVKSAL 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDR-FYIKGGQKYKSP 245
      L+A A G + I+ S + E R+++ FG      R IK G
Sbjct: 179 LLAGLNASGTTSV--IEPASSRDHTE---RMLKAFGADISIRGELGRNIVIKSGSNLIGQ 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      +  + GD SSAS+++ A+I V ++ G + + V++ MG + S
Sbjct: 234 R-VLIPGDISSAFWMIAASIVPNSEVVIQNVGLNPTRTGI--LNVMDSMGCNYEILDKS 290

Query: 305 VTVTGPMPREPFGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVAS 355
      T+ G EP G      +L++ V + +P D L V A F G + I+D
Sbjct: 291 -TIAG---EPIGSIKVKTSNNLRSFTVEGDILPKLIDEIPILTVAACFCSGVSEIKDAQE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
      RVKET+R+ + +L K GA + E D II K + +D+ DHR+AM+ ++A+
Sbjct: 347 LRVKETDRLKVMARQLQKFGAEITEKEDGLIINGQSKFHSAEVDSETDHRVAMSLAIASL 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVL 439
      A+ I R ++P +++ L
Sbjct: 407 LAKGTSKIMRADAARVSYPTEFWHEEL 431

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>ref|ZP_03983417.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
HH22]
gb|EEI58465.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecalis
HH22]
Length = 428

```

Score = 129 bits (325), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 203/435 (46%), Gaps = 27/435 (6%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K + GT+ +P KS+S+R ++ A+S G T + N L ED L A R+LG+++E D
Sbjct: 9 VKHLQGLTMVPSDKSISHRSIMFGAISSGKTTITNFLRGEDCLSTLAAFRSLGVNIEDDG 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G ++ AK + + GN+G +R + + AG L G + +
Sbjct: 69 TT---ITVEGRGFAGLKKAKNTIDV---GNSGTTIRLMLGIL--AGCPFETRLAGDASIAK 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ +++ L Q+GA+ T+ PP+ + G L + + S+Q SA+L AA
Sbjct: 122 RPMNRVMLPLNQMGAEQGVQQTEFPPIISIRGTQNLQPIDYTMPVA-SAQVKSAILFAAL 180

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + ++K + + E +R +FG E + + G Q+ + +N V
Sbjct: 181 QAEGTSVV--VEKEKTRDHEEMIR---QFGGTLEVD--GKKIMLTGFPQL-TGQNVVVP 232

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETSVTVTG 309
GD SSA++FL AG + + ++ G Q +V++ MG VT E +G
Sbjct: 233 GDISAFAFLVAGLVVPDSEILLKNVGLN--QTRTGILDVKNMGGSVTILNEDEANHS 290

Query: 310 PPREFGRKHLKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVA 366
L A ++ +P + L ++AL A G T IRD +VKET R+ A
Sbjct: 291 DLL--VKTSQLTATEIGGAIIPRLIDELPIIALLATQATGTTIIRDAEELKVKETNRIDA 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRD 424
+ ELT LGA + D II P L+ + +Y DHR+ M +AA V +
Sbjct: 349 VAKELTILGADITPTDDGLIIHGPTSLHGGRVTSYGDHRIGMMLQIAALLVKGGTVELDK 408

Query: 425 PGCTRKTFPDYFDVL 439
++P +FD L
Sbjct: 409 AEAHSVSYPAFFDDL 423

>ref|ZP_02084436.1| hypothetical protein CLOBOL_01962 [Clostridium bolteae ATCC BAA-613]
gb|EDP17722.1| hypothetical protein CLOBOL_01962 [Clostridium bolteae ATCC BAA-613]
Length = 426

Score = 129 bits (325), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 123/438 (28%), Positives = 196/438 (44%), Gaps = 27/438 (6%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
G +++PG KS+S+R ++ ++++G T + N L D + +G+ +E +K
Sbjct: 8 HFKGEIRVPGDKSISHRAVMFGSVAQGLTEIHNFLQGADCLSTIACFEKMGIDIE-NKGG 66

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
K V+ G +A EV L GN+G R ++ + G N L G + +RP
Sbjct: 67 K---VLVHGRGLHGLNAPREV-LDCGNSGTTTRLISGIL--CGQNFVTLTGDESICKRP 120

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L +GA + C P+ + G G G S S+Q SA+++A A
Sbjct: 121 MKRIMEPLAMMGARITSIKDNGCAPLLIKG--GPVHGIHYDSRVASAQVKSAILLAGLYA 178

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D + + +S + E+ LRL FG A+ S IK + V GD
Sbjct: 179 --DSPTSVTEPYVSRNHSELMRL---FG--AQVSTEGTTAVIKPANELHG-NQVMVPGD 230

Query: 254 ASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+YF+AG + G V+ G + + V MGA+ S TG P
Sbjct: 231 ISSAAYFIAGGLMVPGSQVLIRNVGINPTRDGI--LRVCRDMGAHIELLNVSOGG-TGEPT 287

Query: 313 EPFGRKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+H L + + +P D +A +A FA+G T IRD +VKE+ R+ +
Sbjct: 288 ADILVRHGSGLHGTVIGSVIPTLIDELPVIAAMACFAEGETVIRDAGELKVKESNRIVAM 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
L +GA V E D II L+ ID+ DHR+AM F++ A CA+ IRD
Sbjct: 348 VQGLAAMGADVTEDEDGMIIRGGAPLHGAVIDSRKDHRIAMTFAVTALCADGITEIRDAD 407

Query: 427 CTRKTFPDYFDVLSTFVK 444

C ++P ++ L +
Sbjct: 408 CVNISYPGFYSDLKKLAQ 425

>ref|ZP_07053534.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria grayi DSM 20601]
gb|EF184547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria grayi DSM 20601]
Length = 429

Score = 129 bits (325), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 116/440 (26%), Positives = 203/440 (46%), Gaps = 25/440 (5%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G +++PG KS+S+R ++ AL+ GTT + + L ++D L A + LG+ +E D
Sbjct: 8 QNLQGNIQVPGDKSISHRSIMFGALANGTTTITHFLRADDCLGTLAAFQKLGVKIEDDGE 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ G G D +V GN+G +R L +T G VL G + R
Sbjct: 68 KVKVHGKGFAG-LEAPDGPIDV----GNSGTTIRLLMGILT--GARIPAVLFGDSSIARR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +++ LK++GA + ++ P+ + G L + + S+Q SA+++A
Sbjct: 121 PMNRVMLPLKEMGASIAKDDSEFAPLTIRDNGKLQAITYDMPVA-SAQVKSAILLAGLQ 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ I ++K + T +++ +FG + R G + + + V G
Sbjct: 180 AEGETVIHELEK-----TRDHTEQMIRQFGGTIQTEGKTIRVT---GNQTLTGQTITVPG 231

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FLA + + + +E G + + +V+E MG V S P
Sbjct: 232 DISSAAFFLAAGLLAENSEIHLENVGINPRTGI--LDVIEQMGGSVQANPSTHQGEPS 289

Query: 312 REPFGFR-KHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
+ R L +++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 290 ADLIVRTSELHGTEISGSLIPRLIDEIPVIALLATQAEGTTVIKDAAELKVKETNRIDAV 349

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDP 425
ELTKLGA +E D II L+ + +Y DHR+ M +AA V +
Sbjct: 350 AAELTKLGARIEPTEDGLIIHGKTALHGNAVTSYGDHRIGMMLQIAALLVTSGEVELDKA 409

Query: 426 GCTRKTFDPDYFDVLSTFVK 445
++P +F L +
Sbjct: 410 EAVSVSYPAFFADLEKLIHQ 429

>ref|ZP_07340631.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS455]
ref|ZP_07344945.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP-BS293]
ref|ZP_07347597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP14-BS292]
ref|ZP_07350239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS397]
ref|ZP_07351779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS457]
ref|ZP_07354014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS458]
emb|CBW34850.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae INV200]
gb|EFL65537.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS455]
gb|EFL67718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP14-BS292]
gb|EFL70365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae SP-BS293]
gb|EFL72642.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS458]
gb|EFL74867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS457]
gb|EFL76358.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus pneumoniae BS455]

pneumoniae BS397]
Length = 427

Score = 129 bits (325), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 208/438 (47%), Gaps = 25/438 (5%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7 IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67 GVITIQVGMAGLKAPQNA-----LNMGNSTGSIIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + + LK++G + D P+R+ G L +L + S+Q SAL+ AA
Sbjct: 120 RPMDRVTLPLKKMGVSISGQTERDLLPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179 QAKG--ESVIEKEYTRNHT---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252 GDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 231 GDISAASFVLVAGLIAPNSRLVLQNVGINETRTGI--IDVIRAMGGKLVKITEID-PVAKS 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAI 367
LK ++ +P + L ++AL A G T I+D +VKET+R+ +
Sbjct: 288 ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQGVTVIKDAEELVKKETDRIQVV 347

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
L +GA + D II L+ ++T+ DHR+ M ++AA A+ V +
Sbjct: 348 ADALNSMGADITPTADGMIKGSALHGARVNTFGDHRIGMMTAIAALLVADGEVELDRA 407

Query: 426 GCTRKTFFPDYFDVLSTFV 443
++P +FD L + +
Sbjct: 408 EAINTSYPSFFDDLES LI 425

>ref|ZP_06555080.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
FSL J2-071]
gb|EFD91725.1| 5-enolpyruvylshikimate-3-phosphate synthase [Listeria monocytogenes
FSL J2-071]
Length = 428

Score = 129 bits (325), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 120/437 (27%), Positives = 219/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEE EI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVRGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQMGAKMHGKDGSEFAPITINGKQSLKRMEYHPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQ + + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQTF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPRTGTI--FDVVEQMGGSLVVKDSSRS-TGKLAGT 291

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIR 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 292 VVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELVKKETNRIDAVAT 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V +
Sbjct: 352 ELNKMGAADITPTEDGLIIRGKTPHAAVNTSYGDHRIGMMLQIAALLVEEGDVELERAEA 411

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 412 VSVSYPTFFEDIRSLK 428

>ref|ZP_08014836.1| hypothetical protein HMPREF9464_00055 [Sutterella wadsworthensis
3_1_45B]
gb|EFW02866.1| hypothetical protein HMPREF9464_00055 [Sutterella wadsworthensis
3_1_45B]
Length = 464

Score = 129 bits (325), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 130/445 (29%), Positives = 205/445 (46%), Gaps = 27/445 (6%)

Query: 13 KEISGTVKLPKSKLSNRILLAAALS--EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+++SGT+ SKS ++R L+ AAL + +V S D+ ALR LG +E
Sbjct: 8 QQLSGTIAAIPSKSWAHRELIAAALGAPDHAVLVRFRGGSNDIEATCRALRGLGAKIER- 66

Query: 71 KAAKRAVVVGCGGKFP-VEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ G G + + A+ + L G +G +R L A G A +
Sbjct: 67 -----LPGTGARVEGISRAERNTRTETPVLDCGESGTTLYLLPVAAALNGPAGVIFT 119

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184
G R+ RP L L++ G +D + + V G L G LSG++SSQ+L
Sbjct: 120 GSGRLPARPQEPPLAGELERHGITLDYAEASPGALLPVRLTGRLPGAYALSGAVSSQFLG 179

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR----FYIKGGQ 240
LL A + G + + D+L S PYV MTL +++ GV+ S + D+ + I G
Sbjct: 180 GLLYALSVLDGPSTLAVKDRLESEPYVRMTLSALQQSGVEIAESRT-DQGLPLWTIAGRG 238

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
P++ VEGD S+A+++L A+T + VEG TSLQGD ++L +GA+V
Sbjct: 239 VLTPPEDVQVEGDWSNAAFWL CAGALTQNPEGIAVEGLSLTSLQGDRAVVDILSRLGAQV 298

Query: 299 TWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRV 358
+ T + P L+ ++ ++PD+ LAV A A+G T R+
Sbjct: 299 ESSSEGRIGTVRVKPKNGAALRGQITIDARQIPDLVPILAVAAGAAEGETRFTHAERLRI 358

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI---ITPPEKLNVTADITYDDHRMAM-AFSLAA 414
KE++R+ + L LG EE PD + I K + I ++ DHR+ M A A
Sbjct: 359 KESDRQLSTAQLHLHLLGVPHEELPDGLVVHGIGSARKFSGGRISSEFKDHRIVMAAAVAGA 418

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVL 439
P+ I K++P +F+ L
Sbjct: 419 SGGAPIVIDGAEDAASYPHFFEDL 443

>ref|YP_002349603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes HCC23]
sp|B8DC03.1|AROALISMH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACK38989.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes HCC23]
Length = 428

Score = 129 bits (325), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 120/437 (27%), Positives = 219/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 12 GAITVPDGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEEIEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSTTIRLMMGIL--AGRDFDTVILGDESIKRPMM 123

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQMQGAKMHGKDGSEFAPITINGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQ + + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQTF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGT 291

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 292 VVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAT 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V +
Sbjct: 352 ELNKMGAADITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERAE 411

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 412 VSVSYPTFFEDIRSLK 428

>emb|CAR84684.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes L99]
Length = 430

Score = 129 bits (324), Expect = 8e-28, Method: Compositional matrix adjust.
Identities = 120/437 (27%), Positives = 219/437 (50%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSKSLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG V+ ++ +
Sbjct: 14 GAITVPGDKSMHSRIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEEEI 71

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRPMN 125

Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+Q+GA + G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 126 RVMLPLQMQGAKMHGKDGSEFAPITINGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQ + + + V GD S
Sbjct: 185 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQTF-TGQEMTVPGDVS 236

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 237 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGT 293

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+ T
Sbjct: 294 VVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAT 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA E V +
Sbjct: 354 ELNKMGAADITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERAE 413

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 414 VSVSYPTFFEDIRSLK 430

>gb|ADO78122.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halanaerobium
praevalens DSM 2228]
Length = 429

Score = 129 bits (324), Expect = 8e-28, Method: Compositional matrix adjust.

Identities = 135/451 (29%), Positives = 228/451 (50%), Gaps = 42/451 (9%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P +ISG +++PG KS+S+R ++LAAL+EG + ++ LL +ED L + LG +
Sbjct: 5  VKPATKISGQIEVPKGSISHSRIILAAALAEESKIEGLLEAEDCLKTLNIMADLGPEIV 64

Query: 69  ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
KA + ++ G +++AK L GN+G +MR LT + A + VL G
Sbjct: 65  KIKAGE--YLIKQGLNGLKEAKN--ILDCGNSGTSMRLLTGLLAAQ--DFYSVLSGDHS 118

Query: 129  MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ ++ L Q+GA + P+ + G L K L + S+Q SA+L+
Sbjct: 119  LLKRPMARIKPLSQMGAKI-WSRKKGLAPLSIQG-QKLKALKYNLPVA-SAQLKSAILL 175

Query: 189  AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKN 247
AA + E II+ +S + E R+++ GV E DR +K +K + P
Sbjct: 176  AALKT--EAETVIEPAVSRDHE---RMLKEAGVDLEIL--ADRIILKQAKKRIKPLR 228

Query: 248  AYVEGDASSASYFLAGAAITG-GTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ + GD SSA++F+A A + G + ++ G Q F EV++ MGA
Sbjct: 229  SKIPGDISSAAFFIAAAILAKKGELLIKNVGIN--QTRSGFLEVIKAMGANFEILNK--- 283

Query: 307  VTGPPREPFGRK-----HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVA 354
+E G K LKA+++ +P D +AV+A+FA+G T I+D A
Sbjct: 284  -----KEEAGEKIADILVRPSTLKAIVEIKGKIIPRLIDELPIIAVLAVFAEGKTVIKDAA 338

Query: 355  SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-VTAIDTYDDHRMAMAFS-L 412
RVKET+R+ A+ TE KLG +E D I P+++ + +Y DHR+AM+ + L
Sbjct: 339  ELRVKETRIKALVTEFRKLIEIEAQADGMEIIGPQQVEGGVQLKSYDHRAMSLAIL 398

Query: 413  AACAEVPTIIRDPGCTRKTFPDYFDVLSTFV 443
A + ++I+ +FP++ +L+ +
Sbjct: 399  ALKTKQGLSIQGSSEIIMTSFPNFKLLAEVI 429
```

```
>ref|NP_923984.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gloeobacter violaceus
PCC 7421]
sp|Q7NLT3.1|ARO_A_GLOVI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC88979.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gloeobacter violaceus
PCC 7421]
Length = 432
```

Score = 129 bits (324), Expect = 8e-28, Method: Compositional matrix adjust.
Identities = 131/455 (28%), Positives = 212/455 (46%), Gaps = 47/455 (10%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + +SG + + G KS+S+R L+LAAL+EG +V++ LL +D LR LG +
Sbjct: 7  ITPARRLSGEIAGVAGDKSISHRALMLAALAEESVIEGLLPGDDPRSTAACLALGAEIS 66

Query: 69  A-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 127
D + R VG G D L +GN+G MR L V A L G
Sbjct: 67  GIDGSPVRVRGVLGRLHEPADV-----LDMGNSGTMR-LMLGVLAGQPGLFCTLTGDR 120

Query: 128  RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+R RP+ +V L+Q+GA + G GG+ L+ + + L A+
Sbjct: 121  SLRSRPMRLRVVSPLRQMGARI-----WGREGGRAPLA--VWGEQLRAID 163

Query: 188  MAAPLALGDVEIEIIDLK-----ISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK 237
+P+A V+ ++ +S P + + R++ FG AE ++
Sbjct: 164  FVSPVASAQVKSAYLLAGLLAAGLTSVSEPVRSDHSEMLRAFG--AEVLVDGTTAAVR 221

Query: 238  GGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G + ++ ++ V GD SSA+++L AG+ + + + G G + V + L MGA
Sbjct: 222  GPARLRA-QSLRVPGDISSAAFVWLVAGSIVPDSQLLLSGVGVNPTRTGV--LDALAAMGA 278

Query: 297  KVTWTETSVTVTGPPREPFGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIR 351
+ E V G P + LKA + +P D LAV A A G T IR
Sbjct: 279  DIA-VENRREVCGEVADLRVRSAPLACTIGGEWIPRLVDEIPVLAVAACCAAGKTVIR 337
```

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS 411
D A RVKE++R+ + EL +LGA +EE PD +I +L +++DDHR+AM+ +
Sbjct: 338 DAAELRVKESDRLATMARELGRLGAHIEERPDGLVIEGGHRLVGAGVESHDDHRVAMSLA 397

Query: 412 LAACAEVPVT-IRDPGCTRKTFPDYFDVLSTFVK 445
+A T I DP C ++P +++ L+ +
Sbjct: 398 VAGLVATGTTEIADPCATVSYPQFYEHRLARVRQQ 432

>ref|ZP_08005469.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp.
2_A_57_CT2]
gb|EFV77580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp.
2_A_57_CT2]
Length = 431

Score = 129 bits (324), Expect = 8e-28, Method: Compositional matrix adjust.
Identities = 122/439 (27%), Positives = 214/439 (48%), Gaps = 27/439 (6%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+K +SG + +PG KS+S+R ++ +++G TVV N L ED + R LG+S+E +
Sbjct: 10 LKGLSGEIAVPGDKSISHRSMVFGSIAKGTVVNTNLLGDCSTIACFRKLGVSIEQE- 68

Query: 72 AAKRAVVVGCGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ ++G G ++ E E L +GN+G +R + + AG VL G +
Sbjct: 69 -GNKVTIMKGK---MDGLHEPEAILDVGNSTTIRLMMGIL--AGRPFHSVLVGDESIA 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L GA + + P+ V G G L G +L + S+Q S+LL A
Sbjct: 122 KRPMTTRVTAPLSLFGAKIYGRKNGEFTPLSVIG-GPLAGAAAYELPVA-SAQVKSLLFAG 179

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G E II+ + + + E R+++FG E + IKGGQ + +V
Sbjct: 180 LQASG--ETVIIPEPMKTRDHT---RMIKQFG--GEVAADGHTIRIKGGQTLTGTE-IHV 231

Query: 251 EGDASSASYFLA-GAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FLA GA + + ++ G + + EVL+ MGA ++ +
Sbjct: 232 PGDISSAAFFLAAGAIVPNSEIKLKNVGLNPTRTGI--IEVLQQMGANISIEPYENGLAE 289

Query: 310 PPREFPGRKH-LKAIDVNMNMPDVMATLAVVALFA---DGPTAIRDVASWRVKETERMV 365
P + R LK + +P + + ++AL A +G T I+D +VKET R+
Sbjct: 290 PAGDITIRTSTLKGTVIEGALIPRLIDEIPIIALLATQAEGETVIKDAEELKVKETNRID 349

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRD 424
+ EL+KLGA + D +I L+ + ++ DHR+ M ++AA ++ V ++
Sbjct: 350 TVVKELSKLGADITATEDGMVIGKGRSSLSGGTVSSGHDHRIGMMLAVAAAISKGEVQLQQ 409

Query: 425 PGCTRKTFPDYFDVLSTFV 443
++P +F+ + +
Sbjct: 410 KEAISVSYPSPFFEHFESLI 428

>ref|ZP_03938367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus brevis
subsp. gravesensis ATCC 27305]
gb|EEI72274.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus brevis
subsp. gravesensis ATCC 27305]
Length = 434

Score = 129 bits (324), Expect = 9e-28, Method: Compositional matrix adjust.
Identities = 127/438 (28%), Positives = 214/438 (48%), Gaps = 34/438 (7%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ A+SEG T + + L +ED L A + LG+S++ D +
Sbjct: 12 LHGELSVPGDKSISHRGIMFGAVSEGRTTLHHFLTAEDCLSTLKAFFQLGVSIRKRD--GE 69

Query: 75 RAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ G G + K L +GN+G R + + AG N L G + +RP+
Sbjct: 70 TVVIEGVGLHGLKQSGKP---LDMGNSGTTTIRLIMGLL--AGQNFDSLTFGDDSLSKRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L ++GAD+ C TD P R++G L +L + S+Q SAL++AA A
Sbjct: 125 KRVSEPLAEMGADI-CV--TDGHLPARIHG-QKLHAIDYQLKVA-SAQVKSALILAAIQA 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEG 252
D +I+KL P T +++ FG + D IK + K + + V G
Sbjct: 180 --DQPSTLIEKL---PTRNHTKMLNFAGANIQ--TMADNVTIKVNPQPKLTGIDLTVP 232

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL A + +T++ G + +L+ MG KV E +G P
Sbjct: 233 DMSSAAFFLVAAATLVPSKLTILKNVGVNETR--TGLLSILKRMGGKV--IERHRNDSGEP 288

Query: 312 REPF--GRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVA 366
LK I++ ++P V L +VAL A+G + I RVKET+R+ A
Sbjct: 289 TADLVVSSAELKPIETGAEEIPAVIDELPLVALLAAKANGISKITGAGELRVKETDRIAA 348

Query: 367 IRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVTIR 423
+ E +KLG ++ E PD +I P ++ T +D++ DHR+ M ++A+ + + +
Sbjct: 349 VVQEFSLGIAIRELPDGFVIDGAKPWRVEKTKLDHSHGHRIGMTLAIASLLDEQLQLN 408

Query: 424 DPGCTRKTFFPDYFDVLST 441
++P+++FD L++
Sbjct: 409 GAESVNISYPEFFDDLAS 426

>ref|YP_003670909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
C56-T3]
gb|ADI26332.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacillus sp.
C56-T3]
Length = 427

Score = 129 bits (324), Expect = 9e-28, Method: Compositional matrix adjust.
Identities = 123/445 (27%), Positives = 211/445 (47%), Gaps = 37/445 (8%)

Query: 12 IKEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ + G +++PG KS+S+R ++L AL+ G TV+D+ L D + R LG+ + D
Sbjct: 7 VSSLRGMIEVPGDKSISHRAVMLGALASGRVIDHFLPGADCLSTIDCFRKLGVDIRQDG 66

Query: 72 AAKRAVVVGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
VV G G P + L +GN+G R L + +A V D + +
Sbjct: 67 TT--VVVEGAG---PGGLREPAAVLDVGNSGTTARLLLGILAGQPFHACLVGD--ESIAK 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSI-SSQYLSALLMAA 190
RP+G + L+++GA +D G + P+ + G P ++ + + S+Q SA+L+A
Sbjct: 120 RPMGRVTKPLREMGARIDGREGGNYTPLSIRGGALRP---LRYTSPVASAQVKSAVLLAG 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
D + + S + E +RL FG E + + G Q+ + + YV
Sbjct: 177 LFT--DGVTSVTEPHRSRDHTERMVRL---FG--GEVNVVDGLTVSVAGPQRLRG-THIYV 228

Query: 251 EGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL AGA + +T++ G + +VL MGA + V
Sbjct: 229 PGDISAAFFLVAGAIVPNSEITLKNVGLNPTR--TGIIDVLTQMGADIAIDN---VRN 282

Query: 310 PPREFPG-----RKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP G L+A+++ + +P + + ++AL A+G T I+D + +VKET
Sbjct: 283 EETEPVGDITVTRTSLRAVEIGGDLIPRLIDEIPIIALLATQAEGTTVIKDASELKVET 342

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEV 418
R+ + TEL KLGA +E D +I P + +D++ DHR+ M ++AAC A+
Sbjct: 343 NRIHTVVTELKKLGADIEATDDGMMIRGKTPLYADGIVVDSHGDHRIKMMLAVAACIAKG 402

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFV 443
V + ++P +F L + +
Sbjct: 403 TVRLERSEAVAVSYPAFFADLRSL 427

>ref|ZP_02713734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP195]
gb|EDT92455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
pneumoniae SP195]
Length = 427

Score = 129 bits (324), Expect = 9e-28, Method: Compositional matrix adjust.

Identities = 118/438 (26%), Positives = 207/438 (47%), Gaps = 25/438 (5%)

```
Query: 12  IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADK 71
      I+ + G+++PG KS+S+R ++ +L+EG T V ++L EDV + R LG+ +E
Sbjct: 7   IRHLHGSIRVPGDKSISHRSIIFGSLAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKD 66

Query: 72  AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
      VG G ++A L +GN+G ++R ++ + AG + + G + +
Sbjct: 67  GVITIQGVGMAGLKAPQNA-----LNMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSK 119

Query: 132  RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+ + + LK++G + D PP+R+ G L +L + S+Q SAL+ AA
Sbjct: 120  RPMDRVTLPLKMGVSISSQTERDLPPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAAL 178

Query: 192  LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G E II+K + + E ++++FG S + ++G QK K V
Sbjct: 179  QAKG--ESVIEKEYTRNHT---DMLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVP 230

Query: 252  GDASSASYFL-AGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
      GD SSA+++L AG + ++ G + + +V+ MG K+ TE V
Sbjct: 231  GDISAASFVLVAGLIAPNSRLVLQNVGINETRTGI--IDVIRAMGGKLEITEID-PVAKS 287

Query: 311  PREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAI 367
      LK ++ +P + L ++AL A T I+D +VKET+R+ +
Sbjct: 288  ATLIVESSDLKGTEICGALIPRLIDELPIIALLATQAQDVTVIKDAEELVKKETDRIQVV 347

Query: 368  RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
      L +GA + D II L+ ++T+ DHR+ M ++AA A V +
Sbjct: 348  ADALNSMGADITPTADGMIKGSALHGARNVTFGDHRIGMMTAIAALLVAGGEVELDRA 407

Query: 426  GCTRKTFFPDYFDVLSTFV 443
      ++P +FD L + +
Sbjct: 408  EAINTSYPSFFDDLES LI 425
```

```
>ref|YP_002572731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
      bescii DSM 6725]
sp|B9MQK4.1|ARO_AANATD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|ACM59958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldicellulosiruptor
      bescii DSM 6725]
      Length = 433
```

Score = 129 bits (324), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 126/448 (28%), Positives = 212/448 (47%), Gaps = 41/448 (9%)

```
Query: 13  KEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      ++I+ V +P KS+S+R +++ +L+ G T ++N L S+D + + L +E
Sbjct: 9   RKINSNVIVPPDKSISHRSIMIGSLANGVTEIENFLFSDDCLATINCFKNLSTDIEIRN- 67

Query: 73  AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
      + +V G G F + K+ L N+G R L ++ + +L G +++R
Sbjct: 68  -DKIIVKGNG--FALSAPKQ--ILDQNSGTTTRLLLGILSTQEFES--ILTGDSLSLKKR 120

Query: 133  PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      P+ + V L Q+GA+ + D P++V G L + L S+Q SAL+ A+
Sbjct: 121  PMKRVTVPLSQMGAEFEFLEKEDFLPIKVGSKKLKPIEYTLPIP-SAQVKSALIFASLK 179

Query: 193  ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR---FYIKGGQKYKSPKNAY 249
      A G I+ K S + E+ L+ + SW++ + ++ S
Sbjct: 180  AEGKSVIKESPK--SRDHTELMLKHA-----GANIKSWEKGVYTVTEILPSQISSIKIK 231

Query: 250  VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      + D SSA++F+ A I G +V +E C + + +VL+ MGA++ + V
Sbjct: 232  IPSDISAFAFFIVLALICEGSSVVIENCILNPTRTGI--IDVLKQMGAEIKIED---VE 285

Query: 309  GPPREPFGR-----KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      E G+ +L+ + V N +P D LAV A FA+G T I + RVKE
Sbjct: 286  NRNGELVGKIVARSSNLRGVKEKNDIPRIIDEIPILAVAAFAEGKTIIDHASSELRVKE 345
```

Query: 361 TERMVAIRTELTKLGA---SVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACA- 416
++R+ L GA +E G + II EKL +++Y DHR+AMA S+ ACA
Sbjct: 346 SDRIKTTVEMLKSFGAECYELENGLE--IIGSREKLKSAVVNSYKDHRIAMAASIMACAV 403

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
E TI D C +FP+++D+L + K
Sbjct: 404 EGESTILDADCVSISFPNFYDILFSSTK 431

>ref|YP_001090863.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9301]
sp|A3PBY7.1|ARO_A_PROM0 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AB017262.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9301]
Length = 436

Score = 129 bits (324), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 121/448 (27%), Positives = 204/448 (45%), Gaps = 44/448 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G +K+PG KS+S+R L++ +++EG T ++ L SED LR LG+++ K
Sbjct: 12 NLKGKIKVPGDKSISHRALIIGSIAEGETTIEGFLYSEDPLSTADCLRKLG VNIPEIKKD 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K + G G + KE ++ GN+G MR L + G ++L G + ER
Sbjct: 72 KPFTISGLG----INGLKEPKEILNCGNSGTTMRLLMGLLAGQEGK-NFILTGDISLNER 126

Query: 133 PIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + + P+ +NG KL G + S+Q SA+
Sbjct: 127 PMGRVKGKPLSLMGGKIFGREKGNKAPISING-----NKLKGCVMGTPVASAQVKSAL 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+A A G + I+ S + E R+++ FG + R IK G
Sbjct: 179 LLAGLKASGTTVS--IEPASSRDHTE---RMLKAFGADITIRGEFGRNVVIKSGGSLIGQ 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETS 304
K + GD SSAS+++ A+I V ++ G + + ++ MG + S
Sbjct: 234 K-ILIPGDISSASFWMIAASIVPNSEVLIQNVGLNPTRTGI--LNIMNSMGCNYEILDKS 290

Query: 305 VTVTGPPEPFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
T+ G EP G +LK+ + + +P D L V A F +G + I+D
Sbjct: 291 -TIAG---EPIGSIKVKTSNNLKSFIIEGDILPKLIDEIPILTVAACFCNGVSEIKDAQE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA- 414
RVKET+R+ + +L K GA + E D II K + +D+ DHR+AM+ ++A+
Sbjct: 347 LRVKETDRLKVMARQLQKFGAEITEKEDGLIINGQSKFHSAEVDSETDHRVAMSLAIASL 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A+ I ++P +++ L+
Sbjct: 407 LAKGTSKIMRADAASVSYPWFWEELAKL 434

>ref|YP_003595106.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter segnis
ATCC 21756]
gb|ADG12488.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter segnis
ATCC 21756]
Length = 443

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 137/448 (30%), Positives = 208/448 (46%), Gaps = 43/448 (9%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G V+ PG KS+S+R ++L AL+ GTT V+ LL +DV A++ G VE
Sbjct: 10 PGGALRGIVRAPGDKSISHRSMILGALATGTTTVEGLLEGDDVLATARAMQAFGARVE-Q 68

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ R + G GG D + GNAG +R + A AAG G +R
Sbjct: 69 EGVGRWRIEGQGGFSEPSDV-----IDCGNAGTGVRLIMGA--AAGFPMCATFTGDSSLR 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+G ++ L ++GA +LG D P+ + G G L G L S+Q SA+L+
Sbjct: 122 GRPMGRVLDPLARMGA---TWLGRDKGRLPLTLKG-GNLRGLNYTLP-MASAQVKSALL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIKGGQKY 242
A A G V E+I+ + + E R++ FG + D + + QK
Sbjct: 177 AGLHAEGGV--EVIEPEATRDHTE---RMLRAFGAEVIVEDRVVGEKTIHRLPESQKL 231

Query: 243 KSPKNAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V GD SSA++ +AG + G VTVEG L+ L MGA + +
Sbjct: 232 TG-THVAVPGDPSSAAFPLVAGLIVPGSEVTVEGVMLNELR--TGLFTTLREMGADLVIS 288

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASW 356
++ +G +H LK + V + P D LA+ A FA+G T +R V
Sbjct: 289 NRRMS-SGEEVGDTARHSLKGVVPPPERAPAMIDEYPILAIAAAFAEGDVTMRGVGEM 347

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTATIDTYDDHRMAMA-FS 411
RVKE++R+ L G VEE P+ I+ PP ++T+ DHR+AM+
Sbjct: 348 RVKESDRIALTAAGLEACGVDEEEPEGFIVHGTGQPPR--GGATVETHGDHRIAMSHLI 405

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVL 439
L A+ PV + +PG +FP + D++
Sbjct: 406 LGMAAQAPVAVDEPGMIATSFPGFADLM 433

>gb|EGD10005.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
vesicatoria ATCC 35937]
Length = 438

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 133/447 (29%), Positives = 212/447 (47%), Gaps = 36/447 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+ V Q + GT+ +PG KS+S+R ++ AAL++G + +D L ED LG
Sbjct: 6 QHWVAQGSALRGTLAIPGDKSVSHRAVMFAALADGISQIDGFLEGEDTRSTAAIFAKLG 65

Query: 65 LSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ ++ A++R V VG G P +A L GNAG MR L + A ++ VL
Sbjct: 66 VRIDTPSASQRIHVGVVDGLQPPTA-----LDCGNAGTGMRLLAGLLAAQRFDS--VL 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSI-SS 180
G + +RP+ + L Q+GA + L D PP+ V+ GG P + + S+
Sbjct: 119 VGDASLSKRPMRRVTGPLAQMGAKI---LTQDDGTPLHVH--GGQPLHGIDFVSQVASA 173

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q SA+L+A A G+ + P + T R++ FG+ S R ++GGQ
Sbjct: 174 QVKSALLAGLYAQGETSVTEPH-----PTRDYTERMLSAFGVEIAFSPGTAR--LRGGQ 226

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ ++ A V D SSA++F+ A+I + V + G + L +MGA ++
Sbjct: 227 RLRATDIA-VPADFSSAAFFIVAASIIPDSEVVLRAVGLNPRR--TGLLAALRLMGADIS 283

Query: 300 WTETSVTVTGPPREPFGRKH--LKAIDVNMNKMPPDVA---MTLAVVALFADGPTAIRDVA 354
E G P ++ L+ + + +PD+ L V A A G T + A
Sbjct: 284 -EENHAEHGGEVADLRVRYAPLQGVQIPEALVPDMIDEFPALFVAAAAAGKTTVTGAA 342

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
RVKE++R+ A+ T L LG V+E PD I + I+++ DHR+AMAF++A
Sbjct: 343 ELRVKESDRLAAMATGLRTLGVQVDETPDGATIH-GGTIGGGVIESHGDHRIAMAFIAAG 401

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVLS 440
C+ V + D +FP FD L+
Sbjct: 402 QCSTGTVQVNDIANVATSFPG-FDTLA 427

>ref|YP_004101072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermaerobacter
marianensis DSM 12885]
gb|ADU50345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermaerobacter
marianensis DSM 12885]
Length = 508

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 138/445 (31%), Positives = 211/445 (47%), Gaps = 37/445 (8%)

```

Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      ++P + + GT+++PG KS+S+R +LAA + G TV+++ D L L LG++V+
Sbjct: 26 VRPGRRLQGTQLQVPGDKSISHRAAMLAAGGRTVLESYAPGRDAASTLACLAALGVTVQ 85

Query: 69 ADKAAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      R V+ G G + P L GN+G MR L + +T D
Sbjct: 86 RPDPG-RVVIDGPGIAGWRAPA-----APLDAGNSGTTMRLLLGLLATRPFRSTLTGDA 138

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      +R RP+G +V L+++GA ++ G P+ V G G L G S S+Q SA
Sbjct: 139 S--LRRRPMGRVVEPLRRMGARIEGQDGGRLAPLHVQG-GDLQGIHHD-SPVASAQVKS 194

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      +L+A A G + + +S + E R++ FGV E ++GG+ ++P
Sbjct: 195 VLLAGLFAAGRTSVR--EPALSRDHTE---RMLPLFGVPVERDGLT--VAVEGGRPLRAP 247

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT--- 301
      + GD S+A+++LA A + + + + G G + F EVLE MGA+V
Sbjct: 248 ARLVIPGDPSSAAAFYLAAILCPDSRIVLPGVGNPTR--TGFLEVENMGARVGMARQA 305

Query: 302 -ETSVTVTGPPPREPFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
      + S P EP L+A+ + + +P D LAV+A A G T IRD
Sbjct: 306 GDGSAGDGPAGEPVADLTAETSALRAVTIGDGLIPLRIDEIPILAVLATQARGTTIRID 365

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
      A RVKET+R+ A+ EL +LGA V+E PD + P L DHRMAMA ++
Sbjct: 366 AAELRVKETDRLRALAEELRRLGARVDEHPDGLDVHGPTPLRGAVCSARGDHRMAMALAV 425

Query: 413 AA-CAEVPVTIRDPGCTRKTFPDYF 436
      A A I D + PD+F
Sbjct: 426 AGLVATGETVILDASSAAVSDPDF 450

```

```

>ref|ZP_01968749.1| hypothetical protein RUMTOR_02328 [Ruminococcus torques ATCC 27756]
ref|ZP_07960258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 8_1_57FAA]
gb|EDK23484.1| hypothetical protein RUMTOR_02328 [Ruminococcus torques ATCC 27756]
gb|EFV18639.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 8_1_57FAA]
Length = 429

```

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 128/447 (28%), Positives = 204/447 (45%), Gaps = 32/447 (7%)

```

Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      L I+ + GTV +PG KS+S+R ++ +++ GTT + N L D + +++G+++E
Sbjct: 3  LAGIQGLKGTVSVPGDKSISHRCIMFGSIANGTTEIHNFLKGADCLATIRCFQSMGINIE 62

Query: 69 ADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      G G P+ L +GN+G R L+ + AG L G
Sbjct: 63 ETDHTITVHGKGLHGLSAPLN-----ILDVGNSTTTRLLSGIL--AGQKFESKLSGDE 114

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSAL 186
      + RP+ ++ L +GA++ L C P+ + G L G + +SS Q S +
Sbjct: 115 SLNSRPMKRIIEPLTMGANISSILRNGCAPLYI-APGNLHG--IHYSVPVSSAQVKSCI 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDR--FYIKGGQKY 242
      L+A A G E + + +S + E+ L+ FG ++ HS S YIK K
Sbjct: 172 LLAGLYAEG--ETSVTEPSLSRNHTEMLK---EFGADIRTLHSLSGTEATAYIKPYPKL 226

Query: 243 KSPKNAYVEGDASSASYFL-AGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
      K V GD SSA+YF+ AG + + +E G + + +V E MG +T
Sbjct: 227 YGQK-IVVPGDISAAYFIAAGLIVPDSEILIEHVGINPTRSGI--LKVCEMDMGDITLL 283

Query: 302 ETSVTVTGPPPREPFG-RHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
      + R L I + + +P D +AV+A ADG T I+D A +
Sbjct: 284 NERCEAGEKIADILVRTSSLHGITIEGDIPTLIDEIPIIAVMAAVADGTTVIKDAEELK 343

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Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAA-CA 416
VKET+R+ + L +G +V D IIT L+ +I T DHR+AMAFS+AA A
Sbjct: 344 VKETDRIETVTDNLKAMGCNVPTEDGMIITGG-TLHGASIHLLDHRIMAFSIAALVA 402

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+ I D C ++P ++D +
Sbjct: 403 DGTTKILDSKCVDSYPTFYDTFEQLL 429

>ref|NP_471371.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria innocua
Clip11262]
sp|Q92A85.1|AROALISIN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAC97267.1| aroE [Listeria innocua Clip11262]
Length = 428

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 217/438 (49%), Gaps = 31/438 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GEITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G D ++ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG-----SDGLKQAEGLPDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRP 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ + G L + + + S+Q SA++ AA A
Sbjct: 123 NRVMPLQEMGAKMHGKDGSEFAPISIIIGNQSLKRMEYHMPVA-SAQVKSIIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K + T ++ +FG + E R +KGGQK+ + V GD
Sbjct: 182 GETIIEHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQKFIG-QEMTVPGDV 233

Query: 255 SSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 234 SSAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 290

Query: 314 PFGRK--HLKAIDVNMKNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIR 368
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 291 TVVVKSELKGTGTEIGGDIIPRLIDEIPVIALLATQAEGTTIKDAELKVKETNRIDAVA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
EL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 351 NELNKMGAIDITPTEDGLIIRGKTPLHAANVTSYGDHRIGMMLQIAALLVEDGDVELDRAE 410

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 411 AVSVSYPTFFEDIRSLK 428

>ref|YP_001187348.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas mendocina
ymp]
gb|ABP84616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas mendocina
ymp]
Length = 746

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 129/437 (29%), Positives = 210/437 (48%), Gaps = 33/437 (7%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+P +SG +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 KPGSSLSGRIRVPGDKSISHSRISIMLSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
R + G G K A L++GN+G +MR L+ + A + VL G +
Sbjct: 377 PHHG-RVTIHGVGLKGLKAPAG---PLYMGNSGTSMRLLSGLLAAQPFDT--VLTGDASL 430

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

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      +RP+  +   L+++GA ++   G +  PP+ + G   L G   ++   + S+Q  S LL+
Sbjct: 431 SKRPMNRVAKPLREMGAVIET--GPEGRPPLTIKGGQRLTGMDYEMPMA-SAQVKSCLLL 487

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
      A  A G   +           P  + T R++ FG  V  E S  +   ++ G K  + +
Sbjct: 488 AGLYAAGRTSVT-----EPAPTRDHTERMLRGFGYPVSVEGSTA----SVESGHKLTATR 538

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      V  D SSA++FL  A+I  G+ + +E  G   +  V   ++L++MG  +T  E
Sbjct: 539 -IEVPADISSAAFFLVAASIAEGSELVLEHVGINPTRTGV--IDILKLMGGDITL-ENQR 594

Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      V G P       +   LK ID+  + +P   D   L V A  A+G T +R       RVKE
Sbjct: 595 EVGGEPVADIRVRSAKLKGIDIPEDLVPLAIDFPPVLFVAAACAEGRTVLRGAEEELRVKE 654

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVP 419
      ++R+  +   L  LG   E  PD  +I           + DHR+AM+FS+A+  A  P
Sbjct: 655 SDRIQVMADGLITLVGKAEPTPDGIVIEGGSIGGGEVW-AHGDHRIAMSFSVASLRASAP 713

Query: 420 VTIRDPGCTRKTFPDYF 436
      + I D           +FP++
Sbjct: 714 IRIHDCANVATSFPNFL 730

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>ref|YP_003796126.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Candidatus Nitrospira
defluviil]
emb|CBK40200.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Candidatus Nitrospira
defluviil]
Length = 442

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Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 124/455 (27%), Positives = 212/455 (46%), Gaps = 33/455 (7%)

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Query: 7   IVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
      + + P + + GT+++PG KS+++R ++L AL+EG + V +   ED   + A ++LG+
Sbjct: 4   LTITPGRPLKGTIRVPGDKSVTHRAIILTALAEGLSQVTDYCRGEDCLNTMRAFQSLGVR 63

Query: 67  VEADKAAKRAVVVCGCKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
      +E           + V   G + + +   +   GN+G  +R  +   + AG  +   VL G
Sbjct: 64  IE---ETPEQLTVHGKGMWGLTEPFGPID--CGNSGTGIRLMAGLL--AGQDFFTFLTGD 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
      +R RP+G +V  L+ +GA +   G +  P+ + G   G  +S  S+Q  S+L
Sbjct: 117 ESIRRRPMGRVVKPLRAMGATIAGRKGELAPLAITGT--RLKGSYVSPVASAQIKSSL 174

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      L AA  A G   I   +  +S  + E  R+  FG+           R  +   ++ S K
Sbjct: 175 LFAALYADGLTTIS--EPRLSRDHTE---RMFAYFGIPFHRDGTVRIEGRPSIRW-SGK 228

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      V  GD S+A++FL  GA+I   + VTV   G   +   ++L  MGA  +   +
Sbjct: 229 TVVVPGLDLSAAFFLVGASIVPDSDVTVLSVGMNPTR--TGLLDILRQMGAHIEVLNSRE 286

Query: 306 TVTGPPPREPFGRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
      P   +   R   L+  + +   ++P   D   L V A  A+G T I       RVKE+
Sbjct: 287 EAGEPVADLRVRSMPLRGVQIGPEQIPQTIDEFPILCVAAVAEGETVITGAEELRVKES 346

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDITYDDHRMAMAFSLAA- 414
      +R+  + TEL  +GA +EE PD  +I   +   L           +Y DHR+AM+ ++ A
Sbjct: 347 DRIATMATELRAMGARIEERPDMVIQGLGRKGANGTLTGATCASYGDRHVAMSVAIGAL 406

Query: 415 CAEVPVTIRDPGCTRKTFPDY----FDVLSTFVK 445
      A  P  I++  C   +FP++           ++L+  VK
Sbjct: 407 TAAQPTQIQNTDCIETSFPNFDRLKLELLTDSVKR 441

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>ref|YP_001172836.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas stutzeri
A1501]
gb|ABP79994.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas stutzeri
A1501]
Length = 706

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Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 126/439 (28%), Positives = 208/439 (47%), Gaps = 33/439 (7%)

Query: 10 QPIKEISGTVKLPKSGSKLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEA 69
P ++G +++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 277 NPGGSLTGHLRVPKDKSISHRSIMLGSLEAGTTEVEGFLEGEDALATIQAFRDMGVVIEG 336

Query: 70 DKAARKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + V VG G P ++LGN+G +MR L+ + A + T L G
Sbjct: 337 PQQGRVTVHGVGLHGLKPPPGP-----IYLGNSGTSMRLLSGLLAAQPFDDT--LTGDAS 389

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + L+++GA ++ PP+ + G L G + + S+Q S LL+
Sbjct: 390 LSKRPMNRVAKPLREMGAVIET-AAEGRPPLTIRGGQRLSGMHYDMPMA-SQVKSCLLL 447

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A I P + T R++ FG V E + ++ G K +
Sbjct: 448 AGLYAADQTSIT-----EPAPTRDHTERMLRGFGYPVTVEGRTA---IVEPGHKLRG-T 497

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++F+ A+I G+ + +E G + V ++L++MG +T E
Sbjct: 498 HIEVPADISSAAFFMVAASIAPGSEIVLEHGVNPNTRTG--IDILKLMGGDITL-ENLR 554

Query: 306 TVTGGPPREPFGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
V G P + LK ID+ + +P D L V A A G T +R RVKE
Sbjct: 555 EVGGEPAADIRVGAQLKGIDIPEDLVPLAIDFPPVLFVAACAQGRITLGAEEELRVKE 614

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG E PD +I + + + DHR+AM+FS+AA A P
Sbjct: 615 SDRIQVMADGLQTLGIKAEPTPDGIVIE-GGMIGSGEVWAHGDHRIAMSFSVAALRASGP 673

Query: 420 VTIRDPGCTRKTFPDYFDV 438
+ I D +FP++ D+
Sbjct: 674 IRIHDCANVATSFNPLDL 692

>ref|NP_636962.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. ATCC 33913]
ref|YP_243712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. 8004]
sp|Q8PA95.1|AROAXANCP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q4UTD1.1|AROAXANCP8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM40886.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. ATCC 33913]
gb|AAY49692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. 8004]
Length = 438

Score = 129 bits (323), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 131/445 (29%), Positives = 209/445 (46%), Gaps = 32/445 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGL 64
+ + Q + G++ +PG KS+S+R ++ AAL++G + +D L ED LG
Sbjct: 6 QHWIAQRGTALQGSALTIPGDKSVSHRAVMFAALADGISKIDFLEGEDTRSTAAIFAQLG 65

Query: 65 LSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E A++R V VG G P + L GNAG MR L + A VL
Sbjct: 66 VRIETPSASQRIHVGVGDGLQPPQGP-----LDCGNAGTGMRLLAGVLAQ--RFDSVL 118

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQY 182
G + +RP+ + L Q+GA ++ PP+RV+G L G + + + S+Q
Sbjct: 119 VGDASLSKRPMRVRTGPLAQMGARIET-ESDGTPLRVHGGQALQG--ITFASPVASQV 175

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SA+L+A A G+ + P + T R++ FGV+ S R ++GGQ+
Sbjct: 176 KSAVLLAGLYATGETSVSEPH-----PTRDYTERMLSAFGVEIAFSPGQAR--LRGGQRL 228

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSQGDVKFAEVLEMMGAKVTWT 301
++ A V D SSA++F+ A+I G+ VT+ G + L +MGA +
Sbjct: 229 RATDIA-VPADFSSAAFFIVAASIIIPGSGVTLRAVGLNPRR--TGLLAALRLMGADIV-E 284

Query: 302 ETSVTVTGPPREPFGGRKH--LKAIDVNMNMKMPDVA---MTLAVVALFADGPTAIRDVASW 356
+ G P ++ L+ + +PD+ L V A A G T + A
Sbjct: 285 DNHAHEHGEPVADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAAARGDTVVSGAAEL 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-C 415
RVKE++R+ A+ T L LG V+E PD I L I+++ DHR+AMAF++A
Sbjct: 345 RVKESDRLAAMATGLRALGIVDETPDGATIH-GGTGSGVIESHGDHRIAMAFIAGQL 403

Query: 416 AEVPTVIRDPGCTRKTFPDYFDVLS 440
+ V + D +FP FD L+
Sbjct: 404 STGTVQVNDVANVATSFPF-FDSL 427

>ref|NP_641982.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas axonopodis pv. citri str. 306]
sp|Q8PLY5.1|AROAXANAC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM36518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas axonopodis pv. citri str. 306]
Length = 440

Score = 128 bits (322), Expect = 1e-27, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 207/440 (47%), Gaps = 36/440 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGS LAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRITPSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G P + L GNAG MR L + A ++ VL G + +RP
Sbjct: 76 RIVHGVGV DGLQPPTVEV----LDCGNAGTGMRLLAGLLAAQRFD--VLVG DASLSKRP 128

Query: 134 IGD LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA ++ PP+ V G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIET-QDDGTPPLHVRGGQALHGIDF-VSPVASAQVKSALLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + P + T R++ FGV+ + S R ++GGQ+ ++ A V D
Sbjct: 187 QGETSVTEPH-----PTRDYTERMLSFAFGVEIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A++ G+ V + G + L +MGA + E G
Sbjct: 239 FSSAAFFIVAASVVPGEVVLRAVGLNPRR--TGLLAALRLMGADI-GEENHAEHGG--- 292

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAM-----TLAVVALFADGPTAIRDVASWRVKETERM 364
EP H++ + ++P+ + L V A A G T + A RVKE++R+
Sbjct: 293 EPVADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAAASGQTVVTGAAELRVKESDRL 352

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTIR 423
A+ T L LG V+E PD I + I+++ DHR+AMAF++A + V +
Sbjct: 353 AAMATGLRTLGIQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAFIAGQLSMGQVQVN 411

Query: 424 DPGCTRKTFPDYFDVLSSTFV 443
D +FP FD L+ V
Sbjct: 412 DVANVATSFPF-FDTLAQDV 430

>gb|AAM16059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16061.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16070.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16071.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
gb|AAM16077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 59

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 59/59 (100%), Positives = 59/59 (100%)

Query: 387 ITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 445
ITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK
Sbjct: 1 ITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 59

>ref|YP_003821881.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
saccharolyticum WM1]
gb|ADL04258.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
saccharolyticum WM1]
Length = 425

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 206/438 (47%), Gaps = 29/438 (6%)

Query: 15 ISGTVKLP GSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ ++++GTT + + L D + R +G+ +E ++
Sbjct: 9 LKGEITIPGDKSISHRSVMFGSI AKGTTEISHFLQGADCLSTIDCFRKMGIENNQ--- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+V G ++ + E L GN+G R ++ + A N T + G +++RP+
Sbjct: 66 NTVIVHKGGLRGLK--RPETILDCGNSGTTTRLISGLLAAQDFNVT--VTGDESIQKRPM 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L +GAD+ L C P+ + G G S S+Q S++L+A A
Sbjct: 122 KRIMEPLSFMGADIKSILDNGCAPLSITG--KRLRGIHYTSPVASAQIKSSILLAGLYAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G E + + +S + E+ L+ FG VK E + + + Y + V G
Sbjct: 180 G--ETRVTEPYVSRNHSEIMLK---HFGANVKTEGTAC---IAPAAELYGN--QIIVPG 229

Query: 253 DASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTVTGPP 311
D SSA+YF+A G + G + ++ G + + V + MGA +T + ++ P
Sbjct: 230 DISSAAYFIAAGLIVPGSEILIKQVGINPTRDGI--IRVCQEMGADITLLDGNMDSGEPT 287

Query: 312 REPFGGRK-HLK AIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ + L + + +P D +A +A FA+G T IRD A +VKE+ R+ +
Sbjct: 288 ADILVKSGLHGVPIGGAIIPTLIDELPIIAAMACFAEGETIIRDAELKVKESNRIDVM 347

Query: 368 RTELTKL GASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
L+ +GA V E D II L+ ID+ DHR+AM F++ CAE I
Sbjct: 348 VKNLSAMGADVRETDDGMIIRGGRPLHGAVIDSKLDHRIAMTFAVTGLCAEGETEILGAE 407

Query: 427 CTRKTFFPDYFDVLSTFVK 444
C ++P ++ L +K
Sbjct: 408 CVNISYPGFYQDLEMLMK 425

>ref|YP_002798775.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Azotobacter vinelandii DJ]
gb|ACO77800.1| 3-phosphoshikimate 1-carboxyvinyltransferase / Prephenate
dehydrogenase [Azotobacter vinelandii DJ]
Length = 752

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 129/439 (29%), Positives = 213/439 (48%), Gaps = 39/439 (8%)

Query: 11 PIKEISGTVKLP GSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P G +++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E
Sbjct: 324 PGGHARGHIRVP GDKSISHRSIMLGS LAEGTTEVEGFLEGEDALATIQA FRDMGVVIEGP 383

Query: 71 KAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V VG G K P L+LGN+G +MR L+ + A + VL G
Sbjct: 384 HHGRVTVHGVGLHLKAP-----PGPLYLGNSGTS MRLLSGLLAAQPFDT--VLTGDAS 435

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA+++ G + PP+ + G L G ++ + S+Q S LL
Sbjct: 436 LSKRPMNRVAKPLREMGAEIEA--GPEGRPPLTIKGRRLTGMHYQMPMA-SAQVKSCLL 492

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G+ + P + T R++ FG VK E S + ++ G K ++
Sbjct: 493 LAGLYAGGETSVS-----EPAPTRDHTERMLRGFGYPVKVEGS----KVTVESGHKLQAT 543

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQ-GDVKFAEVLEMMGAKVTWTET 303
+ V D SSA++FL A I + + +E G + G + E+L++MGA +T E
Sbjct: 544 Q-IEVPADISSATFFLVAATIAEDSELLLEHVGINPRTGTGSI--EILKLMGADITL-EN 598

Query: 304 SVTVTGPPREPFGFRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V G P + L+ I++ ++ +P D L V A A+G T +R RV
Sbjct: 599 PREVGGEFVADIRVRSARLQGIPIPLDLVPLAIDEFPVLFVAAACAEGRTVLRGAELRV 658

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AE 417
KE++R+ + L LG E PD I ++ DHR+AM+FS+A+ A
Sbjct: 659 KESDRIQVMADGLRALGVKAETPDGIAIEGGPIGGGEIY-SHGDHRIAMSFSIASLRAS 717

Query: 418 VPVTIRDPGCTRKTFPDYF 436
P+ I D +FP++
Sbjct: 718 APIRIHDCANVATSPFNFI 736

>gb|AAM16066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 60

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 59/60 (98%), Positives = 59/60 (98%)

Query: 386 IITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSFVKV 445
IITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV IRDPGCTRKTFPDYFDVLSFVKV
Sbjct: 1 IITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVAIRDPGCTRKTFPDYFDVLSFVKV 60

>ref|YP_004094876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
cellulosilyticus DSM 2522]
gb|ADU30145.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
cellulosilyticus DSM 2522]
Length = 428

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 212/439 (48%), Gaps = 39/439 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG KS+S+R ++ A+++ G + + L ED + ++ LG+++ +
Sbjct: 13 LNTISVPGDKSISHRAVMFASIANQSEITGFLKGEDCLSTISCMKQLGVTIREED--D 70

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ +VVG G V+ KE L +GN+G +R L+ + A + VL G + +RP
Sbjct: 71 KIIIVVGK-----VKQLKEPNTILDVGNSGTTIRLLSGIL--ASLPFSSVLIGDDSIKRP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + LK + A VD P+ + G G G +S S+Q S++L+AA A
Sbjct: 125 MARVTGPLKMMNATVDGRENGRFTPLFIRG--GQLQGVHYVSPIASAQVKSSILLAALNA 182

Query: 194 LGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G + + P+ + T R+++ FGV E + +KGGQ + N V
Sbjct: 183 KGTTTV-----TEPHRSRDHTERMLKTFGVSVVEVD--GESVSLKGGQAL-TAANIAVP 232

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA++ L AAI + VT+ G + + +VLE MGA + T+
Sbjct: 233 GDISSAAFLLVAAAIVNKSEVTITNVGINPRTGTI--LDVLENMGADIRITDERFY---- 286

Query: 311 PREPFGRKHLKAIDVN-----MNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP +K +N + ++ D +AV+A A+G T I+D +VKET
Sbjct: 287 GEEPVANITIKYTQLNATTIAGEIIPRLIDEIPAIAVLATQANGVTVIKDAEELVKETN 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ + +L LGA++E D I P L +++Y DHR+ MA +L ++ V
Sbjct: 347 RIDTMVHQLKSLGANIEATSDGMKIIIGPTPLRGGNVESYGDHRIGMAMALCGLISGDVK 406

Query: 422 IRDPGCTRKTFPDYFDVLS 440
I + ++P+++F+ L+

Sbjct: 407 IENTEIAVSYPNFFEHLN 425

>gb|EFR93399.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria innocua FSL
J1-023]
Length = 428

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 118/437 (27%), Positives = 217/437 (49%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GEITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ E L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG---FDGLKQAEGLDIGNSGTTIRLMMGIL--AGRDFDTVLGDSEIAKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+++GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQEMGAKMHGKDGSEFAPISIIGNQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQKFIG-QEMTVPGDVS 234

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGT 291

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 292 VVVKSELKGTIEIGDIIPLRIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAN 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
EL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 352 ELNKMGAADITPTEDGLIIRKGTPLHAANVTSYGDHRIGMMLQIAALLVEDGDVELDRAEA 411

Query: 428 TRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 412 VSVSYPTFFEDIHSLK 428

>gb|EFR90248.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria innocua FSL
S4-378]
Length = 430

Score = 128 bits (322), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 118/437 (27%), Positives = 217/437 (49%), Gaps = 29/437 (6%)

Query: 17 GTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 14 GEITVPGDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 71

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ E L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTG---FDGLKQAEGLDIGNSGTTIRLMMGIL--AGRDFDTVLGDSEIAKRPMN 125

Query: 136 DLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+++ L+++GA + G++ P+ + G L + + + S+Q SA++ AA A G
Sbjct: 126 RVMLPLQEMGAKMHGKDGSEFAPISIIGNQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ I +K + T ++ +FG + E R +KGGQK+ + V GD S
Sbjct: 185 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGQKFIG-QEMTVPGDVS 236

Query: 256 SASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA++F+ IT G + + G + + +V+E MG + ++S + TG
Sbjct: 237 SAAFFIVAGLITPGSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGT 293

Query: 315 FGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369

K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 294 VVVKSSSELKGTIEGGDIIPRLIDEIPVIALLATQAEGTTIIKDAAELKVKETNRIDAVAN 353

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
 EL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 354 ELNKMGAADITPTEDGLIIRGKTPHAAANVTSYGDHRIGMMLQIAALLVEDGDVELDRAEA 413

Query: 428 TRKTFPDYFDVLSTFVK 444
 ++P +F+ + + +K
Sbjct: 414 VSVSYPTFFEDIRSLK 430

>sp|Q1IKI5.2|AROA_ACIBL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 427

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 136/459 (29%), Positives = 214/459 (46%), Gaps = 51/459 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
 + + +QP I G+V PG KS+S+R +LAAL+EGT+ N D L + LG
Sbjct: 2 KSVRVQPASNILGVSFPGDKSISHRYGMLAALAEGTSRFGKNFSTGADCASTLSCMEQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 V K V G G+ K QL GN+G +MR L+ + A ++ + D
Sbjct: 62 AKV-THKDDGVIEVEGVAGQL----RKSATQLDCGNSGSSMRMLSGILAAQPFDSSELMGD 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG-----IGGLPGGKVKLSG 176
 + RP+ +V LKQ+G D++ G P+RV G I +P +VK
Sbjct: 117 A--SLSRPMRRIVDPLKQMGDIETTDGH--APLRVRGSKLTAIDYITPVPSAQVK--- 169

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISI-PYVEMTLRLMERFGVKAHSDSWDRFY 235
 S +L A A G I +D+ I + E+ L+ FG + E +R
Sbjct: 170 -----SCVLFAFAAAG---ITSVDEAIRTRDHGEIALKA---FGAEVERR--QNRVS 214

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
 ++GG K+++ + A V GD SSA++FL AA+ T + G +VL MG
Sbjct: 215 VRGGAKFRAIE-AVVPDGISSAAFFLCAALFP-TSNLVFDGILLNPSRAAILDVLASMG 272

Query: 296 AKVTWTETSV-----TVTGPPREPFGFRKHLKAIDVNM-NKMPDVAMTLAVVALFADGP 347
 AK + + T+T P G K + ++ +++P LA + +
Sbjct: 273 AKPKFLQVQEQHGELVGTITLAPAGLSGLKISGGLTASLIDELP----VLAAGAYTRYG 328

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMA 407
 IRD RVKE++R+ + L +GA VEE D + +KL+ I+++DHR+A
Sbjct: 329 IEIRDAKELRVKESDRIAVVCANLRAMGAEEVEFDDGLRVKGSQKLHGAEIESHEDHRIA 388

Query: 408 MAFSLAAC-AEVPVTIRDPGCTRKTTPDYFDVLSTFVK 445
 MAF++AA AE I C ++P+++FD L+ V+
Sbjct: 389 MAFAVAALRAEGETVINGADCVAISYPEFFDTLNKVVER 427

>ref|YP_592689.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Koribacter
versatilis Ellin345]
gb|ABF42615.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Koribacter
versatilis Ellin345]
Length = 435

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 136/459 (29%), Positives = 214/459 (46%), Gaps = 51/459 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
 + + +QP I G+V PG KS+S+R +LAAL+EGT+ N D L + LG
Sbjct: 10 KSVRVQPASNILGVSFPGDKSISHRYGMLAALAEGTSRFGKNFSTGADCASTLSCMEQLG 69

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 V K V G G+ K QL GN+G +MR L+ + A ++ + D
Sbjct: 70 AKV-THKDDGVIEVEGVAGQL----RKSATQLDCGNSGSSMRMLSGILAAQPFDSSELMGD 124

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG-----IGGLPGGKVKLSG 176


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      + RP+ +V LKQ+G D++ G P+RV G I +P +VK
Sbjct: 125 A--SLSRPMMRIVDPLKQMGDIETTDGH--APLRVRGSKLTAIDYITPVPSAQVK--- 177
Query: 177 SISSQYLSALLMAAPLAGDVEIEIIDKLISI-PYVEMTLRLMERFGVKAHSDSWDRFY 235
      S +L A A G I +D+ I + E+ L+ FG + E +R
Sbjct: 178 -----SCVLFAGAFAG---ITSVDEAIRTRDHGEIALKA---FGAEVERR--QNRVS 222
Query: 236 IKGGQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
      ++GG K+++ + A V GD SSA++FL AA+ T + G +VL MG
Sbjct: 223 VRGGAKFRAIE-AVVPGLISSAAFFLCAAALFP-TSNLVFDGILLNPSRAAILDLVLSMG 280
Query: 296 AKVTWTETSV-----TVTGPPREPFGFRKHLKAIDVNM-NKMPDVAMTLAVVALFADGP 347
      AK + + T+T P G K + ++ +++P LA + +
Sbjct: 281 AKPKFLQVQEQHGELVGTITLAPAGLSGLKISGGLTASLIDELP----VLAIGAYTRYG 336
Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMA 407
      IRD RVKE++R+ + L +GA VEE D + +KL+ I+++DHR+A
Sbjct: 337 IEIRDAKELRVKESDRIAVVCANLRAMGAEEVEFDDGLRVKGSQKLHGAEIESHEDHRIA 396
Query: 408 MAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
      MAF++AA AE I C ++P++FD L+ V+
Sbjct: 397 MAFAVAALRAEGETVINGADCVAISYPEFFDTLNKVVER 435

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>ref|ZP_05620446.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enhydrobacter
aerosaccus SK60]
gb|EEV22181.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enhydrobacter
aerosaccus SK60]
Length = 744

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Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 124/452 (27%), Positives = 220/452 (48%), Gaps = 33/452 (7%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      + V+ P ++ G+ + G KS+S+R ++ +L++GTT V L ED L A R +G
Sbjct: 301 QTYVIAPAQQFEGSHTVAGDKSISHRSIMFGSLAKGTTTGTGFLGEDALATLQAFRDMG 360
Query: 65 LSVEADKAAKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
      + +E R V+ G G G P D L++GN+G +MR L+ ++A ++ V
Sbjct: 361 VVIEGPNQG-RVVIHGVLHGLKPSHDP-----LYMGNSGTSMRLLSGILSAQKFDS--V 412
Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      + G P + +RP+ + L+++GA + PP+ + G L G + ++ + S+Q
Sbjct: 413 MTGDPSLSKRPMERVAKPLREMGAKIQTTEGKGTTPPISITGNQTLTGIRYEMPMA-SAQV 471
Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQ 240
      S LL+A A G +I+ ++ + E R++ FG V + ++ + GG
Sbjct: 472 KSCLLLAGLWAQGT--TVIEPEVTRDHTE---RMLTAFGYPTVTVKVHNGNQISVTGGG 526
Query: 241 KYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
      + + A V D SSA++F+ AGA G VT++ G + V ++L++MGA +T
Sbjct: 527 ELTACDIA-VPADISSAAFFMVAGAIQQGNVTIKKVGINPRTGTG--IDILKLMGADLT 583
Query: 300 WTETSVTVTGPPREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVA 354
      + TV G P K L+ I++ + +P D L V A A G T + A
Sbjct: 584 LINET-TVGGEPVADIVVKSSKLQGIPEHLVPLAIDEFPVLFVAASCATGKTVLHGAA 642
Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITP----PEKLNVTATIDTYDDHRMAMAF 410
      RVKE++R+ + L LG + D I + I+ + DHR+AM+F
Sbjct: 643 ELRVKESDRIQVMADGLKTLGIACTVLDGIEIEGRGDVAQVFGGGEIECHHDHRIAMSF 702
Query: 411 SLAAC-AEVPVTIRDPGCTRKTFPDYFDVLST 441
      ++A+ A +TI +FP++ +++++
Sbjct: 703 TMSLRASDTITIHGTETVNTSFPNFAELVNS 734

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>ref|YP_002461505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus
aggregans DSM 9485]
sp|B8GC95.1|AROACHLAD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

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gb|ACL23069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus
aggregans DSM 9485]
Length = 435

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 139/458 (30%), Positives = 220/458 (48%), Gaps = 44/458 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
EI L K + G +++PG KS+S+R +LL A++ G+ + N L D + +R+LG+
Sbjct: 3 EITLTAPKRLRGVIQVPGDKSISHRSVLLNAIATGSAHITNPLPGADCLSSVACVRSILGV 62

Query: 66 SVEADKAAKRAVV---VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+VE + +R ++ VG GG D L GN+G +R L ++ G V
Sbjct: 63 TVE--QPHERELIIGHVGLGLRESTDV-----LDCGNSGTTLRLLAGILS--GQPFSSV 113

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G +R RP +V L+ +GA +D D P+ + G L GG+ +L+ + S+Q
Sbjct: 114 LSGDSSLRSRPQRRVVGPLRAMGAQIDGRADGDRAPLAIRG-STLRGGQYELTIA-SAQV 171

Query: 183 LSALLMA-----APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
SALL+A PL LG I + T R++ GV E + S DR +
Sbjct: 172 KSALLLAALYADGPLTLGG-----RIDSRDHTERMLAAMGV--EITVSPDRITLH 219

Query: 238 GGQKYKSPK--NAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEM 293
+P + V GD SSA+++ AAI VT C + G + +VL
Sbjct: 220 PPTAATAPVALSLRVPDPSSAAFVWVAAIHPDAELVTPGVCLNPTRTGAL---DVLRA 276

Query: 294 MGAQVTVTETSVTVTGPPREPFGKRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTA 349
MGA++ + + + R L+ + + +P D LAV A ADG T
Sbjct: 277 MGAEIEIMNERLEGSELVGDVVVRSSVLRGTIAGSLIPRLIDEIPVLAVAAACADGETV 336

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPEKLNVTADITYDDHRMAM 408
IRD R KET+R+ + L+ LG +VE D +IT P++L + +Y DHR+AM
Sbjct: 337 IRDAQELRAKETDRITTVAAAGLSALGVTVEPTIDGMVITGKPDQLTGATLHSHYDHRLAM 396

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
A+++AA A TI +P ++PD++ L+ ++
Sbjct: 397 AWAVAALVARGETTIVEPAAVVISYPDFWQTLAAIQED 434

>ref|YP_607169.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas entomophila L48]
emb|CAK14359.1| putative prephenate dehydrogenase, putative/3-phosphoshikimate
1-carboxyvinyltransferase AroA [Pseudomonas entomophila
L48]
Length = 746

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 130/440 (29%), Positives = 212/440 (48%), Gaps = 39/440 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SG +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 QPGGRVSGRIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAARKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P L++GN+G +MR L+ + A + T + G
Sbjct: 377 PHHGRVTIIGHVGLHGLKPPPG-----PLYVGNSTSMRLLSGLLAAQPFDDT--MTGDAS 429

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVK-LSGSI---SSQYL 183
+ +RP+ + L+++GA V+ G + PP+ + G G K+K L+ ++ S+Q
Sbjct: 430 LSKRPMNRVANPLREMGAVVET--GPEGRPPLTIRG-----GHKLKALNYTLPMASQVK 482

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S LL+A A G + P + T R++ FG + + ++ G K
Sbjct: 483 SCLLLAGLYAEGTTTVT-----EPAPTRDHTERMLRGFGYSVQSNGPV--ASLQAGGKL- 534

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
S V D SSA++FL A+I G+ + +E G + V ++L +MG +T E
Sbjct: 535 SATRIEVPADISSAFLVAASIAQGSSELVLEHVGINPRTGTG--IDILRLMGGDITL-E 591

Query: 303 TSVTVTGPPREPFGGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357

V G P + LK I++ + +P D L V A A+G T +R R
Sbjct: 592 NQREVGGEVPADLRVRGAKLKGIEIPEHLVPLAIDFPPVLFVAAACAEGRTVLRGAEEELR 651
Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-A 416
VKE++R+ + L LG E PD II ++ + + DHR+AMAFS+A+ A
Sbjct: 652 VKESDRIQVMADGLITLGVKCEPTPDGIIIE-GGQIGGGEVHGHDHRIAMAFSVASLRA 710
Query: 417 EVPVTIRDPGCTRKTFPDYF 436
P+ I D +FP++
Sbjct: 711 SAPIVIHDCANVATSPFNFL 730

>emb|CBL23833.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus obeum
A2-162]
Length = 424

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 121/437 (27%), Positives = 210/437 (48%), Gaps = 26/437 (5%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ GT+ +PG KS+S+R ++ +L++GTT + + L D + R +G+ +E + A
Sbjct: 8 NLRGTLTVPGDKSISHRAVMFGSLAKGTTIRISHFLEGADCLSTITCFRKMGIIDIE--RNA 65
Query: 74 KRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V G G A + + L +GN+G R ++ + AG N LDG +R RP
Sbjct: 66 SEIMVHGKG--LHGLSAPDSI-LDVNGSGTTTRLISGIL--AGQNFISELDGDDSIIRTRP 120
Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L +GAD+ C P+ ++G L G S S+Q S +L+A A
Sbjct: 121 MKRIMTPLTSMGADIVSKQDNGCVPLVIHG-KTLHGIHYD-SPVASAQVKSCVLLAGMYA 178
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + + +S + E+ ++ FG K + + + + V GD
Sbjct: 179 DGITSVT--EPFLSRNHTEI---MLNYFGAKVTSEGTASIV---PEPTLNGREIQVPGD 230
Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+YF+A +T G+ + ++ G + + +V MGA +T S T P
Sbjct: 231 ISSAAYFIAAGLLTPGSEILLKNVGINPTRAGI--LKVCMDMGADITLFNES-TEGEPTA 287
Query: 313 EPFGR-KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+ R LK + +P D +AV+A FADG T IRD +VKE++R+ +
Sbjct: 288 DLLIRTSSLKGTTEGGIIPTLIDEIPMIAVMAAFADGTTVIRDARELKVKESDRITVMV 347
Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGC 427
L ++GA +E D II L+ ID++ DHR+AM+F++A + V I + C
Sbjct: 348 DNLKRMGADIEGTEDGMIHGRPLHGATIDSHLDHRVAMSFVAGTICDGTVDILNGDC 407
Query: 428 TRKTFPDYFDVLSTFVK 444
+ ++P++++ L + K
Sbjct: 408 VKISYPEFYNDLYSLNK 424

>ref|ZP_06188741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
longbeachae D-4968]
ref|YP_003455274.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
longbeachae NSW150]
gb|EEZ94679.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
longbeachae D-4968]
emb|CBJ12177.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
longbeachae NSW150]
Length = 439

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 122/439 (27%), Positives = 213/439 (48%), Gaps = 26/439 (5%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+ +P+ I G + +PG KS+S+R ++ ++++GTTV++ L+ +D L A + +G
Sbjct: 4 HNFISKPVVSIKGEITVPGDKSISHRSIIFGSIAGTTVINGFLDGDCLATLKAFQAMG 63
Query: 65 LSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+++E ++ VV+ GK+ ++ K E + GN+G ++R L + A ++ L

Sbjct: 64 VTIEGPD--EQQVVIYGVGKYGLK--KPEQVIDCGNSGTSIRLLAGLLAAQAFDSQ--LT 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L +GAD+ G PP+ + G L G + + S+Q S

Sbjct: 118 GDESLLKRPMLRISKPLTLMGADISTIDGK--PPITIKGGKKLHGIDYVMPEA-SAQVKS 174

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L+A A G E I + +S + E+ L+ + +K S + I + +

Sbjct: 175 CILLAGLYAEG--ETLITETGVS RDHTELMKYFS-YPIKR---SGNTLVINS DHECLA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVT-WTE 302
+ YV GD SSA++F+ A I G+ V + G Q +L MGAK+T +

Sbjct: 228 TE-IYVPGDISAAFFIVAATIIPGSDVLIRNVGIN--QTRTGIIHILLEMGAKITLLNQ 284

Query: 303 TSVTVTGPPREPFGKRHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V H LK I+++ N +P D + + A A G T +R + R K

Sbjct: 285 RQVGEEWVADLRVQYHLKGINISANMVLAIDEFVIFIAAACARGQTTLRGASELRFK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLA-ACAEV 418
E++R+ A+ L KLG E D I L +++ DDHR+AM+F++A A A

Sbjct: 345 ESDRIAAMVDGLKKG IQA-EALDDGIFIEGGTLQGGIVESRDDHRIAMSFAGAVASA 403

Query: 419 PVTIRDPGCTRTKTFPDYFD 437
PVT+R+ +FP + +

Sbjct: 404 PVTVRNCANVATSFPLFVE 422

>ref|YP_001250157.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila str. Corby]
ref|YP_003618699.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila 2300/99 Alcoy]
sp|A5IBR1.1|AROA_LEGPC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ54811.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila str. Corby]
gb|ADG24747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila 2300/99 Alcoy]
Length = 433

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 213/439 (48%), Gaps = 32/439 (7%)

Query: 6 EIVLQPIKEISGTVKLP GSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
+ +P+ + G + +PG KS+S+R ++ A++ GT+V+D L+ ED L A +++G+

Sbjct: 3 NFISKPVVCLKEITVPGDKSISHRSIIFGAIAIGTSVIDGFLDGEDCIATLKAFQSMGV 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E K+ V++ GK+ ++ + + GN+G +MR L + A ++ L G

Sbjct: 63 RIEGPD--KQRVVIHGVGKYGLKQPQNIID--CGNSGTSMRLLAGLLAAQQFDSQ--LTG 116

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+ + L Q+GADV G PP+ + G L G + + S+Q S

Sbjct: 117 DESLLKRPMLRISRPLSQMGADVTTQDGK--PPILIKGGKKLNGIHVMP EA-SAQVKSC 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS---WDRFYIKGGQKY 242
LL+A A G + +I + +S + E R++ F + D DR G+ +

Sbjct: 174 LLLAGMYAEG--QTKITENAVSRDHT E---RMLRTFSYPVQIQDGVIVIDR---NGECH 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWT 301
+ N + GD SSA++F+ A+IT G+ + + G + + +L MGA +

Sbjct: 225 GTRLN--IPGDISAAFFIVAASITPGSDILIRNVGINPTRTGI--IHILTEMGADIKVL 280

Query: 302 ETSVTVTGPPREPFGFR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
P + R LK ID+ ++ +P D + + A A G T + R

Sbjct: 281 NQRAYGEEPVADLHIRYSQLKGIDIPVSMVPLAIDEFPVIFIAAACAQGKTTLHGAKELR 340

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLA-ACA 416
+KE++R+ A+ L +LG EG D I+ + +++ DHR+AM+F++A A A

Sbjct: 341 LKESDRIGAMVDGLNQLGVHA-EGFDDGILIEGGSIQGGEVNSRGDHRIAMSFAGAVA 399

Query: 417 EVPVTIRDPGCTRKTFPDY 435
PVTI++ +FP +
Sbjct: 400 SAPVTIKNCANVATSFPSF 418

>ref|YP_811504.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. cremoris SK11]
sp|Q02XD1.1|AROA_LACLS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ73391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. cremoris SK11]
Length = 430

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 118/439 (26%), Positives = 212/439 (48%), Gaps = 27/439 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+PG KS+S+R ++ ++++G T++ ++L EDV + A R LG+ +E D
Sbjct: 10 LKGHLKVPGDKSISHRSIMFGSIAGKGTIIHDILRGEDVLTIEAFRALGVEIEDD---- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ L G+ + + E L +GN+G + R L+ + AG L G + +RP+
Sbjct: 66 -GQVITVHGQGISKLEKEKALDMGNSGTSTRLLSGIL--AGLPFETTLFGDDSLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA++ P+ + G L L + S+Q SA++ AA A
Sbjct: 123 DRVATPLQMMGAIEIVGQTDKVKLPMTIKGSAHLKAIDYVLPVA-SAQVKS AVIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++++K + + E ++ +FG + + SD + GGQK + V GD
Sbjct: 182 GLT--KVVEKEKTRSHTE---EMLVQFGGEIKVSDKTS--LVPGGQKLMG-QEVTVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTWTSETSVTVTGPPRE 313
SSA+++L AG + + +E G + + EV++ MG ++ E V
Sbjct: 234 SSAAFWLAVAGLVVENSELILENVGINETRTGI--LEVIQAMGGQLEILEQD-EVAKAATL 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAIRTE 370
LK +++ + +P + L ++AL A+G T IRD A +VKET+R+ +
Sbjct: 291 KVKASQKLGTEISGDLIPRLIDELPIIALLATQAEGKTIIRDAAELKVKETDRIAVVADA 350

Query: 371 LTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
L +GA++E D II KL+ AI+T DHR+ M ++AA + +
Sbjct: 351 LNSMGANIEPTDDGMIIQGGTKLHAPENAINTLGDHRIGMMVAIAALLVENGEIELELRAE 410

Query: 427 CTRKTFPDYFDVLSTFVKN 445
+ ++P +FD L +N
Sbjct: 411 AIQTSYPSFFDDLEKLSN 429

>ref|ZP_06703798.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas fuscans
subsp. aurantifolii str. ICPB 11122]
gb|EFF44621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas fuscans
subsp. aurantifolii str. ICPB 11122]
Length = 440

Score = 128 bits (321), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 129/434 (29%), Positives = 211/434 (48%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGS LAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRIETPSASQ 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R +V G G VE + ++ GNAG MR L + A ++ VL G + +RP
Sbjct: 76 R-IVHGVG---VEGLQAPTEVLDCGNAGTGMRLLAGLLAAQRFD--VLVG DASLSKRP 128

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA ++ PP+ V+G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIET-QDDGTPPLHVHGGQALNGIDF-VSPVASAQVKS AVLLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV+ + S R ++GGQ+ ++ A V D
Sbjct: 187 QGETSVTEPH-----PTRDYTERMLSAFGVEIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I G+ V + G + + A L +MGA++ E G P
Sbjct: 239 FSSAAFFIVAASIVPGSEVVLRAVGLNPRRTGLLAA--LRLMGAEI-GEENHAEHGGEPV 295

Query: 313 EPFGRKH--LKAIDVNMNKMMPDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 296 ADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAASGQTVVTGAAELRVKESDRLAAM 355

Query: 368 RTELTKLGSVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 356 ATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAFIAGQLSTGQVQVNDVA 414

Query: 427 CTRKTFPDYFDVLS 440
+FP FD L+
Sbjct: 415 NVATSFPG-FDSLA 427

>ref|ZP_02177238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenivirga sp.
128-5-R1-1]
gb|EDP75779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenivirga sp.
128-5-R1-1]
Length = 435

Score = 127 bits (320), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 125/450 (27%), Positives = 220/450 (48%), Gaps = 29/450 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E ++ + + + G +++P KS+S+R +++ AL+ G T V + L SED L +R LG
Sbjct: 3 ELVIEKRVS RVKELRVPSDKSISHRAVIIGALARGKTTVHDWLRSEDTLATLNMVRMLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V + V+ GK + + ++ L N+G R + ++ + L
Sbjct: 63 VEVYDSGS-----VLEIEGKNYLFEEPTDI-LDARNSGTTARLMLGVLSTQPPFSA--LT 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+ +V L+ +GA +D + PV V G G L G + S+Q S
Sbjct: 115 GDES LRGRPMLRVVDPLRSMGATIDGREQGNKLPVAVRG-GKLRGISF-FNKKASAQVKS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKY 242
++L+A A G E+ ++ ++S + E +++ FG + + + ++GGQ+
Sbjct: 173 SILLAGIKAEGITEV--VEPVMSRDHTE---KMLSFFGAEIVSVPEKEGHIVKLGGQEL 227

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K + Y D SSA++F A A +T GG + + + F L MGA++++
Sbjct: 228 KGSE-VYCPADPSSAAFFCALALLTEGGELVLRDVLNPNTRDG--FYRKL RDMGAELSY- 283

Query: 302 ETSVTVTGPPREPFF---GRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVAS 355
E ++G P G K LKA+ V+ ++P D LAVV A+G ++R
Sbjct: 284 ENQREISGEPIADIVVRGSKRLKAVKVDAEEIPAMIDEIPVLAVVMALAEGKSSVRGARE 343

Query: 356 WRVKETERMVAIRTELTKLGSVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
RVKE++R+ AI L +G V+E D I ++L I T+ DHR+AMAF++A
Sbjct: 344 LRVKESDRIRAIVENLRAMGVKVDEYEDGFDIEGTDRLKGAHIKTFGDHRIAMAF TVAGL 403

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSFVK 444
A+ I D C ++P++ + + V+
Sbjct: 404 LADGRTIIDDVECVNISYPNFLRDIDSVVE 433

>ref|YP_220088.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas abortus
S26/3]
sp|Q5L5F4.1|AROCHA_CHLAB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH64137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlamydomonas abortus
S26/3]
Length = 445

Score = 127 bits (320), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 210/435 (48%), Gaps = 29/435 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISG V +P SKS + R + A+++GT+++ + L S D M+ A + LG K K
Sbjct: 11 ISGRVSVPPSKSHTLRAIFWASVAQGTSHHHLASPDSEAMIQACKQLGA-----KILK 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVLGDGVPRMRERPI 134
++ + G P + + G++GI R TA AA + + +++ RPI
Sbjct: 66 KSTHLEITGT-PHLILPKNTTINAGSSGIVFRFFTA--LAAIFSEKITITESQLQRRPI 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L+ GA P V +G + G ++ G SQY SAL +A LA
Sbjct: 123 APLIQALENFATFSYEGEPYSLPFVS--LGPMSGGYTEVIGE-DSQYASALAIACSLAE 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-VEGD 253
G I++ P+ +TL ++ G+ S+ D + +G K + +Y V GD
Sbjct: 180 GPFSFTILNPK-ERPWFALTLLWLDLGLIPYAQSE--DTYSFEG--KTRPQAFSYTVGGD 234

Query: 254 ASSASYFLAGAAI--TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
SSA++ A A + + +E +QGD + +L+ +GA +T+ E + + P
Sbjct: 235 FSSAAFLAAALLSQSPHPTYLENLNIDDIQDKELFLLKKLGANITF-ENNTIIFPS 293

Query: 312 REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
G +++M+ D LAV+ FA + + + S + KE++R++AI EL
Sbjct: 294 TFSGG-----NIDMDPFIDALPILAVLCCFATSSSYLYNARSANKESDRIIAITQEL 346

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRK 430
K+GA ++ D +I P L ++ ++ DHR+AMA S+AA A I D C +K
Sbjct: 347 QKMGACIQPCHDGLLIN-PSPLYGASMHSKDHRIAMALSIAAMHASGDSIIYDTCVKK 405

Query: 431 TFPDYFDVLSTFVK 445
TFP++ +L++ N
Sbjct: 406 TFPNFIQILNSLHTN 420

>ref|ZP_05898407.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sputigena
ATCC 35185]
gb|EEX77706.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sputigena
ATCC 35185]
Length = 436

Score = 127 bits (320), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 136/466 (29%), Positives = 215/466 (46%), Gaps = 54/466 (11%)

Query: 1 MAGAEIEIVLQPIKE-ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGA 59
MA +EI +P K ++G +++PG KS+S+R ++ +A+++G V N L + D
Sbjct: 3 MAEGKEI--RPAKRGLTGKIRVPGDKSVSHRSVMFSAIAKGQVHVRNFLEADCLSTAAC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGN 118
+R LG VE +A +V G G + KE + L GN+G +R L + A
Sbjct: 61 MRALGAGVE-RQADGSLLVTVGVG----LHGLKEPQGVLDAGNSGTTLRLLLLGILAAQ--P 113

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADV-----DCFLGTDCCPPVRVNGIGGLPGGKVK 173
L G + RP+G +V L ++GA + D FL P+ V G
Sbjct: 114 FFSALTGDASLSRRPMGRVVEPLTRMGAAIRGRGSDRFL-----PLAVLPHEGSLRAMDY 168

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
S S+Q SA+L+A A + + + +S + E R++ FG + E + +
Sbjct: 169 ESPVASAQVKSAVLLAGLYA--ERATCLTEPALSRDHTTE---RMLSAFGARIEREGET--K 221

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLE 292
I+ + +P+ V GD SSA+Y+L A+ I G + ++ G + + +VL
Sbjct: 222 VTIEPADELFAPEEICVPGDISSAAYWLVAASLIEGSDIILQDVGVNPTRTGI--LDVLS 279

Query: 293 MMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVN-----MNKMPDVAMTLAV 339
MGA +T RE G + L I V + ++ D LAV
Sbjct: 280 DMGANITICSE-----RESGG-EALADIRVRSALRGASFGGEIIPRLIDEIPILAV 330

Query: 340 VALFADGPTAIRDVASWRVKETERMVAIRTELTKLG-ASVEEGPDYCIITPPEKLNVTAI 398

ALFADG T I A RVKET+R+ A+ EL + +VE D +I L+ +
Sbjct: 331 AALFADGDTVISGAELRVKETDRLAAVTAELNRFAPGAVEAKEDGMVIHGGRTLSPLASC 390

Query: 399 DTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVLSFVK 444
TYDDHRMAM+ ++A VT+ P C ++P ++ L V+
Sbjct: 391 RTYDDHRMAMSLAVAGAVGEGVTLDPSCVNISYPSFYQTLGLVQ 436

>ref|ZP_07453238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris
ATCC 35239]
gb|EFM45141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris
ATCC 35239]
Length = 465

Score = 127 bits (320), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 136/484 (28%), Positives = 212/484 (43%), Gaps = 85/484 (17%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ LPGSKSLS R LLL+A+ + + V+ LL + D M+ AL+ LG + A V
Sbjct: 1 MHLPGSKSLSARELLLSAIGDTSRVEGLLYARDTDLMVRLQGLGARISPWPAGNPVE 60

Query: 79 V-----GCG-----GKFP-VEDAKEEVQLFLGNAGIAMRSL 108
+ G G P + ++ VQ+ G AG MR L
Sbjct: 61 IQPIPLWEETKQSGVSSNSGAGLEALASSDSLHNPPELEQPVQIECGLAGTVMRFL 120

Query: 109 TAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPC-----PVRVNG 163
A V A G A + D +RP+ L+ L LGA+ + +D P P +N
Sbjct: 121 PALVVALGVPARFTADAA--ANKRPLRGLLEALASLGANWE----SDDPLDGIFPFTINS 174

Query: 164 IGGPLPGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERFG 222
G + + + SSQ++SALL++APL + I ++ S+P+++MTL + G
Sbjct: 175 RRGDVPEVITVDTAASSQFVSALLLSAPLWGKPLTIRCKTPVVPSPHIQMTLEALSLRG 234

Query: 223 VKAEHSDSWDRFYIKGGQKYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTVEGC- 276
+ A S D + Q P + + +E D S+A FLA A I GG V+V G
Sbjct: 235 INATGSIQSDGTW---QWRVEPDSDVFGQDLAIEPDLSNAGPFLAAAGIIGGVVSVPGWP 290

Query: 277 GTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMT 336
TS GD+ + ++L G +V T G L+A+ ++ ++ ++ T
Sbjct: 291 AHTSQVGDL-WRQILPQFGMQVRHRCGVFTARG-----TGVLRVSLDCSQCGELVPT 342

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 396
+A +A A G + + ++ R ET+R+ A+ EL KLG C ITP + L +
Sbjct: 343 IAALAAHASGVSHLEGLSHLRGHETDRLNALYQELQKLGIR-----CAITPEDGLEII 395

Query: 397 AID-----TYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDYFDVL 439
I Y+DHRMA +L + I D G T KT PD+ +
Sbjct: 396 GIPRTQLGARLPDQPLMMRAYEDHRMATFAALMGLYRT-IQIDDIGATTKTLPDFPQMW 454

Query: 440 STFV 443
+ +
Sbjct: 455 AQVI 458

>ref|YP_002871287.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas fluorescens
SBW25]
emb|CAY47896.1| putative bifunctional protein (prephenate dehydrogenase +
3-phosphoshikimate 1-carboxyvinyltransferase)
[Pseudomonas fluorescens SBW25]
Length = 748

Score = 127 bits (320), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 127/441 (28%), Positives = 210/441 (47%), Gaps = 41/441 (9%)

Query: 10 QPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P +SG +++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+ +E
Sbjct: 319 NPGGRLSGRIRVPGDKSISHRSIMLGSLAEGVTEVEGFLEGEDALATLQAFRDMGVVIEG 378

Query: 70 DKAACKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P ++LGN+G +MR L+ + A ++ VL G

Sbjct: 379 PHHGRVTIHGVGLHGLKPAPGP-----IYLGNSTSMRLLSGLLAAQRFDS--VLTGDAS 431

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+ +GA ++ G + PP+ + G L G + + S+Q S LL

Sbjct: 432 LSKRPMNRVAKPLRDMGAVIET--GPEGRPPLTIRGGQALKGLTYAMPMA-SAQVKSCLL 488

Query: 188 MAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G + P + T R++ FG V E + + ++ G +

Sbjct: 489 LAGLYAEGKTAVT-----EPAPTRDHTERMLRGFGYPVAVEGATA----SLESGHALIA- 538

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SS+++FL A+I G+ + +E G + V E+L +MGA +T E

Sbjct: 539 THIEVPGDISSAFFLVAASIAEGSELLEHVGVNPTRTGV--IEILRLMGADITL-ENQ 595

Query: 305 VTVTGPPEPFRGRKHLKAIDVNMNKMPPDVAMTLA-----VVALFADGPTAIRDVASW 356
V G EP ++A + ++P+ + LA V A A+G T +R

Sbjct: 596 REVGG--EPVADLRVRAASLKGIEIPEALVPLAIDFPPVLFVAAACAEGRTVLRGAQEL 652

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC- 415
RVKE++R+ + L LG E PD II + + + DHR+AMAFS+A+

Sbjct: 653 RVKESDRIQVMADGLLALGVKCEPTPDGIIID-GGLMGGGDVHAHGDHRIAMAFSVASLR 711

Query: 416 AEPVVTIRDPGCTRKTFFDYF 436
A P+ I D +FP++

Sbjct: 712 AAAPIRIHDCANVATSFNFL 732

>ref|XP_002538414.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Ricinus communis]
gb|EEF23969.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Ricinus communis]
Length = 193

Score = 127 bits (320), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 80/180 (44%), Positives = 107/180 (59%), Gaps = 8/180 (4%)

Query: 24 SKSLSNRILLLA-ALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGG 82
++LS LLA AL++G TV+ +LL S+D ML AL LG+ +E + V GCG

Sbjct: 21 QQALSEMTSLLAQALADGVTVIRDLLASDDTARMLEALTALGVKLE-NIGENAWQVTGCG 79

Query: 83 GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLK 142
G FP ++ LFLGNAG A R LTAA+ +GG+ Y L G+ RM ERPIGDLV LK

Sbjct: 80 GNFP---NKKADLFLGNAGTAFRPLTAALAFSGGD--YHLHGIARMHERPIGDLVDALK 133

Query: 143 QLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEII 202
Q GA VD PP++++ +K+ G +SSQ+L+ALLMA PL IE++

Sbjct: 134 QAGAQVDYLANEGYPPLQISPAQLDVSQPIKIRGDVSSQFLTALLMALPLTGQAASIEVV 193

>ref|NP_422383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter crescentus CB15]
ref|YP_002519077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter crescentus NA1000]
sp|Q9A2H2.1|ARO_ACAUCR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B8H6A8.1|ARO_ACAUCN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAK25551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter crescentus CB15]
gb|ACL97169.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caulobacter crescentus NA1000]
Length = 443

Score = 127 bits (320), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 139/446 (31%), Positives = 209/446 (46%), Gaps = 39/446 (8%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G V+ PG KS+S+R ++L AL+ GTT V+ LL +DV A++ G +E +

Sbjct: 10 PGGALRGIVRAPGDKSISHRSMILGALATGTTTVEGLLEGDDVLATARAMQAFGARIERE 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + G + PV+ + GNAG +R + A AT+ D +R
Sbjct: 70 GVGRWRIEGKGGFEEPVD-----VIDCGNAGTGVRLIMGAAAGFAMCATFTGD--QSLR 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPV---PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+G ++ L ++GA +LG D P+ + G G L G L S+Q SA+L+
Sbjct: 122 GRPMGRVLDPLARMGA---TWLGRDGRPLPLTLKG-GNLRGLNYTLP-MASAQVKSALL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFY----IKGGQKY 242
A A G V E+I+ + + E R++ FG V E + D+ + + GQK
Sbjct: 177 AGLHAEGGV--EVIEPEATRDHTE---RMLRAFGAEVIVEDRKAGDKTFRHVRLPEGQKL 231

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
A V GD SSA++ L A I G+ VTVEG L+ L+ MGA + +
Sbjct: 232 TGTHVA-VPGDPSAAFPVLVAILVPGSEVTVEGVMLNELR--TGLFTTLQEMGADLVIS 288

Query: 302 ETSVTVTGPPREPFGFR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
V + R LK + V + P D LAV A FA G T +R V R
Sbjct: 289 NVRVASGEEVDITARYSQLKGVVPPERAPSMIDEYPILAVAAAFASGETVMRGVGEMR 348

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVTATIDTYDDHRMAMA-FSLA 413
VKE++R+ L G V E P+ I+T P K T + T+ DHR+AM+ L
Sbjct: 349 VKESDRISLTANGLKACGVQVVEEPEGFIVTGTGQPPKGGATVV-THGDHRIAMSHLILG 407

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVL 439
A+ V + +PG +FP + D++
Sbjct: 408 MAAQAEVAVDEPGMIATSFPGFADLM 433

>ref|ZP_03913621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
mesenteroides subsp. cremoris ATCC 19254]
gb|EEJ42831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
mesenteroides subsp. cremoris ATCC 19254]
Length = 434

Score = 127 bits (319), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 130/447 (29%), Positives = 210/447 (46%), Gaps = 48/447 (10%)

Query: 15 ISGTVKLPKSGKSLNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R L+ A++EG TV+DN L S+DV + +G R LG VE D
Sbjct: 12 LHGEITVPGDKSISHRALMFGAIAEGKTVIDNFLMSDDVMHTMGVFRALG--VEIDHTES 69

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+A V+G G F A L +GN+G + R L ++ + G + +RP
Sbjct: 70 QAKVIGKGLTNFKAPSAG---LDMGNSGTSNRLLMGLLSKQPFDLNIF--GDSSLSKRP 123

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPV---RVNGIG-GLPGGKVKLSGSISSQYLSALL 187
+G + L + A + P V +NGI +P S+Q SA+L
Sbjct: 124 LGRVADPLSMNAQFELSNDEFLPAVIKANTELNGITYHMP-----VASAQVKSAIL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPK 246
+A A G E II+ L P + T R++ +FG + + D I ++ K S +
Sbjct: 176 LAGIQAEG--ETIIIEGL---PSRDHTEMLRQFGGQIK---TDNGVITVKKQSKLSGQ 226

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++F+ IT +T++ G + V ++LE MGA++ T+ +
Sbjct: 227 HVLVPSDISAFAFFMVAGLITPNSIEITIKKGVNPNTRDGV--IKLLERMGAEI--TQKPI 282

Query: 306 TVTGPPEPFGFRK--HLKAIDVNMNKMMPDVAMTLAVVALFAD--GPTAIRDVASWRVKE 360
G P K L I + +P L ++AL A G T I RVKE
Sbjct: 283 ASDGEPLADITVKAQTLHGIAITAEDIPGAVDELPIALALATQAVGDTIISGAELRVKE 342

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---TAIDTYDDHRMAMAFSLAA-C 415
T+R+ + +ELTKLGA ++E PD +I L+ T +D++ DHR+ M +A+
Sbjct: 343 TDRISTVISELTKLGADIDEKPDGMVHGGTLLHTSNGSTLLDSHGDHRIGMMNVIASLI 402

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
E V + ++P + + +S+
Sbjct: 403 TEGDVVLTGEEAMSVSYPGFVEDVSSI 429

>ref|YP_004218168.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium sp.
MP5ACTX9]
gb|ADW69388.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium sp.
MP5ACTX9]
Length = 432

Score = 127 bits (319), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 128/450 (28%), Positives = 198/450 (44%), Gaps = 40/450 (8%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ P + + G++ LPG KS+S+R +LA L+EGTT + N D H LG + LG
Sbjct: 5 IIHPARSLQGSVLVLPKDKSISHRYAMLAGLAEGTTKLSNFSFGADPHSSLGCMAALG--A 62

Query: 68 EADKAAKRAVVVCGGKGF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
E V G G G F P D L GN+G MR L+ + A T+ L G
Sbjct: 63 EVKDLGTHIEVTGVGGSFRQPTGD-----LDCGNSGSTMRMLSGLI--ASHPHTFTLIG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLS 184
+ RP+ + L+Q+GA + G P+ +NG P + I S+Q +
Sbjct: 115 DHSLTVRPMERIRKPLEQMGARIALVDGH--APITINGG---PLKAIDFDTPIPSAQVKT 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYK 243
A+L A A G + + + + E LR FG K + R I GGQK K
Sbjct: 170 AVLFAGLQAEGTTSLS--EAITTRDHTHEALR--AFGAKLTRETGERPRLVIAGGQK 244

Query: 244 SPKNAYVEGDASSASYFLAGAAI-TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + A V GD SSA++FL A + + + + G + +V+ +GAK+
Sbjct: 225 AIE-ATVPGDLSSAAFLCAALLFPDSNLILDSLGMNPTRS--ALLDVVAALGAKIKVLN 281

Query: 303 T-----SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDV 353
++ V P R ++ ++ D LA +A + IRD
Sbjct: 282 VEEQHGLIGLTIQVNAAP--ALSRGPMIEISGALTAQLIDELPVLAAIAPYTRHGMIIRDA 339

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
RVKE++R+ + L +GA++ E D I + L+ ID+ DHR+AMAFS+A
Sbjct: 340 KELRVKESDRIDLVARNLAMGATLTEHEDGMEIPGGQTLHGAQIDSGSDHRIAMAFSIA 399

Query: 414 ACAEVPVT-IRDPGCTRKTFPDYFDVLSTF 442
T I +FP++F L
Sbjct: 400 GLRATSATEINGAEAAAIISFPEFFTHLRNL 429

>ref|ZP_03994372.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris
ATCC 35243]
gb|EEJ53410.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mobiluncus mulieris
ATCC 35243]
Length = 465

Score = 127 bits (319), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 137/485 (28%), Positives = 212/485 (43%), Gaps = 87/485 (17%)

Query: 19 VKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ LPGSKSLS R LLL+A+ + + V+ LL + D M+ AL+ LG + A V
Sbjct: 1 MHLPGSKSLSARELLLSAIGDTNSRVEGLLYARDTDLMLVRLQGLGARISPWPAGNPVE 60

Query: 79 V-----GCG-----GKFPVEDAKEEVQLFLGNAGIAMRS 107
+ G G + P E ++ VQ+ G AG MR
Sbjct: 61 IQPIPLWEETKQSGVSSNYGAGLEALASSDSLNRNPPPE-LEQPVQIECLAGTVMRF 119

Query: 108 LTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVN 162
L A V A G A + D +RP+ L+ L LGA+ + +D P P +N
Sbjct: 120 LPALVVALGVPARFTADAA--ANKRPLRGLLEALASLGANWE----SDDPLDGIFPFTIN 173

Query: 163 GIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI-SIPYVEMTLRLMERF 221
G + + + SSQ++SALL++APL + I + S+P+++MTL +
Sbjct: 174 PRRGDVPEVITVDTAASSQFVSALLSAPLWGKPLTIRCKTPAVPSLPHIQMTLEALSLR 233

Query: 222 GVKAEHSDSWDRFYIKGGQKYKSPKNAY-----VEGDASSASYFLAGAAITGGTVTVEGC 276
G+ A S D + Q P + + +E D S+A FLA A I GG V+V G
Sbjct: 234 GINATGSIQSDGTW----QWRVEPDVSFGQDLAIEPDLNAGPFLAAAGIIGGVVSVPGW 289

Query: 277 -GTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAM 335
TS GD+ + ++L G +V T G L+A+ ++ ++ ++
Sbjct: 290 PAHTSQVGDL-WRQILPQFGMQVRHRCGVFTARG-----TGVLRVSLDSCQCGELVP 341

Query: 336 TLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN 395
T+A +A A G + + ++ R ET+R+ A+ EL KLG C ITP + L +
Sbjct: 342 TIAALAAHASGVSHLEGLSHLRGHETDRLNALYQELQKLGIR-----CAITPEDGLEI 394

Query: 396 TAID-----TYDDHRMAMAFSLAACAEVPTIRDPGCTRKTTFPDYFDV 438
I Y+DHRMA +L + I D G T KT PD+ +
Sbjct: 395 IGIPRTQLGARLPSPDQPLMMRAYEDHRMATFAALMGLYRT-IQIDDIGATTKTLPDFPQM 453

Query: 439 LSTFV 443
+ +
Sbjct: 454 WAQVI 458

>ref|YP_001541657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldivirga
maquilingensis IC-167]
sp|A8MB38.1|AROA_CALMQ RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|ABW02667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caldivirga
maquilingensis IC-167]
Length = 414

Score = 127 bits (319), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 122/418 (29%), Positives = 196/418 (46%), Gaps = 36/418 (8%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAakra 76
G+VK P SKS + R++LL+A+S+ T + ++ +S+D L + LG V R
Sbjct: 12 GSVKAPRSKSWAIRLILLSAISDEETTICSIIPDSDDTEAALRMIEVLGSKVIRQGN CIRV 71

Query: 77 V--VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ + CGG V G +G MR L A+ ++ N ++DG ++ RPI
Sbjct: 72 IPNLRQCGGYNV-----GSGTVMR-LGVALASSCRNPV-IIDGETLKRRI 118

Query: 135 GDLVVLGKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+L+ L+ LG +V+ D PV +NG + G V++ G ++SQY+S L+M ++
Sbjct: 119 RELLESRLSLGVNVN----GDSLPVAING--PVKGNVVEIRGDLTSQYISGLIMLGLVS- 171

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ I +I L+S YV++T R++E G S+ D + S N V GD
Sbjct: 172 -GITIRVIGDLVSRQYVDLRRRIIEESGCSVGVS--DVITVNECIPRISLSN--VPGDY 226

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREP 314
+ + ++ A A TGG VTV G GD + GA+ ++ +V G
Sbjct: 227 ALSGFYALALATGGLVTVTGLPKPLGYGDDSLVNIFSNAGARSVFSNGDWSVEGG---- 282

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
L+ I V++ PD+A +A +A FA G T I V KE+ R+ I L
Sbjct: 283 ---GELRGIVDLKDSPDLAPVVASIAPFASGETVITGVRHLAFKESNRLETISDSLRAF 339

Query: 375 GASVEEGPDYCIITPPEKLVNTAIDTYDDHRMA-MAFSLAACAEVPTIRDPGCTRKT 431
G +V G D I+ + I +DHR+A M+ +AA + I + C K+
Sbjct: 340 GVNVDHGDSDLRIS-GSITHGALIKCPNDHRIAMMSGVVAAGSNGESIIHNAECVNKS 396

>sp|Q608S5.2|AROA_METCA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 437

Score = 127 bits (319), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 132/448 (29%), Positives = 204/448 (45%), Gaps = 45/448 (10%)

Query: 11 PIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G +++PG KS+S+R ++L +L+EG T V L +ED + A R +G+ +E
Sbjct: 12 PGGRMQGDIRVPGDKSISHRVMLGSLAEGVTEVSGFLQAEDCLATMAAFRAMGVEIEGP 71

Query: 71 KAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ R VG G P L LGN+G +MR L+ + AG L G +
Sbjct: 72 TEGRLRIHGVLHGLKP-----PAAPLDLGNSGTSMRLLSGLL--AGQAFDITLTGDASL 124

Query: 130 RERPIGDLVVLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+ + L+ +GA +D GT P+R+ G L G + + S+Q S LL+
Sbjct: 125 VRRPMRRVTEPLRAMGARIDTTEAGT--APLRIAGGSRLKGIDYAMPVA-SAQVKSCLLL 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G + P + T R++ FG + +R I+ G K S
Sbjct: 182 AGLYAEKTCVT-----EPAPTRDHTERMLAGFGYPV--ARDGNRVCIQSGGKL-SATRI 233

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAI+ G+ V + G + V E+L MGA +
Sbjct: 234 DVPADISSAAFFMIGAAISP GSDVFLRHVGINPRTGTG--IEILREMGADIEILA----- 286

Query: 308 TGPPREPFGFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVAS 355
PRE G + L+ I + + +P D L + A A G T +
Sbjct: 287 ---PREVGGEVADLRIRYRELRGIRIPEHTVPLAIDFEPALFIAACATGETVLTGAEE 343

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC 415
RVKE++R+ A+ LT LG PD +I A+D+ DHR+AM+FS+AA
Sbjct: 344 LRVKESDRIQAMADGLTTLGIDARPTPDGMVIR-GGSFRGGAVDSRGDHRIAMSFSAAL 402

Query: 416 -AEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A +P+ I D +FP++ ++ T
Sbjct: 403 RAPIPIEIHDCANVATSFNPFVELARTL 430

>ref|ZP_04294221.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH621]
gb|EEK74108.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
AH621]
Length = 424

Score = 127 bits (319), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 119/443 (26%), Positives = 212/443 (47%), Gaps = 43/443 (9%)

Query: 15 ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + +PG KS+S+R ++ A++EGTT V N L ED + + LG+ +E +
Sbjct: 10 LNGKIVVPGDKSISHRSVMFGAIAEGTTKVSNFLLEDCLSTIACFQKLGQIE--QFGN 67

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ G G + + +E + L +GN+G +R + + ++T + D + +RP
Sbjct: 68 DVTIYGKG---LHNLQEPKGVLDVNGSGTTIRLMLGILANTPFHSTIIGDA--SIGKRP 121

Query: 134 IGDVLVGLKQLGADVDCFGLTDCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALLMA 189
+ + L ++ A +D P+ + G GVK S S+Q SA+L+A
Sbjct: 122 MKRVTDPLSKMNAQIDGRENGQYTPLSIRG-----GKVKGMHYHSPVASAQVKSALLA 175

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
G+ + + + S + E R++ FG + + ++GGQ+ K +
Sbjct: 176 G--LQGEGITTVTEPMQSRDHTE---RMLRAFCTVDVNGRT--VSLQGGQQLKGA-DIE 227

Query: 250 VEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FL AGA + + +E G + V +VL MGA ++ +
Sbjct: 228 VPGDISAFAFLVAGAIVQNSKLVLENVGLNPRTGTG--LDVLTKMGALISIDH----IR 281

Query: 309 GPPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
EP G LK I++ +P + + V+AL A +G T I++ +VKE
Sbjct: 282 NEEFEPGCDITIETSKLKGIEGGTLPRLIDEIPVIALLATQAEGITVIKNAEELKVKE 341

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
T R+ + EL KLGA +E PD II + L ++++ DHR+ M ++A+C +
Sbjct: 342 TNRIDTVVDELKGLGAKIEATPDGMIIYGKQSLKGNTVNSHGDHRIGMMLAIASCIIDGE 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
V I + ++P++F+ L+
Sbjct: 402 VKIENSDAVAVSYPEFFEQLAAL 424

>ref|NP_299603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
9a5c]
sp|Q9PB21.1|AROA_XYLFA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAF85123.1|AE004043_7 3-phosphoshikimate 1-carboxyvinyltransferase [Xylella fastidiosa
9a5c]
Length = 454

Score = 127 bits (318), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 130/432 (30%), Positives = 205/432 (47%), Gaps = 35/432 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ AAL++GT+ +D L +ED L LG+ +E + +
Sbjct: 29 LHGVLSIPGDKSISHRAVMFAALADGTSRIDGFLEAEDTCSTAEILARLGVRITPLSTQ 88

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V VG G + L GNAG MR L + A ++ VL G + +RP
Sbjct: 89 RIVHGVGV DGL-----QASHIPLDCGNAGTGMRLLAGLLVAQPFDS--VLVGDAASLSKRP 141

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+R+ G G L G +S S+Q SA+L+A A
Sbjct: 142 MRRVTDLPSQMGARIDTS-DDGTPPLRIYG-GQLLHGIDFISPVASAIKSAVLLAGLYA 199

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ + P + T R++ FGV + S R ++GGQ+ + + + D
Sbjct: 200 RNETVVREPH-----PTRDYTERMLTAFGV DIDDVSTGCAR--LRGGQRLCA-TDITIPAD 251

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++L A + I G +T+ G + + VL +MGA + E++ G
Sbjct: 252 FSSAAFYLVAA SVIPGSDITLRAVGLNPRR--IGLLTVLRLMGANI--VESNRHEQGG-- 305

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP ++ + ++P D L V A A+G T + A RVKE++R+
Sbjct: 306 EPVVDLVRVYAPLQGTTRVPEDLVADMIDEFPALFVAAAAAEGQTVVSGAAELRVKESDRL 365

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP-VTIR 423
A+ T L LG V+E D I + I+++ DHR+AMAFS+A V V I
Sbjct: 366 AAMVTGLRVLVGVQVDETADGATIH-GGPIGHGTINSHGDHRIAMAFSIAGQLSVSTVRIE 424

Query: 424 DPGCTRKTFPDY 435
D +FPDY
Sbjct: 425 DVANVATSFDPY 436

>emb|CBL25232.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruminococcus torques
L2-14]
Length = 432

Score = 127 bits (318), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 125/446 (28%), Positives = 199/446 (44%), Gaps = 27/446 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L I + G V +PG KS+S+R ++ +++ GTT + N L+ D + R LG+ +E
Sbjct: 3 LCNITGLKGVKTIPGDKSISHRCIMFGSIANGTTQIHNFSLGADCLATIRCFRELGEIE 62

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ +V G G A E++ L +GN+G R ++ + AG L G
Sbjct: 63 VESDYSSVIVHGKG--LHGLSAPEKI-LDVNGSGTTTRLISGIL--AGQPFDSKLSGDES 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ ++ L Q+GA + L C P+ + L G S S+Q S LL+
Sbjct: 118 LNSRPMKRIIEPLAQMGAHISSILRNCGAPLYITP-AQLHGIHYD-SPVASAQVKSCLLL 175

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A D E + + +S + E+ L+ FG A+ +++ K + +
Sbjct: 176 AGLYA--DGETSVTEPSLSRNHTEMLK---EFG--ADIHSTFEIGSSKATAIRPCEEL 228

Query: 249 Y-----VEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
Y V GD SSA+YF+A G + + VE G + + V E MG +T

Sbjct: 229 YGQEITVPGDISAAYFIAAGLIVPDSEILVENVGINPTRAGI--LRVCEDMGGDITLLN 286

Query: 303 TSVTVTGPPREPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ R L + + +P D +AV+A A+G T I+D A +V

Sbjct: 287 ERTEGGERIADVLVRSRLHGTTEIGDIIPTLIDEIPVIAVMAAMAEGTTIIKDAELKV 346

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KET+R+ + L +G V D II L+ +I T DHR+AMAFS+AA AE

Sbjct: 347 KETDRIETVTDNLKAMGCDVPTEDGMIINGGRPLHGASIHLLDHRIAMAFSIAALVAE 406

Query: 418 VPVTIRDPGCTRKTFFDYFDVLSTFV 443

I D C ++P ++D +

Sbjct: 407 GTTKILDSKCDVSYPTFYDTFEQLL 432

>ref|ZP_07829261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sp. oral
taxon 137 str. F0430]
gb|EFR41290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sp. oral
taxon 137 str. F0430]
Length = 438

Score = 127 bits (318), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 127/431 (29%), Positives = 197/431 (45%), Gaps = 30/431 (6%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PG KS+S+R ++LA L + N L++ D +G +R LG+ VE A VV G

Sbjct: 20 IPGDKSISHRSVMLAGLGSTPVHIKNFLHAADCLSTVGVMRALGVRVEF-PADGELVVVG 78

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
G E A L GN+G +R + + T+ D + RP+G +++

Sbjct: 79 RGLHGLSEPAS---VLDAGNSGTTLRMMGLLAPQPFFLTFTGDA--SLSRPMGRVLLP 133

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-SISSQYLSALLMAAPLALG---D 196
L Q+GA + + P+ + +P GK KL G S S SA + +A L G D

Sbjct: 134 LGQMGAIYGRNDNNLPLSI-----VPAGK-KLCGISYDSPVASAQVKSAILLAGLYTD 187

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNAYVEGDAS 255
+ + +S + E R++ FGV+ E R Y + + Y +P+ V GD S

Sbjct: 188 APTSVTEPFVSRDHTE---RMLAGFGRVVEREGCTARVYPVTREEDYIAPEEITVPGDIS 244

Query: 256 SASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA+YFL G +I G+ + ++ G + + +VL MGA + + T G

Sbjct: 245 SAAYFLVGGSIKGRLLLNKNGINLRTGTI--LDVLAQMGAHIA-VKNERTSGGEALAD 301

Query: 315 FGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ L + V MP D LA ALFA+G T I RVKET+R+ AI

Sbjct: 302 ISVETAEHLGVRVGAIEIMPRVLDEIPILAAAALFAEGDVTITGAGELRVKETDRLRAIAD 361

Query: 370 ELTKLG-ASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
E K+ S+EE D II + + + DHRMAM+ ++ A I +P

Sbjct: 362 EFGKIAPGSIEELEDGLIIRGKRPICKARVHSRSDHRMAMSLAVLGAADGAEIEEPDSV 421

Query: 429 RKTFFPDYFDVL 439

+ ++P +F+ L

Sbjct: 422 QISYPAFFEQL 432

>ref|YP_003924935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
plantarum subsp. plantarum ST-III]
gb|ADN98841.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
plantarum subsp. plantarum ST-III]
Length = 432

Score = 127 bits (318), Expect = 4e-27, Method: Compositional matrix adjust.
Identities = 131/453 (28%), Positives = 211/453 (46%), Gaps = 46/453 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

+++ +QP + G + +PG KS+S+R L+L A+S+GTT + + L + D L AL+ LG

Sbjct: 3 KKLSIQPASGLQGDLSVPGDKSVSHRGLILGAISQGTTLHHFLPADCLSTLTALQKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+ + K V + G + ++ L +GNAG A R LT + AG L
 Sbjct: 63 VPI---KRVDTTVTISGRGLRGLTQPQQP--LDMGNAGTATRLLTGLL--AQPPFETTLV 115
 Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
 G + +RP+ + L+ +GA V G P+ + G L G + ++ + S+Q S
 Sbjct: 116 GDTSLSQRPMEVRVQPLQAMGAQVQLTAG--HLPMTITG-RTLHGSRTMQVA-SAQVKS 171
 Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
 AL++AA A D II+KL P + T RL+++FG + E + ++ Q
 Sbjct: 172 ALILAALQA--DQASTIIIEKL---PTRDHTERLLQQFGGQIETAPDQRTITVQ-PQPALV 225
 Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
 ++ + GD SSA++F+ A I + V + G + F +L MG +VT
 Sbjct: 226 GQSLTIPGDFSSAAFFVTAATIIPNSHVRLTNVGLNPTR--TGFLNILRRMGQVTVDE 283
 Query: 304 SVTVTGPPREPFGFR-----KHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVAS 355
 EP G L + V ++P V L +VAL A+G + I A
 Sbjct: 284 HRM-----GEPVGTLDVRFAQLHPVQVTATEIPAVIDELPLVALLAATANGISTISGAAE 338
 Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPEKLNVTATIDYDDHRMAM 408
 RVKET+R+ I TEL KLG + PD +I P E L ++ DHR+ M
 Sbjct: 339 LRVKETDRIATIVTELKRLGVQITSQPDGFVIDGRKSWRQPTPLA-----SHGDHRIGM 393
 Query: 409 AFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
 ++AA P + ++P +F+ L+
 Sbjct: 394 MMAIAALRLAAPAELESAAEAVNISYPFFEDLA 426

>ref|YP_143723.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus thermophilus
 HB8]
 sp|Q5SL36.1|ARO_A_THET8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 dbj|BAD70280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus thermophilus
 HB8]
 Length = 427

Score = 127 bits (318), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 143/440 (32%), Positives = 208/440 (47%), Gaps = 34/440 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
 L P + G +++PG KS+++R L+L AL+EG + L + D L+ LG E
 Sbjct: 6 LAPCGPLRGLRVPGDKSVTHRGLMLLALAEGERLFYPLKAGDTLSTARVLQALG--AE 63
 Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
 + +V G G +F + E L GNAG MR L + VL G
 Sbjct: 64 VREEGPHFLVRGRGLRF---QEPEDVLDCGNAGTLMRLLGLLAGQE-GLFAVLTDGAS 118
 Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 +R RP+G +V L+ +GA VD + P+ V G L G + L S+Q SALL+
 Sbjct: 119 LRRRPMGRVAPLRAMGARVDGREEGERAPLAVRG-APLRGLRYTLP-VPSAQVKSALLL 176
 Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
 A A G E+E P + T RL FG+ E R + G + + K+
 Sbjct: 177 AGLFAEGVTEVEE-----PTPTRDHTERLFRHFGLPLEVEGRKVRTWRTG--PFPA-KDL 228
 Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
 V GD SSA++FL A +T G+ V VEG G + VL+ MGA + W +
 Sbjct: 229 VVPGDFSSAAFFLVAALVTPGSEVVVEGVGLNPTR--TGLLTVLKAMGADLEWQ----VL 282
 Query: 308 TGPPREPFG---RKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
 G EP G +H LK + V+ +P D LA A +A+G T I ++ RVK
 Sbjct: 283 EGEAGEPVGWVRARHSLKGVAVDPGLIPLMVDEVVLA AAAA WAEGETYIPGLSELRVK 342
 Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAIEVP 419
 E++R+ AI L LG VEEGPD+ I + + + DHR+AMAF++A V
 Sbjct: 343 ESDRVRAIAENRALGVEVEEGPDWLIR-GGGVRPGRVRPFHDHRIAMAFAVAGLP-VG 400
 Query: 420 VTIRDPGCTRKTFPDYFDVL 439
 V + +P ++P +F L
 Sbjct: 401 VEVEEPHWAEISYPGFFQDL 420

>ref|NP_785560.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus plantarum WCFS1]
sp|Q88VL2.1|AROA_LACPL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD64409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus plantarum WCFS1]
Length = 432

Score = 127 bits (318), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 131/453 (28%), Positives = 211/453 (46%), Gaps = 46/453 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ +QP + G + +PG KS+S+R L+L A+S+GTT + + L + D L AL+ LG
Sbjct: 3 KKLSIQPASGLQGDLSVPGDKSVSHRGLILGAISQGTTLHHFLPAADCLSTLTALQKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + K V + G + ++ L +GNAG A R LT + AG L
Sbjct: 63 VPI---KRVDTTVTISGRGLRGLTQPQQP--LDMGNAGTATRLTGLL--AGQPFETTLV 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L+ +GA V G P+ + G L G + ++ + S+Q S
Sbjct: 116 GDTSLSRPMERVRQPLQAMGAQVQLTAG--HLPMTITG-RTLHGSRTMQVA-SAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
AL++AA A D II+KL P + T RL+++FG + E + ++ Q
Sbjct: 172 ALILALQA--DQASTIIEKL---PTRDHTERLLQQFGGQIETAPDQRTITVQ-PQPALV 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++ + GD SSA++F+ A I + V + G + F +L MG +VT
Sbjct: 226 GQSLTIPGDFSSAAFFVTAATIIIPNSHVRLTNVGLNPT--TGFLNILRRMGQVTVDE 283

Query: 304 SVTVTGPPREPFGF-----KHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVAS 355
EP G L + V ++P V L +VAL A+G + I A
Sbjct: 284 HRM-----GEPVGTLDVRFAQLHPVQVTATEIPAVIDELPLVALLAATANGISTISGAAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDYDDHRMAM 408
RVKET+R+ I TEL KLG + PD +I P E L ++ DHR+ M
Sbjct: 339 LRVKETDRIATIVTELKQLGVRITSQPDGFVIDGRKSWRQPTEPLA-----SHGDHRIGM 393

Query: 409 AFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
++AA P + ++P +F+ L+
Sbjct: 394 MMAIAALRLAAPAELESAEAVNISYPTFFEDLA 426

>emb|CBK74531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Butyrivibrio fibrisolvens 16/4]
Length = 493

Score = 127 bits (318), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 114/449 (25%), Positives = 210/449 (46%), Gaps = 35/449 (7%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ + +K + G + +PG KS+S+R ++ A+S+GTT + L+ D + + +G+
Sbjct: 1 MAITKVKSLKGEISVPGDKSISHRGVMFGAISKGTTELGTGFLDGADCRSTISCFKAMGID 60

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ ++ V+ G G + K + +GN+G R ++ + AG L+G
Sbjct: 61 I--NQNGDHVVIHNG---LHGLKAPSSMLDVGNSTTTLISGIL--AGQPFISSLNG 112

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLS 184
++ RP+G ++ L ++GA + C P+ IGG + + ++S Q S
Sbjct: 113 DESIQRRPMGRIITPLSEMGAIKSLKDNGCTPLE---IGGQSLHSIHNSPVASQVKS 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY 242
+L+A A G + + +IS ++ E+ ++ FG +K+E + I G
Sbjct: 170 CVLLAGLYADGITSVT--EPVISRNHTEL---MLSGFGANIKSEGLTAT----IVGNPTL 220

Query: 243 KSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301

K A V GD SSA+YF+ AG + ++ T + + +V + MG +
 Sbjct: 221 NGQKIA-VPGLDISAAYFIVAGLICENSDDLKKNVNTNPTRAGI--IKVAQAMGGNIELL 277
 Query: 302 ETSVTVTGPPPREPF--GRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
 + V+G P +L +V + +P D +AV+A A+G T I+D A
 Sbjct: 278 NERI-VSGEPVADIHVSTSNLHGCEVKGDIIPALIDEIPVIAVMAACAEGQTIIKDAAEL 336
 Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-C 415
 +VKE+ R+ + L +G + D II + L+ T I TY DHR+AM+F++A
 Sbjct: 337 KVKNESNRIATVTENLANMGCDIISTDDGMIINGGKPLHGTNIKTYLDHRIAMSFAIAGLV 396
 Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
 A+ T + C + ++PD+F+ + +
 Sbjct: 397 ADGETTFDNEACCQISYPDFPETIKNYTN 425

>ref|NP_441799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechocystis sp. PCC
 6803]
 sp|Q59975.1|AROA_SYNY3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 emb|CAA53074.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechocystis sp. PCC
 6803]
 dbj|BAA18477.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechocystis sp. PCC
 6803]
 Length = 447

Score = 127 bits (318), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 131/439 (29%), Positives = 208/439 (47%), Gaps = 27/439 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 ++G +++PG KS+S+R L+L A++ G T+++ LL ED R +G + ++ ++
 Sbjct: 26 LTGRLRVPGDKSISHRALMLGAIATGETIIEGLLLGEDPRSTAHCFRAMGAEI-SELNSE 84
 Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
 + +V G G G+ + L GN+G MR L + A + + + G +R RP
 Sbjct: 85 KIIIVQGRGLGQL----QEPSTVLDAGNSGTTMR-LMLGLLAGQKDCFLTFTVTDGDSLRRHP 139
 Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
 + ++ L+Q+GA + P+ V G P + I+S Q S LL+A
 Sbjct: 140 MSRVIIQPLQMQGAKIWARSNKGFPAPLAVQGSQKLP---IHYHSPIASAQVKSCLLLAGLT 196
 Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
 GD + + +S + E R+++ FG K D G + + + V G
 Sbjct: 197 TEGDTTV--TEPALSRDHSE---RMLQAFGAKLT-IDPVTHSVTVHGAHLTGQRVVVP 250
 Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
 D SSA+++L A+I G+ + VE G + V EVL MGA +T E VTG P
 Sbjct: 251 DISSAAFVWVAASILPGSELLVENVGINPTRTGTV--LEVLAQMGADIT-PENERLVTGEP 307
 Query: 312 REPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
 + HL+ +P D LAV A FA+G T I D A RVKE++R+ A
 Sbjct: 308 VADLRVRASHLQCGCTFGGEIIPRLIDEIPILAVAAAFAGETTRIEDAAELRVKESDRLAA 367
 Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
 I +EL K+GA V E D I L +D+ DHR+AMA ++AA TI +
 Sbjct: 368 IASELGKMGAKVTEFDDGLEIQGGSPLQGAEVDSLTDHRIAMALAI AALGSGGQTIINRA 427
 Query: 427 -CTRKTFPDYFDVLSTFVK 444
 ++P++F L +
 Sbjct: 428 EAAAISSYPEFFGTGLGQVAQ 446

>ref|NP_692701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanobacillus
 iheyensis HTE831]
 sp|Q8EQC1.1|AROA_OCEIH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 dbj|BAC13736.1| 5-enolpyruvylshikimate-3-phosphate synthase [Oceanobacillus
 iheyensis HTE831]
 Length = 429

Score = 127 bits (318), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 130/460 (28%), Positives = 217/460 (47%), Gaps = 56/460 (12%)

Query: 7 IVLQPIK-EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ LQPI + GT+K+PG KS+S+R ++ ++++GTT V N L+ ED + A + +G+
Sbjct: 4 LALQPISGSLHGTIKVPGDKSISHSRIFGSIAGTTTVTNFLDGEDCMRTIDAFKEMGV 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
++ K + G G +E KE L GN+G R + + N T D
Sbjct: 64 PIQ--KNGSNVTIEGTGLSGLMEPNKE--LDFGNSGTTTIRLMLGLLAGLPFNTTVYGDA 118

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIG-----GLPGGKVKLSGSIS 179
+ +RP+ +V L+ +GA +D + P+ + G LP VK S
Sbjct: 119 --SLSKRPMNRVVDPLRLMGATIDGKEQGNYLPLTITGTSLSIDYDLP---VK-----S 168

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAE-HSDSWDRFYI 236
+Q SALL+A L I+ + P T +++ FG +K++ H+ S
Sbjct: 169 AQVKSALLLAG---LHSENTTIVRE--KSPTRNHTETMLQAFGANIKSDGHTTSI----- 218

Query: 237 KGGQKYKSPKNAYVE--GDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
K + +VE GD SSA++F+ A + G V ++ G + + +++
Sbjct: 219 ---SKTDDLQGHVEVPGDISAFAFVVAACMVPGEVILKDVGLNETRTGI--IDIVLQ 273

Query: 294 MGAKVTWTETSVTVTGPPREPFG----RKHLKAIDVNMNMKMP---DVAMTLAVVALFAD 345
MGAK+T + V G E G L + + + +P D LA++A AD
Sbjct: 274 MGAKLTIQNERI-VGG---EKIGDILIISSPLTGVITIEGDAIPRLIDEIPILALLATQAD 329

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHR 405
G T I+D +VKET+R++A+ LT+LGA V D II KL ++DDHR
Sbjct: 330 GTTIIDAEELKVKETDRLLAVSENLTQLGADVTPTEGMIIRGNTKLKGGNFKSFDDHR 389

Query: 406 MAMAFSLAA-CAEVPVTIRDPGCTRKTFFPDYFDVLSTFVK 444
+AM +A+ E V + + C ++P++ + L + +K
Sbjct: 390 IAMMGIASLVTEDTVVDNIDCINISYPNFVNDLQSILK 429

>ref|YP_003465144.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria seeligeri
serovar 1/2b str. SLCC3954]
emb|CBH28060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria seeligeri
serovar 1/2b str. SLCC3954]
Length = 428

Score = 126 bits (317), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 217/438 (49%), Gaps = 31/438 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GEITVPGDKSMHSRISIMFGAIAEGKTIVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G G P L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTGFAGLKPAAAGP-----LDIGNSGTTIRLMMGIL--AGSHFDTVILGDESIKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ ++G L + + + S+Q SA++ AA A
Sbjct: 123 NRVMPLPLREMGAKMHGKDGSEFAPITISGNQALKQIEYHMPVA-SAQVKSIIIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K +T ++ +FG + E R +KGGQ + + + V GD
Sbjct: 182 GETIHEKEK-----TRDTEHMIRQFGGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDV 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+ AG I + + G + + +V+E MG + ++S + TG
Sbjct: 234 SSAAFFIVAGLIIPKSEIELTHVGLNPRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 290

Query: 314 PFGRK--HLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIR 368
K LK ++ + +P + + V+AL A +G T I++ A +VKET R+ A+
Sbjct: 291 TVVVKTSDLKGTEIGGDIIIPRLIDEIPVIALLATQAEGTTVIKNAELKVKETNRIDAVA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPG 426

TEL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 351 TELNKMGAADITPTEDGLIIRGKTPLHAAKVTSYGDHRIGMMLQIAALIVEDGEVELDRAE 410

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K

Sbjct: 411 AVSVSYPTFFEDIHSLK 428

>ref|YP_091968.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus licheniformis ATCC 14580]
ref|YP_079558.3| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus licheniformis ATCC 14580]
ref|ZP_07999507.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. BT1B_CT2]
sp|Q65I39.1|AROABACL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|AAU41275.1| AroE [Bacillus licheniformis ATCC 14580]
gb|AAU23920.3| 5-enolpyruvylshikimate-3-phosphate synthase [Bacillus licheniformis ATCC 14580]
gb|EFV73877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus sp. BT1B_CT2]
Length = 428

Score = 126 bits (317), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 122/446 (27%), Positives = 213/446 (47%), Gaps = 36/446 (8%)

Query: 12 IKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
I + G + +PG KS+S+R ++ A++EG TV+ N L D + R +G+ +E +
Sbjct: 6 ISSLKGEHLHIPGDKSISHRSVMFGAMAEGKTVIKNPLPGADCLSTIACFRKMGEVEIQN- 64

Query: 72 AAKRAVVVGCGKGFVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V G G ++ E +L +GN+G +R + + AG + G +
Sbjct: 65 -GSDVTVRGKG----LDQLAEPAELLDVGNSTTIRLMLGIL--AGRPFHSTVAGDESIA 117

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+++GA +D G + P+ V G G L + S S+Q SA+L+A
Sbjct: 118 KRPMKRVTEPLRKMGAKIDGRAGGEYTPLSVRG-GHLKAIDFQ-SPVASAQIKSAVLLAG 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + K + T R++ FGV ++ I+GGQ+ K+ + +V
Sbjct: 176 LQAEGTTTVTEPHK-----SRDHTERMLSMFGVSLREDETS--VSIEGGQQLKAAE-VFV 227

Query: 251 EGD-ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD +S+A + A + + G V + G + + +VL+ MGA + E T
Sbjct: 228 PGDISSAAFFLAAASLVPGEVVLNRNVLNPTRTGI--IDVLKEMGADLEIEEKDTGNT- 284

Query: 310 PPREFPG-----RKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKET 361
EP+G LKA +++ + +P + + ++AL A+G T I+D A +VKET
Sbjct: 285 ---EPYGLRIKTTSSLKAAEISGDLIPRLIDEIPIIALLATQAEGTTVIKDAEELVKET 341

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ADTYDDHRMAMAFSLAAC-AEVP 419
R+ + +EL K+GA++E D I L A + ++ DHR+ M +AAC E P
Sbjct: 342 NRIDTVASELKKIGANIEPTEDGMKIHGKTPLTGGAKVSSHGDHRIGMMLGIAACICEQP 401

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 445
+ I P ++P +F+ + +
Sbjct: 402 IDILQPEAVSVSYPSFFEHIKLAEK 427

>ref|ZP_06729331.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas fuscans subsp. aurantifolii str. ICPB 10535]
gb|EFF49547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas fuscans subsp. aurantifolii str. ICPB 10535]
Length = 440

Score = 126 bits (317), Expect = 5e-27, Method: Compositional matrix adjust.
Identities = 129/434 (29%), Positives = 211/434 (48%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++

Sbjct: 16 LQGS LAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRIETPSASQ 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF--LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R +V G G VE + ++ GNAG MR L + A ++ VL G + +RP

Sbjct: 76 R-IVHVG-VEGLQAPTEVLDCGNAGTGMRLLAGLLAAQRFDS--VLVDASLSKRP 128

Query: 134 IGD LVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA ++ PP+ V+G L G +S S+Q SA+L+A A

Sbjct: 129 MRRVTGPLAQMGARIET-QDDGTPPLHVHGGQALYGIDF-VSPVASAQVKS AVLLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV+ + S R ++GGQ+ ++ A V D

Sbjct: 187 QGETAVTEPH-----PTRDYTERMLSFAFGEIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I G+ V + G + + A L +MGA++ E G P

Sbjct: 239 FSSAAFFIVAASIVPGSEVVLRAVGLNPRRTGLLAA--LRLMGA EI-GEENHAHEHGGE PV 295

Query: 313 EPFGRKH--LKAIDVNMNKM PDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+

Sbjct: 296 ADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAAASGQTVVTGAE LRVKESDR LAAM 355

Query: 368 RTELTKLGSVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D

Sbjct: 356 ATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAF AIAQQLSTGQVQVNDVA 414

Query: 427 CTRKTFPDYFDVLS 440
+FP FD L+

Sbjct: 415 NVATSFPG-FDSL A 427

>gb|AAM16073.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 59

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 58/59 (98%), Positives = 58/59 (98%)

Query: 387 ITPPEKLNVT AIDTYDDHRMAMAFSLAA CAEVPVTIRDPGCTRKTFPDYFDVLS TFVKN 445
ITPPEKLNVT AIDTYDDHRMAMAFSLAA CAEVPV IRDPGCTRKTFPDYFDVLS TFVKN

Sbjct: 1 ITPPEKLNVT AIDTYDDHRMAMAFSLAA CAEVPVAIRDPGCTRKTFPDYFDVLS TFVKN 59

>ref|YP_001224755.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 7803]
sp|A5GKJ3.1|ARO A_SYN PW RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS

emb|CAK23458.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 7803]
Length = 439

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 129/448 (28%), Positives = 207/448 (46%), Gaps = 47/448 (10%)

Query: 15 ISGTVKLPGSKSLSNRI LLLAALSEGTTVDNLLNSE DVHYMLGALRTLGLSVEADKAAK 74
+ G V++PG KS+S+R LL A+++G T ++ LL +ED LR +G +

Sbjct: 17 LKGAVRVP GDKSISHRALLFGAIADGVT TIEGLLP AEDPISTAACL RAMGA EI SPIGEGD 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G D +E L GN+G MR + + G +VL G +R R

Sbjct: 77 LIRVTGVG-----LDGLQEPD TVLDCGNSGTMRMLGLLAGRDGR-HFVLTGDASLRRR 130

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+ + L LGA+V + P+ V G +L G++ S+Q SAL

Sbjct: 131 PMQRVGGPLAMLGA EVRGRGDGN YAPLAVQG-----RRLRGAVVGTPVASAQVKSAL 182

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSP 245
L+AA A G + + P + + R+++ FG R +K G + +

Sbjct: 183 LLAALTADGPTTV-----IEPAPSRDHSERMLKAFGADLT VG GEMGRHISVKPGARLQG- 236

Query: 246 KNAYVEGDASSASYFL-AGAAITGGT VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET- 303

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      ++ V GD SSA+++L AGA + G +TVE G + V +VLE MGAK+
Sbjct: 237 QHVVPVPGDISSAAFVLVAGALVPGADLTVENVGLNPTRTGV--LDVLEQMGAKIEVLNRR 294

Query: 304 -----SVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVAS 355
      + VT P +PF + + M ++ D L V A F +G + I A
Sbjct: 295 DVAGEPVGDLHVTSGPLQPF-----RFGEIIMPRLVDEVPIITVAACFCEGESHISGAAE 349

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
      RVKET+R+ + +L +GA ++E PD +I L A+D+ DHR+AM+ ++A+
Sbjct: 350 LRVKETDRLAVMARQLKTMGADLDETDPGLVIRGGRLRGAALDSETDHRVAMSLAVASL 409

Query: 415 CAEVPVTIRDPGCTRKTTFPDYFDVLSTF 442
      A T+ ++P ++D L+
Sbjct: 410 LASGDSTLERSDAAVSYPSFWDDLRL 437

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>ref|ZP_07078084.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus plantarum subsp. plantarum ATCC 14917]
gb|EFK29406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus plantarum subsp. plantarum ATCC 14917]
Length = 432

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 131/453 (28%), Positives = 211/453 (46%), Gaps = 46/453 (10%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      +++ +QP + G + +PG KS+S+R L+L A+S+GTT + + L + D L AL+ LG
Sbjct: 3 KKLSIQPASGLQGDLSVPGDKSVSHRGLILGAISQGTTLHHFLPAADCLSTLTALQKLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + + K V + G + ++ L +GNAG A R LT + AG L
Sbjct: 63 VPI---KRVDTTVTISGRGLRGLTQPQQP--LDMGNAGTATRLTGLL--AGQPFETTLV 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGLPGGKVKLSGSISSQYLS 184
      G + +RP+ + L+ +GA V G P+ + G L G + ++ + S+Q S
Sbjct: 116 GDTSLSQRPMEVRVRLQPLQAMGAQVQLTAG--HLPMTITG-RTLHGSRTMQVA-SAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      AL++AA A D II+KL P + T RL+++FG + E + ++ Q
Sbjct: 172 ALILAALQA--DQASTIIIEKL---PTRDHTERLLQQFGGQIETAPDQRTITVQ-PQPALV 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      ++ + GD SSA++F+ A I + V + G + F +L MG +VT
Sbjct: 226 GQSLTIPGDFSSAAFFVTAATIIPNSHVRLTNVGLNPTR--TGFLNILRRMGGQVTVVDHE 283

Query: 304 SVTVTGPPREPFGR-----KHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVAS 355
      EP G L + V ++P V L +VAL A+G + I A
Sbjct: 284 HRM-----GEPVGTLDVRFAQLHPVQVTATEIPIAVIDELPLVALLAATANGISTISGAAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAM 408
      RVKET+R+ I TEL KLG + PD +I P E L ++ DHR+ M
Sbjct: 339 LRVKETDRIATIVTELKRLGVQITSQPDGFFVIDGRKSWRQPTEPLA-----SHGDHRIGM 393

Query: 409 AFSLAACA-EVPVTIRDPGCTRKTTFPDYFDVLS 440
      ++AA P + ++P +F+ L+
Sbjct: 394 MVAIAALRLAAPAELESAEAVNISYPTFFEDLA 426

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>ref|ZP_00787486.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus agalactiae CJB111]
gb|EAO73814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus agalactiae CJB111]
Length = 427

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 117/437 (26%), Positives = 206/437 (47%), Gaps = 27/437 (6%)

```

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + GT+++PG KS+S+R ++ ++S+G T + ++L EDV + A + +G+ +E D
Sbjct: 10 LKGTIRVPGDKSISHRAIIFGSISQGVTRIVDVLRGEDVLSTIEAFKQMGVLIEDDGE-- 67

```

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVLGDGVPRMRERPI 134
++ GK + L +GN+G +MR L A V A G + G + +RP+
Sbjct: 68 ---IITIYGKGFAGLTQPNLLDMGNSGTSMR-LIAGVLA-GQEFVETMVGDNLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ + L ++GA + D PP+++ G L L + S+Q SAL+ AA
Sbjct: 123 DRIALPLSKMGARISGVNTRDLPLKLQGTCKLKPIFYHLPVA-SAQVKSALIFAALQTK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNAYVEGD 253
G E I++K + + E +R +FG H D D+ + GGQ ++ V GD
Sbjct: 182 G--ESLIVEKEQTRNHTEDMIR---QFG---GHLDIKDKEIRLNGGQSLVG-QDIRVPGD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++++ AG I + +E G + + +V+ MG K+ + V
Sbjct: 233 ISSAAFVWIVAGLIIPNSHIILENVGINETRTGI--LDVVSKMGGKIKLSSVDNQVKSATL 290

Query: 313 EPFGRKHLKADVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
HL+A ++ +P + L ++AL A G T I D +VKET+R+ +
Sbjct: 291 -AVDYSHLQATHISGAMIPRLIDELPIALLATQAQGTTVIADAQELKVKETDRIQVVVE 349

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
L ++GA + D II L+ ++D + DHR+ M ++AA E V +
Sbjct: 350 SLKQMGADITATADGMIIRGNTPLHAASLDCHGHRIGMMIAIALLVKEGEVDLSGEEA 409

Query: 428 TRKTFPDYFDVLSTFVK 444
++P++ + L V
Sbjct: 410 INTSYPNFLEHLEGLVN 426

>gb|EFR99623.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria seeligeri
FSL N1-067]
Length = 430

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 217/438 (49%), Gaps = 31/438 (7%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 14 GEITVPGDKSMHSRISIMFGAIAEGKTIVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 71

Query: 77 VVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVLGDGVPRMRERPI 134
+V G G G P L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 72 IVHGTGFAGLKPAAGP-----LDIGNSGTTIRLMMGIL--AGSHFDTVILGDESIKRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ ++G L + + + S+Q SA++ AA A
Sbjct: 125 NRVMLPLQEMGAKMHGKDGSEFAPITISGNQALKQIEYHMPVA-SAQVKSALIFAALQAE 183

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K + T ++ +FG + E R +KGGQ + + + V GD
Sbjct: 184 GETIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDV 235

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+ AG I + + G + + +V+E MG + ++S + TG
Sbjct: 236 SSAAFFIVAGLIIPKSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 292

Query: 314 PFGRK--HLKADVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIR 368
K LK ++ + +P + + V+AL A +G T I++ A +VKET R+ A+
Sbjct: 293 TVVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTVIKNAELKVKETNRIDAVA 352

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
TEL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 353 TELNKMADITPTEDGLIIRGKTPLHAAKVTSYGDHRIGMMLQIAALIVEDGEVELDRAE 412

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 413 AVSVSYPTFFEDIHSLK 430

>ref|YP_001748251.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas putida W619]

gb|ACA71882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida
W619]
Length = 746

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 128/436 (29%), Positives = 208/436 (47%), Gaps = 31/436 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E
Sbjct: 317 QPGGRLTGRIIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 376

Query: 70 DKAARKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P +++GN+G +MR L+ + AG + + G
Sbjct: 377 PNHGRVTIHGVLHGLKPPPG-----PIYVGNSGTSMRLLSGLL--AGQSFVDTMTGDAS 429

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+ + L+++GA V+ G D PP+ + G L L + S+Q S LL
Sbjct: 430 LSKRPMNRVANPLREMGAVVET--GPDGRPPLTIRGGHTLKALTYTLPMA-SAQVKSCLL 486

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A A G + P + T R++ FG E + ++ G K + +
Sbjct: 487 LAGLYAEGKTTVT-----EPAPTRDHTERMLRGFGYAVESNGPVA--SLQSGGKLTA-TH 538

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++FL A+I G+ + +E G + V ++L +MG +T E
Sbjct: 539 IEVPADISSAAFFLVAASIAQGSELVLEHVGINPTRTGTV--IDILRLMGGDITL-ENQRE 595

Query: 307 VTGPPPREPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPATAIRDVASWRVKET 361
V G P + LK ID+ + +P D L V A A+G T +R RVKE+
Sbjct: 596 VGGEPVADLVRVGAKLKGIDIPPEHLVPLAIDEFPVLFVAAACAEGRTVLRGAEEELRVKES 655

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPV 420
+R+ + L LG E PD II ++ + + DHR+AMAFS+A+ A P+
Sbjct: 656 DRIQVMADGLIALGVKCEPTPDGIIID-GGQIGGGEVHGHGDHRIAMAFSVASLRASAPI 714

Query: 421 TIRDPGCTRKTFPDYF 436
I D +FP++
Sbjct: 715 RIHDCANVATSFNPL 730

>ref|YP_001212170.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelotomaculum
thermopropionicum SI]
sp|A5D1R9.1|ARO_A_PELTS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAF59801.1| 5-enolpyruvylshikimate-3-phosphate synthase [Pelotomaculum
thermopropionicum SI]
Length = 431

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 134/445 (30%), Positives = 206/445 (46%), Gaps = 46/445 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
+ + GTV +PG KS+S+R ++L AL+ G T+++N L ED + R LG+ + D
Sbjct: 9 RGLRGTVAVPGDKSISHRAVMLGALASGETTIENFLPGEDCLSTIDCFRKLGEINGPDN 68

Query: 72 AAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
R G G PV+ L GN+G MR + + AG V+ G +R
Sbjct: 69 NTVRVRGRGLDGLSEPVD-----VLDTGNSGTTMRLILGVL--AGQPFFSVITGDSSLR 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSGSISSQYLSAL 186
RP+G + L +GA +D + P+ V G G ++ +S S+Q SA+
Sbjct: 121 RRPMPGRVTGPLISMGAKIDGRQNGNLAPLAVRG-----GTLRPINFVSPVASAQVKS AV 174

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-----GQK 241
L+A G + + + T R++ FG E S+ +KG G+K
Sbjct: 175 LLAGLFTDGVTAVTEAYR-----TRDHTERMLRAFGAGVEVSEGT--VAVKGRPRLTGRK 227

Query: 242 YKSPKNAYVEGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV-- 298
K P GD SSA++ L A+ I G +T+ G G + + EVL MGA++
Sbjct: 228 VKVP-----GDISAFLVAASLIPGSDLTLTGTVGNPTR--IGIIEVLSSMGAIEIRL 279

Query: 299 -TWTETSVTVTGPPREPFGGRKHLKAIDVNM-NKMPDVAMTLAVVALFADGPTAIRDVASW 356
E V GR A+ + ++ D LAV A A+G T IRD A
Sbjct: 280 FNLREEEEPVADIRVRYNGRLCGTAVGGEIIPRLIDEVPALAVAAALAEGKTIVIRDAEL 339

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-C 415
+VKE++R+ A+ L K GA VEE PD ++ L +++ DHR+AMA ++A
Sbjct: 340 KVKESDRIAAVAGMLAKFGADVEELPDGLLVGRSRLKGCVCESHGDRIAMAAAVAGLL 399

Query: 416 AEVPTVIRDPGCTRKTFPDYFDVLS 440
AE +R C +FP + D+L+
Sbjct: 400 AEGKTIVRGAECISVSFPGFSDLLA 424

>ref|YP_004182677.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Terriglobus saanensis
SP1PR4]
gb|ADV82683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Terriglobus saanensis
SP1PR4]
Length = 434

Score = 126 bits (317), Expect = 6e-27, Method: Compositional matrix adjust.
Identities = 134/451 (29%), Positives = 202/451 (44%), Gaps = 42/451 (9%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
++P K + G+V+LPG KS+S+R +LA L+EGT+V+ N D H L + LG +V
Sbjct: 11 TIRPAKNLRGSRVRLPGDKSISHRYAMLAGLAEGTSVLANFSTGADPHSSLACMEALGATV 70

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
K V G G+F + + L GN+G MR L + A T+ L G
Sbjct: 71 -VKKDDGTIAVTGTTGQF----KQPLIDLDCGNSGSTMRMLAGLI--APHPHTFRLIGDA 123

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSAL 186
+ RP+ + L ++GA +D G P+ V+G P + I S+Q +A+
Sbjct: 124 SLTPRPMERIRGPLSKMGAKIDLTDGH--APITVHGG---PLQAITFDTPIPSAQVKTAI 178

Query: 187 LMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L A A G I + + + + E LR FG AE + S D I+GGQK S
Sbjct: 179 LFAGLQANGTTTIS--ESVTRRDHSEHALR---AFG--AELTRSADAISIEGGQKLHS-L 230

Query: 247 NAYVEGDASSASYFLAGAAI-----TGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
N V GD SSA++FL A + T + L VK + E
Sbjct: 231 NLTVPGMSSAAFFLCAALLFPESNLVDDLGMNPNRSALLDVLVGLGLKVKVLNLEHH 290

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVA 354
G + + + + E G + ID ++P LA +A + IRD
Sbjct: 291 GELIGSLQINSSAQLKGAIEISGGLSAQLID----ELP----VLAAIAPYTRDGIKIRDAK 342

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
RVKE++R+ + L +GA E D I + L+ AID+ DHR+AMAFS+AA
Sbjct: 343 ELRVKESDRIALVAKNLKVMGAVFTENEDGLDIPGGQTLHGAAIDSGLDHRIAMAFSIAA 402

Query: 415 C-AEVPTVIRDPGCTRKTFPDYFDVLSFVK 444
AE I +FP+++ +L + +
Sbjct: 403 LRAEGETEIHGAEEAAISFPEFYTLDSLCE 433

>gb|EFS02708.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria seeligeri
FSL S4-171]
Length = 428

Score = 126 bits (317), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 217/438 (49%), Gaps = 31/438 (7%)

Query: 17 GTVKLPKSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV EADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GEITVPGDKSMHSRIMSFGAIAEGKTIVIRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERPI 134
+V G G G P L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTGFAGLKPAAGP-----LDIGNSGTTIRLMMGIL--AGSHFDTVILGDESIKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ ++G L + + + S+Q SA++ AA A
Sbjct: 123 NRVMPLPQEMGAKMHGKDGSEFAPITISGNQALKQIEYHMPVA-SAQVKSALIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K + T ++ +FG + E R +KGGQ + + + V GD
Sbjct: 182 GETIIEHEKEK-----TRDHTHEMIRQFGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDV 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE 313
SSA++F+ AG I + + G + + +V+E MG + ++S + TG
Sbjct: 234 SSAAFVIVAGLIIPKSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 290

Query: 314 PFGRK--HLKAIDVNMNMPDVMATLAVVALFA--DGPTAIRDVASWRVKETERMVAIR 368
K LK ++ + +P + + V+AL A +G T I++ A +VKET R+ A+
Sbjct: 291 TVVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAE GTTVIKNAELKVETNRIDAVA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
TEL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 351 TELNKMADITPTEDGLIIRGKTPLHAAKVTSYGDHRIGMMLQIAALIVEDGEVELDRAE 410

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 411 AVSVSYPTFFEDIHSLK 428

>ref|NP_687654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 2603V/R]
ref|YP_329343.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae A909]
ref|ZP_00781183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 18RS21]
ref|ZP_00783206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae H36B]
ref|ZP_00784488.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae COH1]
ref|ZP_00790443.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 515]
sp|Q8E0U0.1|AROAS TRA5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q3K2B0.1|AROAS TRA1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM99526.1|AE014219.18 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 2603V/R]
gb|ABA45909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae A909]
gb|EA062214.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 18RS21]
gb|EA070815.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae 515]
gb|EA076715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae COH1]
gb|EA078052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae H36B]
Length = 427

Score = 126 bits (317), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 117/437 (26%), Positives = 206/437 (47%), Gaps = 27/437 (6%)

Query: 15 ISGTVKLPGSKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ ++S+G T + ++L EDV + A + +G+ +E D
Sbjct: 10 LKGTIRVPGDKSISHRAIIFGSISQGVTRIVDVLRGEDVLSTIEAFKQMGVLIEDDGE-- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ GK + L +GN+G +MR L A V A G + G + +RP+
Sbjct: 68 ---IITIYGKGFAGLTQPNLLDMGNSGTSMR-LIAGVLA-GQEFVETMVGDNLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ + L ++GA + D PP+++ G L L + S+Q SAL+ AA
Sbjct: 123 DRIALPLSKMGARISGVTNRDLPLKLQGTKKLKPIFYHLPVA-SAQVKSALIFAALQTK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNAYVEGD 253
G E I++K + + E +R +FG H D D+ + GGQ ++ V GD
Sbjct: 182 G--ESLIVEKEQTRNHTEDMIR---QFG---GHLDIKDKEIRLNGGQSLVG-QDIRVPGD 232

Query: 254 ASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++++ AG I + +E G + + +V+ MG K+ + V
Sbjct: 233 ISSAAFVIVAGLIIPNSHIILENVGINETRTGI--LDVVSMMGGKIKLSSVDNQVKSATL 290

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRT 369
HL+A ++ +P + L ++AL A G T I D +VKET+R+ +
Sbjct: 291 -TVDYSHLQATHISGAMIPRLIDELPIIALLATQAQGTTVIADAQELKVKETDRIQVVVE 349

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
L ++GA + D II L+ ++D + DHR+ M ++AA E V +
Sbjct: 350 SLKQMGADITATADGMIIRGNTPHAAASLDCHGDHRIGMMIAIAALLVKEGEVDLSGEEA 409

Query: 428 TRKTFPDYFDVLSTFVK 444
++P++ + L V
Sbjct: 410 INTSYPNFLEHLEGLVN 426

>ref|YP_001483896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9215]
sp|A8G3X9.1|ARO_A_PROM2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV50310.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9215]
Length = 436

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 117/444 (26%), Positives = 204/444 (45%), Gaps = 42/444 (9%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G +K+PG KS+S+R L++ ++++G T ++ L+SED LR LG+++
Sbjct: 12 KLKGIKIKVPKGSISHRALIIGSIAGNNTTIEGFLHSEDPLSTADCLRKLGVNIPKIIKD 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G G ++ KE ++ GN+G MR L + A G ++L G + ER
Sbjct: 72 EPFTISGKG---LDGLKEPKEILNCGNSGTTMRLLMGLLAAQEGK-NFILTGDASLNER 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + + P+ +NG KL G + S+Q SA+
Sbjct: 127 PMGRVKGPLSLMGGKISGREGNKAISING-----EKLKGCVIGTPVASAQVKSAL 178

Query: 187 LMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G + I+ S + E R+++ FG R + +
Sbjct: 179 LLAGLNASGTTSV--IEPASSRDHTE---RMLKAFGADISIRGELGRNIVITSGNLIQ 233

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ GD SSAS+++ A+I V ++ G + + V++ MG + S
Sbjct: 234 RILIPGDISSASFWMIAASIVPNSEVLIQNVGLNPRTGTI--LNVMSMGNCNYEILDKS- 290

Query: 306 TVTGPPREPFGFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
T+ G EP G +L++ V + +P D L V A F G + I+D
Sbjct: 291 TIAG---EPIGSIKVKTSNNLRSFTVEGDILPKLIDEIPILTVAACFSGVSEIKDAQEL 347

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-C 415
RVKET+R+ + +L K GA + E D II K + +D+ DHR+AM+ ++A+
Sbjct: 348 RVKETDRLKVMARQLQKFGAKITEKEDGLIINGQSKFSAEVDSETDHRVAMSLAIASLL 407

Query: 416 AEVPVTIRDPGCTRKTFPDYFDVL 439
A+ I G ++P +++ L
Sbjct: 408 AKGTSKIMRAGAASVSYPFWHEEL 431

>ref|YP_001918207.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natranaerobius
thermophilus JW/NM-WN-LF]
gb|ACB85619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Natranaerobius
thermophilus JW/NM-WN-LF]

Length = 484

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 117/460 (25%), Positives = 208/460 (45%), Gaps = 39/460 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
+ + + G++ +PG KS+++R +L ++ G + ED L L+ +G +
Sbjct: 30 QKFRSLKGSLLHVPKDKSITHRSYILGSLVPGVVKIKGRALGEDCEATLECLKAMGAEGSS 89

Query: 70 DKAARAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + + P E L GN+G R L + +G N + G +
Sbjct: 90 NSEDEDEYITSHSLYEPSE-----VLDAGNSGTTARLLGLI--SGLNLFACITGDDSL 141

Query: 130 RERPIGDLVVGLKQLGADV-----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
++RP+ ++ L +LG D+ + L PV + K + +I +Q S
Sbjct: 142 KKRPMRDRVISPLAKLGDIDRQNNKLPAAIIPVEMQNQSTTVKSISKSTPTIKTQVSS 201

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG-----VKAHSDSWDR---- 233
A + +A L L ++ + I+ + S + T R++ G ++ EH D+
Sbjct: 202 AQVKSALLLASLKTGGINVIESQQTTRDHTERMLSFMGFVLENVMQNEHEPESDQNVHQ 260

Query: 234 FYIKGGQKYKSPKNAYV---EGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAE 289
+ GGQ K YV GD SSA++ + A + G V + CG + F +
Sbjct: 261 ITLPGGQLSKLPRDYVLDIPGDLSSAAFLITAALLVPGSQVKLLNCGLNPT--TGFVK 318

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFRGRH---LKVIDNMNMPDVAMTL---AVVALF 343
+L+ +GA++T T + T+ PR ++ L+ + N +PD L AV+A+
Sbjct: 319 ILQQLGARITITNTT-TLAAEPRGDINVEYSPCLQGFQLGKNLVPDTIDELPLLAVIAVL 377

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDD 403
+ G T + R KE++R+ AI ELTKLGA + E D I+ P +L +D++ D
Sbjct: 378 SHGTTKVSAGAEELRYKESDRISAITQELTKLGADITETQDGFIVNGPTQLTGNVVDVSHGD 437

Query: 404 HRMAAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
HR+AMA ++AA A+ I++ C ++P + L+
Sbjct: 438 HRIAMALTVAALTAQGKTIKNSDCINISYPGFIQDLTKL 477

>ref|YP_113872.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylococcus
capsulatus str. Bath]
gb|AAU92307.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylococcus
capsulatus str. Bath]
Length = 422

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 131/444 (29%), Positives = 203/444 (45%), Gaps = 45/444 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R ++L +L+EG T V L +ED + A R +G+ +E +
Sbjct: 1 MQGDIRVPGDKSISHRSVMLGSLAEGVTEVSGFLQAECDLATMAAFRAMGVEIEGPTAGR 60

Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G P L LGN+G +MR L+ + AG L G + RP
Sbjct: 61 LRIHVGVLHGLKP----PAAPLDLGNSTSMRLLSGLL--AGQAFDTTLTGDAASLVRRP 113

Query: 134 IGDVVGLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ + L+ +GA +D GT P+R+ G L G + + S+Q S LL+A
Sbjct: 114 MRRVTEPLRAMGARIDTTEAGT--APLRIAGGSRLKGIDYAMPVA-SAQVKSCLLLAGLY 170

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G + P + T R++ FG + +R I+ G K S V
Sbjct: 171 AEGKTCVT----EPAPTRDHTERMLAGFGYPV--ARDGNRVCIQSGGKL-SATRIVPA 222

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F+ GAAI+ G+ V + G + V E+L MGA + P
Sbjct: 223 DISSAAFFMIGAAISPGSDVFLRHVGINPRTGTG--IEILREMGADIEILA-----P 272

Query: 312 REPFGR-----KHLKVIDNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
RE G + L+ I + + +P D L + A A G T + RVK
Sbjct: 273 REVGGEPVADLRIRYRELGRIRIPEHTVPLAIDFPAIFIAAACATGETVLTGAEEELRVK 332

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEV 418
E++R+ A+ LT LG PD +I A+D+ DHR+AM+FS+AA A +
Sbjct: 333 ESDRIQAMADGLTTLGIDARPTPDGMVIR-GGSFRGGAVDSRGDHRIAMSFSIAALRAPI 391

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
P+ I D +FP++ ++ T
Sbjct: 392 PIEIHDCANVATSFPPNFVELARTL 415

>ref|ZP_08030107.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas artemidis
F0399]
gb|EFW30535.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas artemidis
F0399]
Length = 438

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 127/431 (29%), Positives = 197/431 (45%), Gaps = 30/431 (6%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+PG KS+S+R ++LA L + N L++ D +G +R LG+ VE A VV G
Sbjct: 20 IPGDKSMHSRVMLAGLGSTPVHIKNFLHAADCLSTVGVMRALGVRVEF-PADGELVVVG 78

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
G E A L GN+G +R + + T+ D + RP+G +++
Sbjct: 79 RGLHGLSEPAS---VLDAGNSGTTLRLMMGLLAPQPFFLTFTGDA--SLSRPMGRVLLP 133

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG-SISSQYLSALLMAAPLALG---D 196
L Q+GA + + P+ + +P GK KL G S S SA + +A L G D
Sbjct: 134 LGQMARIYGRNDDNNLPLSI-----VPAGK-KLCGISYDSPVASAQVKSAILLAGLYTD 187

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNAYVEGDAS 255
+ + +S + E R++ FGV+ E R Y + + Y +P+ V GD S
Sbjct: 188 APTSVTEPFVSRDHT---RMLAGFGVRVEREGCTARVYPVTREEDYIAPEEITVPGDIS 244

Query: 256 SASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA+YFL G +I G+ + ++ G + + +VL MGA + + T G
Sbjct: 245 SAAYFLVGGSIKGRLLLNKVGINLRTGTI--LDVLAQMGAHIA-VKNERTSGGEALAD 301

Query: 315 FGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ L + V MP D LA ALFA+G T I RVKET+R+ AI
Sbjct: 302 ISVETAEHLHGVRVGAIEIMPRVDEIPILAAAALFAEGDVTITGAGELRVKETDRLRAIAD 361

Query: 370 ELTKLG-ASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
E K+ S+EE D II + + + DHRMAM+ ++ A I +P
Sbjct: 362 EFGKMAPGSIEELEDGLIIRKRPICKARVHSRGDHRMAMSLAVLGAAADGAEIEEPDSV 421

Query: 429 RKTFFPDYFDVL 439
+ ++P +F+ L
Sbjct: 422 QISYPAFFEQL 432

>ref|YP_004112024.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfurispirillum
indicum S5]
gb|ADU65468.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfurispirillum
indicum S5]
Length = 432

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 119/441 (26%), Positives = 209/441 (47%), Gaps = 33/441 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+ + KS+++R ++ ++L++G +++ N L +D A + +G+ V+
Sbjct: 10 LKGITIAVASDKSITHRAIMFSSLAQGSIIISNPLMGDDNISTCKAFQAMGVDVQL---VH 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A+++ G + +A++ L GN+G R + ++ G V+ G +R+RP+
Sbjct: 67 NAIIINSPGVDGLREAEV--LDFGNSGTTTTLMLGILS--GLPLFSVITGDQYLRKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L+Q+GA +D G P V G G L G S S+Q SAL++A A
Sbjct: 123 MRVIDPLRQMGARIDGRDGRLLPASVRG-GDLQGITYH-SPVASAQVKSALVLAGIFAR 180

Query: 195 GDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G ++S P + + T R++ +GV + + GGQ+++ P+N V G
Sbjct: 181 GTT-----VVSEPEISRDHTEMLPFYGVGVKVEGKT--VSVTGGQRFE-PRNMEVPG 230

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL A++ G VT+ G + V ++L+ MGA + E V G P
Sbjct: 231 DISSAAFFLVAASVVPGSQVTLNNGINPRTGTG--LDILQQMGADIRL-ENQRLVCGEP 287

Query: 312 REPFGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
H L+A + +P D LAV FA G + ++D RVKET+R+V
Sbjct: 288 VCDIVITHAPLEAAHIFGEMVPRILDEIPALAVAMCFARGKSIVKDAKELRVKETDRIVT 347

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACAEVPTIR 423
L LG VEE D +T + + +D+Y DHR+ M+ L + + + +
Sbjct: 348 TLANKLALGVEVEYEDGFAVTGNPDFQLPSGVTLDSYGDHRIGMSAYLFSLLQRNIIVD 407

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
C +FP++ L+ +
Sbjct: 408 GMECVSVSFPNFQKFLAQLQR 428

>ref|YP_818635.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
mesenteroides subsp. mesenteroides ATCC 8293]
sp|Q03X10.1|AROA_LEUMM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ62262.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
mesenteroides subsp. mesenteroides ATCC 8293]
Length = 434

Score = 126 bits (316), Expect = 7e-27, Method: Compositional matrix adjust.
Identities = 129/447 (28%), Positives = 209/447 (46%), Gaps = 48/447 (10%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R L+ A++EG TV+DN L S+DV + +G R LG VE D
Sbjct: 12 LHGEITVPGDKSISHRALMFGAIAEGKTVIDNLFMSDDVMHTMGVFRALG--VEIDHTES 69

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+A V+G G F A L +GN+G + R L ++ + G + +RP
Sbjct: 70 QATVIGKGLTNFKAPSAG---LDMGNSGTSTRLLMGLLSKQPFDLNIF--GDSSLSKRP 123

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPV-----RVNGIG-GLPGGKVKLSGSISSQYLSALL 187
+ + L + A + P V +NGI +P S+Q SA+L
Sbjct: 124 LRRVADPLSMMAQFELSNDEFLPAVIKANTELNIGITYHMP-----VASAQVKSAIL 175

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPK 246
+A A G E II+ L P + T R++ +FG + + D I ++ K S +
Sbjct: 176 LAGIQAEG--ETTIIEDL---PSRDHTEMLRQFGGQIK---TDNGVITVKKQSKLSGQ 226

Query: 247 NAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++F+ IT +T++ G + V ++LE MGA++ T+ +
Sbjct: 227 HVLVPSDISSAAFFMVAGLITPNSITIKKGVNPNTRDGV--IKLLERMGAEI--TQKPI 282

Query: 306 TVTGPPPREPFGRK--HLKAIDVNMNKMPPDVAMTLAVVALFAD--GPTAIRDVASWRVKE 360
G P K L I + +P L ++AL A G T I RVKE
Sbjct: 283 ASDGEPLADITVKAQTLHGIAITAEDIPGAVDELPILALAATQAVGDTIISGAEEELRVKE 342

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---TAIDTYDDHRMAMAFSLAA-C 415
T+R+ + +ELTKLGA ++E PD +I L+ T +D++ DHR+ M +A+
Sbjct: 343 TDRISTVISELTKLGADIDEKPDGMVHGGTLLHTSNGSTLLDSHGDHRIGMMNVIASLI 402

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
E V + ++P + + +S+
Sbjct: 403 TEGDVVLTEGEEAMSVSYPGFVEDVSSI 429

>ref|YP_001033191.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. cremoris MG1363]
sp|P43905.1|AROA_LACLM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
emb|CAA55180.1| 5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus lactis]
emb|CAL98495.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. cremoris MG1363]
gb|ADJ60903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. cremoris NZ9000]
Length = 430

Score = 126 bits (316), Expect = 8e-27, Method: Compositional matrix adjust.
Identities = 118/439 (26%), Positives = 210/439 (47%), Gaps = 27/439 (6%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+PG KS+S+R ++ +++G T++ ++L EDV + A R LG+ +E D
Sbjct: 10 LKGRLLKVPKSGKSLSHRSIMFGSIAGKGTIIHDILRGEDVLSTIEAFRALGVEIEDD---- 65
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ G+ + + E L +GN+G + R L+ + AT L G + +RP+
Sbjct: 66 -GQVITVHGQGISKLEKEKALDMGNSGTSTRLLSGILAGLPFEAT--LFGDDSLSKRPM 122
Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA++ P+ + G L L + S+Q SA++ AA A
Sbjct: 123 DRVATPLQMMGAEIVGQTDKVKLPMTIKGSAHLKAIDYILPVA-SAQVKS AVIFAALQAE 181
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++++K + + E ++ +FG + SD + GGQK + V GD
Sbjct: 182 GLT--KVVEKEKTRSHTE---EMLVQFGGEITVSDKT--ILVPGGQKLLG-QEVTVPGLDI 233
Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA+++L AG + + +E G + + EV++ MG ++ E V
Sbjct: 234 SSAAFWLVLVAGLVVENSGLILENVGINETRTGI--LEVIQAMGGQLEILEQD-EVAKAATL 290
Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAIRTE 370
LK +++ + +P + L ++AL A+G T IRD A +VKET+R+ +
Sbjct: 291 KVKASQLKGTESGDLIPRLIDELPIIALLATQAEGKTIIRDAAELVKETDRIAVVADA 350
Query: 371 LTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
L +GA++E D II KL+ AI+T DHR+ M ++AA + +
Sbjct: 351 LNSMGANIEPTDDGMIIQGGTKLHAPENAINTLGDHRIGMMVAIAALLVENGEIELERAE 410
Query: 427 CTRKTFPDYFDVLSTFVK 445
+ ++P +FD L N
Sbjct: 411 AIQTSYPSFFDDLEKLSGN 429

>ref|YP_095448.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
pneumophila subsp. pneumophila str. Philadelphia 1]
sp|Q5ZVM1.1|AROALLEGPH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAU27501.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
pneumophila subsp. pneumophila str. Philadelphia 1]
Length = 433

Score = 126 bits (316), Expect = 8e-27, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 208/439 (47%), Gaps = 32/439 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ +P+ + G + +PG KS+S+R ++ A++ GT+V+D L+ ED L A +++G+
Sbjct: 3 NFISKVPKGLKGEITVPGDKSISHSIIFGAIAIGTSVIDGFLDGEDCIATLKAFQSMGV 62
Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E K+ V++ GK+ ++ + + GN+G +MR L + A ++ L G
Sbjct: 63 RIEGPD--KQRVIIHGVGKYLKQPQNIID--CGNSGTSMRLLAGLLAAQQFDSQ--LTG 116
Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+ + L Q+GADV G PP+ + G L G + + S+Q S
Sbjct: 117 DESLLKRPLRISRPLSQMGADVTTQDGK--PPIVIKGGKLNIGIHYVMPEA-SAQVKSC 173
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG---GQKY 242
LL+A A G + +I + +S + E R++ F + D G G +
Sbjct: 174 LLLAGMYAEG---QTKITENAVSRDHTE---RMLRTFSYPVQIQDGAIIDCNGECHGTRL 228

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
P GD SSA++F+ A+IT G+ V + G + + +L MGA +
Sbjct: 229 NIP-----GDISA AFFIVAASITPGSDVLIRNVGINPTRTGI--IHILTEMGADIRVL 280

Query: 302 ETSVTVTGPPREPFGFR-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
P + R LK ID+ + +P D + + A A G T + R
Sbjct: 281 NQRAYGEEPVDLHIRYSQLKGIDIPASMVPLAIDFPPVIFIAAACAQKTTLHGAKELR 340

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA-ACA 416
+KE++R+ A+ L +LG EG D I+ + +++ DHR+AM+F++A A A
Sbjct: 341 LKESDRIGAMVDGLNQLGVHA-EGFDDGILIEGGSIQGGEVNSRGDHRAMSFIAIAGAVA 399

Query: 417 EVPVTIRDPGCTRKTFPDY 435
PVTI++ +FP +
Sbjct: 400 SAPVTIKNCANVATSFPSF 418

>ref|ZP_02462400.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
thailandensis MSMB43]
Length = 451

Score = 126 bits (316), Expect = 8e-27, Method: Compositional matrix adjust.
Identities = 120/431 (27%), Positives = 189/431 (43%), Gaps = 31/431 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL--LSVEADKA 72
+SGT+ LP SKS S R LL AAL+ G + + N+ + + M LG S E D
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPGISTIRNVATGFNSNAMKHNCERLGASFSSSEGDTT 79

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V V + V D GN+G+ +R L V + +V + R
Sbjct: 80 VVKGVDVVHVRKIVFDP-----GNSGVVLR-LLMGVAGYLPDTEFVTQYRSLGVR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
++V L++L + + P+ + L G ++S SSQ+LS LL +
Sbjct: 131 SQAEMVAALRRLNVECEAVGPEARLPISIRSTREL-GRHTEVSCKKSSQFLSGLLYLGAI 189

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
D+EI+++D + + V T+ + GV E+ + RF++ G +++ P V
Sbjct: 190 GERDLEIDVVDHITAPSMVHTTINNLAHAGVAVEYDAPFRRFFVPGRRHFE-PSEFTVGA 248

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTVTGPP 311
D +S + LA VT+ G F E GA + + T+T + P
Sbjct: 249 DPASTAAILALCGSLASDVTLNG-----FFEEELGSGAVIRYLTDGTGLIDELP 297

Query: 312 REPF---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G ++A D + + PD LA A FADG + ++ R KE++R+ R
Sbjct: 298 GNRIRIRGGASIRAQDFDGLAPDAVPALAGRAAFADGTSTFYNIEHIRYKESDRISDFR 357

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF-SLAACAEVPVTIRDP 425
EL KLG EE D II P +D + DH + MA ++ E PV I++P
Sbjct: 358 RELDKLGVSRSEKLDQLIIGHNPRGYRGGA VVDGHYDHGLIMALTITGLHCEHPVLIKEP 417

Query: 426 GCTRKTFPDYF 436
+T+PDYF
Sbjct: 418 HHVGQTYPDYF 428

>ref|YP_126720.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
pneumophila str. Lens]
sp|Q5WWS9.1|AROALLEGPL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH15610.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
pneumophila str. Lens]
Length = 433

Score = 126 bits (316), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 212/439 (48%), Gaps = 32/439 (7%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

+ +P+ + G + +PG KS+S+R ++ A++ GT+V+D L+ ED L A +++G+
 Sbjct: 3 NFISKVPVGLCKGEITVPGDKSISHRSIIFGAIAIGTSVIDGFLDGEDCIATLKAFQSMGV 62
 Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
 +E K+ V++ GK+ ++ + + GN+G +MR L + A ++ L G
 Sbjct: 63 RIEGPD--KQRVIIHGVGKYGLKQPQNIID--CGNSGTSMLLAGLLAAQQFDSQ--LTG 116
 Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
 + +RP+ + L Q+GADV G PP+ + G L G + + S+Q S
 Sbjct: 117 DESLLKRPMLRISRPLSQMGADVTTQDGK--PPIVIKGGKKLNGVHYVMPEA--SAQVKSC 173
 Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS---WDRFYIKGGQKY 242
 LL+A A G + +I + +S + E R++ F + D DR G+ +
 Sbjct: 174 LLLAGMYAEG--QTKITENAVSRDHTE---RMLRTFSYPVQIQDGTIVIDR---NGECH 224
 Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
 + N + GD SSA++F+ A+IT + V + G + + +L MGA +
 Sbjct: 225 GTRLN--IPGDISSAAFFIVAASITPDSVDLIRNVGINPTRTGI--IHILTEMGADIRIL 280
 Query: 302 ETSVTVTGPPPREPFGR-KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
 P + R LK ID+ ++ +P D + + A A G T + R
 Sbjct: 281 NQRAYGEEPVDLHIRYSQKLGIDIPVSMVPLAIDEFPVIFIAAACAQGKTTLHGAKELR 340
 Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLA-ACA 416
 +KE++R+ A+ L +LG EG D I+ + +++ DHR+AM+F++A A A
 Sbjct: 341 LKESDRIGAMVDGLNQLGVHA-EGFDDGILIEGGSIQGGEVNSRGDHRIAMSFIAIAGAVA 399
 Query: 417 EVPVTIRDPGCTRKTFPDY 435
 PVTI++ +FP +
 Sbjct: 400 SAPVTIKNCANVATSFPSF 418

>ref|YP_001377406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter sp.
 Fw109-5]
 sp|A7H6S6.1|AROANAD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABS24422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaeromyxobacter sp.
 Fw109-5]
 Length = 430

Score = 126 bits (316), Expect = 9e-27, Method: Compositional matrix adjust.
 Identities = 136/434 (31%), Positives = 204/434 (47%), Gaps = 33/434 (7%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G++++PG KS+S+R LL ALS G T V LL++EDVH A+ LG +V A+ +
 Sbjct: 13 LRGSIEVPGDKSISHRALLFGALSTGETRVRLDADVDHATRRRAVEALGATVRAE--GE 70
 Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
 VVV P +E + GN+G ++R LT ++ G +L G +R RP
 Sbjct: 71 ELVVV-----PPPALREPGDVVDCGNSGTSRLRLTGVLSGVPG--LSILTGDA SLRRP 122
 Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
 + ++ L+++GAD+ G PPV V G L G + L + S+Q SA L+A A
 Sbjct: 123 VRRVIEPLRRMGADLSARDGRLPPVVVRGRP-LRGARHVLEVA--SAQVKSACLLAGLFA 180
 Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
 G E +++ S + E R++ GV D + V GD
 Sbjct: 181 EG--ETTVVEPERSRDHTE---RMLAGMGVPR---VDGLEVTVAPARPRGGRVDVPGD 231
 Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
 SSA++FL AA G+ VTV G + +VL MGA ++ V G PR
 Sbjct: 232 ISSAAFFLCAAAALPGSEVTVRNGLVNPTR--TGLLDVLGAMGAALSRANER-EVAGEPR 288
 Query: 313 EPFGRKH--LKAIDVNMNKMMPDVAMTLAVV---ALFADGPTAIRDVASWRVKETERMVAI 367
 + L ++ +P + L VV A A G T IRD RVKE++R+ ++
 Sbjct: 289 ADVTVRAAALHGTEIGGAIIPRLIDELPVVMVMTAQARGRTVIRDAKELRVKESDRILASM 348
 Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDP 425
 L + GA +E D C I P L A+ T DHR+AM+ ++A V + D
 Sbjct: 349 GEALARAGAKIELFEDGCAIEGPTPLRGVAVQTRLDHRIAMSMAVAQLLAGGEEVVLDDV 408

Query: 426 GCTRKTFFPDYFDVL 439
C +FP +F +L
Sbjct: 409 ACVATSFPSFFALL 422

>ref|ZP_05041335.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Alcanivorax
sp. DG881]
gb|EDX88756.1| 3-phosphoshikimate 1-carboxyvinyltransferase, putative [Alcanivorax
sp. DG881]
Length = 752

Score = 125 bits (315), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 129/441 (29%), Positives = 209/441 (47%), Gaps = 37/441 (8%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
V+ P ++ G +++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+
Sbjct: 323 FVVTPGQQLQGRLRVPGDKSMHSRIMLGSLAEGVTQVEGFLEGEDALATLQAFRDMGVV 382

Query: 67 VEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + + VG G K P + L++GN+G +MR LT + AG L
Sbjct: 383 IEGPHNQVVTIHGVGLHGLKAPGK-----ALYMGNSGTSMLLLTGLL--AGQAFDVELT 434

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L+++GA + PPVR+ G L G L + S+Q S
Sbjct: 435 GDASLSKRPMERVAKPLREMGAIITTGE-QGRPPVRIRGGQPLKGFHYDLPMA-SAQVKS 492

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+ A G+ + P + T R++ FG + + + GG +
Sbjct: 493 AVLLGGLYADGETSV-----TEPAPTRDHTERMLGGFGYEVRRDGATS--ALTGGGTLSA 545

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
K V D SSA++FL GA+I + VT+ G + V ++L++MGA + E
Sbjct: 546 GK-LEVPADISSAAFFLVGASIAADSEVTLPHVGINPRTGTG--IDILKLMGADIRL-EN 601

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLA-----VVALFADGPTAIRDVAS 355
G EP +KA + ++P+ + LA + A A+G T +R
Sbjct: 602 QRDAGG---EPVADLVVKAAPLKGIEPEALVPLAIDFPAIFIAAACAEGETILRGAE 658

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC 415
RVKE++R+ + L LG S E D IT E + ++ DHR+AM+F++AA
Sbjct: 659 LRVKESDRIQVMADGLAALGVSHEVFEDGIRITGGE-FGGGEVQSHGDHRIAMSFAMAAL 717

Query: 416 -AEVPVTIRDPGCTRKTFFDY 435
A P+TI D +FP +
Sbjct: 718 RATGPITIHDCANVATSFPGF 738

>ref|YP_850146.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria welshimeri
serovar 6b str. SLCC5334]
sp|A0AK35.1|AROALISW6 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAK21367.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria welshimeri
serovar 6b str. SLCC5334]
Length = 428

Score = 125 bits (315), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 118/438 (26%), Positives = 219/438 (50%), Gaps = 31/438 (7%)

Query: 17 GTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + +PG KS+S+R ++ A++EG TV+ + L ++D + A + LG+ +E + +
Sbjct: 12 GNITVPGDKSMHSRIMFGAIAEGKTIVRHFLRADDCLGTIKAFKALGVKIE--ETDEEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+V G G + K+ + L +GN+G +R + + AG + V+ G + +RP+
Sbjct: 70 IVHGTG---FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIKRP MN 123

Query: 136 DLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLAL 194
+++ L+++GA + G++ P+ + G L +V+ ++S Q SA++ AA A
Sbjct: 124 RVMLPLQEMGAKMHGKDGSEFAPITILGKQSLK--RVEYHMPVASAQVKSATIFAALQAD 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I +K + T ++ +FG + E R +KGGQK+ + V GD
Sbjct: 182 GETIIHEKEK-----TRDTEHMIRQFGGEIEMDGLTIR--VKGGQKFIG-QEMTVPGDV 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+ AG + + + G + + +V+E MG + ++S + TG
Sbjct: 234 SSAAFFIVAGLIMPNSEIELTHVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAG 290

Query: 314 PFGRK--HLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIR 368
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A+
Sbjct: 291 TVVVKSELKGTGTEIGGDIIPRLIDEIPVIALLATQAE GTTIKDAELKVKETNRIDAVA 350

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
TEL K+GA + D II L+ + +Y DHR+ M +AA + V +
Sbjct: 351 TELNKMGA DITPTEDGLIIRKTPHAA NVTSYGDHRIGMMLQIAALLVEDGDVELDRAE 410

Query: 427 CTRKTFPDYFDVLSTFVK 444
++P +F+ + + +K
Sbjct: 411 AVSVSYPTFFEDIRSLK 428

>ref|ZP_01312238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfuromonas
acetoxidans DSM 684]
gb|EAT16267.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfuromonas
acetoxidans DSM 684]
Length = 430

Score = 125 bits (315), Expect = 9e-27, Method: Compositional matrix adjust.
Identities = 117/435 (26%), Positives = 211/435 (48%), Gaps = 24/435 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G + +PG KS+S+R ++ +L++G T V L ED + A R +G+++ D+
Sbjct: 11 RGLRGEITVPGDKSISHR SVMFGSLAKGVTRVSGFLQGEDNLSTVKA FRAMGV TI--DQP 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+V+ G +++ + L GN+G +R ++ + AG + VL G +R+R
Sbjct: 69 GDGELVIHGLGVHSLQEPAD--VLDCGNSGTTIRLMSGLL--AGQSFFSVLTGDQYLKRK 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+G +V L +GA + P+ ++G L + S S+Q SA+L+A
Sbjct: 125 PMGRIVAPLAGMGASIRGRQQQYAPLAIDG-QQLKATSYQ-SPVASAQVKS AVLLAGLY 182

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A D + + +S + E R++ FGV+ D + GGQ+ + ++ V G
Sbjct: 183 A--DGVTTVYEPHLSRDHSE---RMLRHFGVEVTSFDGG--VSLAGGQEL-TARDLLVPG 234

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F+ AG + + ++ G + V ++L+ M + P
Sbjct: 235 DISSAAFFMVAGLIVPDSELLIKNVGINPTRCGV--IDILKMN GSIELVNEREMAGEPV 292

Query: 312 REPFGKRKH-LKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ + LK I++ +P D ++V A A+G T IRD RVKET+R+ A+
Sbjct: 293 ADLLVKSSDLKGIEIGGEDVPRAIDFPVISVAAACAEGTTVIRDAKELRVKETDRIDAA 352

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPG 426
L+ G +V D + E+L +++ DHR+AM+ ++AA A+ V I D
Sbjct: 353 ADVLSTFGVTVTTAEDGMTVQGAERLQGGRVNSCGDHRIAMSSAIAALRADGDVVIEDTQ 412

Query: 427 CTRKTFPDYFDVLST 441
CT +FP+++ +L T
Sbjct: 413 CTATSFNFWQLLGT 427

>ref|NP_228156.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga maritima
MSB8]
Length = 421

Score = 125 bits (315), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 124/450 (27%), Positives = 205/450 (45%), Gaps = 52/450 (11%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P K++ G + +P KS+++R L+L+AL+E + + NLL D L LG E D
Sbjct: 5 PAKKVEGVLSPVPPDKSITHRALILSALAETESTLYNLLRCLDTERTHDILEKLGTRFEGD 64

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP A+ LF GN+G R ++ + A VL G P +
Sbjct: 65 WEKMKV-----FPKPPFAEPIEPLFCGNSGTTTRLMSGVL--ASYEMFTVLYGDPSLS 114

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ ++ L+ +GA P ++ N + G+ K ++ S+Q SA+L+A
Sbjct: 115 RRPMMRVIEPLEMMGARFMARQNNYLPMAIKGNHLSGI-SYKTPVA---SAQVKSAVLLA 170

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-- 247
A G +I+ S + E R+++ GV E ++G + P
Sbjct: 171 GLRASG--RTIVIEPAKSRDHTE---RMLKNLGVPE-----VEGTRVVLEPATFR 216

Query: 248 ---AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V GD SSA++F+ GA +TV G + EV+++MGA + W T
Sbjct: 217 GFTMKVPGDISAFAFFVVLGAIHPNARITVTDVGLNPTR--TGLLEVMMKLMGANLEWEIT 274

Query: 304 SVTVTGPPREPFQ-----RKHLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVA 354
+ EP G +LK + V + +P + L +VAL FA+G T +R+
Sbjct: 275 EENL-----EPIGTVRVETSPNLKGVVPEHLVPLMIDELPLVALLGVFAEGETVVRNAE 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
R KE++R+ + +LG +EE D I + + ++D DHRMAM FS+A
Sbjct: 330 ELRKESDRIRVLVENFKRLGVEIEEFKDGFKIVGKQSIKGSVDPEGDHRMAMLFISIAG 389

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+E V ++D C +FP++++L V
Sbjct: 390 LVSEEGVDVKDEHCVASFNPFIYELLERVV 419

>ref|ZP_05127216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium
NOR5-3]
gb|EED33763.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium
NOR5-3]
Length = 436

Score = 125 bits (315), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 132/452 (29%), Positives = 208/452 (46%), Gaps = 48/452 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E ++ P I G ++PG KS+S+R ++L AL+ G T V L ED + A R LG+
Sbjct: 2 EFLVAPGGSIHGEARVPGDKSISHRSVMLGALATGETTVTGFLQGEDALATVAAFRALGV 61

Query: 66 SVEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ K A R VG G + L +GN+G +MR L + AG N L
Sbjct: 62 EIDGPRKGALRIQGVGFELRAASSS-----LDMGNSGTSMRLLAGIL--AQQNFASELV 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ ++ L ++GA ++ G PP+R+ G L G L + S+Q S
Sbjct: 115 GDVSLMGRPMQRVITPLARMGASIESGDGGR-PPLRIAGGSKLHGIHYDLPLMA-SAQVKS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L+A A G+ + P + T R++ FG + E +S ++GG +
Sbjct: 173 CVLLAGLFAEGETSVT-----EPAPTRDHTEMLRGFGYQLESRESS--VSLRGGGQLHG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT---VTVGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V D SSA++ L A+I G+ +T G T +L +MGA +T +
Sbjct: 226 -CDIDVPSDISAFAFLVAASIAPGSELLLTHVGVNPNTR----TGVISILRLMGADITLS 280

Query: 302 E-----TSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTA 349
+ VT P L+ ID+ + +P D L + A A+G T
Sbjct: 281 NEREIGGEPVADILVTSAP-----LRGIDIPRDLVPLAIDFVPLFIAAACAEGRTV 332

Query: 350 IRDVASWVRKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
+R RVKE++R+ ++ L LG E D II L+ + T+ DHR+AM+
Sbjct: 333 LRGAEEELRVKESDRIASMAEGLRTLGVNR-NEVLDDGIIIEGGTSLSGGTVRTFHDHRIAMS 391

Query: 410 FSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLS 440

F++AA AE P+ + D +FP FD L+
Sbjct: 392 FAVAALRAEGPIRVLDCHVATSFPG-FDSLT 422

>ref|NP_953651.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
sulfurreducens PCA]
sp|Q749Y6.1|ARO_A_GEOSL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAR35978.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
sulfurreducens PCA]
gb|ADI85356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Geobacter
sulfurreducens KN400]
Length = 429

Score = 125 bits (315), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 125/436 (28%), Positives = 196/436 (44%), Gaps = 25/436 (5%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P + + G + +PG KS+S+R ++L +++ G T V L ED L A R +G+ V
Sbjct: 7 HPARALRGEIAVPGDKSISHRSIMLGSIGRVTTVSGFLRGEDNIATLDAFRAMGVQVHD 66

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
D R G G ED + GN+G ++R LT + A VL G +
Sbjct: 67 DGETLRIEGKGLHLTEAEDVID----CGNSGTSIRLLTGLMAAQ--RFYTVLTGDRYL 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMA 189
R RP+ +V L ++GA C G D I G P + ++S + + LM
Sbjct: 120 RRRPMRRVVEPLSRMGA---CIHGRDNGEKAPLAIVGRPLTGIAIDSPVASAQVKSALML 176

Query: 190 APLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A L D + + +S + E R+ FG + E + Y GG + ++
Sbjct: 177 AGL-YADGATRVTEPHLSRDHSE---RMFRHFGARLETDAGVTYV--GGHELDG-RDIV 229

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++FL A I G + + G G + ++L MG V +
Sbjct: 230 VPGDISAFAFLVAALIVPGSELLIRGVGNPTR--TGILDILAAMGGSVELLDQREVSG 287

Query: 309 GPPREPFGGRKH-LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + R LK I++ + +P D + V A A+G T IRD RVKET+R+
Sbjct: 288 EPVADLLVRSSALKGIEIGGDVVPRAIDFPPVICVAAALAEAGTTVIRDARELRVKETDRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
A+ L GA++ E D II +LN ++++ DHR+AM+ +A A +T+
Sbjct: 348 AAMAANLRAAGATITETADGMIEGTGRLNGVTVESFGDHRIAMSLVAGLAASGAITVS 407

Query: 424 DPGCTRKTFFPDYFDVL 439
D C +FP + +L
Sbjct: 408 DTECIATSFPTFTALL 423

>ref|ZP_05362235.1| 3-phosphoshikimate 1-carboxyvinyltransferase/prephenate
dehydrogenase [Acinetobacter radioresistens SK82]
ref|ZP_06072718.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
radioresistens SH164]
gb|EET81136.1| 3-phosphoshikimate 1-carboxyvinyltransferase/prephenate
dehydrogenase [Acinetobacter radioresistens SK82]
gb|EEY86932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acinetobacter
radioresistens SH164]
Length = 748

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 128/445 (28%), Positives = 205/445 (46%), Gaps = 41/445 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K G +PG KS+S+R ++ A++EGTT V L ED L A R +G+S+E K
Sbjct: 314 KTFQKGKFTVPGDKSVSHRSIMFGAIAEGTTHVTGFLGEDALATLQAFRDMGVSIEGPKN 373

Query: 73 AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + VG G K P L++GN+G +MR L+ + A + V+ G +
Sbjct: 374 GEVTIHGVGMHGLKAPAS-----ALYMGNSGTSMRLLSGMLAAQKFD--VMTGDASLS 425

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDPCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + L+ +GA + PPV ++G L G L S+Q S +L+A
Sbjct: 426 KRPMERIAKPLRLMGAQIQTTGEKGTTPVVISGQQKLHGIHYDLMP-SAQVKS GILLAG 484

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G+ + + P + T R++ FG VK E + + GG K +
Sbjct: 485 LWAEGETSVTEPE----PTRDHTERMLRAFGEVTE----GHKISLIGGKLVGTE-I 534

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ GAAIT + V +E G + + E+L+ MGA +T E
Sbjct: 535 QVPSDISSAAFFMVGAAITQNSDVLLLEAVGINPTRTGI--IEILKQMGADLT-VENERIA 591

Query: 308 TGPPREPF---GRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
G P G + LK I + +++P D L V A A+G T + A RVKE+
Sbjct: 592 GGPEIADIHIRGSRITLKGIIHPEDQVPLAIDFPAALFVAAACAEGQTVLTGAAELRVKES 651

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAA 414
+R+ + L +G D II K+ + I+++ DHR+AM+FS+A
Sbjct: 652 DRIQVMADGLGIDCTPTEDGIIIEGKIGDWSAVFTGGEIESHHDHRIAMSFMSAG 711

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
+ + I +FP + ++
Sbjct: 712 LRSSGTINIMGTETVATSFPTTEL 736

>ref|ZP_02243759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas oryzae
pv. oryzaicola BLS256]
Length = 437

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 130/434 (29%), Positives = 203/434 (46%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++
Sbjct: 16 LQGSALAPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGRIETLSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMMRERP 133
R V VG G P L GNAG MR L + A VL G + +RP
Sbjct: 76 RIVHGVGVGDQLGPPTGV-----LDCGNAGTGMRLLAGLLAAQ--RFDSVLVGDESLSKRP 128

Query: 134 IGDVLVGLKQLGADVDCFLGTDPCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA +D PP+RV+G L G +S S+Q SA+L+A A
Sbjct: 129 MRRVTGPLAQMGARIDT-QDDGTPPLRVHGGQALHGIDF-VSPVASAQVKS AVLLAGLYA 186

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ + P + T R++ FGV + S R ++GGQ+ ++ A V D
Sbjct: 187 QGETSVTEPH-----PTRDYTERMLSAFGVDIDFSPGSAR--LRGGQRLRATDIA-VPAD 238

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A+I + V + G + L +MGA ++ E G P
Sbjct: 239 FSSAAFFIVAASIVPDSEVVLRAVGLNPRR--TGLLAALRLMGADIS-EENHAHEHGGEPV 295

Query: 313 EPFGRKH--LKAIDVNMNKMPPDVA---MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
++ L+ + +PD+ L V A A G T + A RVKE++R+ A+
Sbjct: 296 ADLRVRYAPLRGAQIPEALVPDMIDEFPALFVAAAASGQTVVTGAAELRVKESDRLAAM 355

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA-CAEVPVTIRDPG 426
T L LG V+E PD I + I+++ DHR+AMAF++A + V + D
Sbjct: 356 ATGLRTLGVQVDETPDGATIH-GGSIGSGVIESHGDHRIAMAFIAGQLSGGSSVRVNDVA 414

Query: 427 CTRKTFPDYFDVLS 440
+FP FD L+
Sbjct: 415 NVATSFPG-FDTLA 427

>ref|YP_002129031.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phenyllobacterium
zucineum HLK1]
sp|B4RCK3.1|AROAPHEZH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ACG76602.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phenylobacterium
zucineum HLK1]
Length = 452

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 141/448 (31%), Positives = 206/448 (45%), Gaps = 55/448 (12%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ GTV+ PG KS+S+R L+L AL+ G T VD LL S+DV A++ G V + A
Sbjct: 14 LKGTVRAPGDKSISHRALILGALASGLTEVDGLLESDVRRATAAMQAFGAGVIRTGEGA 73

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V G GG D + GNAG +R + A AAG + G +R RP
Sbjct: 74 WR--VEGKGGFAEPGVID-----CGNAGTGVRLIMGA--AAGFDLAATFTGDSSSLRGRP 124

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG----SISSQYLSALLMA 189
+ ++ L ++GA C G P L GG +K S+Q SA+L+A
Sbjct: 125 MNRVLKPLGEMGASWICRAGGRLPLT-----LKGGLSLKRIAYRLPEPSAQVKSALLMA 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEE--HSDSWDRFYIKGGQKYKSPKN 247
A G E+ + + T R++ FG + + + R + GGQ K +
Sbjct: 178 GLSADGGAEEV-----FEAEATRDHTEMLRGFGAEVDVTEESAGRRIVLPGGQALKGTR- 231

Query: 248 AYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT----- 301
V GD SSA++ L A +T G VTVEG L+ + E L MGA ++ T
Sbjct: 232 IRVPGDPSSAAFPVLAALVTPGSQVTVEGMLLNPLR--IGLLETGLDMGADLSVTNVRDE 289

Query: 302 --ETSVTVTGPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
ET VT +H L+ ++ + P D LAV A FA G T +R +
Sbjct: 290 GGETVADVTA-----RHSALEGVETPPERAPSMIDEYPILAVAAAFASGRTVMRGIG 341

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDYDDHRMAMA-FS 411
RVKE++R+ + L G VEE P+ I+T I T+ DHR+AM+
Sbjct: 342 EMRVKESDRIALMAAGLAACGVEVEEPEGMIVTGRGGAVRGGGRIITHGDHRIAMSHLV 401

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVL 439
L AE PV++ +PG +FP + +++
Sbjct: 402 LGMAAEEPVSVDPEPGMIATSFPGFVEMM 429

>ref|ZP_01904632.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
AzWk-3b]
gb|EDM69814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
AzWk-3b]
Length = 469

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 137/443 (30%), Positives = 208/443 (46%), Gaps = 34/443 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
++GT +PG KS+S+R L+L ALS G T+V LL +DV A+R G V D
Sbjct: 38 LAGTADIPGDKSISHRALILGALSVMGTGVLLEGQDVLDATARAMAFGAEEVVRDDGT 97

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG A+ + + GN+G +R + A+ + AT+ D + +RP
Sbjct: 98 WRIHGVGVGGF-----AEPDQVIDCGNSGTGVRLIMGAMATSPVTATFTGDA--SLNKR 150

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+ + L GA G P V LP V+ + + S+Q SA+L+A
Sbjct: 151 MARVTDPLALFQAQAVGRSGGRLPMTIVGARDPLP---VRYTVPVPSAQVKSALLLAGLN 207

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+ + + E R++ FG + D+ + R GQ SP+ V
Sbjct: 208 APG--QTVVIEHEATRDHTE---RMLAGFGAQITTEDTAEGRIITLEGQPELSPQTIAVP 262

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ + A IT G+ V V G + L+ MGA +++ E G
Sbjct: 263 RDPSSAAFPVCAALITEGSDVLVPNIGLNPTN--AGLFTTLQEMGADLSY-ENLREEGGE 319

Query: 311 P----REFPGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F LK I+V + M D L+VVA FA G T +R V RVKE++R

Sbjct: 320 PVADLRASF-SPDLKGIEVPPERAASMIDEYPVLSVVAFAQGATVMRGVKELRVKESDR 378

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADIT--YDDHRMAMAF-SLAACAEVP 419
+ A+ T L G VE+GPD+ I+ +V T + DHR+AM+F + A P

Sbjct: 379 IEAMATGLRANGIKVEDGPDWWIVHGRGHGDPGGATCASHLDHRIAMSFLVMGLAANQP 438

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
VT+ D G +FP + ++++

Sbjct: 439 VTVDDGGPIATSFPIFEPLMASL 461

>ref|YP_123698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila str. Paris]
sp|Q5X5E6.1|AROA_LEGPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAH12525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella pneumophila str. Paris]
Length = 433

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 211/439 (48%), Gaps = 32/439 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ +P+ + G + +PG KS+S+R ++ A++ GT+V+D L+ ED L A +++G+

Sbjct: 3 NFISKPVGCLKGEITVPGDKSISHRSIIFGAIAIGTSVIDGFLDGEDCIATLKAFQSMGV 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E K+ V++ GK+ ++ + + N+G +MR L + A ++ L G

Sbjct: 63 RIEGPD--KQRVIIHGVGKYGLKQPQNIIDCV--NSGTSMLLAGLLAAQQFDSQ--LTG 116

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSA 185
+ +RP+ + L Q+GADV G PP+ + G L G + + S+Q S

Sbjct: 117 DESLLKRPMLRISRPLSQMGADVTTQDGK--PPIVIKGGKKLNGIHYVMPEA-SAQVKSC 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDS---WDRFYIKGGQKY 242
LL+A A G + +I + +S + E R++ F + D DR G+ +

Sbjct: 174 LLLAGMYAEG--QTKITENAVSRDHTE---RMLRTFSYPVQIQDGAIVIDR---NGECH 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ N + GD SSA++F+ A+IT G+ V + G + + +L MGA +

Sbjct: 225 GTRLN--IPGDISSAAFFIVAASITPGSDVLIRNVGINPTRTGI--IHILTEMGADIRVL 280

Query: 302 ETSVTVTGPPPREPFGR-KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWR 357
P + R LK ID+ + +P D + + A A G T + R

Sbjct: 281 NQRAYGEEPVDLHIRYSQLKGIDIPASMVPLAIDFFVIFIAACAQGGKTTLHGAKELR 340

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA-ACA 416
+KE++R+ A+ L +LG EG D I+ + +++ DHR+AM+F++A A A

Sbjct: 341 LKESDRIGAMVDGLNQLGVHA-EGFDDGILIEGGSIQGGEVNSRGDHRIAMSFAIAGAVA 399

Query: 417 EVPVTIRDPGCTRKTFPDY 435
PVTI++ +FP +

Sbjct: 400 SAPVTIKNCANVATSFPSF 418

>ref|ZP_07895932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus italicus DSM 15952]
gb|EFU73869.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus italicus DSM 15952]
Length = 436

Score = 125 bits (314), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 124/433 (28%), Positives = 204/433 (47%), Gaps = 24/433 (5%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L K ++GT+ +P KS+S+R ++ A+++G TVV N L +ED L A + LG+S+E

Sbjct: 12 LHQAKSLNGTLAVPADKSISHRSIMFGAIAKGETTVTNFLEAEDCLSTLKAFQDLGVSIE 71

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
++ + G G P AKE L +GN+G R + + A +L G

Sbjct: 72 RKGSSSLKIQAGFGKFSP---AKEP--LDMGNSGTTTRLIMGIL--ANQPFQSILVGDD 124

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ ++ LKQ+ A + + P+ ++ L + + S+Q SA+L

Sbjct: 125 LSKRPMNRVIDPLKQMNALKTGKNESGYAPITISPSESLQPIHYTMPVA-SAQVKSAILF 183

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A D E II+K P T ++++FG E I G Q+ + +

Sbjct: 184 AALQA--DGESTIIEKE---PSRNHTEEMIKQFGGTIE--VEGKTIKISGPQEL-TGQTV 235

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL AGA + ++ G + + +VL MGA++T

Sbjct: 236 TVPGDISAFAFLVAGAIGKDSRLVLKNVGNPRTGTI--LDVLNKMGARLTILNEDTHN 293

Query: 308 TGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERM 364
E L A ++ +P + + V+AL A G T I++ +VKET R+

Sbjct: 294 QAADIE-IRSELVATEIGGEIIPRLIDEIPVIALLATQAKGTIIKNAEELKVKETNRI 352

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
A EL KLGA++E D II P KL+ + ++ DHR+ M +AA + + +

Sbjct: 353 DATVNELRKLGANIEPTADGLIYGPTKLHGHHVSSHGDHRIGMMLQIAALLTDETELE 412

Query: 424 DPGCTRKTFPDYF 436
P ++P +F

Sbjct: 413 HPEAVSISYPQFF 425

>ref|YP_004063.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus thermophilus
HB27]
sp|Q72LH1.1|ARO_A_THET2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAS80436.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermus thermophilus
HB27]
Length = 427

Score = 125 bits (313), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 142/440 (32%), Positives = 207/440 (47%), Gaps = 34/440 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L P + G +++PG KS+++R L+L AL+EG + L + D L+ LG E

Sbjct: 6 LAPCGPLRGLRVPGDKSVTHRGLMLLALAEGERLFYPLKAGDTLSTARVLQALG--AE 63

Query: 69 ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ +V G G +F + E L GNAG MR L + VL G

Sbjct: 64 VREEGPHFLVRGRGLRF---KEPEDVLDGNGATLMRLLGLLAGQE-GLFAVLTDGAS 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+G +V L+ +GA VD + P+ V G L G + L S+Q SALL+

Sbjct: 119 LRRRPMGRVAVPLRAMGARVDGREGERAPLAVRG-APLRGLRYTLP-VPSAQVKSALLL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G E+E P + T RL FG+ E R + G + + K+

Sbjct: 177 AGLFAEGVTEVEE-----PTPTRDHTERLFRHFGLEVEGRRVRTWRTG--PFPA-KDL 228

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++FL A +T G+ V VEG G + VL+ MGA + W +

Sbjct: 229 VVPGDFSSAAFLVLAALVTPGSEVVVEGVGLNPTR--TGLLTVLKAMGADLEWR----VL 282

Query: 308 TGPPREPFG---RKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G EP G +H LK + V+ +P D LA A +A+G T I ++ RVK

Sbjct: 283 EGEAGEPVGWVRARHSLLKGVAVDPGLIPLMVDEVVLA AAAA WAEGETYIPGLSELRVK 342

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
E++R+ AI L LG VEEGPD+ I + + + DHR+AMAF++ V

Sbjct: 343 ESDRVRAIAENLRALGVEVEEGPDWLRIIR-GGGVRPGRVRPFHDHRIAMAFVVGLP-VG 400

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
V + +P ++P +F L

Sbjct: 401 VEVEEPHWAESISYPGFFQDL 420

>ref|ZP_06604224.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas noxia
ATCC 43541]
gb|EFF65391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas noxia
ATCC 43541]
Length = 411

Score = 125 bits (313), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 116/419 (27%), Positives = 189/419 (45%), Gaps = 37/419 (8%)

Query: 33 LLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGK-----FPV 87
+ A L + + N L++ED +G +R LG+ +E + VV G G F V
Sbjct: 1 MFAGLGDTFVHIRNFLHAEDCLSTVGVMRALGVDIEFLNEHE-LVVKGNNGPHGLSEPFVS 59

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGAD 147
DA GN+G +R + + +T+ G + RP+G +++ L Q+GA
Sbjct: 60 LDA-----GNSGTTLRLLMGLLAPQPFSTF--SGDDSLTRRPMGRVLLPLAQMGAK 109

Query: 148 VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLIS 207
+ G + P+ + G G S S+Q SA+L+A A D + + IS
Sbjct: 110 IFGRSGNNNPLTLPAEGKLHGIYYESPVASAQVKSAILLAGLYA--DAPTTVTEPYIS 167

Query: 208 IPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAI 266
+ E +++ FGV+ E S + + + Y++P V GD SSA+YFL AG+ I
Sbjct: 168 RDHTE---QMLANFGVRLERSRTSVTIFPVETETYRAPNEIIVPGDISSAAYFLTAGSII 224

Query: 267 TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVN 326
G + + G + + +VL MGA +T + EP ++A ++
Sbjct: 225 PGSRLLLNNVGINLRTGI--LDVLSEMGAHITLRNKRQSGG---EPVADIEVQAAQLH 278

Query: 327 -----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG-AS 377
M ++ D LA A FA+G T I RVKET+R+ AI E +K+ S
Sbjct: 279 GVSFGAEIMPRILIDEIPILAAAFFAEGDTVISGAELRVKETDRLDAIAAEFSKIAPGS 338

Query: 378 VEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYF 436
+EE D +I KL + + DHRMAM+ ++ A A + +P ++P +F
Sbjct: 339 IEEREDGLVIHGQRKLRRKVVSSRGDHRMAMSLAVLAAAGKAVLENPDSVNISYPTFF 397

>ref|YP_003063283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
plantarum JDM1]
gb|ACT62586.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
plantarum JDM1]
Length = 432

Score = 125 bits (313), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 131/453 (28%), Positives = 210/453 (46%), Gaps = 46/453 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++ +QP + G + +PG KS+S+R L+L A+S+GTT + + L + D L AL+ LG
Sbjct: 3 KKLSIQPASGLQGDLSVPGDKSVSHRGLILGAISQGTTLHHFLPADCLSTLTALQKLG 62

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + K V + G + ++ L +GNAG A R LT + AG L
Sbjct: 63 VPI---KRVDTTVTISGRGLRGLTQPQPP--LDMGNAGTATRLLTGLL--AQPPFETTLV 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L+ +GA V G P+ + G L G ++ + S+Q S
Sbjct: 116 GDTSLSRPMEVRVRQPLQAMGAQVQLTAG--HLPMTITG-RTLHGSCTEMQVA-SAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
AL++AA A D II+KL P + T RL+++FG + E + ++ Q
Sbjct: 172 ALILAALQA--DQASTIIIEKL---PTRDHTERLLQQFGGQIETAPDQRTITVQ-PQPALV 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++ + GD SSA++F+ A I + V + G + F +L MG +VT
Sbjct: 226 GQSLTIPGDFSSAAFFVTAATIIIPNSHVRLTNVGLNPTR--TGFLNILRRMGQVTVVDHE 283

Query: 304 SVTVTGPPREPFGR-----KHLKAIDVMNMKMPDVAMTLAVVALF---ADGPTAIRDVAS 355
EP G L + V ++P V L +VAL A+G + I A
Sbjct: 284 HRM-----GEPVGTLDVRFAQLHPVQVTATEIPAVIDELPLVALLAATANGISTISGAAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAM 408
RVKET+R+ I TEL KLG + PD +I P E L ++ DHR+ M
Sbjct: 339 LRVKETDRIATIVTELKRLGVQITSQPDGFVIDGRKSWRQPTEPLA-----SHGDHRIGM 393

Query: 409 AFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
++AA P + ++P +F+ L+
Sbjct: 394 MMAIAALRLAAPAELESAEAVNISYPTFFEDLA 426

>gb|AAM16087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 57

Score = 125 bits (313), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 57/57 (100%), Positives = 57/57 (100%)

Query: 389 PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN
Sbjct: 1 PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 57

>gb|AAM16058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 58

Score = 125 bits (313), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 57/58 (98%), Positives = 57/58 (98%)

Query: 388 TPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
TPPEKLNVTADITYDDHRMAMAFSLAACAEVPV IRDPGCTRKTFPDYFDVLSTFVKN
Sbjct: 1 TPPEKLNVTADITYDDHRMAMAFSLAACAEVPVAIRDPGCTRKTFPDYFDVLSTFVKN 58

>ref|NP_735069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae NEM316]
sp|Q8E6F8.1|ARO_A_STR3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAD46254.1| Unknown [Streptococcus agalactiae NEM316]
Length = 427

Score = 124 bits (312), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 116/437 (26%), Positives = 205/437 (46%), Gaps = 27/437 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ ++S+G T + ++L EDV + A + +G+ +E D
Sbjct: 10 LKGTIRVPGDKSISHRAIFGSISQGVTRIVDVLRGEDVLSTIEAFKQMGVLIEDDGE-- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ GK + L +GN+G +MR L A V A G + G + +RP+
Sbjct: 68 ---IITIYGKGFAGLTQPNLLDMGNSGTSMR-LIAGVLA-GQEFVMTMGDNSLSKRPM 122

Query: 135 GDLVVGKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ + L ++GA + D PP+++ G L L + S+Q SAL+ AA
Sbjct: 123 DRIALPLSKMGARISGVTNRDLPLKLQGTKKLKPIFYHLPVA-SAQVKSALIFAALQTK 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNAYVEGD 253
G E I++K + + E +R +FG H D D+ + GGQ ++ V GD
Sbjct: 182 G--ESLIVEKEQTRNHTEDMIR---QFG---GHLDIKDKEIRLNGGQSLVG-QDIRVPGD 232

Query: 254 ASSASYFLA-GAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA+++ G I + +E G + + +V+ MG K+ + V
Sbjct: 233 ISSAAFVIVVGLIIPNSHIILENVGINETRTGI--LDVVSKMGGKIKLSSVDNQVKSATL 290

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRT 369
HL+A ++ +P + L ++AL A G T I D +VKET+R+ +
Sbjct: 291 -TVDYSHLQATHISGAMIPRLIDELPIIALLATQAQGTTVIADAQELKVKETDRIQVVVE 349

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGC 427
L ++GA + D II L+ ++D + DHR+ M ++AA E V +
Sbjct: 350 SLKQMGADITATADGMIIRGNTPLHAASLDCHGHRIGMMIAIAALLVKEGEVDLSGEEA 409

Query: 428 TRKTFPDYFDVLSTFVK 444
++P++ + L V
Sbjct: 410 INTSYPNFLEHLEGLVN 426

>ref|YP_191032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconobacter oxydans
621H]
sp|Q5FTC0.1|ARO_A_GLUOX RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW60376.1| 3-Phosphoshikimate 1-carboxyvinyltransferase [Gluconobacter oxydans
621H]
Length = 442

Score = 124 bits (312), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 132/443 (29%), Positives = 210/443 (47%), Gaps = 33/443 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG ++PG KS+S+R L+ AAL+ G T V LL EDV A+R LG ++ + A
Sbjct: 14 KGLSGRTRVPGDKSISHRSLMFAALASGRTYVTGLLEGEDVLRATADAMRALGATITREGA 73

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V+ G G E A L +GN+G A R L+ +++ N+ ++ G +R R
Sbjct: 74 DW--VIEGRGVGALTEPAD---VLDMGNSGTAAARLLSGILSSHAFNS--IMTGDASLRSR 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + V L G++ G P+ + G G + +L + S+Q SA+L+A
Sbjct: 127 PMRRVTVPPLAANGSEFLTREGGRL-PAIRGTGEAKPIEYRLPVA-SAQVKSAILLAGLN 184

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS--DSWDRFYIKGGQKYKSPKNAYV 250
A G +E + + + + E LR FGV+ + S D+ R G + ++ V
Sbjct: 185 AHGTTTVE--EPVATRDHTENMLR---HFGVEVDVSRIDAGGRRIALTGPVQMTARDVTV 239

Query: 251 EGDASSASY-FLAGAATGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++ +A + G + +EG G L+ + F ++E MGA ++ V
Sbjct: 240 PGDPSSAAFPVIAALLVPGSDIWIIEGVLNPLRTGL-FTTLIE-MGASLSIENERVEGG- 296

Query: 310 PPREFPGRKH-----LKAIDVNMNMKMP---DVAMTLAVVALFADGPATIRDVASWRVKET 361
EP G H LK +DV + P D LAV FA+G + +R + RVKE+
Sbjct: 297 ---EPVGDHLVRYSKLKGVDVPPERAPSMIDEYPVLAVACAFAGASRLRGLEELRVKES 353

Query: 362 ERMVAIRTELTKLGASVEE-GPDYCIITPPEKLNVTADITYDDHRMAM-AFSLAACAEVP 419
+R+ + L GA E G D + L + T+ DHR+AM A L A+ P
Sbjct: 354 DRLASTVALLNVNGAETEVIGDDLIVKGYHGLPGGTQVTHMDHRLAMSAAVVLGLAAQKP 413

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
V + D +FP + D+++
Sbjct: 414 VNVDATAFIETSFPFGFVLDLMNAL 436

>ref|YP_616539.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingopyxis
alaskensis RB2256]
sp|Q1GT16.1|ARO_A_SPHAL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF53206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingopyxis
alaskensis RB2256]
Length = 446

Score = 124 bits (312), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 209/445 (46%), Gaps = 38/445 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G + +PG KS+S+R L+L+AL+ G + V LL DV A+R +G + D
Sbjct: 17 LKGRIAPGDKSISHRSLMLSALAVGESRVAGLLEGHDVLATAAAMRAMGADIARRDDGE 76

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R VG GG A L +GN+G + R L V + AT+V D + RP
Sbjct: 77 WRIHGVGVGGLLQPRGA-----LDMGNSGTSTRLLMGLVASHPITATFVGDA--SLSGRP 129

Query: 134 IGDVLVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALL 187

+G ++ L Q+GAD+ G P+ V G+ + LS + S+Q SA+L
Sbjct: 130 MGRVIDPLTQMADISASPGARGAKTLPLMVRGL----APAIPLSYRLPMASQVKSAIL 185
Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSWDRFYIK-GGQKYKSP 245
+A G E+ + +P + + R++ FG D+ +I+ G+ P
Sbjct: 186 LAGLNTPGVTEV-----IEVPTRDHSEMLGAFGADLTVIDAGGTRHIRIRGEADLKP 240
Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SSA++F+ A I G+ VT+ G + EVL+ MG + +
Sbjct: 241 QAIIVPGDPSSAAFFIVAALIVPGSDVTIANVGLNPTR--AGLVEVLKAMGGDIELDDR 298
Query: 305 VVTGTGPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ G P +H LK I+V+ P D L V A A+G T + RVK
Sbjct: 299 -EIGGEPVADLVRHVSVLKGEVDPVAVAPSMIDEFPVLFVAATLAEGRTVTTGLDELVRVK 357
Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT-IDENTYDDHRMAMAFSLAA-C 415
E++R+ + T L +GA VEE D +I T + L A I + DHR+ M+F++A
Sbjct: 358 ESDRLAVMATGLKAIGARVEESQDGLVIDGTGGDPLAGGATIAGHLDRICMSFAIAGLV 417
Query: 416 AEVPVTIRDPGCTRKTFPDYFDVLS 440
++ PVT+ D +FP++ +L+
Sbjct: 418 SKAPVTVDDIAPVATSFNFEALLA 442

>ref|ZP_03953584.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
hilgardii ATCC 8290]
gb|EEI24612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
hilgardii ATCC 8290]
Length = 434

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 125/438 (28%), Positives = 209/438 (47%), Gaps = 34/438 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ A+SEG T + + L +ED L A + LG+ ++ D
Sbjct: 12 LHGELSVPGDKSISHRGIMFGAVSEGRTTLHHFLTAEDCLSTLKAFQQLGVPIKRDGETV 71
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG G + L +GN+G R + + AG N L G + +RP+
Sbjct: 72 EIEGVGLHGL-----KQSGNPLDMGNSGTTTTLIMGLL--AGQNFDSLFGDDSLSKRPM 124
Query: 135 GDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L ++GAD+ C TD P R++G L +L + S+Q SAL++AA A
Sbjct: 125 KRVSEPLAEMGADI-CV--TDGHLPARIHG-QKLHAIDYQLKVA-SAQVKSALILAAIQA 179
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEG 252
D +I+KL P T +++ FG + D IK + K + + V G
Sbjct: 180 --DQPSTLIEKL---PTRNHTKMLNAFGANIQ--TMADNVTIKVNPPKLTGIDLTVPG 232
Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS SVTVTGPP 311
D SSA++FL A + +T++ G + +L+ MG KV E +G P
Sbjct: 233 DMSSAAFFLVAATLVPN SKLTLKNVGVNETR--TGLLSILKRMGGKV--IERHRNDSGEP 288
Query: 312 REPF--GRKHLKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVA 366
LK I++ ++P V L +VAL A+G + I RVKET+R+ A
Sbjct: 289 TADLVSSAELKPIEIGAEIIPAVIDELPLVALLAAKANGISKITGAGELRVKETDRIAA 348
Query: 367 IRTELTKLGASVEEGPDYCI--TPPEKLNVT-IDENTYDDHRMAMAFSLAA-CAEVPVTIR 423
+ E +KLG ++ E PD +I P + T +D++ DHR+ M ++A+ + + +
Sbjct: 349 VVQFESKLGIAIRELPDGFVIDGAKPWHVEKTKLDSHGDRIGMTLAIASLLLDLQQLN 408
Query: 424 DPGCTRKTFPDYFDVLS 441
++P++FD L++
Sbjct: 409 GAESVNISYPEFFDDLAS 426

>ref|YP_002731486.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Persephonella marina
EX-H1]
sp|C0QS40.1|ARO_A_PERMH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|AC004095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Persephonella marina
EX-H1]
Length = 432

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 119/447 (26%), Positives = 203/447 (45%), Gaps = 29/447 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ + I G +++P KS+S+R ++L +L++G +VV N L + D L R LG+S+
Sbjct: 5 ISKVSRIKIGELRVPSDKSISHRSIIITSLADGVSVVKNFLKAGDTTLTLNVYRKLGSII 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+K + V G ED L +GN+ + +G L G
Sbjct: 65 EEKGVLIKIGVNLKGFKEPEDI-----LDMGNS--GTTTRLTLGLLSGQEFFSALTGDSD 117

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R+RP+G + L+ +GA +D P+ V G L G + S S+Q SALL+
Sbjct: 118 LRQRPMGRVADPLRSMGAKIDGRQDGKLLPLSVRG--SSLKGIQFYNKRS--SAQVKSALLI 175

Query: 189 AAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKS 244
A LA G ++ + PY+ + T ++++ G + E D + I G +K +
Sbjct: 176 AGLLAEGKTKV-----TEPYISRDHTEKMLDAMGADIHIERDDEYS-VTISGSKKLEG 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ +S+A + A I + ++ + F L+ MG + +T
Sbjct: 228 IEIDVPADPSSAAFFAAAVLIPDSELLKLDVLINPTRDG--FFRKLKEMGGDIRYTNIR 285

Query: 305 VVTGTPPREPFGR--KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
P + + R LK I + +P D L++VA A+G T I RVK
Sbjct: 286 EKAKEPVADIYVRYSPDLKGRIRIKKEDVPSMVDEIPLLSIVATQAEGETIITGAELRVK 345

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEV 418
E++R+ A+ L LG VEE PD +I +K+ +D+Y DHR+AM FS L +E
Sbjct: 346 ESDRIKAVVENLKNLGDVEELPDGMVIGKQKVKGGVVDSYKDHRIAMGFSILGLISEE 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVKN 445
+ I+D ++P++++ L + N
Sbjct: 406 GIKIKDADSVFISYPEFYEHLEIRIISN 432

>ref|YP_003376188.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (epsp
synthase) (epsps) protein [Xanthomonas albilineans GPE
PC73]
emb|CBA16198.1| probable 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (epsp
synthase) (epsps) protein [Xanthomonas albilineans]
Length = 437

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 130/438 (29%), Positives = 212/438 (48%), Gaps = 38/438 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E ++
Sbjct: 16 LQGTTLTVPGDKSVSHRAVMFAALADGVSRIIDGFLLEGEDTRSTAAIFAKLGVRIETPSPSQ 75

Query: 75 RAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R V VG G + P + +L GNAG MR L + A N+ VL G + +R
Sbjct: 76 RLVHGVGVDGLRAP-----QGELDCGNAGTGMRLLAGLLAAQPFNS--VLVGDA SL SKR 127

Query: 133 PIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L +GA +D PP+R++G L +S S+Q SA+L+A
Sbjct: 128 PMRRVTEPLALMGARIDT-AANGVPPRLIHGGQALRAIDF-VSPVASAQVKSAVLLAGLY 185

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G ++ P + T R++ FGV+ + R ++GGQ+ ++ A V
Sbjct: 186 AEGVTVFQEPH-----PTRDYTERMLSAFGVEIAFAPQAR--LRGGQRLRATDIA-VPA 237

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F+ A+I G+ +T++ G + + A L +MGA + E + + G
Sbjct: 238 DFSSAAFFIVAASIIIPGSDITLKAVGLNPRRTGLLAA--LRLMGADI--VEHNHSEHGG- 292

Query: 312 REPFGGRKHLKAIDVNMNMPDVAM-----TLAVVALFADGPTAIRDVASWRVKETER 363
EP ++ + K+P+ + L + A A G T + A RVKE++R
Sbjct: 293 -EPVADLRVRYALLRGAKIPETVVPDMIDEFPALFIAAAAAQGRTTVSGAAELRVKESDR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ A+ T L LG V+E PD I L I+++ DHR+AMAF++A A+ V I
Sbjct: 352 LAAMATGLRTLGIIVDETPDGATIH-GGTLGAGTIESHGDHRIAMAFIAAGQLAQGEVRI 410

Query: 423 RDPGCTRKTFPDYFDVLS 440
+ +FP FD L+
Sbjct: 411 EEVANVATSFPG-FDALA 427

>ref|ZP_03941378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
buchneri ATCC 11577]
gb|EEI20794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
buchneri ATCC 11577]
Length = 434

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 125/438 (28%), Positives = 209/438 (47%), Gaps = 34/438 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++ A+SEG T + + L +ED L A + LG+ ++ D
Sbjct: 12 LHGELSVPGDKSISHRGIMFGAVSEGRTTLHHFLTAEDCLSTLKAFQQLGVPIKRDGETV 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG G + L +GN+G R + + AG N L G + +RP+
Sbjct: 72 EIEGVGLHGL-----KQSGNPLDMGNSGTTTRLIMGLL--AGQNFDSLTFGDDSLSKRPM 124

Query: 135 GDLVVLGKQLGADVDCFLGTDGP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L ++GAD+ C TD P R++G L +L + S+Q SAL++AA A
Sbjct: 125 KRVSEPLAEMGADI-CV--TDGHLPARIHG-QKLHAIDYQLKVA-SAQVKSALILAAIQA 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEG 252
D +I+KL P T +++ FG + D IK + K + + V G
Sbjct: 180 --DQPSTLIEKL---PTRNHTKMLNAFGANIQ--TMADNVTIKVNPQPKLTGIDLTVPG 232

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL A + +T++ G + +L+ MG KV E +G P
Sbjct: 233 DMSAAFFLVAAATLVPSKLT LKNVGVNETR--TGLLSILKRMGGKV--IERHRNDSGEP 288

Query: 312 REPFGGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVA 366
LK I++ ++P V L +VAL A+G + I RVKET+R+ A
Sbjct: 289 TADLVSSAELKPIEIGAEIIPAVIDELPLVALLAAKANGISKITGAGELRVKETDRIAA 348

Query: 367 IRTTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
+ E +KLG ++ E PD +I P + T +D++ DHR+ M ++A+ + + +
Sbjct: 349 VVQEFSLGLIAIRELPDGFVIDGAKPWHVEKTKLDSHGDHRIGMTLAIASLLLDEQLQLN 408

Query: 424 DPGCTRKTFPDYFDVLS 441
++P++FD L++
Sbjct: 409 GAESVNISYPEFFDDLAS 426

>ref|ZP_05636000.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tabaci ATCC 11528]
Length = 268

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 92/290 (31%), Positives = 143/290 (49%), Gaps = 37/290 (12%)

Query: 161 VNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIP-YVEMTLRLME 219
+ G GGL G++++ G++SSQY+SALLMA G VE+ + I YV++TL M+
Sbjct: 2 IKKGGLLEAGRIEIDGNLSSQYVSALLMAGACGKGPVEVALTGSEIGARGYVDLTAAAMQ 61

Query: 220 RFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCG 277
FG V+A +W Y++ + ++E DAS+A+Y A A+T G + +
Sbjct: 62 AFGAEVQAIGETAWK----VSATGYRA-TDFHIEPDASAATYLWAAQALTEGDIDLGVAS 116

Query: 278 TTS LQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTL 337
Q D +++++ P P A+ ++ ++M D TL
Sbjct: 117 DAFTQPDALASQIIASF-----PNMP-----AV-IDGSQMQDAIPTL 152

Query: 338 AVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL--GASVEEGPDYCIITPPEKLV 395
AV+A F P +A+ RVKE +R+ A+ L + G +VEEG D + P
Sbjct: 153 AVLAAFNRQPVRFVGIANLRVKECDRISALSHGLCAIAPGLAVEEGDLLVHANPALAGT 212

Query: 396 TA---IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
T IDT+ DHR+AM F+LA + I DP C KT+P Y+D L++
Sbjct: 213 TVDALIDTHSDHRIAMCFALAGLKIAGIRILDPDCVGKTYPGYWDALASL 262

>ref|YP_001262955.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingomonas wittichii RW1]
gb|ABQ68817.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingomonas wittichii RW1]
Length = 479

Score = 124 bits (311), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 134/437 (30%), Positives = 205/437 (46%), Gaps = 33/437 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+ G++ +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R +G S+E D
Sbjct: 48 LRGSIAVPGDKSISHRALMLSALAIGESRVEGLLTGEDVLATAAAMRAMGASIERGDDDV 107

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG E A E +GN+G + R L V + AT+ D + +RP
Sbjct: 108 WRIHGVGVGGLLQPEGALE----MGNSGTSTRLLMGLVASHAITATFTGDA--SLSKRP 160

Query: 134 IGDVLVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAA 190
+ ++ L +GADV G P+ + GI P + + S+Q SA+L+A
Sbjct: 161 MNRVIEPLSLMGADVDTATPGGKGGTLPMLRGIS--PAVPIDYRLPVASAQVKSALLAG 218

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKYKSPKNA 248
G +I+ + + + E R++ FG + E D R G+ P++
Sbjct: 219 LNTPGIT--RVIEPVATRDSHSE--RMLRGFGAELEVEQDADGARIISIRGEAELQPQHI 273

Query: 249 YVEGDASSASY-FLAGAAITGGTVTVEGCGTTS LQGDVVKFAEVLEMMGAKVTWTETSVTV 307
V GD SSA++ +A + G VT+ G + +VL MMG + + V
Sbjct: 274 VVPGDPSSAAPPVVAALLVPGSAVTIANVGLNPTR--AALFDVLRMMGGDIEFANPR-EV 330

Query: 308 TGPPREPFGGRKH--LKAIDV---NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P +H LK I+ + M D L V A A+G T R + RVKE++
Sbjct: 331 GGEPVADIVVRHSTLKGIEPTVETVASMVDEYPILFVAAALAEGRVARGLEELRVKESD 390

Query: 363 RMVAIRTELTKLGASVEEGPDYCI--TPPEKLVNTA-IDTYDDHRMAMAFSLAA-CAEV 418
R+ + L +GA VEE D II T + L A I DHR+AM+F++A ++
Sbjct: 391 RIAVMAEGLRAIGARVEELEDGLIIDGTGGDPLPGGATIAARLDHRIAMSFVAVAGLVSKA 450

Query: 419 PVTIRDPGCTRKTFFPDY 435
VTI D G +FP +
Sbjct: 451 AVTIDDMGPVATSFPGF 467

>ref|ZP_06861446.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citromicrobium bathyomarinum JL354]
Length = 446

Score = 124 bits (310), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 130/446 (29%), Positives = 202/446 (45%), Gaps = 33/446 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+P +G++ +PG KS+S+R L+L A++ G T V LL EDV A+R +G V
Sbjct: 10 FRPAGPLRGSITVPGDKSISHRSLILGAMAVGETRVSGLLEGEDVLATAAAMRAMGADVH 69

Query: 69 ADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
D A V VG GG + E + GN+G + R L V + G T+ D
Sbjct: 70 RDDDATWHVHVGVGGLL----QPEAAIDCGNSGTSARLLMGLVASHGIAVTFTGDA-- 122

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSAL 186


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      + +RP+G ++ L Q+GA      G P +      G P ++      + S+Q SA+
Sbjct: 123 SLSKRPMPGRVIDPLSQMGARFTSPGGTmplmle---GAHPAVPIRYRLPVASAQVKS AV 179

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSWDRFYIKGGQKYKSP 245
      L+A      G      +      +P + + R++ FG + E DS R      GQ P
Sbjct: 180 LLAGLNTPG-----VTSVIEPVPTRDHSEMLRGFGAELEIGEDSGARVICLTGQVDLRP 234

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + V GD SSA++F+ A + G+ +T+ G +      +VL MGA + +
Sbjct: 235 QILTVPGDPSSAAFFMVAATLVEGSDLTIRNVGMNPTR--AGLVDVLRQMGANIEELDAR 292

Query: 305 VTVTGPMPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
      V G P      +H L I+V+ P D      L V A A G T R + RVK
Sbjct: 293 -EVGGPEVADLVRHAPLTGIEVDPALAPSMIDFVPLFVAAALAKGTTVTRGLDELVRVK 351

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT---IDTYDDHRMAMAFSLAA 414
      E++R+ + L +GA VEE D I T E L +A + T+ DHR+AM+ ++A
Sbjct: 352 ESDRLATMTAALETIGARVEEREDGLTIHGTGGEPLRGSANARVKTHLDHRIAMSMVAVAG 411

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVL 439
      + V + D      +FP + +L
Sbjct: 412 LVSRDGEVDDTSPIATSFPGFESLL 437

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>ref|YP_003443611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Allochro-
      vinosum DSM 180]
gb|ADC62579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Allochro-
      vinosum DSM 180]
      Length = 488

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Score = 124 bits (310), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 126/447 (28%), Positives = 207/447 (46%), Gaps = 35/447 (7%)

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Query: 8 VLQPIKEISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
      ++ P + G +++PG KS+S+R ++L+A++EG T V L D L A R +G+S+
Sbjct: 54 LISPGGSLRGLRVPKDKSISHSIMLSAIAEGRTQVSGFLEGADALATLAAFRAMGVSI 113

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      E + V+ G G + + L +GN+G AMR L + G AT V D
Sbjct: 114 EGPDSGE-LVIEGVGMR---GLRAPDTTLDMGNSGTAMRLLVGLLAGQGFTATLVGDD-- 167

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      + RP+ + L +GA + T P+ + + L G + +L + S+Q S L+
Sbjct: 168 SLTRRPMRRVTEPLALMGAQIRTS-PTGTAPLTIEPVDHLNGLLEYRLPMA-SAQVKSCLM 225

Query: 188 MAAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      +A A G+ VE E P + T R++ FG R + GG + +
Sbjct: 226 LAGLYAEGETCIVEPE-----PTRDHTERMLTAFGYSVRRQGL--RVCLTGGGRLTA 275

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      + + D SSA++FL GA+I G+ + +E G + V ++ MGA + +
Sbjct: 276 CR-LRIPADISSAAFFLVGASAPGSDLLLEAVGINPTR--VGVINIMRAMGADIELLDK 332

Query: 304 SVTVTGPMPREPFGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
      T G P K L+ I + ++++P D L + A A+G T + RV
Sbjct: 333 R-TAGGEFVADIRVKSARLRGIRIPVDQVPLAIDEFPALFIAAACAEGETVLTGAELRV 391

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIDTYDDHRMAMAFSLAAC 415
      KE++R+ + LTKLG E PD I T AI+ + DHR+AM+F++A
Sbjct: 392 KESDRIQVMADGLTKLGIQAETPDGIRIQGGTLGSATGENAIEAHGDHRIAMSFAIAGL 451

Query: 416 -AEVPVTIRDPGCTRKTFPDYFDVLST 441
      A P+ +RD +FP + + S
Sbjct: 452 RASGPIEVRDCANVETSFPGFQQLASN 478

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>ref|NP_267900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
      subsp. lactis Il1403]
sp|Q9CEU0.1|AROALACLA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS

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gb|AAK05842.1|AE006404_9 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. lactis Il1403]
Length = 430

Score = 124 bits (310), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 209/439 (47%), Gaps = 27/439 (6%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+PG KS+S+R ++ ++++G TV+ ++L EDV + A R +G+ +E DK
Sbjct: 10 LKGRLLKVPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ GK E E L +GN+G + R L+ + AG L G + +RP+
Sbjct: 68 ---VITVHGKGISELKAPEKALDMGNSGTSTRLLSGIL--AGLPFETTLFGDDSLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA++ P+ + G L L + S+Q SA++ AA A
Sbjct: 123 DRVATPLQLMGAEITGQTDKVKLPMTIKGSTHLKAIDYVLPVA-SAQVKS AVIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G ++++K + + E ++ +FG + + SD + GGQK K V GD
Sbjct: 182 GLT--KVVEKEKTRSHTE---EMLVQFGGELKVSDKT--ILVPGGQKLVGQK-VVVPGLDI 233

Query: 255 SSASYFLAGA-AITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA+++L A + + +E G + + EV++ MG ++ E V
Sbjct: 234 SSAAFWLVAALVVENSELILENVGVNENETRTGI--IEVIQAMGGQLEILEQD-NVAKAATL 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAIRTE 370
LK +++ + +P + L ++AL A G T IRD A +VKET+R+ +
Sbjct: 291 KVKASQLKGTESGDLIPRLIDELPIIALLATQAQGGTIIRDAAELKVKETDRIAVVANA 350

Query: 371 LTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
L +GA ++ D II KL+ +I+T DHR+ M ++AA + +
Sbjct: 351 LNSMGAKIQPTDDGMIIQGGTKLHAPENSINTLGDHRIGMMAAIAALLVKNGEIELELRAE 410

Query: 427 CTRKTFPDYFDVLSTFVK 445
+ ++P +FD L +N
Sbjct: 411 AIQTSYPSFFDDLEQLSEN 429

>ref|YP_349802.1| 3-phosphoshikimate 1-carboxyvinyltransferase / prephenate
dehydrogenase [Pseudomonas fluorescens Pf0-1]
gb|ABA75811.1| putative bifunctional protein, prephenate dehydrogenase:
3-phosphoshikimate 1-carboxyvinyltransferase
[Pseudomonas fluorescens Pf0-1]
Length = 735

Score = 124 bits (310), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 125/438 (28%), Positives = 209/438 (47%), Gaps = 35/438 (7%)

Query: 10 QPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SG +++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+ +E
Sbjct: 306 QPGGRLSGRIRVPGDKSISHRSIMLGS LAEGVTEVEGFLEGEDALATLQAFRDMGVVIEG 365

Query: 70 DKAARAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + VG G P ++LGN+G +MR L+ + A ++T L G
Sbjct: 366 PHHGRVTIHGVLHGLKPAPGP-----IYLGNSGTSMRLLSGLLAQDFDST--LTGDAS 418

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + L+++GA ++ PP+ + G L G + + S+Q S LL+
Sbjct: 419 LSKRPMNRVANPLREMGAVIET-AAEGRPPMTIRGGHKLKGLTYTMPMA-SAQVKSCLLL 476

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G + P + T R++ FG S + ++ G K + +
Sbjct: 477 AGLYAEKTTT---EPAPTRDHTERMLRGFGYPV--SVNGATASVESGGKLT-THI 528

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS+++FL A+I G+ + +E G + V ++L +MGA +T E V
Sbjct: 529 EVPGDISSAFFLVAASIAEGSELVLEHVGINPRTGTG--IDILRLMGADITL-ENQREV 585

Query: 308 TGPPPREPFGRKHLKAIDVNMNMPDVAMTLA-----VVALFADGPTAIRDVASWRVK 359

G EP ++A + ++P+ + LA V A A+G T + RVK
Sbjct: 586 GG---EPVADLRVRAAKLKGI EIP EALVPLAIDEFPVLFVAAACAEGRTVLTGAEEELRVK 642

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEV 418
E++R+ + L LG E PD II ++ + + DHR+AMAFS+A+ A

Sbjct: 643 ESDRIQVMADGLLALGVKCEPTPDGI IID-GGQIGGGEVHGHGDHRIAMAFSVASLRATA 701

Query: 419 PVTIRDPGCTRKTFPDYF 436
P+ I D +FP++

Sbjct: 702 PIRIHDCANVATSFPNFL 719

>ref|ZP_04929449.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [Pseudomonas aeruginosa C3719]
gb|EAZ53568.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [Pseudomonas aeruginosa C3719]
Length = 747

Score = 124 bits (310), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 125/416 (30%), Positives = 204/416 (49%), Gaps = 36/416 (8%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SGT+++PG KS+S+R ++L +L+EGTT V+ L ED + A R +G+ +E

Sbjct: 318 QPGGSLSGTIRVPGDKSISHRSIMLGSLAEGTTEVEGFLEGEDALATIQA FRDMGVVIEG 377

Query: 70 DKA AKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ + V VG G K P ++LGN+G +MR L+ + A ++T L G

Sbjct: 378 PQNGRVTVHGVGLHGLKAP-----PGPIYLGNSGTSMRLLSGLLAAQPF DST--LTGDA 429

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + L+++GA ++ G + PP+ + G L G + + S+Q S L

Sbjct: 430 SLSKRPMNRVAKPLREMGAVIET--GPEGRPPMTIRGGQRLTGMHYDMPMA-SAQVKSCL 486

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKA EHSDSWDRFYIKGGQKYKS 244
L+A A G+ + P + T R++ FG V E S + ++ G K S

Sbjct: 487 LLAGLYAAGETS VT-----EPAPTRDHTERMLRGFGYPVVVEG STA----KVESGHKL-S 536

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTET 303
+ V D SSA++FL A+I G+ + ++ G + V E+L +MG ++ E

Sbjct: 537 ATHIEVPADISSAAFFLVAASIAEGSELVLQHVGINPTR--VG VIEILRLMGDL SL-EN 593

Query: 304 SVTVTGPPREPFG RK--HLKAIDVN MNKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V G P + LK ID+ + +P D L V A A+G T +R RV

Sbjct: 594 QREVGGEFPVADIRVRSARLKGIDIPEDLVPLAIDEFPVLFVAAACAEGRTVLRGAEE LRV 653

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA 414
KE++R+ + L LG E PD +I + + DHR+AM+FS+A+

Sbjct: 654 KESDRIQVMADGLKALGVKA EPTPDGIVIE-GGAFGGGEVWAHGDHRIAMSF SVAS 708

>ref|ZP_01123903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH
7805]
gb|EAR18538.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH
7805]
Length = 417

Score = 124 bits (310), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 123/437 (28%), Positives = 201/437 (45%), Gaps = 37/437 (8%)

Query: 21 LPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA AKRAVVVG 80
+PG KS+S+R LL A++EG T ++ LL +ED LR +G + V G

Sbjct: 1 MPGDKSISHRALLFGAIAEGVT TIEGLLPAEDPISTAACLRAMGAEISPIAEGSLIHVQG 60

Query: 81 CGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G D +E L GN+G MR L + A + +VL G +R RP+ +

Sbjct: 61 VG-----LDGLQEPD TVLDCGNSGTTMR-LMLG LLAGRHDRHFVLTGDASLRRRPMQ RVG 114

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L LGA+V + P+ V G +L G++ +++ + + L L +

Sbjct: 115 HPLAILGA EVRGRGNGNYAPLAVQG-----RRLRGAVVGTPVASAQVKSALLLAALT 166

Query: 199 IEIIDKLIS-IPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNAYVEGDASS 256
E +I P + + R+++ FG R ++ G + K ++ V GD SS
Sbjct: 167 AEGTTTVEIPAPSRDHSERMLKAFGADLTVGEMGRHISVQPGAQLKG-QHVVVPGDISS 225

Query: 257 ASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET-----SVT 306
A+++L AGA + G +TVE G + V +VLE MGAK+ +
Sbjct: 226 AAFWL VAGALVPGADLTVENVGLNPTRTGV--LDVLEQMGAKIDVLNRRDVAGEPVGDRL 283

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
VT P +PF + + M ++ D L V A F DG + I A RVKET+R+
Sbjct: 284 VTCGPLQPF-----RFGEIIMPRLVDEVPILTVAACFCDGESHISGAAELRVKETDRLAV 338

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ +L +GA ++E PD +I L +D+ DHR+AM+ ++A+ A+ T+
Sbjct: 339 MARQLKAMGADLDETPDGLVIRGGRPLRGAVLDSETDHRVAMSLAVASLMAKGDSTLERS 398

Query: 426 GCTRKTFFPDYFDVLSTF 442
++P ++D L+
Sbjct: 399 EAAAVSYPSFWDDLARL 415

>ref|YP_430188.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moorella
thermoacetica ATCC 39073]
gb|ABC19645.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moorella
thermoacetica ATCC 39073]
Length = 435

Score = 124 bits (310), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 131/441 (29%), Positives = 206/441 (46%), Gaps = 34/441 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++QP + G ++ PG KS+S+R ++ AL+EGTTV+D L D L LR LG+
Sbjct: 2 RLIIQPPPSLEGNIQPPGDKSISHRAAIGALAEGTTVIDGFLAGADCLSTLNCLRALGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + V ++ KE E L GN+G MR L + AG V++
Sbjct: 62 DIAGPDGGRVVVR----GGGLDSLKEPETVLDAGNSGTTMRLLLGLV--AQQPFYSVIN 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVK-LSGSI---SS 180
G +R RP+G + L+ +GA + + P+ V G GK++ L+ ++ S+
Sbjct: 115 GDESLLRRRPMGRVTGPLRSMGAAIWGRQNGELAPLSVRG-----GKLEPLAYTLPVASA 168

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q SALL+A G E + + S + E LR A+ R I+G +
Sbjct: 169 QVKSALLLAGLFTSG--ETIVTEPCRSRHSERMLR-----AAGADLRVEGLRVRIRGRK 221

Query: 241 KYKSPKNAYVEGDASSASYFL-AGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAK-- 297
K P V GD S+A++FL AG +T+E + +VL MGA
Sbjct: 222 PLK-PLTINVPGDISAAFFLVAGCLHPRAALTLEKVNLPTR--TGIIDVLTAMGAPLE 278

Query: 298 -VTWTETSVTVTGPPREPFGRKH-LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVAS 355
+ ET+ G R GR H L+ + ++ D LAV A A+G T IR A
Sbjct: 279 IIPGEETAGEPAGSIRVTSGRHLHGLEVGAMIPRLIDEIPVLAVAAALAEGETLIRGAAE 338

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
+VKE++R+ + EL ++GA + PD I +L +D++ DHR+AMA ++A
Sbjct: 339 LKVKESDRIAMVAGELARMGAEIYARPDGFRIGVRRRLRGAVVDSHGDHRLAMALAMAGL 398

Query: 415 CAEVPVTIRDPGCTRKTFFPDY 435
AE +R C ++P +
Sbjct: 399 VAEGTTEVRGAECIAISYPGF 419

>ref|ZP_07740278.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aminomonas
paucivorans DSM 12260]
gb|EFQ24167.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aminomonas
paucivorans DSM 12260]
Length = 430

Score = 123 bits (309), Expect = 5e-26, Method: Compositional matrix adjust.
Identities = 140/452 (30%), Positives = 206/452 (45%), Gaps = 46/452 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ + P + G ++PG KS+S+R L+ ALS V+ D L L LG
Sbjct: 4 RDVTVAPRGVLRGMREVPGDKSVSHRAALMGALSREGVEVEGFAPGADCASTLRCLALG 63

Query: 65 LSVEADKAAKRAVVVGCG--GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V+ + + V G G G V DA GN+G R L + G T V
Sbjct: 64 ARVQ--RRGDRVRVARGEPLGAAAVLDA-----GNSGTTARLLCGLLAGQPGTFT-V 113

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ G + RP+ +V L+ LGA +D G P+ V G L GG V G+ S+Q
Sbjct: 114 IQGDESLSRPMRRVVDPLRTLGRIDGREGGGLPLSVRGTS--LSGG-VCTPGAPSAQV 171

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY----IKG 238
SALL+A A G V + + L + + E+ L+E GV + Y + G
Sbjct: 172 KSALLLAGLSARGSVTV--AEPLKTRDHTI---LLEHLGVPLRREGAAVTVYPLEDLPG 226

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAI--TGGTVTVGCGGTSLSLQGDVKFAEVLEMMGAK 297
G +K P GD SSA++++ AA+ G +T+ G + L MG
Sbjct: 227 GT-WKVP-----GDFSSAAFWITAAALLPEGDLTLPEVGLNPTR--TGLLSALGRMG-- 275

Query: 298 VTWTETSVTVTGPPREPF-----RKHLKAIDVNMNKM---DVAMTLAVVALFADGPTA 349
+ + T + ++G EP G L+ V+ ++P D LAV A+ A G T
Sbjct: 276 LDYGVTDLALSGG--EPLGTLQVRSSSLEGTVVDAPALVDELPIAVALAVRAKGVTE 333

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
IR R KE +R+ A+ L LGA VEE D I+ P +L +D++ DHR+AMA
Sbjct: 334 IRGARELRFKCEDRIAAMAEGRLTLGAEEVEREDGWILRGPCRLRGGEVDSFGDHRVAMA 393

Query: 410 FSLAA-CAEVPVTIRDPGCTRTFPDYFDVLS 440
+AA AE PV IR C ++P +F+ LS
Sbjct: 394 LGVAALTAEGPVRIRGAACADISYPGFEEALS 425

>ref|ZP_05104162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylophaga
thiooxidans DMS010]
gb|EEF80156.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylophaga
thiooxidans DMS010]
Length = 439

Score = 123 bits (309), Expect = 5e-26, Method: Compositional matrix adjust.
Identities = 124/445 (27%), Positives = 212/445 (47%), Gaps = 32/445 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ ++ P +I G +++PG KS+S+R ++L +L+EGTT V L ED L R +G
Sbjct: 7 KKYIVHPGGQIQGELRVPGDKSISHRSIMLGSLAEGTTKVTGFLEGEDALATLATFRAMG 66

Query: 65 LSVEA-DKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ + DK VG G K P E + ++GN+G ++R L+ ++ + T
Sbjct: 67 VDIIGPDKGKVTIHVGVMQGLKAP-----EKEFYVGNSTGTSIRLLSGLLSGQQFDCT-- 118

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + L +GA +D G PP++++G L G L + S+Q
Sbjct: 119 LSGDKSLSGRPMKRVTDPLALMGAKIDTKEGK--PPLKIHGSSSLKGIDYLLPMA-SAQV 175

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S LL+A A G + P + T R++ G + S I GG K
Sbjct: 176 KSCLLLAGMYAEGKTSVT-----EPAPTRDHTERMLSGMGYAVDVEGST--ISITGGGKL 228

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGGTSLSLQGDVKFAEVLEMMGAKVTWT 301
+ N V D SSA++F+ AAI G+ +T++ G + + +L++MGA ++ T
Sbjct: 229 TA-TNIDVPADISSATFFMVAAAIAPGSDITLKHVGINPTR--IGVINILKLMGADISLT 285

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASW 356
+ T G P ++ LK I + ++P D L + A A+G T +
Sbjct: 286 NEAET-GGEPVADIRVRYAPLKGIQIPEDQVPLAIDFFPALFIAAACAEGQTVLTGAEEEL 344

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC- 415
RVKE++R+ + L LG + D +I + +D++ DHR+AM+F++AA
Sbjct: 345 RVKESDRIQVMADGLQTLGIDAKPTEDGIVIH-GGIIGSGEVDSHSDHRIAMSFAIAALQ 403

Query: 416 AEVPVTIRDPGCTRKTFFDYFDVLS 440
A + I D +FP + ++ S
Sbjct: 404 AGGSIQINDCANVATSFPGFVEMAS 428

>gb|ABE11079.1| EPSP synthase 3-p [uncultured Prochlorococcus marinus clone
HF10-11A3]
Length = 449

Score = 123 bits (308), Expect = 6e-26, Method: Compositional matrix adjust.
Identities = 117/448 (26%), Positives = 205/448 (45%), Gaps = 44/448 (9%)

Query: 14 EISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G VK+PG KS+S+R L++ ++++G T ++ L+SED LR LG+ + K
Sbjct: 25 NLRGNVKVPKDKSISHRALIIGSIKGETTIEGFLHSEDPLSTADCLRKLGVKIPKIKKN 84

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G G ++ KE ++ GN+G MR L + G ++L G + ER
Sbjct: 85 EPFTISGLG---LDGLKEPKEILNCGNSGTTMRLMGLLAGQEGK-NFILTGDISLNER 139

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + + P+ ++G KL G + S+Q SA+
Sbjct: 140 PMGRVKGPLSLMGGKIFGREKGNKAPISIDG-----NKLKGCVIGTPVASAQVKSAL 191

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+A A G + I+ S + E R+++ FG R IK G
Sbjct: 192 LLAGLKASGTTSV--IEPASSRDHTE---RMLKAFGADISIRGELGRNVVKSAGDLIGQ 246

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + GD SSAS+++ A+I V ++ G + + V++ MG + S
Sbjct: 247 R-ILIPGDISSASFWMIAASIVPNSEVLIQNVGLNPTRTGI--LNVMDSMGCNYEILDKS 303

Query: 305 VTVTGPPEPFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
T+ G EP G +L++ + + +P D L V A F +G + I+D
Sbjct: 304 -TIAG---EPIGSIKVKTSNNLRSFTIEGDILPKLIDEIPILTVAACFCNGVSEIKDAQE 359

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA- 414
R+KET+R+ + +L K GA + E D II K + +D+ DHR+AM+ ++A+
Sbjct: 360 LRIKETDRLKVMARQLQKFGAEITEKEDGLIINGQSKFHSAEVDSETDHRVAMSLAIASL 419

Query: 415 CAEVPVTIRDPGCTRKTFFDYFDVLSTF 442
A+ I ++P +++ L+
Sbjct: 420 LAKGTSKIMRADAASVSYPFWHEELAKL 447

>ref|NP_214059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aquifex aeolicus VF5]
sp|O67494.1|ARO_AQUAE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAC07443.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Aquifex aeolicus
VF5]
Length = 431

Score = 123 bits (308), Expect = 6e-26, Method: Compositional matrix adjust.
Identities = 128/453 (28%), Positives = 210/453 (46%), Gaps = 57/453 (12%)

Query: 9 LQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ IK + G +++P KS+++R +L AL+ G T+V L S D L L+ + V
Sbjct: 4 IEKIKRVKGLRVPSDKSITHRAFILGALASGETLVRKPLISGDTLATLEILKAIRTKVR 63

Query: 69 ADKAAKRAVVVGCGGKF----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
K + ++ G F V DAK N+G R ++ ++ + VL
Sbjct: 64 EKG--EEVLIEGRNYTFLEPHDVLDAK-----NSGTTARIMSGVLSTQPFPS--VLT 111

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G ++ RP+ +V L+++GA +D + P+ + G G L G + S+Q S
Sbjct: 112 GDESILNRPMLRVVEPLREMGAKIDGREGNKLPIAIRG-GNLKGISY-FNKKSSAQVKS 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY 242
ALL+A A G E+ ++ +S + E L+L FG V + IKGGQ+
Sbjct: 170 ALLLAGLRAEGMTEV--VEPYLSRDHTERMKL---FGAEVITIPEERGHIVKIKGGQEL 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM----- 293
+ + Y D SSA+YF A A T + +G+++ EVL
Sbjct: 225 QGTE-VYCPADPSSAAYFAALA-----TLAPEGEIRLKEVLLNPNTRDGFYRK 270

Query: 294 ---MGAKVTWTETSVTVTGPPREPFG--KHLKAIDVNMNKM---DVAMTLAVVALFAD 345
MG +++ P + R +LK + V+ ++P D LAV+ FAD
Sbjct: 271 LIEMGGDISFENYRELSNEPMADLVVRPVDNLKPKVKSPEEVPTLIDEIPIILAVLMAFAD 330

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHR 405
G + ++ R KE++R+ AI T L KLG VEE D I +++ I+T+ DHR
Sbjct: 331 GVSEVKGAKELRYKESDRIKAIVTNLRKLGQVEEFEDGFAIHGTKEIKGGVIETFKDHR 390

Query: 406 MAMAFS-LAACAEVPTIRDPGCTRKTFPDYFD 437
+AMAF+ L E V I P C ++P++++
Sbjct: 391 IAMAFAVLGLVVEEVIIDHPECVTVSYPEFWE 423

>ref|ZP_05293336.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Acidithiobacillus
calculus ATCC 51756]
gb|EET26811.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Acidithiobacillus
calculus ATCC 51756]
Length = 432

Score = 123 bits (308), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 213/439 (48%), Gaps = 39/439 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+ G + +PG KS+S+R+++L A+++G T + LL DV + A +++G+ +E D+
Sbjct: 11 LRGQISVPGDKSISHRVMLGAIADGVTEAEGLEGLADVLATIAAFQSMGVHMEGPDGRH 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G D + GN+G AMR L + AG + L G +R RP
Sbjct: 71 LRIEGVLRLGLRAPSDIID-----CGNSGTAMRLLAGLL--AGQEFSCTLTGDAASLRPP 123

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLMAAPLA 193
+G ++ L Q+GA ++ G P+ ++G L G L + S+Q SA+L+A A
Sbjct: 124 MGRVLAPLAQMGAIEAEDGR--APLHIHGR-PLQGIHYDLPVA-SAQVKSAILLAGLYA 179

Query: 194 LGDVEIEIIDKLISIPYEMTLRLMERFG--VKAHSDSWDRF--YIKGGQKYKSPKNAY 249
GD + P + + R+++ FG V+ E + R +++ GQ + P
Sbjct: 180 TGDTCVR-----EPAPTRDHSERMLQGFGQPVVRVEGAQRCLRSAGHLR-GQSLRVP---- 229

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
GD SSA++FL GA+I + + +EG G + E+L MGA++ V
Sbjct: 230 --GDISSAAFFLLGASIAPKSDDLLEGGVGINPTR--TGIVEILTRMGARIDLRLR-EVG 284

Query: 309 GPPREPFGKRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P ++ L+ ID+ +P D + + A A+G T IR RVKE++R
Sbjct: 285 GEPVADLRVRYAQLRGIDIPTRLVPLAIDEFPAIFIAAAAEGVTRIRGAEEELRVKESDR 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ + L LG +VEE D II L + ++ DHR+AMAF++A A V I
Sbjct: 345 IAVMAAGLRTLGIAVEELADGAIH-HGGVLGGGEVASHGDHRIAMAFAMAGLVARESVRI 403

Query: 423 RDPGCTRKTFPDYFDVLST 441
D +FP++ ++ T
Sbjct: 404 TDCTNVATSFNFAELART 422

>ref|YP_003346483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga
naphthophila RKU-10]
gb|ADA67069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga
naphthophila RKU-10]
Length = 421

Score = 123 bits (308), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 125/451 (27%), Positives = 206/451 (45%), Gaps = 54/451 (11%)

Query: 11 PIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P K++ G + +P KS+++R L+L+AL+E + + NLL D L LG E D

Sbjct: 5 PAKKVEGVLSPDPKSIITHRALILSALAETESTLYNLLRCLDTERTHDILEKLGTRFEGD 64

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP A+ LF GN+G R ++ + A VL G +

Sbjct: 65 WEKMKV-----FPKPFAPFIEPLFCGNSGTTTRLMSGVL--ASYEMFTVLYGDSLS 114

Query: 131 ERPIGDLVVGLKQLGADVDCFLG--TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+ ++ L+ +GA F+ + P+ + G L G + K + S+Q SA+L+

Sbjct: 115 RRPMPRVIEPLEMMGAR--FMARQNNYLPMAIKG-NHLSGIRYK-TPVASAQVKSALL 169

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN- 247
A A G +I+ S + E R+++ GV E ++G + P

Sbjct: 170 AGLRASG--RTIVIEPAKSRDHTE---RMLKNLGVPE-----VEGTRVVLEPATF 215

Query: 248 ----AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTE 302
V GD SSA++F+ GA +TV G + EV+++MGA + W

Sbjct: 216 RGFTMKVPGDISAFAFFVVLGAIHPNARITVTDVGLNPTR--TGLLEVMMKLMGANLEWEI 273

Query: 303 TSVTVTGPFPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVAL---FADGPTAIRDV 353
T + EP G +LK + V + +P + L +VAL FA+G T +R+

Sbjct: 274 TEENL----EPIGTVRVETSPNLKGVVPEHLVPLMIDELPLVALLGVFAEGETVVRNA 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
R KE++R+ + +LG +EE D I + + ++D DHRMAM FS+A

Sbjct: 329 EELRKKESTRIRVLVENFKRLGVEIEEFKDGFKIVGKQSIKGSVDPEGDHRMAMLFSLA 388

Query: 414 A-CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+E V ++D C +FP++++L V

Sbjct: 389 GLVSEEGVDVKDHECVAVSFPNFYELLERVV 419

>ref|YP_002533868.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga
neapolitana DSM 4359]
sp|B9KBV6.1|ARO_A_THENN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACM22502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga
neapolitana DSM 4359]
Length = 421

Score = 122 bits (307), Expect = 8e-26, Method: Compositional matrix adjust.
Identities = 123/450 (27%), Positives = 204/450 (45%), Gaps = 52/450 (11%)

Query: 11 PIKEISGTVKLPKSKLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P K++ G + +P KS+++R L+L+AL+E + + NLL D L LG E D

Sbjct: 5 PAKKVEGVLSPDPKSIITHRALILSALAESESTLYNLLRCLDTERTHDILEKLGTRFEGD 64

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP A+ LF GN+G R ++ + A VL G +

Sbjct: 65 WEKMKV-----FPKPFAPFIEPLFCGNSGTTTRLMSGVL--ASYEMFTVLYGDSLS 114

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ ++ L+ +GA P ++ N + G+ K ++ S+Q SA+L+A

Sbjct: 115 RRPMPRVIEPLEMMGARFMARQNNYLPMAIKGNHLSGI-SYKTPVA---SAQVKSALLA 170

Query: 190 APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-- 247
A G +I+ S + E R+++ GV E ++G + P

Sbjct: 171 GLRASG--RTIVIEPAKSRDHTE---RMLKNLGVPE-----VEGTRVVLEPATFR 216

Query: 248 ----AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTET 303
V GD SSA++F+ GA +TV G + EV+++MGA + W T

Sbjct: 217 GFTMKVPGDISAFAFFVVLGAIHPNARITVTDVGLNPTR--TGLLEVMMKLMGANLEWEIT 274

Query: 304 SVTVTGPFPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVAL---FADGPTAIRDVA 354
+ EP G +LK + V + +P + L +VAL FA+G T +R+

Sbjct: 275 EENL----EPIGTVRVETSPNLKGVVPEHLVPLMIDELPLVALLGVFAEGETVVRNAE 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R KE++R+ + +LG +EE D I + + ++D DHRMAM FS+A

Sbjct: 330 ELRKKESTRIRVLVENFKRLGVEIEEFKDGFKIVGKQSIKGSVDPEGDHRMAMLFSLA 389

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+E V ++D C +FP++++L V
Sbjct: 390 LVSEEGVDVKDHECVAVSFNPFYELLERVV 419

>emb|CBY95001.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Weltevreden str. 2007-60-3289-1]
Length = 162

Score = 122 bits (307), Expect = 8e-26, Method: Compositional matrix adjust.
Identities = 76/159 (47%), Positives = 99/159 (62%), Gaps = 5/159 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LPGSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESITLQPIARVDGAINLPKSGKSVSNRALLAALACGKTVLTNLLSDDDRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++ R + G GG A ++LFLGNAG AMR L AA+ G VL
Sbjct: 62 INYTLSADTRCDITGNGGALRAPGA---LELFLGNAGTAMRPLAALCL--GQNEIVLT 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG 163
G PRM+ERPIG L+ L+Q GA++D + PP+R+ G
Sbjct: 117 GEPRMKERPIGHLIDSLRQGGANIDYLEQENYPPLRLRG 155

>ref|YP_003354315.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. lactis KF147]
gb|ADA65490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactococcus lactis
subsp. lactis KF147]
Length = 430

Score = 122 bits (307), Expect = 8e-26, Method: Compositional matrix adjust.
Identities = 119/439 (27%), Positives = 208/439 (47%), Gaps = 27/439 (6%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+PG KS+S+R ++ ++++G TV+ ++L EDV + A R +G+ +E DK
Sbjct: 10 LKGRLLKVPKSGKSIHSRISIMFGSIAGKGTVIYDILRGEDVLSTIEAFRAMGVEIE-DKGE- 67

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ GK E E L +GN+G + R L+ + AG L G + +RP+
Sbjct: 68 ---VITVHGKGISELKAPEKALDMGNSGTSTRLLSGIL--AGLPFETTLFGDDSLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA++ P+ + G L L + S+Q SA++ AA A
Sbjct: 123 DRVATPLQLMGAETIGQTDKVKLPMTIKGSTHLKAIDYVLPVA-SAQVKS AVIFAALQAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPNAYVEGDA 254
G ++++K + + E ++ +FG + SD + GGQK K V GD
Sbjct: 182 GLT--KVVEKEKTRSHTE---EMLVQFGGELMVSDKI--ILVPGGQKLVGQK-VVPGDI 233

Query: 255 SSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA+++L A + + +E G + + EV++ MG ++ E V
Sbjct: 234 SSAAFWLVAALVENSELILENVGVNETRTGI--IEVIQAMGGQLEILEQD-NVAKAATL 290

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAIRTE 370
LK +++ + +P + L ++AL A G T IRD A +VKET+R+ +
Sbjct: 291 KVKASQLKGTESGDLIPRLIDELPIIALLATQAQGETIIRDAAELVKETDRIAVVANA 350

Query: 371 LTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPG 426
L +GA ++ D II KL+ +I+T DHR+ M ++AA + +
Sbjct: 351 LNSMGAKIQPTDDGMIIQGGTKLHAPENSINTLGDHRIGMMAAIALLVKNGEIELERA 410

Query: 427 CTRKTFPDYFDVLSTFVN 445
+ ++P +FD L +N
Sbjct: 411 AIQTSYPSFFDDLEQLSEN 429

>ref|ZP_07396389.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sp. oral
taxon 149 str. 67H29BP]
gb|EFM24228.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Selenomonas sp. oral
taxon 149 str. 67H29BP]

Length = 434

Score = 122 bits (307), Expect = 9e-26, Method: Compositional matrix adjust.
Identities = 123/442 (27%), Positives = 194/442 (43%), Gaps = 49/442 (11%)

Query: 16 SGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
G + +PG KS+S+R ++ A L + N L++ D +G +R LG++VE K
Sbjct: 15 QGIIDIPGDKSISHRVFMFAGLNTPVHIKNFLHAADCLSTVGVMRALGVNVEFLN-EKE 73

Query: 76 AVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G + + E + + GN+G +R + ++ V G + RP+
Sbjct: 74 LIVTGRG----LHGLSEPLTVLDAGNSGTTLRMMGLLSPQ--PFLSVFSGDASLTHRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-----SISSQYLSALLM 188
G + L +GA + + P+ + +P K +L G S+Q SA+L+
Sbjct: 128 GRIRRLPLSTMGIYGRNENNNLPLTI-----VPSEK-ELHGIHYDSPVASQVKSAILL 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A D ++ IS + E +++ FGV E S + + +P
Sbjct: 182 AGLYA--DAPTTVTPEYISRDHTE---QMLTGFVHLERSGTSVTIFPVEEDSFHAPGEI 236

Query: 249 YVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V GD SSA+YFL AG I G + + G + + +VL MGA ++
Sbjct: 237 TVPGDISSAAYFLVAGTIIAGSRLRLNNVGINPRTGTI--LDVLRDMGAHISVHNERESG 294

Query: 303 ----TSVTVTGPPREPFGGRKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVAS 355
+ V P L + MP D LAV ALFA+G T I
Sbjct: 295 GECVADLLVEAAP-----LHGVSFGEIIMPRLLIDEIPVLAVALFAEGDTIITGAGE 346

Query: 356 WRVKETERMVAIRTELTKLG-ASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAA 414
RVKET+R+ AI TEL KL S+EE D +I ++ + +YDDHRMAM+ ++
Sbjct: 347 LRVKETDRLHAIAATELQKLSPGSIEEREDGLVIHGKSEIRRAQVKSYDDHRMAMSLAVLG 406

Query: 415 CAEVPVTIRDGPCTRKTFPDYF 436
A I +P ++P +F
Sbjct: 407 AAGAGALIENPESVNISYPTFF 428

>ref|ZP_08020996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
australis ATCC 700641]
gb|EFV99069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
australis ATCC 700641]
Length = 427

Score = 122 bits (306), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 211/438 (48%), Gaps = 41/438 (9%)

Query: 13 KEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G +++PG KS+S+R ++ +L+ GTT V ++L EDV + R LG+S++ D
Sbjct: 8 KGLNGIIRVPGDKSISHRSIIFGSLAHGTTKVYDILRGEDVLSTIQVFRDLGVS IQDD-- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V+ GK + + L +GN+G + R L A V A G + G + +R
Sbjct: 66 ---GQVITIEGKGFEAFQQPKNDLDMGNSGTSTR-LIAGVLA-GSPFPVTMVGDSDL SKR 120

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + + L+++G V D P+ ++G L L + S+Q SALL AA
Sbjct: 121 PMDRVAIPLREMGVTVQGQTERDMLPLHLHGTKDLQPIHYSLPVA-SAQVKSALLFAAMQ 179

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G E I++K ++ + E ++++FG + D R ++G Q +++ + V G
Sbjct: 180 AEG--ESVILEKELTRNHT---DMIQQFGGRISVKDKAIR--LRGPQSFQACE-VTVPG 231

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L AG + + +E G + + EV+E MG K+ +
Sbjct: 232 DISSAAFVWLAVGLIVPNSQIRLENVGINETRTGI--LEVIEKMGKQLQILDL----- 281

Query: 312 REPFGR-----KHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
+P + L +++ + +P + L ++AL A G T I+D +VKE
Sbjct: 282 -DPLAKAATLVVETSDLHGTEISGDLIPRLIDELPIALLATQASGKTIKDAEELKVKE 340

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEV 418
T+R+ + L +GAS+ D II L+ ++ T+ DHR+ M ++AA ++
Sbjct: 341 TDIRQVVADSLNAMGASITPTEDGMIIEGKTPLHGASLQTFGDRIGMMGAIAALLVSDG 400

Query: 419 PVTIRDPGCTRKTFPDYF 436
V + ++P +F
Sbjct: 401 EVELARAEAINTSYPSFF 418

>ref|ZP_01103672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Congregibacter
litoralis KT71]
gb|EAQ96789.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Congregibacter
litoralis KT71]
Length = 420

Score = 122 bits (306), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 127/429 (29%), Positives = 205/429 (47%), Gaps = 32/429 (7%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAAKRAVVV 79
+PG KS+S+R ++L A++ G T V L ED + A R LG+ +E K A R V
Sbjct: 1 MPGDKSISHRSVMLGAMATGETSVKGFLQGEDALATVAAFRALGVEIEGPRKGAMRIRGV 60

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
G G + +L +GN+G +MR L + AG + L G + RP+ ++
Sbjct: 61 GLRGL-----REASTRLDMGNSGTSMRLLCGIL--AGQEFSELVGDASLMGRPMQRVIT 113

Query: 140 GLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L ++GA + G PP++++G L G L + S+Q S +L+A A G+ +
Sbjct: 114 PLTRMGATIVSGDGR-PPLKISGGSSLRGIHYDLPMA-SAQVKSCVLLAGLFAEGETSV 171

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASY 259
P + T R++ FG + + D ++GG + + + V D SSA++
Sbjct: 172 T-----EPAPTRDHTERMLRGFGYELQSRDGV--SLRGGGQLRGCE-IDVPSDISSAAF 223

Query: 260 FLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
+ A+I G+ +T G T +L++MGA +T + P + F
Sbjct: 224 LMVAASIAPGSELLLTHVGNPTR---TGVISILKLMGADITLSNEREVGGEPVADIFV 279

Query: 317 RK-HLKVIDNMMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
R L+ ID+ + +P D L + A A+G T +R RVKE++R+ ++ LT
Sbjct: 280 RSASLRGIDIPRDLVLAIDFFVFLFAAACAEGRTVLRGAEEELRVKESDRIASMAEGLT 339

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
LG S E D II ++ I T+ DHR+AM+F++AA AE + I D +
Sbjct: 340 TLGVS-NEVLDDGIIIDGGPISGGTIRTFHDHRIAMSFABAALRAENEIRILDCDHVATS 398

Query: 432 FPDYFDVLS 440
FPD FD L+
Sbjct: 399 FPD-FDALT 406

>ref|YP_001244172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga petrophila
RKU-1]
ref|YP_001738626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga sp. RQ2]
sp|A5IK73.1|AROA_THEP1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B1L9E5.1|AROA_THESQ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ46596.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga petrophila
RKU-1]
gb|ACB08943.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotoga sp. RQ2]
Length = 421

Score = 122 bits (306), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 123/450 (27%), Positives = 204/450 (45%), Gaps = 52/450 (11%)

Query: 11 PIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P K++ G + +P KS+++R L+L+AL+E + + NLL D L LG E D
Sbjct: 5 PAKKVEGVLSVPPDKSITHRALILSALAETESTLYNLLRCLDTERTHDILEKLGTRFEGD 64

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP A+ LF GN+G R ++ + A VL G +
Sbjct: 65 WEKMKV-----FPKPFAPIEPLFCGNSGTTTRLMSGVL--ASYEMFTVLYGDSLS 114

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ ++ L+ +GA P ++ N+ G+ K ++ S+Q SA+L+A
Sbjct: 115 RRPMMRVIEPLEMMGARFMRQNNYLPMIAIKGNHLSGI-SYKTPVA---SAQVKSALLA 170

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN-- 247
A G +I+ S + E R+++ GV E ++G + P
Sbjct: 171 GLRASG--RTIVIEPAKSRDHE---RMLKNLGVPE-----VEGTRVVLEPATFR 216

Query: 248 ---AYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V GD SSA++F+ GA +TV G + EV+++MGA + W T
Sbjct: 217 GFTMKVPGDISAFAFFVVLGAIHPNARITVTDVGLNPTN--TGLLEVMMKLMGANLEWEIT 274

Query: 304 SVTVTGPPREPFG-----RKHLKAIDVNMNKMMPDVAMTLAVVAL---FADGPTAIRDVA 354
+ EP G +LK + V + +P + L +VAL FA+G T +R+
Sbjct: 275 EENL-----EPIGTVRVETSPNLKGVVPEHLVPLMIDELPLVALLGVFAEGETTVVRNAE 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R KE++R+ + +LG +EE D I + + ++D DHRMAM FS+A
Sbjct: 330 ELRKESDRIRVLVENFKRLGVEIEEFKDGFKIVGKQSIKGSVDPEGDHRMAMLFISIAG 389

Query: 415 -CAEVPVTIRDPGCTRTFPDYFDVLSTFV 443
+E V ++D C +FP++++L V
Sbjct: 390 LVSEEGVDVKDHECVAVSFPPNFYELLERVV 419

>ref|YP_003703062.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophothermus
lipocalidus DSM 12680]
gb|ADI02497.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Syntrophothermus
lipocalidus DSM 12680]
Length = 430

Score = 122 bits (306), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 129/438 (29%), Positives = 208/438 (47%), Gaps = 28/438 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + GT+ LP KS+S+R ++LAAL++G + V N L + D + +R LG+++ +
Sbjct: 10 KGLRGTTITLPADKSISHSVMLAALAQGKSRVKNFLRARDTLATVRCVRLGVNIMDNGE 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
G GG ED L N+G MR ++ ++A + VL G +R R
Sbjct: 70 DLIEGRGLGGFLQPEDI-----LDCENSGTTMRLMSGTSLAC--SFFSVLTGDSSLSR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L+ +GA +D G P+ + G G L G L S+Q SA+L+A
Sbjct: 123 PMARVVEPLRLMGARIDGRDGGRLAPLAIRG-GNLKGIDYTLF-VPSAQVKSALLAG-- 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
LG VE E + + +P + T R++ G+ AE ++ G++ + P + V
Sbjct: 179 -LG-VEGETVVRE-KVPSRDHTERMAL--GMGAEIFAENGVIRLQPGRELE--PFDMSVPA 232

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++++ A + + V + G G + V VL MGA++ V V G P
Sbjct: 233 DISSAAFVIVAATLVPESEVLIPGVGNPTRSGV--LRVLASMGARIELQNQRV-VGGEP 289

Query: 312 REPF---GRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+L V +P D LAV A G + +RD + RVKET+R++
Sbjct: 290 VADIRVVSAGNLIGTTVAGEIVPSLIDEIPVLAVAMAMARGESVVRDASELRVKETDRIL 349

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRD 424
A+ T L +LG VEE D + +L +D+Y DHR+AMA +A AE ++
Sbjct: 350 AVCTCLRRLLGVEVEETEDGFYVRGQGRLTGAKVDSYGDHRIAMAMGIAGLVAEGETIVKG 409

Query: 425 PGCTRTKTFPDYFDVLSTF 442
++P ++ L+ F
Sbjct: 410 AEAVNISYPGFWAELARF 427

>ref|ZP_01080057.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Synechococcus sp. RS9917]
gb|EAQ69038.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Synechococcus sp. RS9917]
Length = 439

Score = 122 bits (306), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 125/448 (27%), Positives = 200/448 (44%), Gaps = 57/448 (12%)

Query: 14 EISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G V++PG KS+S+R LL A++EGTT ++ LL +ED LR +G + +A
Sbjct: 16 RLGGRVRVPGDKSISRALLFGAIAEGTTTIEGLLPAEDPISTAACLRAMGAVISPIEAG 75

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G G ++ +E ++ GN+G MR + + G +VL G +R R
Sbjct: 76 AVIEVQGVG----LDGLQEPSEVLDCGNSGTTMRLMLGLLAGREGR-HFVLSGDASLRRR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L +GA+V G + P+ V G Q L ++ P+
Sbjct: 131 PMQVRVQPLALMGAEVRGRNGNFAPLAVQG-----QPLHGAVVGTPV 173

Query: 193 ALGDVEIE-----IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKG 238
A V+ +I+ S + E R++ FG E R ++
Sbjct: 174 ASAQVKSALLLAALTAKGPSTVIEPAHSRDHSE---RMLRAFADLEVGGEMGRHITVRP 230

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
G + ++ V GD SSA+++L AGA + G +T+E G + V VLE M A+
Sbjct: 231 GANLRG-QHVVPVGDISSAFLVAGALVPGADLTENVLNPTRTGV--LAVLEQMQR 287

Query: 298 VTWTETSVTVTGPPREPF-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTA 349
+ V G EP G + L+ + MP D LAV A F DG +
Sbjct: 288 IEVLNRR-DVAG---EPVGDLRVRQGLQPFNFGEIEMPRLVDEVPIAFAACFCGVS 343

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMA 409
I + RVKET+R+ + +L +GAS++E D I L A+D+ DHR+AM+
Sbjct: 344 ISGASELRVKETDRLAVMARQLKAMGASIDEHDDGLTIHGGHPLRGAALDSETDHRVAMS 403

Query: 410 FSLAA-CAEVPVTIRDPGCTRTFPDYF 436
++AA AE T+ ++P ++
Sbjct: 404 LAVAAMLAEGDSTLARSEAAVSYPGFW 431

>ref|YP_397110.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Prochlorococcus marinus str. MIT 9312]
sp|Q31BS1.1|ARO9_PROM9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB49674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9312]
Length = 436

Score = 122 bits (305), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 115/448 (25%), Positives = 206/448 (45%), Gaps = 44/448 (9%)

Query: 14 EISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G +K+PG KS+S+R L++ ++++G T ++ L+SED LR LG+++ K
Sbjct: 12 NLKGKIKVPKDKSISRALIIGSIAQGETTIEGFLHSEDPLSTADCLRKLGVNIPDIKED 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + G G ++ KE ++ GN+G MR L + G ++L G + ER
Sbjct: 72 EPFTISGLG----LDGIKEPKEILNCGNSGTTMRLMLGLLAGQEGK-NFILTGDTSLNER 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSAL 186
P+G + L +G + + P+ + G KL G + S+Q SA+
Sbjct: 127 PMGRVNKPLSLMGIIISGREGNKAISIIYG-----NKLKGCVIGTPIASAQVKS 178

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L+A A G + I+ S + E R+++ FG R IK G
Sbjct: 179 LLAGLKASGTTTSV--IEPASSRDHTE---RMLKAFGANISIRGELGRNVVKS GGNLIGQ 233

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + GD SSAS+++ A+I V ++ G + + V++ MG + S
Sbjct: 234 R-ILIPGDISSASFWMIAASIVPNSEVLIKNVGLNPTRTGI--LNVMSMGCNYEILDKS 290

Query: 305 VTVTGPPEPFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVAS 355
T+ G EP G +L++ + + +P D L V A F +G + I+D
Sbjct: 291 -TIAG---EPIGSIKVKTANNLRSFTIEGDILPKLIDEIPILTVAACFCNGVSEIKDAQE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA- 414
R KET+R+ + +L+K GA + E D II K + +D+ DHR++M+ ++A+
Sbjct: 347 LRFKETDRCLKVMAQLSKFGAEITEKEDGLIINGQSKFHSAEVDSETDHRVMSLSLAIASL 406

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A+ I + ++P +++ L+
Sbjct: 407 VAKGTSKIMRADASYVSPSWEDLAKL 434

>ref|ZP_05746273.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus antri
DSM 16041]
gb|EEW53162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus antri
DSM 16041]
Length = 428

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 128/442 (28%), Positives = 210/442 (47%), Gaps = 36/442 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ LPG KS+S+R +++ +L+ G T +D ED + A R LG+ ++ +K
Sbjct: 11 LAGTISLPGDKSMHRAVMIGSLATGLTTIDQFAQGEDCQTTVNACRALGVQIDQEK-- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV G G + ++ A + +Q + N+G R L + AG N T L G + +RP+
Sbjct: 69 RLVVHGVGLRG-LKKAPDPLQ--MNNSGTTTLLMGIL--AGQNFTSCLLGDRSLSQRPM 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L G +V P V + G L G +L ++S L + L+ A L
Sbjct: 124 KRVSDPLTLFGGEVQLSAAAGTLPVAV-IRG-HFLHGANYQL--PVASAQLKSALLFA-ALL 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D II+KL + + E+ LR +FG A+ + DR I K + V GD
Sbjct: 179 ADRPSRIIEKLPTNRHTEIMLR---QFG--ADVKTNGDREIIVHPAKALVARTLRVPGDI 233

Query: 255 SSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS SVTVTGPPE 313
SSA+++L AG + + + G + + +VL MGA + T+ E
Sbjct: 234 SSAAFWLTAGTLVPHSQIRLSKVGLNPYRTGI--LKVLTRMGANLAIQRPAD-----GE 286

Query: 314 PFG-----RKHLKAIDVNMNKMMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMV 365
P G HL+ I + +P V L +VAL A G ++IR R KET+R+
Sbjct: 287 PIGDVVVRSGHLRPITLGPADIPAVIDELPLVALLAASVPGQSSIRGAGELRFKETDRIK 346

Query: 366 AIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTI 422
A L +LG +V E PD +IT P ++ D++ DHR+ M ++AA A+ P+ +
Sbjct: 347 ATIAILRQLGVTVTELPGDMVITGKPDWQVMDPVFDSFGDHLGMMVAVAALKAKQPLFL 406

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ ++P +F L+ ++
Sbjct: 407 ANSAAIDVSYPRFFADLRLMR 428

>ref|YP_003855771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parvularcula
bermudensis HTCC2503]
gb|ADM10629.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parvularcula
bermudensis HTCC2503]
Length = 441

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 136/442 (30%), Positives = 203/442 (45%), Gaps = 37/442 (8%)

Query: 12 IKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ ++G + PG KS+S+R L+L L+EGTT + LL ++DV +R G +VE +
Sbjct: 10 VGPLNGAISPPGDKSVSHRALILGGLAEGTTTITGLEADDVLRATSCVRGFGAAVE-RQ 68

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V G P + L+ GN+G R L A AAG + DG +R
Sbjct: 69 GEGSWVTGASWSSPAQ-----ALYCGNSGTGARLLMGA--AAGQGVSVTFDGDQSLRG 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++G + D G PVR+ +GG P G S+Q SA+L+A
Sbjct: 121 RPYMERILAPLREMGIESDAREGK--LPVRL--VGGPRGIEYRLPKPSAQIKSAVLLAGL 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
A G+ IE +P + T R++ +FG + R + G Q+ +
Sbjct: 177 GAEGETVIE-----EPVPCRDHTERMPLQFGGRLTIEPLGGGRRRLRPGAQRLTAGGIV 231

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVWTETSVTV 307
V GD SSA++ LA AAI G+ VT+ G T + F E L MGA + ++V V
Sbjct: 232 PVPGDPSAFLPLAAAAIVDGSVVTLRGVMTNPHR--TGFFEALSAMGADL----STVPV 285

Query: 308 TGPPREPFGRKHLK-----AIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G E L+ AI + +K P D L VVA FA G + + RVK
Sbjct: 286 GEEGEAIADLRLRYAPLTAIHITADKAPGLIDEYPLCVVAFAAGTSRFDGLGELRVK 345

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM-AFSLAACAEV 418
E++R+ A L G V G D+ I A+ T+ DHR+AM A +
Sbjct: 346 ESDRLAATAALLRANGVDVRTGEDWIEIDGGRPGGGGAVATHHHRIMASALVMGMATAA 405

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
PVTI D +FP + D+++
Sbjct: 406 PVTIDDADMIATSFPGFIDL MN 427

>ref|ZP_00239462.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
G9241]
gb|EAL12903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus
G9241]
Length = 399

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 119/427 (27%), Positives = 197/427 (46%), Gaps = 43/427 (10%)

Query: 33 LLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKE 92
+ A++EG T + L D + + +G+ + + VVG G +E +E
Sbjct: 1 MFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVDIVQN--GDEVTVVGKG----LEGLQE 54

Query: 93 -EVQLFLGNAGIAMRSLTAAVTAAGGNATYV--LDGVPRMRERPIGDLVVGLKQLGADV 149
+ L +GN+G +R ++ + N + + G + +RP+ + LKQ+GA++D
Sbjct: 55 PKAVLDVGNSTTIRLMSGIL----ANTPFFSCVQGDASIAKRPMKRVNTNPLKQMGANID 110

Query: 150 CFLGTDCPPVRVNGIGGLPGGKVK----LSGSISSQYLSALLMAAPLALGDVEIEIIDKL 205
P+ + G G +K S S+Q SA+L+A A G +
Sbjct: 111 GREEGTFTPLTIRG-----GDLKAIEYTPVASAQVKSAILLAGLRAEGVTAV----- 158

Query: 206 ISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL-A 262
+ P++ + T R++E FGK + + GGQK + + V GD SSA++FL A
Sbjct: 159 -TEPHISRDHTERMLEAFGVKVTREGKTVK--LAGGQKL-TATDVQVPGDVSSAAFFLVA 214

Query: 263 GAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE-PFGRKHLK 321
GA I + ++ G + + +VLE MGA T + + P LK
Sbjct: 215 GAIIPNSKLVQNVGMNPTRTGI--IDVLEKMGATFTVEPINEGASEPAANITITETSSLK 272

Query: 322 AIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
I++ + +P + + V+AL A +G T I+D +VKET R+ + ELTKLGA +
Sbjct: 273 GIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDAHELKVKETNRIDTVVAELTKLGARI 332

Query: 379 EEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFD 437
E D II L +++Y DHR+ M ++A C AE TI D ++P +F+
Sbjct: 333 EATDDGMIYIGKSALKGNTVNSYGDHRIGMMLAIAGCIAEGKTTIEDAEAVGVSYPTFFE 392

Query: 438 VLSTFVK 444
L K
Sbjct: 393 ELQKLAK 399

>ref|ZP_01167045.1| still frameshift 3-phosphoshikimate 1-pcarboxyvinyltransferase
prephenate dehydrogenase [Oceanospirillum sp. MED92]
gb|EAR60806.1| still frameshift 3-phosphoshikimate 1-pcarboxyvinyltransferase
prephenate dehydrogenase [Oceanospirillum sp. MED92]
Length = 738

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 124/440 (28%), Positives = 213/440 (48%), Gaps = 35/440 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP +SG +++PG KS+S+R ++L +L++G T V L ED L + R +G+ +E
Sbjct: 310 QPGGSVSGKIRVPGDKSISHRSIMLGLADGVTEVSGFLEGEDSLATLQSFDMGVVIEG 369

Query: 70 DKAACKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VG G + P L++GN+G +MR L+ + A + L G
Sbjct: 370 PVDGNVTIYGVGLNGLQAP-----PGPLYVGNSGTSMRLLSGLLAAQQFDTE--LTGDA 421

Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ +RP+G + L+ +GA+++ PP+++ G L G + + S+Q S LL
Sbjct: 422 SLTKRPMGRVADPLRLMGAEIET-AENGRPPLKIKGGQPLKGIHYDMPMA-SAQVKSCLL 479

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G+ + P + T R++ FG VK E + + GGQ + +
Sbjct: 480 LAGLYAEGETSV-----TEPAPTRDHTERMLTGFYGVKQEGAQAA--VSPGGQLHATK 531

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V D SSA++F+ AAI G+ +T+E G + + +L +MGA +
Sbjct: 532 ID--VPADISSATFFMVAAAIAPGSDLTLEHVGINPTR--IGIINILRLMGANLELLNER 587

Query: 305 VTVTGPMPREPFRGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V G P ++ LK I + +++P D L V A A+G T + RVK
Sbjct: 588 -EVGGEPPVADIRIQYAPLKGHIHPEDQVPLAIDEFPALFVAAACAEGTTIVSGAEELRVK 646

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEV 418
E++R+ ++ L LG +E PD II + ++++DDHR+AM+F +A+ A
Sbjct: 647 ESDRIQSMVDGLKTLGVDIEGTPDGAIIQ-GGTIGGGVVESHDDHRIAMSFVSLRATD 705

Query: 419 PVTIRDPGCTRKTFPDYFDV 438
+TI D +FP + ++
Sbjct: 706 TITINDCANVATSFPGFVEL 725

>ref|ZP_02354547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
oklahomensis E0147]
ref|ZP_02361741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
oklahomensis C6786]
Length = 451

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 120/435 (27%), Positives = 188/435 (43%), Gaps = 39/435 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ LP SKS S R LL AAL+ G + + N + + M LG S ++
Sbjct: 20 LSGTIDLPAKSSSTRALLTAALTPIGISTIRNAATGFNSNAMKHNCERLGASFSS--GD 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV--LDGVPRMRE- 131
VV G ++ GN+G+ +R L G A Y+ D V + R
Sbjct: 78 TVVVGKVDAMH----VDRKIVFDPGNSGVVLRLLM-----GVAGYLPETDFVTQYRYS 126

Query: 132 ---RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
R ++V L++L + + P+ + L G ++S SSQ+LS LL
Sbjct: 127 LGVRSQAEMVAALRLNVECEAVGPEARLPIGIRSTREL-GKHEVSCRKSSQFLSGLLY 185

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
+ D+EI+++D + + V T+ + GV E+ + F++ G ++K P
Sbjct: 186 LGAIGDRDLEIDVVDHITAPSMVHTTINNLAHAGVAIEYDARFRHFFVPGSDRFK-PSEF 244

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TETSVTV 307
V D +S + LA VT+ G F E GA + + T+T +
Sbjct: 245 TVGADPASTAAILALCGSLASDVTLNG-----FFEEELGNGAVIRYLTDGTGLI 293

Query: 308 TGPPREFP---GRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P G ++ D + + PD LA A FADG + ++ R KE++R+
Sbjct: 294 DELPGNRIRIRIKGGASIRPQDFDGLAPDAVPALAGRAAFADGTSTFYNIEHIRYKESDRI 353

Query: 365 VAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-SLAACAEVPT 421
R EL KLG EE D II P +D + DH + MA ++ E PV
Sbjct: 354 SDFRRELDKLGVRSEEKLDQLIIHGNGRGRGAVVDGHYDHGLIMALTTVGLHCEHPVL 413

Query: 422 IRDPGCTRKTFFDYF 436
I++P +T+PDYF
Sbjct: 414 IKEPFHVGTYPDYF 428

>ref|ZP_08129288.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp. D5]
gb|EGB93661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp. D5]
Length = 430

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 118/446 (26%), Positives = 202/446 (45%), Gaps = 29/446 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L I + G V +PG KS+S+R ++ +++G T + N L D + R +G+ ++
Sbjct: 3 LTNITGLKGEVNIPGDKSISHRCVMFGSIAGKITEIHNFLGADCLATIDCFRKMGIIDIQ 62

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+K + V G + KE L +GN+G R ++ + +G + L G
Sbjct: 63 Q---SKDTITVHGKGLRGLSAPKE--ILDVGNSGTTTRLISGIL--SGQSFDKSLSGDES 115

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ ++ L +GA++ L C P+ + G L G + S S+Q S +L+
Sbjct: 116 LNSRPMKRIIEPLTLMGANISSILRNGCAPLYITK-GDLHGIHYE-SPVASAQVKSCVLL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKSPKNA 248
A A D E + + ++S + E+ ++ FG A+ + + D K + +
Sbjct: 174 AGLYA--DSETAVTEPILSRNHTL---MLAEFG--ADIT'THDLDDSTKATASLRPCEEL 226

Query: 249 Y-----VEGDASSASYFLA-GAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
Y V GD SSA+YF+A G + + ++ G + + +V E MG +T
Sbjct: 227 YGRKITVPGDISAAYFIAAGLLVPDSEILIKNTGINPTRAGI--LKVCEDMGGDITLLN 284

Query: 303 TSVTVTGPPREFPGR-KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ R L V + +P D ++V+A A+G T IRD A +V
Sbjct: 285 ERTEGGEKIADILVRTSRLHGTTVEGDIPTLIDEIPVISVMAAMAEGTTVIRDAELKV 344

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
KET+R+ + L +G V D II +L+ I T DHR+AMAFS+AA A+
Sbjct: 345 KETDRIETVTDNLRAMGCEVTPTFDGMIIEGKPLHGATIHTLLDHRIAMAFSIAALVAD 404

Query: 418 VPVTIRDPGCTRKTFFDYFDVLSTFV 443
I D C ++P ++D +
Sbjct: 405 GNTNILDSCVDVSYPTFYDTFEQLL 430

>ref|YP_003181690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eggerthella lenta DSM
2243]
gb|ACV55301.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eggerthella lenta DSM
2243]
Length = 442

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 126/449 (28%), Positives = 204/449 (45%), Gaps = 35/449 (7%)

Query: 4 AEEIVLQPI-KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
A V+ P+ + G+ +PG KS+S+R +L AA++EGT+ + +L+SEDV + A+
Sbjct: 5 ANATVVNPLPAPLRGSASVPGDKSISHRAVLFAAMAEGTSRLSGVLDSEDVRSSIRAVGQ 64

Query: 63 LGLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
LG V +K ++ G G ++ E + GN+G +R L + A N
Sbjct: 65 LGAQVSLEKQPDGSLAGGVTGWGAAGPSQPEAPIDCGNSGTTVRLLMGVL--APWNVRVE 122

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G ++ RP+ + L ++GA + G + P+ V G GL + S+Q
Sbjct: 123 LTGDDSLQRRPMRRITAPLMKMGARFEFE-GRETLPPLTVCGSEGLRAITYD-APMASAQL 180

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+A+L+A A G + P T ++ FGV + + DR G
Sbjct: 181 KTAVLLAGVYARGTTTLNEPS-----PSRNHTELMLEPFGVT--TTAADRTASVTGPAA 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
V GD SSA++ + A + ++ VE + + + F LE MGA ++
Sbjct: 233 LRACEVQVPGDPSSAAFLVCAAVLKPDSIIQVENVSLNTAR--IGFTRTLERMGADISVR 290

Query: 302 ETSVTVTGPPREFFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
T +EP+G +L +V +K+ D LAVVA A G T R+
Sbjct: 291 HTGAA----GKEPYGIVSACYTPNLHGCEVPADKIATIVDEVVLAHVAAHARGVTVFRE 346

Query: 353 VASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLN---TAIDTYDDHRMAM 408
V+ RVKET+R+ AI L LG +G D + P L V A D+ +DHR+AM
Sbjct: 347 VSELRVKETDRLAAIVEGLETLGVDWIDGNDLFVEGQP-GLQVPVGAADFSDKNDHRLAM 405

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++LA C PV + + + ++P +
Sbjct: 406 TWALAGLCGNAPVEVENFDSVKISYPQFL 434

>ref|YP_003460455.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thioalkalivibrio sp.
K90mix]
gb|ADC71719.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thioalkalivibrio sp.
K90mix]
Length = 434

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 200/439 (45%), Gaps = 30/439 (6%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
+QP +SG ++PG KS+S+R ++L AL+EG T V L D L A R +G+ +E
Sbjct: 6 VQPGGTLSGVARVPGDKSISHSIMLGALAEGETRVTFLEGADCLATLEAFRAMGVPIE 65

Query: 69 ADKAAKRAVVVCGCGK-FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
K V+ G G + D L +GN+G AMR L + AG + L G
Sbjct: 66 -RKGPGEVVIQGRGLQGLQAPDRP----LDMGNSGTAMRLLCGVL--AGQSFDELIGDE 118

Query: 128 RMRERPIGDLVVLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + L +GA ++ GT PP+R+ G L G L S+Q SA+
Sbjct: 119 SLTRRPMRRVTEPLALMGAQIETSEAGT--PPLRIRGGAPLRGTDHVLQ-VASAQVKSAI 175

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A A G + P + T R++ FG + + + GG + ++
Sbjct: 176 LLAGLWADGKTCV-----TEPAPTRDHTERMLNGFGCVV--TRDGPACVTTGGGRLQA-S 227

Query: 247 NAYVEGDASSASYFLAGAAI-TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++FL GA+I TG + +E G + V ++L +MGA + E
Sbjct: 228 SVDVPADISSAAFFLVGASIAATGSQMRLEHVGINPRTGV--IDILRLMGADI-RVENER 284

Query: 306 TVTGPPREPF--GRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
G P LK I++ +P D + V A A+G T + RVKE
Sbjct: 285 EAGGEPVADIEVHATRLKGIEIPTTELPLAIDEFPAIFVAAACAEGEVTLTGAEELRVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVP 419
++R+ + L LG D I E ID++ DHR+AM+F++A A P
Sbjct: 345 SDRIQVMADGLQALGVQCSVQRDGIIRILGGEGFAGGEIDSHGDHRIAMSFAMAGLRASGP 404

Query: 420 VTIRDPGCTRKTFPDYFDV 438
+ IRD +FP + D+
Sbjct: 405 IRIRDCANVATSFPGFVDL 423

>ref|YP_002753305.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium
capsulatum ATCC 51196]
gb|AC033530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidobacterium
capsulatum ATCC 51196]

Length = 433

Score = 121 bits (304), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 133/446 (29%), Positives = 203/446 (45%), Gaps = 37/446 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E V+ P + I G+++LPG KS+S+R LL L+EGT+ N D L + LG
Sbjct: 7 ERVISPARNIDGSLRLPGDKSISHRYALLGGLAEGTSRFSNFSTGADPSSSLACVEALGA 66

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+V D V G GG F L GN+G MR L + A G + L G
Sbjct: 67 TVVNDGKGN-VEVTGVGGTFHAPAGA---LDCGNSGSTMRMLAGFLAAQSGE--FTLIG 119

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + L+Q+GA++D G +R + + S+Q SA
Sbjct: 120 DESLTRPRMERVRKPLQQMGAEIDLTDGHAPMTIRGRKLHAMD----YTTVPVSAQVKSA 175

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L A A G + + + + + E+ LR FG AE + + D I GGQK +
Sbjct: 176 VLFAGLQAEGVTTVR--EAVRTRDHSSELALRA---FG--AELTRTVDSVSITGGQKLTAI 228

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGA----- 296
+ A V GD SSA++FL AA+ G + + G + +VL +GA
Sbjct: 229 E-AKVPGDMSSAAFFLCAAALFPGSNLIFFDLGLNPTR--ASLLDVLTAALGAHIGVINLE 285

Query: 297 -KVTWTETSVTVTGPPREPFGRKHLKAIDVNM-NKMPDVAMTLAVVALFADGPTAIRDVA 354
K + +V + P G + + +P LA +A + IRD
Sbjct: 286 DKASELIGTVQINAPANGLTGTTVSGGLAAQLIDELP---VLAAIAPYTQNGIRIRDAR 341

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
RVKE++R+ + L +GA VEE D + ++L+ ID DHR+AMAFS+AA
Sbjct: 342 ELRVKESDRIALVAQNLRAMGAEEVEEFEDGLDVPGGQQLHGAEIDAGGDHRIAMAFSVAA 401

Query: 415 C-AEVPVTIRDPGCTRKTFFPDYFDVL 439
AE IR +FP++FD+L
Sbjct: 402 LRAEGETLIRGAESAASISFPEFFDLL 427

>ref|YP_002560520.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Macroccoccus
caseolyticus JCSC5402]
dbj|BAH17824.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Macroccoccus
caseolyticus JCSC5402]
Length = 433

Score = 121 bits (303), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 212/442 (47%), Gaps = 35/442 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V +PG KS+++R ++LA+LS+G TV+ L ED + R LG+ + + +
Sbjct: 9 LTGEVSVPGDKSITHRAIMLASLSKGTVISKPLLGEDCVSTINIFRKLGVQISTE---E 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+V G E +E + L+ GN+G R L + AG VLDG + +RP
Sbjct: 66 DNVIVDSPG---YEQFREPAEVLYTGNSGTTTLLCGLL--AGLPFKTVLDGDASIGQRP 120

Query: 134 IGDVLVGLKQLGADVDCFLGTDCP--PVRVN--GIGGLPGGKVKLSGSISSQYLSALLMA 189
+G ++ L+++G ++ G D P+ +N GI + G + S+Q SA+L+A
Sbjct: 121 MGRVIEPLREMGVNIK---GRDNQFTPIIINDGGISKVQGINYMPVK-SAQVKSAILLA 176

Query: 190 APLALGDVEIEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A + E+ I ++ IS + E+ + + + E +D G K K+
Sbjct: 177 GLYA--EDEVRITEQDISRNHTEL---MFKNSNIDIEVNDRTILLKNGIHAIKM-KDIE 230

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ GD SSA++F+ A I G +T++ GT + + EV++MMG + + V T
Sbjct: 231 IPGDISSAAFFIVAALIIPGSKITLQDVGTVNTRSGI--LEVVKMMGGNIQVID-KVQQT 287

Query: 309 GPPREPFGF--KHLKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETER 363
P + +L I + + +P + + V+AL A G + IRD +VKET R
Sbjct: 288 EPVSDIVVSYTHNLTGITIEGSLIPKLIDEIPVIALLLAHAQKGSEIRDAEELKVKETNR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAE-VPV 420
+ + +EL LG ++ D ++ K T D+Y DHR+ M ++AA E V +
Sbjct: 348 IDTVVSELNALGYKIQTDDGGVVYGVKVDERTDFTDSYGDHRIGMMLAVAALLETVEI 407

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I ++P + + ++
Sbjct: 408 EINQFEAVNISYPSFMEHINQL 429

>ref|ZP_08017442.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lautropia mirabilis
ATCC 51599]
gb|EFV96105.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lautropia mirabilis
ATCC 51599]
Length = 441

Score = 121 bits (303), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 127/441 (28%), Positives = 206/441 (46%), Gaps = 41/441 (9%)

Query: 11 PIKEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P ++ G +++PG KS+S+R ++L AL+EG T V L D R +G+ ++
Sbjct: 9 PGGQVRGDIRVPGDKSISHRAIMLGALAEGVTEVHGFLGADALATAQIFRAMGVRIDGP 68

Query: 71 KAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + V VG G + P D L GN+G +MR L + AG + G
Sbjct: 69 EQGQVKVHGVGLHGLQAPAGD-----LDCGNSGTSMLRLCGIL--AGQRFATRMVGDAS 120

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ ++ L ++GA +D G PP++V + GL +KL+ S+Q SALL+
Sbjct: 121 LSRRPMRRVIDPLSRMGARIDSQDGK--PPLQVQVPDGLTAVDLKLA-VASAQVKSALLL 177

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G+ + P + T R++ FGK + ++GGQ ++ +
Sbjct: 178 AGLYADGETRVT-----EPAPTRDHTERMLTAFGVKVGREGAT--ASVQGGQVLRAAR-V 229

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++FL AAI G+ + + G + V VL MGA + TE++ +
Sbjct: 230 DVPADISSAAFLVAAAICPGSDLVLRHVGMPNTRTGV--LHVLRAMGADI--TESNPQL 285

Query: 308 TGPPREPFGGRKH-----LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
G EP H LK I ++ +P D L + A A+G T +R RVK
Sbjct: 286 VGG--EPVADLHVRGGRKLGITIDPAWVPLAIDEFPALFIAAACAEGVTELRGAEEELRVK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIIT----PPEKLNVT AIDTYDDHRMAMAFSLAAC 415
E++R+ + L +G V PD I ++ + DHR+AM+F++AA
Sbjct: 344 ESDRIQVMADGLAAVGLPVTVLPDGMRIEGRGGEAHPFAGGTVEAHGDHRIAMSFTVAAL 403

Query: 416 -AEVPVTIRDPGCTRKTFPDY 435
+ P+ +RD +FP +
Sbjct: 404 RSRGPIHVRDTANVGTSFPGF 424

>ref|YP_864107.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Magnetococcus sp.
MC-1]
sp|A0L408.1|ARO_A_MAGSM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK42701.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Magnetococcus sp.
MC-1]
Length = 445

Score = 120 bits (302), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 122/442 (27%), Positives = 213/442 (48%), Gaps = 34/442 (7%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADK 71
+ +SGT++ KS+S+R ++ AL+EG T V +L EDV + A RT+G+S+E ++
Sbjct: 16 QNLSGTRPADAKSISHRSVIFGALAEGETHVKGMEGEDVLRITITAFRTMGISIERCNE 75

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R G G +D L +GN+G AMR L + + ++ +L G +R
Sbjct: 76 GEYRIQQGLDGLKEPDDV-----LDMGNSGTAMRLLCGLLASQPFHS--ILTGDHSLRS 128

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAA 190
 RP+G +V L ++GA + G P+ + G +P + + I S+Q SA+++A
 Sbjct: 129 RPMGRVVQPLTKMGARIRGRDGGRLAPLAIEGTELVP---ITYNSPIASAQVKSAILAG 185

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
 G E II+ +S + E R++ FG AE + ++ I+G + + V
 Sbjct: 186 LNTAG--ETIIIEPAVSRDHTe--RMLIAFG--AEVTRDGNQVTIEGWPNLQG-QEIEV 237

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
 D S+A++ + A IT G+ + +E G + ++L MG + V G
 Sbjct: 238 PADISAAAFPMVAALITPGSDIILENVGMNPTR--TGILDLLAMGGNIQRLNER-EVGG 294

Query: 310 PPREFPGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 P ++ L+ I+++ +P D V A A G T ++ RVKE++R+
 Sbjct: 295 EPVADLQVRSYQLQIEIDPTVVPRAIDFPPVFFVAAALAQQTTLVQGAELRVKESDRI 354

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAA--CAEVPV 420
 A+ L LGA +EE PD +IT P ++D++ DHR+AM+ +A C E V
 Sbjct: 355 TAMANGLKALGAIIEERPDGALITGNPDGLAGGASVDSFTDHRIAMSLLVAGLRCKE-SV 413

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
 ++ +FP + +++
 Sbjct: 414 LVQRCDNINTSFPSFSQLMNSL 435

>ref|ZP_07655500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacter
 tundripaludum SV96]
 gb|EFO04593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacter
 tundripaludum SV96]
 Length = 453

Score = 120 bits (302), Expect = 3e-25, Method: Compositional matrix adjust.
 Identities = 125/442 (28%), Positives = 199/442 (45%), Gaps = 36/442 (8%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
 +QP ++ G ++PG KS+S+R ++L +L+EG T V L +ED L A R +G+ +E
 Sbjct: 23 VQPGGKLQGEARVPKDKSMHSRIMLSLAEGVTHVKGFLAEDALATLQAFRDMGVEIE 82

Query: 69 ADKAAKRAV--VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
 + + V G K P D L+LGN+G +MR L+ + N+ VL G
 Sbjct: 83 GPVNGELTIHGVGKHLKAPTND-----LYLGNSGTSMRLLSGLLAGQAFNS--VLTGD 134

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
 + RP+ + L +GAD+ P+ + G G G S+Q S L
 Sbjct: 135 KSLSGRPMKRVTEPLAAMGADIKT-TEKGTAPLHITGRAGQLTGIDYAMPIASAQVKSL 193

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
 L+A A G + P + T R++ F + + +G +
 Sbjct: 194 LLAGMYAQG-----VTSVTEPAPTRDHTERMLSGFNYPVKQEGNKVSITAEGSL---TAT 245

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
 + V D SSA++FL GA+I G+ + ++ G + + ++L +MGA +
 Sbjct: 246 DIDVPSDISSAAFFLVGASIAPGSDLLKHHVGNPTR--IGVIDILRLMGANIEVLNER- 302

Query: 306 TVTGPPREFPGRKH-----LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
 TV G EP H LK ID+ + +P D L V A A+G T + R
 Sbjct: 303 TVGG---EPVADLHVVSALKGIDIPEHLVPLAIDFPPVLFVAAACAEGQTRLTGAEELR 359

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-A 416
 VKE++R+ + L LG + D II I ++ DHR+AM+FS+A A
 Sbjct: 360 VKESDRIQVMADGLQILGVDAQSTEDGMIIQGGSIGGGEVI-SHGDHRIAMSFISIAGLRA 418

Query: 417 EVPVTIRDPGCTRKTFPDYFDV 438
 P+TI D +FP++ D+
 Sbjct: 419 NAPITTYDCENVNTSFPEFRDL 440

>ref|YP_004167349.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitratifactor
 salsuginis DSM 16511]
 gb|ADV45600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitratifactor
 salsuginis DSM 16511]

Length = 430

Score = 120 bits (302), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 136/451 (30%), Positives = 210/451 (46%), Gaps = 50/451 (11%)

```
Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
          QP + T+ KS+S+R + + S+ + V N L ED L R LG VE
Sbjct: 11 QPFDTVLDTIA--PDKSISHRCAMFSLFSDRPSTVRNFKGEDTLASLSIARQLGAEEVEE 68

Query: 70 DKAACKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
          D+A + PVE + + L GNAG MR + AG ++VL G +
Sbjct: 69 DEAGTLRITP-----PVELREPDDILDGCGNAGTGMRLYCGLL--AGVEGSFVLTGDRYL 120

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL----SGSISSQYLSA 185
          R RP+ + L+ +GA +D + P+ + G GK+K S S+Q SA
Sbjct: 121 RSRPMPKRVTPQLQSIGAKIDGREEGNLAFLHIRG-----GKLKAFRYESPIDSAQVKSA 174

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
          +++AA GD + +S + E LR M G E +D+ +K K +P
Sbjct: 175 MILAA--LRGDAPSYRENFLSRDHTERMLRGM---GASIE-TDAEGWIVVKPLTKPLNP 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLMMGAKVTWT--ET 303
          + V D SSA +F AAI G V G T ++ +VLE MGA V + E
Sbjct: 229 LDITVPADPSSAFFFAVAAAIVPGA-KVRIPGVTLNPTRIEAYKVLEAMGAAYEYALRED 287

Query: 304 SVTVTGPPREPFG-GRKHLKAIDVN-----MNKMPDVAMTAVLAVFADGPTAIRDVASW 356
          G R + GR L A++V+ ++++P +A+ +A A+G + +R+ A
Sbjct: 288 RYEPIGEIRVAYDGR--LSAVEVSHRIAWLIDELPALAVAMAT----AEGVSRVRNAAEL 341

Query: 357 RVKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLAA- 414
          RVKE++R+ + T L G EE PD Y I L ID++ DHR+AM+F++A
Sbjct: 342 RVKESDRIATVVTALKACGIEAEYPDGYAIRG--GTLRRAVIDSHGDHRIAMSFAIAGL 399

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
          C + I D C +FP++F++LS +
Sbjct: 400 LCG---MEIEDIDCVATSFPPNFFEILSNLTE 427
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>ref|ZP_07415893.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu001]
ref|ZP_07420614.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu002]
ref|ZP_07424422.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu003]
ref|ZP_07428789.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu004]
ref|ZP_07441702.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu008]
ref|ZP_07486336.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu010]
ref|ZP_07490554.2| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu011]
gb|EFO73499.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu001]
gb|EFP13881.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu002]
gb|EFP18101.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu003]
gb|EFP21933.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu004]
gb|EFP37189.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu008]
gb|EFP45768.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu010]
gb|EFP49767.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis SUMu011]
Length = 352
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Score = 120 bits (302), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 101/333 (30%), Positives = 163/333 (48%), Gaps = 18/333 (5%)

Query: 114 AAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK 173
AA G+ DG + R RPI L+ L++LG VD GT P RV G G L GG V
Sbjct: 8 AALGSVPVTFDGDQQARGRPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVA 63

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSD 232
+ S SSQ++S LL++A + ++ L S P++ MT ++ + GV + S +
Sbjct: 64 IDASASSQFVSGLLLSAASFDTGLTVQHTGSSSLPSAPHIAMTAAMLRQAGVDIDDSTP-N 122

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 292
R+ ++ G + + +E D ++A FL+ A ++GGTV + G S+Q +L
Sbjct: 123 RWQVRPGFV--AARRWDIEPDLTNAVAFLSAAVVSOGTVRITGWPRVSVQPADHILAILR 180

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR- 351
+ A V ++S+ V GP DV++ + ++ ++A +A A + R
Sbjct: 181 QLNAVVIHADSSLEVRGP-----TGVDGFDVLDRAVAGELTPSVAALAALASPGSVSRL 233

Query: 352 -DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
+A R ET+R+ A+ TE+ +LG + E PD +IT L Y DHRMAMA
Sbjct: 234 SGIAHLRGHETDRLAALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAG 292

Query: 411 SLAACAEPVPTIRDPGCTRKTFFDYFDVLSTFV 443
++ V + D T KT P++ + + V
Sbjct: 293 AIIGLRVAGVEVDDIAATTKTLPEFPRLWAEMV 325

>ref|ZP_07577691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotogales
bacterium mesG1.Ag.4.2]
gb|EFN46356.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermotogales
bacterium mesG1.Ag.4.2]
Length = 419

Score = 120 bits (302), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 130/457 (28%), Positives = 208/457 (45%), Gaps = 71/457 (15%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
L P K++ G + +P KS+S+R L++ ++S G +VV NLL SED LRT
Sbjct: 3 LLPSKKVVGEIAVPPDKSISRHALMCMSSSGVSVVHNLESED-----TLRTF----- 51

Query: 69 ADKAAKRAVVVGCGGKF-----PVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGN 118
++ GG F + KE ++ L GN+G R + ++ G
Sbjct: 52 -----RIIGELGGNFRGGFDRMEISLASWKESLRPLDCGNSGTTARLMAGVLS--GKE 102

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADV----DCFLGTDCPPVRVNGIGGLPGGKVKL 174
+VL G + RP+ +V LK++GA + D L P+ + G G L G + L
Sbjct: 103 GFHVLFGDDSLSGRPMERVVRPLKEMGASISARQDSSL-----PMCITG-GKLSGSEHSL 156

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSD 232
S + S+Q SA+L+A A G + + P+ + T RL+ G K S S
Sbjct: 157 SVA-SAQVKSAILLAGIQAEGTTAV-----TEPHCSRDRHTERLLRSMGAKI--SVSNK 206

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAI-TGGTVTVEGCGTTSLQGDVKFAEVL 291
R ++ + P + GD SSA++ +A A + G VT+ G QG F +L
Sbjct: 207 RVEVEKSELL--PIRFSIPGDVSSAAPPALAVLHENGKVTIREVGLN--QGRGTGLRLLL 262

Query: 292 EMMGAKVTWTETSVTVTGPPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVAL---F 343
MGA + E V + P EP G L ++V + +P + L ++AL F
Sbjct: 263 IKMGADI---EMEVEESLP--EPVGTIVARSSRLIGVEVGSIDLIPSMIDELPLIALAGVF 317

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDD 403
A+G T +R R KE++R+ ++G + E D + P+++ +D+Y D
Sbjct: 318 AEGTTTVRGAGELRKESDRISVTVQNFRRIGVEILEHEDGFSVEGPGQRTGGKVDYSYGD 377

Query: 404 HRMAMAFSLAA-CAEVPVTIRDPGCTRKTFFDYFDVL 439
HR+AM FSLA + V + + +FP +F L
Sbjct: 378 HRIAMLFSLAGPLSREGVEVTNSNAVNVSPFGFFKTL 414

>gb|EDZ39285.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospirillum sp.
Group II '5-way CG']
Length = 454

Score = 120 bits (301), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 131/454 (28%), Positives = 210/454 (46%), Gaps = 48/454 (10%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+SGTV++PG KS+S+R L+L ++ G TVV L S+D L A LG+ + + D
Sbjct: 26 HRVSGTVRVPGDKSISHRSLILGGMASGKTVVTGFLPDDCLRTLSTAFSRLGVQIRQQQD 85

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ G G + + L GN+G A R + + AG + V+ G +R
Sbjct: 86 ETVLELESPGLSGL-----QEPDSILDFGNSGTASRLMCGVL--AGTSFFTVMTGDDSLR 138

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ +V L +GA +D P+ + G G + S+Q S++L+A
Sbjct: 139 KRPMKRVVDPLGMMGAKIDGPGSGSRLPLAIRGTA--LKGISFFNAHKSAQVKSSVLLAG 196

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +E + L + + E RL+ FG K Y + +V
Sbjct: 197 LNASGSTTVE--EPLQTRDHTE---RLLPLFGGKVLREGLRTTVY----PSRLTGTAHV 247

Query: 251 EGDASSASYFLAGAAIT-GGTVTEGCGTTSLQGDVKFAEVLEMMGAK----VTWTETSV 305
GD SSA++FLA +T G ++T+EG G + +VLE M A+ + T+ S+
Sbjct: 248 PGDFSSAAFFLALGGLTPGSSLTLEGVGLNPSR--TGLLQVLEAMKARSLRILPSTDPSL 305

Query: 306 TVTGPPREPFGFR-----KHLKAIDVNMNMKMPDV---AMTLAVVALFADGPTAIRDVASWR 357
EP+G L+ IDV +P++ LA A A G T IR A R
Sbjct: 306 Q-----SEPYGNIQVGFSELEGIDVPEWIPNIIDEIPILAACAACARGTTTIRGAELR 360

Query: 358 VKETERMVAIRTELTKLGASVEEGPD-YCI--ITPPEKLNVTADITYDDHRMAMAFSLAA 414
VKE++R+ I + L LG +E PD + I + P +L ID+ +DHR+AM+ ++
Sbjct: 361 VKESDRIRGIVSALQVLGVPCKEFPDGFADGLGPDRLTGTTIDSLNDHRIAMSMVAVLG 420

Query: 415 CAEVP----VTIRDPGCTRKTFPDYFDVLSTFVK 444
+ +P +TIR +FP + + + V+
Sbjct: 421 -SRLPESEILTIRGTDVFSTSFPGFSKLFNQVVE 453

>ref|ZP_04157452.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock3-17]
ref|ZP_04163100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock1-4]
gb|EEM05081.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock1-4]
gb|EEM10790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus mycoides
Rock3-17]
Length = 434

Score = 120 bits (301), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 117/441 (26%), Positives = 202/441 (45%), Gaps = 39/441 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ A+++G T + L D + R +G VE +
Sbjct: 13 LRGTIRIPGDKSISHRAVMFGAIAQGGKTTIKGFLPGADCLSTISCFREMG--VEISQNGD 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+V+G G +E +E + +GN+G +R ++ + A + G + +RP
Sbjct: 71 EVIVMGKG---LEGLQEPKNVLDVGNSTTIRLMSGIL--ANTPFHSCIQGDSSIGKRP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALLMA 189
+ + L + A +D P+ + G G +K S S+Q SA+L+A
Sbjct: 125 MKRVTNPLGLMRAKIDGREEGTFTPLTIRG-----GSLKAIDYTSPPVASAQVKSAILLA 178

Query: 190 APLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
A G + + P++ + T R++E FGV D I GGQK +
Sbjct: 179 GLTAKGVTTV-----TEPHISRHDHTERMLEAFGVTVTREDKT--VKIAGGQKLIG-TD 228

Query: 248 AYVEGDASSASYFL-AGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++FL AGA + + ++ G + + +VL MGAK+ +
Sbjct: 229 IQVPGDVSSAAFFLVAGAVVPNSKLVLQNVGMNPTRTGI--IDVLTKMGAKLEIQPINKD 286

Query: 307 VTGPPRE-PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETE 362
+ P L+ I++ + +P + + ++AL A +G T I+D +VKET

Sbjct: 287 ASEPAANITETSSSLQIEIGDIIIPRLIDEIPIIALAATQAEGITVIKDAHELKVKETN 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA-ACAEVPVT 421
R+ + ELTKLGA +E D II L +++++ DHR+ M +A + AE

Sbjct: 347 RIDTVVAELTKLGARIEATDDGMIIYGKSSSLKGNKVNSHGDHRIGMMLGIAGSIAEGKTV 406

Query: 422 IRDPGCTRKTFFDYFDVLSTF 442
+ D ++P +F LS

Sbjct: 407 LGDAEAVGVSYPTFFKELSKL 427

>ref|YP_003640350.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermincola sp. JR]
gb|ADG82449.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermincola potens
JR]
Length = 428

Score = 120 bits (301), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 124/441 (28%), Positives = 206/441 (46%), Gaps = 32/441 (7%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ GT+ +PG KS+S+R +++ +L+EG T ++N L D + R +G+ + +K
Sbjct: 10 KLRGTIAVPGDKSISHRAVMIGSLAEGPTRIENFLMGADCLSTIRCFRANGIEISIEKD- 68

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+VG G + E L +GN+G +R +T ++ G + G +R+RP
Sbjct: 69 NIVTLVKGKGLRGLQEPGD---ILDVGNSGTTIRLMTGILS--GQPFSSVTGDESIRKRP 123

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + + L ++GA + P+ + G P V S S+Q SA+L+A A
Sbjct: 124 MDRVTTIPLTRMGAGHIWGRENGRLAPLAIKGGELYPIDFV--SPVASAQVKSAVLLAGLFA 181

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G +E + + T R++ FG E +R + G + + + V GD
Sbjct: 182 SQQTRVEE-----PVKSRDHTERMLRYFGADIEVE--GNRTTVTGFPPEL-TGREVRVPGD 233

Query: 254 ASSASYFL-AGAAITGGTGTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ AG G + + G + + +VL MG ++ V+G
Sbjct: 234 ISSAAFFIVAGLTTPGSELMLREVGLNPTRDGI--IDVLRQMGGRIEILNER-EVSG--- 287

Query: 313 EPFG-----RKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP G L+ +++++ +P D LAV A ADG T IRD A +VKET R+
Sbjct: 288 EPVGDILVKSSLLRGVEIDGAIIPRLIDEIPVLAVAAVADGETVIRDAELKVKETNRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
+ EL K G V+E PD I KL D++ DHR+AMA ++A AE TI
Sbjct: 348 ATVTMELAKFGVEVDELDPGLRIKGRKLQAAFCDSHGDHRIAMAMAVAGLVAEGETTID 407

Query: 424 DPGCTRKTFFDYFDVLSTFVK 444
T +FP++ ++L +
Sbjct: 408 GWEATDVSFPNFGELLEKIAR 428

>ref|YP_001839953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira biflexa
serovar Patoc strain 'Patoc 1 (Paris)']
ref|YP_001963580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira biflexa
serovar Patoc strain 'Patoc 1 (Ames)']
sp|B0SM47.1|AROA_LEPBP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B0SDL8.1|AROA_LEPBA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABZ95002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira biflexa
serovar Patoc strain 'Patoc 1 (Ames)']
gb|ABZ98677.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira biflexa
serovar Patoc strain 'Patoc 1 (Paris)']
Length = 428

Score = 120 bits (301), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 127/453 (28%), Positives = 214/453 (47%), Gaps = 45/453 (9%)

Query: 8 VLQPIKEISGT--VKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+LQP +++ + +PG KS+S+R +L ALS+G + + L ED + L ++GL
Sbjct: 1 MLQPQIKLNKNEIYVPGDKSISHRVTLFCALSQKGSEIHGFLEGEDPLHTLRFCFESMGL 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVL 123
SV + +VV GK + K L GNAG +R L+A + A G NAT L
Sbjct: 61 SVSSLGKGSYSVV--SPGKQNLNSPKG--VLDFGNAGTGIR-LSAGLLAGLPGMNAT--L 113

Query: 124 DGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LSGSIS 179
G + +RP+ ++ L+++GA V G D P+R+ G ++K +S S
Sbjct: 114 TGDASLCKRPMARIMNPLQEMGASVISVEGNDRAPLRIE-----GKQLKDYSYVSPIAS 167

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+Q SAL++AA LA D+ IE + +S + E +R + G HS F +K
Sbjct: 168 AQIKSALVLAA-LA-SDISIEYKESEVSRDHTENMIRFLG--GTITHHSSV--HFTVKPP 221

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAK 297
++ K + GD SSA++F+ GG+ + ++ G + + VL+ MG K
Sbjct: 222 YHFEGTKYV-IPGDISAAFFIVFGLCVGSGEPLLIKNIPLNPSR--IGILTVLQNMGGK 278

Query: 298 VTWTETSVTVTGPPREPFGFGR----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTA 349
+ V E G LK + + +P D L + LF++G
Sbjct: 279 IEIIAKRVECG---EEIGDLLVYPSKLKRTVITEDLIPSIIDEIPILTIAGLGFSEGGFQ 334

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMA 409
I R KE++R+ ++ + L +LG V+E D + I+T+ DHR+AM+
Sbjct: 335 ISHAHEELRAKESDRIRSMVSNLERLGVKVKVENDGYEFDEVGTIQNAKIETFMDHRIAMS 394

Query: 410 FS-LAACAEVPVTIRDPGCTRKTFPDYFDVLST 441
F+ L+ + V ++ D +FP +F++L +
Sbjct: 395 FAILSKLSGVSLSFDDTSWVDTSFPGFFFEILKS 427

>ref|YP_003809163.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfarculus baarsii
DSM 2075]
gb|ADK86569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Desulfarculus baarsii
DSM 2075]
Length = 421

Score = 120 bits (301), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 136/441 (30%), Positives = 205/441 (46%), Gaps = 38/441 (8%)

Query: 14 EISGTVKLPGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G + PG KS+S+R+ LL+ L++G V S D L A+ LG VE +
Sbjct: 2 KLVGQLTPPGDKSISHRGLLSLLAQGRCEVGGFSPSADCASTLA AVALGGGVE--RVG 59

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+R ++ G G+ + + GN+G MR L + AGG +VLDG +R RP
Sbjct: 60 ERVILSGAAGRL----RPGQTIDCGNSGTTMRFLMGLLAGAGGR--FVLDGDESLRGRP 112

Query: 134 IGDVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L+++GA V+C G PPV + G GGL GG+ L S+Q SALL+A A
Sbjct: 113 MERVAEPLRRMGARVECAAGGR-PPVIIQG-GGLRGQFDLP-VASAQLKSALLLAGLQA 169

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + + S + E RL+ ++G + D G + P + D
Sbjct: 170 DGPTTVN--EPAASRDHTE---RLLAQWGAQIRR-DGLSCTVWPG--LLRLPAQIWPAD 221

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE 313
AS+A++F GAAI G+ V G + + + VLE MG V V G E
Sbjct: 222 ASAAAFCCGAAILPGSRLVAQ-GVLLNENRLGWLRVLERMGGCV----DVRREQDDPE 275

Query: 314 PFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P+G L+A++V ++ D A LA+ A G + R V RVKE++R+
Sbjct: 276 PWGDIGVEFSPELRAVEVGAAEIAAIDEAPILALTASQCHGVSVFRQVQVGLRVKESDRL 335

Query: 365 VAIRTELTKLGASVE-EGPDYCIITP-PEKLNVTATIDYDDHRMAMAFSLAA-CAEVPVT 421
AI +L LGA + EG D + P P +L + ++ DHR+AM +A A
Sbjct: 336 AAIIGQLGALGADLRAEGDDLIVRGPTPLRLPDAPLKSFGDHRIAMVLRVAGLLAGGWPR 395

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442

I D C + P + D L
Sbjct: 396 IDDEACMAISHPAFNDDLRL 416

>ref|ZP_01156384.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanicola granulosus
HTCC2516]
gb|EAR51437.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanicola granulosus
HTCC2516]
Length = 451

Score = 120 bits (301), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 133/441 (30%), Positives = 203/441 (46%), Gaps = 34/441 (7%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G ++PG KS+S+R L+L AL+ G T + LL+ EDV A+R G +
Sbjct: 18 LTGEAQVPGDKSISHRSLILGALAVGETTITGLLDGEDVLDTAAAMRAFGAEITEAGGVW 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG D + GN+G +R + ++ AT+ D +R RP+
Sbjct: 78 TVHGVGTGGFAEPADVID-----CGNSGTGVRLLIMGSMATTPITATFTGDA--SLRSRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLA 193
G + L GA G P V +P V+ + + S+Q SA+L+A A
Sbjct: 131 GRVTDPLAAGFARAHGRQGGRRLPLTLVGAADPVP---VRYAVPVPSAQVKSALLLAGLNA 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G E +I++ + + E R++ FG + + + R GQ SP+ V
Sbjct: 188 PG--ETVVIEREATRDHTE---RMLAGFGARITTETTNEGRVITLTGQPELSPQTITVPR 242

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTWETS SVTVTGPP 311
D SSA++ + A +T G+ V V G + E L MGA +T+ E G P
Sbjct: 243 DPSSAAFPVCAALVTEGSDLVVPNIGLNPTR--AGLFETLRDMGADLTY-ENLREEGGEP 299

Query: 312 ----REFPGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
R F L+ I+V + M D L+VVA FA+G T +R V RVKE++R+
Sbjct: 300 VADLRARFS-PDLRGIEVPPERAASMIDEYPVLSVVAFAEGRTVMRGVKELRVKESDRI 358

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN---TAIDTYDHRMAMAF-SLAACAEVPV 420
A+ L G VEEG D+ I+T +V +++ DHR+AM+F L + PV
Sbjct: 359 DAMAQLRAAGVEVEEGEDWWIVTGRGFGDVPGGVTVESRLDHRIAMSFLILGLASNRPV 418

Query: 421 TIRDPGCTRKTFPDYFDVLST 441
T+ D +FP F+ L T
Sbjct: 419 TVDDAAPATSFPP-VFEPLMT 438

>ref|ZP_07836976.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermaerobacter
subterraneus DSM 13965]
gb|EFR61663.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermaerobacter
subterraneus DSM 13965]
Length = 560

Score = 120 bits (301), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 134/426 (31%), Positives = 201/426 (47%), Gaps = 45/426 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+ ++P +++ GT+ +PG KS+++R LLAA + G V+D D L L LG++
Sbjct: 66 VRVRPARDLRGTLVPVPGDKSIAHRAALLAAAAGGRVVLDRYAPGRDAASTLACLAALGVT 125

Query: 67 VEADKAAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V A + V+ G G + P L GN+G MR L + + AT
Sbjct: 126 VR-RPAPHQVVLEGGPIAGWQAPA-----APLDAGNSGTTMRLLLGLLASRPFTATLTG 178

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QY 182
D + RP+ +V L+++GA + G P+ + G GGL + ++S Q
Sbjct: 179 DAS--LCRRPMDRVVEPLRRMGARISGREGRRAPLTIRG-GGL--RAIHHDSPVASAQV 233

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
SA+L+A A G + + +S + E RL+ FGV E + GGQ
Sbjct: 234 KSAILLAGLFAAGRTSVR--EPALSRDHTE---RLLPLFGVAVERDGPM--VAVDGGQVL 286

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVT-- 299
+P+ + GD S+A+++LA A + G+ +T++G G + F EVL+ MGA+V
Sbjct: 287 AAPERLAIPGDPSSAAAFYLAALLCPGSRITLQGVGVNPNTR--TGFLEVLQAMGARVRVE 344

Query: 300 -----WTETSVTVTGPPREPFG-----RKHLKAIDVNMNKMPP--DVAMTLAVVAL 342
S G P EP L+A+DV + +P D LAV+A
Sbjct: 345 AVRELQPGGGPAGSSATAGGPGEVADLTAETSELRAVDVGGDLIPRLIDEIPILAVLAT 404

Query: 343 FADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
A G T IRD A RVKET+R+ AI EL +LGA V+E P I P L + +
Sbjct: 405 QARGTTRIRDAAELRVKETDRLTAIAEELRRLGARVDEHPGGLDIHGPTPLRGAVVSSRG 464

Query: 403 DHRMAM 408
DHRMAM
Sbjct: 465 DHRMAM 470

>ref|YP_004011289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodomicrobium
vannielii ATCC 17100]
gb|ADP70190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodomicrobium
vannielii ATCC 17100]
Length = 459

Score = 120 bits (300), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 132/436 (30%), Positives = 203/436 (46%), Gaps = 37/436 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V +PG KS+S+R L+L AL+EG T + LL +ED+ AL LG VE D
Sbjct: 19 LQGAUVVPGDKSISHRALILGALAEGRTRITGLLEADILCTARALEALGAGVERDADGA 78

Query: 75 RAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V G GG P D L GN+G R + V AG G +++R
Sbjct: 79 WTVTGRGLGGLAAPAGD-----LDFGNSGTGARLMMGVV--AGHPLAARFTGDASLQKR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMA 189
P+G ++ L+ +G ++ G + P+ + G G L V +S + S+Q SA+L+A
Sbjct: 131 PMGRVLAPLQSMGLAIEEE-GRNTLPLTLVGTGDL---VPISYRLPVPSAQVKSAVLLA 185

Query: 190 APLALGDVEIEIIDLKISIPYEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247
A G E +I+ S + E LR FG + E + R ++G + +
Sbjct: 186 GLFASG--ETSVIESEKSRDHTEKMLRY---FGAEISVEPFEGGLRIALEGRRTLQGGPV 240

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
A V GD SSA++ +A A IT + + V+ + F E L MGA +++ E
Sbjct: 241 A-VPGDPSAAFLVAAALITPASDILVKNVLNPNTR--TGFYETLAEMGADISF-ENERE 296

Query: 307 VTGPPREPFGGRK--HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V+G P + L+ + V + P D LA +A A+G T + +A RVKE+
Sbjct: 297 VSGEVADIRARTSELRGVTVPAARAPSMIDEYPMLAALATLAEGETLMEGLAELRVKES 356

Query: 362 ERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAF-SLAACAEVP 419
+R+ A+ L GA G ++ P+ I T+ DHR+AM+F L E P
Sbjct: 357 DRLAAMVDGLVACGAIAHARGDTLTVLGLPKVRGGATIKTHMDHRIAMSFLVLGLATEEP 416

Query: 420 VTIRDPGCTRKTFFPDY 435
VT+ D +FP++
Sbjct: 417 VTVDDASMIATSFPEF 432

>ref|YP_003151076.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cryptobacterium
curtum DSM 15641]
gb|ACU94394.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cryptobacterium
curtum DSM 15641]
Length = 443

Score = 120 bits (300), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 125/458 (27%), Positives = 214/458 (46%), Gaps = 39/458 (8%)

Query: 5 EEIVLQPIK-EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E+V++P+ + GT +PG KS+S+R +L +A++EGT+ V +L+S DV + A++ L
Sbjct: 7 DELVIEPLAGPLLGTTSVPGDKSISHRSVLFSAEAGTSQVSGVLDSDGVRSSIAAVQQL 66

Query: 64 GLSVEADKAAKRAV---VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
G V +K ++ + G G P + + L GN+G R L + A +
Sbjct: 67 GAQVALEKQVDGSLAGGITGWSAGPTQPTR---ALDCGNSGTTARLLMGVL--APWDIA 121

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
LDG +R RP+ + L ++G G++ PV G L S S+
Sbjct: 122 VTLDGDDSLRRRPMRRIYAPLMKMGVTF-TPAGSEGLPVTEKGSRLKALSVD-SPMASA 179

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
Q +ALL+A A G E + + S + E+ ++ +FGV+ + + +R G
Sbjct: 180 QLKTALLLAGLGAEG--ETRVCEPAASRNHTEL---MLPQFGVQ---TTAGERTASVIGP 231

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ +V GD SSA++ + A + V +EG + + F LE MGA V+
Sbjct: 232 CQLTASEVHVPDGPSSAAFIVCAAVLARDSAVQIEGVSLNPAR--IGFTRTLERMGADV 289

Query: 300 WTETSVTVTGPPREPFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
T T ++ +EP+G + L+ ++ +K+ D LA+VA A G T
Sbjct: 290 ITRTGMS----GKEPYGIIERWTEDLRGCEIPADKIASLVDEIPVLALVAHAHAGITVF 345

Query: 351 RDVASWRVKETERMVAIRTELTKLGASV-EEGPDYCIITPP--EKLNVTAIDTYDDHRMA 407
R V+ +VKE+ R+ A+ L +LG EG D I P + D++ DHR+A
Sbjct: 346 RQVSELKVKESNRLAAVIEGLRGLGVDANNEGDDLYIEGQPSLQYPCDLVFDSSHDRHLA 405

Query: 408 MAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLFSTFK 444
M ++L PVT+ + ++P + + V+
Sbjct: 406 MTWALVGLTGPNPVTVTGFDSVKISYPGLASMEGLVR 443

>gb|EGC89612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eggerthella sp. HGA1]
Length = 442

Score = 120 bits (300), Expect = 5e-25, Method: Compositional matrix adjust.
Identities = 125/449 (27%), Positives = 204/449 (45%), Gaps = 35/449 (7%)

Query: 4 AEEIVLQPI-KEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
A V+ P+ + G+ +PG KS+S+R +L AA++EGT+ + +L+SEDV + A+
Sbjct: 5 ANATVVNPLPAPLRGSASVPGDKSISHRAVLFAAMAEGTSRLSGVLDSEDRSSIRAVGQ 64

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
L G V +K ++ G G ++ E + GN+G +R L + A N
Sbjct: 65 LGAQVSLEKQPDGSLAGGVTGWGAAGPSQPEAPIDCGNSGTTVRLLMGVL--APWNVRVE 122

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G ++ RP+ + L ++GA + G + P+ V G GL + S+Q
Sbjct: 123 LTGDDSLQRRPMRRIYAPLMKMGARFEPE-GRETLPITVCGSEGLRAITYD-APMASAQL 180

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+A+L+A A G + P T ++ FGV + + DR G
Sbjct: 181 KTAVLLAGVYARGTTTLNEPS-----PSRNHTEMLMPEFGVT---TTAADRTASVTGPAA 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
V GD SSA++ + A + ++ VE + + + F LE MGA ++
Sbjct: 233 LRACEVQVPGDPSSAAFIVCAAVLKPDSIIQVENVSLNTAR--IGFTRTLERMGADISVR 290

Query: 302 ETSVTVTGPPREPFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
T +EP+G +L +V +K+ D LA+VA A G T R+
Sbjct: 291 HTGAA----GKEPYGIVSACYTPNLHGCEVPADKIATIVDEVPVLALVAHAHARGVTVFRE 346

Query: 353 VASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLN---TAIDTYDDHRMAM 408
V+ RVKET+R+ AI L LG +G D + P L V A D+ +DHR+AM
Sbjct: 347 VSELRVKETDRLAAIVEGLETLGVDWIDGNLDFVEGQP-GLQVPVGAAFDKNDHRLAM 405

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++LA C PV + + + ++P +
Sbjct: 406 TWALAGLCGNAPVEVENFDSVKISYPQFL 434

>ref|ZP_01622155.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lyngbya sp. PCC 8106]
gb|EAW35794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lyngbya sp. PCC 8106]

Length = 448

Score = 120 bits (300), Expect = 6e-25, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 200/437 (45%), Gaps = 27/437 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+++PG KS+S+R L+L AL+ GTT+++ LL D +G + ++ K
Sbjct: 28 LHGSIEIPGDKSISHRALMLGALATGTIIIEGLLLGADPRSTASCFSQMGAQI-SELNEK 86

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R V G G G+ A L GN+G +R L + A+ + + + G + RP
Sbjct: 87 RVEVRGIGLQGLHEPTAV---LDAGNSGTTLR-LMLGILASHPDRFFTTVTDHSLVRRP 141

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPL 192
+ +V L+++GA + G P+ + G P + I+S Q S +L+A +
Sbjct: 142 MDRVVKPLQEMGIWREGGSFAPLAIQGGRLNP---IHYKSPIASAQVKSCVLLAGLM 198

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G E + + +S + E R++ FG + G + + V G
Sbjct: 199 AEG--ETTVTEPLSRDHSE---RMLRAFGATVTVDPETHSATVIGPATLQG-QPVVVP 252

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA+++L AGA I G + ++ G + + + LEMM A + E V G P
Sbjct: 253 DISSAAFWLVAGAIIPGSELLIQNVGNPRTGTI--LDALEMMEADIQL-ENQREVAGEP 309

Query: 312 REPFGRKH--LKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
K+ LKA + +P D LAV A A G T IRD RVKE++R+
Sbjct: 310 VADLRVKYSQKACTLEGALIPRLIDEIPILAVAATSAQGTIIIRDAEELRVKESDRITV 369

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDP 425
+ EL ++GA + E PD I L +D+Y DHR+AM+ ++AA A TI
Sbjct: 370 MAAELNRMGAKISELPDGMIEVGGTALTGAEVDSYTDHRIAMSLAIAALKASGKTTIGRA 429

Query: 426 GCTRKTFPDYFDVLSTF 442
++P + L
Sbjct: 430 EAASISYPQFTTTLQOI 446

>ref|YP_001233179.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidiphilium cryptum
JF-5]
sp|A5FUH8.1|AROACICJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ29260.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidiphilium cryptum
JF-5]
Length = 445

Score = 119 bits (299), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 133/442 (30%), Positives = 196/442 (44%), Gaps = 32/442 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE- 68
+P ++GT+ +PG KS+S+R L+ A L+ G T + LL EDV A+R LG +VE
Sbjct: 13 RPATPLTGTITVPGDKSISHRALMFAGLAVGETRISGLLEGEDVLRATAAMRALGATVER 72

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A RA G GG +D L +GN+G A R L + A + V+ G
Sbjct: 73 TGPGAWRASGP GIGGLQSPDDV-----LDMGNSGTARLLCGIL--ASHDIFAVMTGDAS 125

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+ ++ L GA G P+ V G +L + S+Q SALL+
Sbjct: 126 LRRPMPRRVIDPLGATGAVFAAREGGRL-PLSVRGAAEAMPLSYRLPVA-SAQVKSALLL 183

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPKN 247
A A G EIE + P + + ++ FG + E + I+ GQ +
Sbjct: 184 AGLNARGITEIEEPE-----PTRDHSENMLRHFGEVEVAAHGTGKLIRLRGQPELRGAD 238

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++ + A I G+ VT+ G G L+ + L MGA + V
Sbjct: 239 VVVPGDPSAAFPIVAALIVPGSRVTIGGVGLNPLRTGLFL--TLREMGAIEI----VN 292

Query: 307 VTGPPREPFG-----RKHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRV 358

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          EP G          L+A+DV  + P  D    LAV    A G + +R +A  RV
Sbjct: 293 AREAGGEPVGDILIVTASDLRAVDVPAERAPSMIDEYPILAVACAMARGSSRLRGLAELRV 352

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM-AFSLAACAE 417
          KE++R+ A    +T G  +   D II          + T+ DHR+AM A  +   E
Sbjct: 353 KESDRLAATLAMITANGVKAQVDGDDLIIEGGGARGGATVATHMDHRLAMSALVMGLATE 412

Query: 418 VPVTIRDPGCTRKTFFPDYFDVL 439
          PVTI D      +FP +  ++
Sbjct: 413 TPVTIDDARFIDTSFPGFLPLM 434

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>ref|ZP_03718009.1| hypothetical protein EUBHAL_03103 [Eubacterium hallii DSM 3353]
gb|EEG35068.1| hypothetical protein EUBHAL_03103 [Eubacterium hallii DSM 3353]
Length = 431

Score = 119 bits (299), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 117/444 (26%), Positives = 198/444 (44%), Gaps = 52/444 (11%)

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Query: 15  ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
          + GT+ +PG KS+S+R ++ +LSEGT +   L  D    +   R +G+S+E    +
Sbjct: 10  LKGTLTVPGDKSISHRAIMFGSLSEGTTTIHGFLLKGADCLSTIDCFRKMGISIE-----E 64

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
          +   +   GK    +K E L +GN+G  R ++ +   AG +   VL G  +   RP+
Sbjct: 65  KDETIYVHGKGLHGLSKPEETLDVGNSGTTTTLISGIL--AGQDFDTVLSGDASLNSRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
          G ++  L  +GADV          C P+ + G          L+A+  +P+A
Sbjct: 123 GRIMKPLSMMGADVTSINNNGCAPLSIKG-----HTLNAIHYDSPVAS 165

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-----IKGGQKYKSP---- 245
          V+  +   L++  Y E T  + E  +   +H++  R +          G    +P
Sbjct: 166 AQVKSCV---LLAGLYAEGTTSVTEP-ALSRDHTERMLRSFGADIVSDGNTCTITPPETL 221

Query: 246 --KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
          ++  V GD SSA++F+   IT    +T++  G    +   +V + MGA +T
Sbjct: 222 HQQHIEVPGDISAFAFFIVAGLITPDSEITIKNVGINDTRAGI--LKVCQDMGADITLLN 279

Query: 303 TSVTVTGPPREPFGFGR-KHLKAIDVNMNKMMPDVAMTLAVVAL---FADGPTAIRDVASWRV 358
          T    P  +   +   L    V  + +P +   L V+AL  FA G T I+D  RV
Sbjct: 280 TREEGGEFVADLLVKTSLKHGTVEGSIPTLIDELPVIALMACFAKGKTIKDAHELRLV 339

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEK-----LNVTAIDITYDDHRMAMAFSLA 413
          KE++R+  +   LT + A V + D II    +   L+  I+  DHR+AM F++A
Sbjct: 340 KESDRIAIMTENLTAMDADVIDTDDGFIINSRSEESIPVLHGAEINCSMDHRIAMTFAIA 399

Query: 414 AC-AEVPVTIRDPGCTRKTFFPDYF 436
          A+    I D C  ++P +F
Sbjct: 400 GLNADGETMITDSDCDVSYPGFF 423

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>ref|ZP_02073823.1| hypothetical protein CLOL250_00573 [Clostridium sp. L2-50]
gb|EDO58549.1| hypothetical protein CLOL250_00573 [Clostridium sp. L2-50]
Length = 397

Score = 119 bits (299), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 113/425 (26%), Positives = 199/425 (46%), Gaps = 48/425 (11%)

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Query: 33  LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE 92
          +L +L++G T V  LN D    +   R +G++++ +   V++  G  ++ KE
Sbjct: 1   MLGSLADGITEVHGFLNGADCISSMNCFREMGVTIDHNG---DTVIIHGKGLHGLQAPKE 57

Query: 93  EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFL 152
          L +GN+G  R L + + AA    + V+ G  +   RP+  ++  L  +GAD+
Sbjct: 58  --TLDVGNSTGTTTR-LMSGILAAQNFKSRVI-GDASICRRPMKRIMTPLSLMGADIVSEN 113

Query: 153 GTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEIIDKLISIPYV 211
          G DC P+ + G    P  +   ++S Q  S +L+A  A D E  + +  +S  +
Sbjct: 114 GNDCAPLLITG---KPLHGIHYDSPVASAQVKSCILLAGLYA--DGETSVTEPYVSRNHT 168

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Query: 212 EMTLRLMERFGVKAHSDSW-----DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAA 265
E+ + + FGV + S + D+ Y GQK P GD SSA+YF+A
Sbjct: 169 EL---MFDAGVDIKTSGTTAIVKPADKLY---GQKIMIP-----GDISSAAYFIAAGL 216

Query: 266 IT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAID 324
IT +T++ G + + + EV++MMG +T+ P EP ++ D
Sbjct: 217 ITPDSCITIKNVGINNTRDGI--LEVVKMMGGTITYDRLD-----QPGEPSADITVQTSD 269

Query: 325 VN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
+ + K+ D +A++A FA G T I+D +VKE+ R+ + L+ +GA
Sbjct: 270 LKGCVIQGSLLIPKLIDEIPIIAIMACFAKGQTVIKDAQELVKESNRIDVMVRNLSAMGA 329

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFFPDY 435
+ D II + L+ ID++ DHR+AM+F++A A+ I C ++P +
Sbjct: 330 DITATDDGMIHGGKPLHGAVIDSHLDHRIAMSFAIAGLNADGDTEILGSDCVNISYPTF 389

Query: 436 FDVLS 440
+ L+
Sbjct: 390 YQDLA 394

>ref|ZP_04433066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus coagulans
36D1]
gb|EEN90822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus coagulans
36D1]
Length = 427

Score = 119 bits (299), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 214/439 (48%), Gaps = 32/439 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+PG KS+S+R ++ AA++ G T+V+N L D + + + +E D
Sbjct: 11 LKGTIKVPGDKSISHRSVMFAAVARGKTMVENFLPGADCLSTIHCQMQMSVPIERD--GT 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V+ G G A+ E L GN+G R + + AG V+ G + +RP+
Sbjct: 69 RVVIAGKGWDGL--AEPETVLDGTGNSGTTTTLMLGLL--AGRPFHSVIAGDESIKRP 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L ++GA +D +G + P+ + G G L G + +L + S+Q SALL+A A
Sbjct: 124 QRVTKPLCEMGAHIDGRMGNGFTPLSIRG-GALQGIEYRLPVA-SAQVKSALLLAGLQAD 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + P + T R++ FG E ++GG + V GD
Sbjct: 182 GTTIVHEPQ-----PTRDHTERMIRAFG--GEVRTEGRTISVRGGTVFHG-TEIVVPGDI 233

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SSA++F+A A++ G+ + + G + + +VL+ MGA + ET G E
Sbjct: 234 SSAAFFMAAASLVPGSEIVLPDVG LNPTRAGI--IDVLKQMGADMEVIETHAPSDG---E 288

Query: 314 PFGR-----KHLKAIDVNMNMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMV 365
G L+ +++ +P + + ++AL A +G T I+D A +VKET R+
Sbjct: 289 QTGTLVIRPAALQGVEIGGGLIPRLIDEIPIIALLATQAEGRTVIKDAAEKVKETNRID 348

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRD 424
+ EL KLGA +E D II P +L+ ++++ DHR+ M ++A+ A+ V ++
Sbjct: 349 TVVRELKKGALHIEATADGMIIEGPCRLSGGTVESHGDRIGMMLAVASLVAKDAVCLKG 408

Query: 425 PGCTRKTFFPDYFDVLSFV 443
++P +FD L + +
Sbjct: 409 AEAIASYPQFFDDLKSVL 427

>ref|ZP_06514727.1| LOW QUALITY PROTEIN: 5-enolpyruvylshikimate-3-phosphate synthase
[Mycobacterium tuberculosis EAS054]
gb|EFD63365.1| LOW QUALITY PROTEIN: 5-enolpyruvylshikimate-3-phosphate synthase
[Mycobacterium tuberculosis EAS054]
Length = 374

Score = 119 bits (298), Expect = 8e-25, Method: Compositional matrix adjust.
Identities = 99/330 (30%), Positives = 161/330 (48%), Gaps = 18/330 (5%)

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G+ DG + R RPI L+ L++LG VD GT P RV G G L GG V +
Sbjct: 33 GSVPTVTFDGDQQARGPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDA 88

Query: 177 SISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S SSQ++S LL++A + ++ L S P++ MT ++ + GV + S +R+
Sbjct: 89 SASSQFVSGLLLSAASFDTGLTVQHTGSSSLPSAPHIAMTAAMLRQAGVDIDDSTP-NRWQ 147

Query: 236 IKGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
++ G + + +E D ++A FL+ A ++GGTV + G S+Q +L +
Sbjct: 148 VRPGPV--AARRWDIEPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLN 205

Query: 296 AKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR--DV 353
A V ++S+ V GP DV++ + ++ ++A +A A + R +
Sbjct: 206 AVVIHADSSLEVRGP-----TGyDGFVDLRAVGEITPSVAALAALASPGSVSRLSGI 258

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLA 413
A R ET+R+ A+ TE+ +LG + E PD +IT L Y DHRMAMA ++
Sbjct: 259 AHLRGHETDRLAALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAI 317

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVLSFV 443
V + D T KT P++ + + V
Sbjct: 318 GLRVAGVEVDDIAATKTLPEFPRLWAEMV 347

>ref|ZP_07774219.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas fluorescens WH6]
gb|EFQ64983.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas fluorescens WH6]
Length = 748

Score = 119 bits (298), Expect = 9e-25, Method: Compositional matrix adjust.
Identities = 124/441 (28%), Positives = 208/441 (47%), Gaps = 35/441 (7%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
V P +SG +++PG KS+S+R ++L +L+EG T V+ L ED L A R +G+
Sbjct: 316 FVANPGGVLSGRIRVPGDKSISHRSIMLGSLAEGVTEVEGFLEGEDALATLQAFRDMGVV 375

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E + V + G ++ A + +LGN+G +MR L+ + A N VL G
Sbjct: 376 IEGPHHGR--VTIHGVLHGLKAAPGPI--YLGNSGTSMRLLSGLLAAQ--NFDSVLTGD 429

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+ + L+++GA ++ G + PP+ + G L G L + S+Q S
Sbjct: 430 ASLSKRPMNRVAKPLREMGAVIET--GPEGRPPLTIRGGQSLTGMTYALPMA-SAQVKSC 486

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+A A G + P + T R++ FG + + ++ G +
Sbjct: 487 LLLAGLYAKGTTAVT-----EPAPTRDHTERMLRGFCPVAINGATA--SVESGHVLT- 538

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SS+++FL A+I G+ + +E G + V ++L +MGA +T E
Sbjct: 539 THIEVPGDISSAFFLVAASIAEGSELLEHVGINPRTGV--IDILRLMGADITL-ENQ 595

Query: 305 VTVTGPPEPFGKRHLKAIDVNMNKMPPDVAMTLA-----VVALFADGPTAIRDVASW 356
V G EP ++A + ++P+ + LA V A A+G T +R
Sbjct: 596 REVGG---EPVADLRVRAAGLKGIEIPEALVPLAIDEFPVLFVAAACAEGRTVLRGAEEL 652

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC- 415
RVKE++R+ + L LG E II + + + DHR+AMAFS+A+
Sbjct: 653 RVKESDRIQVMADGLLALGVKCEP-TPDGIIDGGPIGGGDVHAHGDHRIAMAFSVASLR 711

Query: 416 AEVPVTIRDPGCTRKTFPDYF 436
A P+ I D +FP++
Sbjct: 712 ATAPIRIHDCANVATSFNPNFL 732

>ref|ZP_03430112.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mycobacterium tuberculosis EAS054]
Length = 350

Score = 119 bits (298), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 99/330 (30%), Positives = 161/330 (48%), Gaps = 18/330 (5%)

Query: 117 GNATYVLGDGVP RMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
G+ DG + R RPI L+ L++LG VD GT P RV G G L GG V +
Sbjct: 9 GSVPVTFDGDQQARGRPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDA 64

Query: 177 SISSQYLSALLMAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S SSQ++S LL++A + ++ L S P++ MT ++ + GV + S +R+
Sbjct: 65 SASSQFVSGLLLSAASFTDGLTVQHTGSSSLPSAPHIAMTAAML RQAGVDIDDSTP-NRWQ 123

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
++ G + + +E D ++A FL+ A ++GGTV + G S+Q +L +
Sbjct: 124 VRPGPV--AARRWDIEPDLTNAVAFLSAAVVSGGTVRITGWPRVSVQPADHILAILRQLN 181

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIR--DV 353
A V ++S+ V GP DV++ + ++ ++A +A A + R +
Sbjct: 182 AVVIHADSSLEVRGP-----TG YDGFVDVLRVAGELTPSVAALALASPGSVSRLSGI 234

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLA 413
A R ET+R+ A+ TE+ +LG + E PD +IT L Y DHRMAMA ++
Sbjct: 235 AHLRGHETDRLAALSTEINRLGGTCRETPDGLVIT-ATPLRPGIWRAYADHRMAMAGAI I 293

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
V + D T KT P++ + + V
Sbjct: 294 GLRVAGVEVDDIAATTKTLPEFPRLWAEMV 323

>ref|YP_393384.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurimonas
denitrificans DSM 1251]
sp|Q30S82.1|AROASULDN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB44149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurimonas
denitrificans DSM 1251]
Length = 428

Score = 119 bits (297), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 205/437 (46%), Gaps = 40/437 (9%)

Query: 18 TVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T ++ KS+S+R + A L++GT+ + N L +ED L ++ LG +++ D
Sbjct: 16 TSEIASDKSISHRCAMFAMLADGTSQITNFLRAEDTMNSLKIVKNLGATIDDD----- 68

Query: 78 VVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLGDGVP RMRERPIG 136
G K + KE ++ GN+G MR +++A G+ +VL G +R RP+
Sbjct: 69 --GETIKISSDGIKESSEVLDCGNSGTGMRLFCGLLSADGH--FVLSGDEYLRRRPMKR 124

Query: 137 LVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
+ L+ +GA +D D P+ + G L + S S+Q SA+++AA A D
Sbjct: 125 ITAPLRDIGAKLDGRENDLAPLSIRG-ASLKAFNYE-SKIASAQVKSAMILAALRA--D 180

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
E + +S + E R+++ G + E + IK +K SP V D SS
Sbjct: 181 GECSFSEPELSRDHTE---RMLKGMGAIEVEGLITK--IKPMKKLSPLKIRVPADPSS 235

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
A +F AAIT V +EG + ++ + LE MGA + + T EP
Sbjct: 236 AFFFAVAAAAITPNSNVVLEGVTLNPNTR--IEAFKALERMGADIRYEATENIY-----EPI 288

Query: 316 GRKH-----LKAIDV--NMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G H LKAI V N++ + D L++ ADG + +++ RVKE++R+ +
Sbjct: 289 GNIHVKYAPLKAITVEDNISWLIDELPALSIAFACADGVSIVKNAQELRVKESDRISTVV 348

Query: 369 TELTKLGASVEEGPD-YCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPG 427
L G V+E D Y + L ID++ DHR+AM+F +A + + D C
Sbjct: 349 NGLKACGIEVDEVDHGYSV--KGGVLKEAKIDSHGDHRIAMSFIIAGVT-CGMRVDDIAC 405

Query: 428 TRKTFPDYFDVLSTFVK 444
+FP++F++L K

Sbjct: 406 INTSFPNFFELLKKITK 422

>ref|ZP_00055501.2| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase
[Magnetospirillum magnetotacticum MS-1]
Length = 445

Score = 119 bits (297), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 126/439 (28%), Positives = 205/439 (46%), Gaps = 31/439 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEAD-KAA 73
++G+ ++PG KS+S+R L+L AL+ G +VV LL +DV +R LG VE +
Sbjct: 15 LAGSARVPGDKSISHRALMLGALAVGESVVTGLLEGDDVLRTAACMRALGAEVERQADGS 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R G GG D L +GN+G R L V + DG +R RP
Sbjct: 75 WRLFGRGVGGLMEPADI-----LDMGNSGTGARLLMGLVATHPFTCFFTGDG--SLRSRP 127

Query: 134 IGDVLVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ ++ L ++GA F+ D P+ V G +L + S+Q SA+++A
Sbjct: 128 MRRVIEPLSRMGAR---FVSRDGGRLPLAVTGTSTQPTPITYELPVA-SAQVKSAILLAGL 183

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G E +I++ + + E+ LR FG V+ E ++ R G + +
Sbjct: 184 NTAG--ETTIVIEREATRDHTEMLR--NFGATVRVEDAEGGGRAVTVVGFELTGRPVV 238

Query: 250 VEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D SSA++ +A + G + + G GT L+ + + +LE MGA + +
Sbjct: 239 VPADPSSAAFPVVAALLVEGSEIRLPGVGTNPLRTGL-YQTLLE-MGADIRFDNPRDQAG 296

Query: 309 GPPREPFGFR-KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + R LK +DV + P D LAV A FA+G T +R +A RVKE++R+
Sbjct: 297 EPVADLVVRASRLKGVDPVPAERAPSMIDEYPILAVAAFAEGTTRMRGLAELRVKESDRL 356

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEV-PVT 421
A+ L G +VEE D I+ ++ + T+ DHR+AM+F + A PV
Sbjct: 357 AAMARGLAACGVAVEEEKDSLIVHGTGRIPDGDATVTTHFDHRIAMSFLVMGMASARPVA 416

Query: 422 IRDPGCTRKTFFDYFDVLS 440
+ D +FP + ++++
Sbjct: 417 VDDAEAIETSFPIFVELMN 435

>dbj|BAJ79378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidiphilium
multivorum AIU301]
Length = 445

Score = 119 bits (297), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 133/442 (30%), Positives = 196/442 (44%), Gaps = 32/442 (7%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE- 68
+P ++GT+ +PG KS+S+R L+ A L+ G T + LL EDV A+R LG +VE
Sbjct: 13 RPATPLTGTITVPGDKSISHRALMFAGLAVGETRISGLLEGDDVLRTAAMRALGATVER 72

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A RA G GG +D L +GN+G A R L + A + V+ G
Sbjct: 73 TGPGAWRASGPGIGGLQSPDDV-----LDMGNSGTAAARLLCGIL--ASHDIFAVMTGDAS 125

Query: 129 MRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+ ++ L GA G P+ V G +L + S+Q SALL+
Sbjct: 126 LRRRPMMRVIDPLGATGAVFAAREGGRL-PLSVRGAAEAMPLSYRLPVA-SAQVKSALLL 183

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPKN 247
A A G EIE + P + + ++ FG + E + I+ GQ +
Sbjct: 184 AGLNARGITEIEEPE-----PTRDHSNMLRYFGAEVEVATHGTGKLIIRLRGQPELRGAD 238

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA++ + A I G+ VT+ G G L+ + L MGA + V
Sbjct: 239 VVVPGDPSAAFPIVAALIVPGSRVTIGGVGLNPLRTGLFL--TLREMGAAIEI----VN 292

Query: 307 VTGPPREPFG-----RKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358

EP G L+A+DV + P D LAV A G + +R +A RV
Sbjct: 293 AREAGGEPVGDILVTASDLRAVDVPAERAPSMIDEYPILAVACAMARGSSRLRGLAELRV 352
Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM-AFSLAACAE 417
KE++R+ A +T G + D II + T+ DHR+AM A + E
Sbjct: 353 KESDRLAATLAMITANGVKAQVDGDDLLIEGGGARGGATVATHMDHRLAMSALVMGLATE 412
Query: 418 VPVTIRDPGCTRKTFPDYFDVL 439
PVTI D +FP + ++
Sbjct: 413 TPVTIDDARFIDTSFPGFLPLM 434

>ref|XP_001619008.1| hypothetical protein NEMVEDRAFT_vlg75553 [Nematostella vectensis]
gb|EDO26908.1| predicted protein [Nematostella vectensis]
Length = 215

Score = 118 bits (296), Expect = 1e-24, Method: Compositional matrix adjust.
Identities = 74/212 (34%), Positives = 120/212 (56%), Gaps = 7/212 (3%)

Query: 98 LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP 157
+G+AG AMR LTA + G +L G RM+ RPI LV LK LGA++ P
Sbjct: 9 IGHAGTAMRFLTAYFSVKEGREV-ILTGSERMQNRPIEILVDALKSLGAIEHYKEKIGYP 67
Query: 158 PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRL 217
P+++ G L V+++G++SSQY+SAL++ A +++E+ K+ S+PY+ MTL+L
Sbjct: 68 PIKIKG-KQLLKDSVQINGNVSSQYISALMLIAASLPNGLQLELQGKITSVPYINMTLKL 126
Query: 218 MERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT--GGTVTVEG 275
++ G++A +S + I+ K + K VE D SSASYF + A++ G +VT+
Sbjct: 127 LQEIGIEAGFCNS--KIVIQPFVK-EVAKKIVVESDWSSASYFYISIALSNIGSSVTLS 183
Query: 276 CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
SLQGD ++ + G + + E S+ +
Sbjct: 184 YKKNLQGDSCLVKIYQHFGVETVFFVENSIVL 215

>sp|Q9WYI0.1|AROA_THEME RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAD35431.1|AE001715_7 3-phosphoshikimate-1-carboxyvinyltransferase [Thermotoga maritima
MSB8]
Length = 410

Score = 118 bits (296), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 200/442 (45%), Gaps = 52/442 (11%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV 78
+ +P KS+++R L+L+AL+E + + NLL D L LG E D +
Sbjct: 2 LSVPPDKSITHRALILSALAETESTLYNLLRCLDTERTHDILEKLGRFEGDWEKMKV-- 59
Query: 79 VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
FP A+ LF GN+G R ++ + A VL G P + RP+ ++
Sbjct: 60 -----FPPKPFAPFIEPLFCGNSGTTTRLMSGVL--ASYEMFTVLYGDPSSLRRPMRRI 111
Query: 139 VGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
L+ +GA P ++ N + G+ K ++ S+Q SA+L+A A G
Sbjct: 112 EPLEMMGARFMAQNNYLPMAIKGNHLSGI-SYKTPVA---SAQVKSALLAGLRASG-- 165
Query: 198 EIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKN-----AYVEG 252
+I+ S + E R+++ GV E ++G + P V G
Sbjct: 166 RTIVIEPAKSRDHTE---RMLKNLGVPE-----VEGTRVVLEPATFRGFTMKVPG 213
Query: 253 DASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F+ GA +TV G + EV+++MGA + W T +
Sbjct: 214 DISSAAFFVVLGAHPNARITVDVGNPTR--TGLLEVMMKLMGANLEWEITEENL---- 267
Query: 312 REPFG-----RKHLKAIDVNMKNMPDVAMTLAVVAL---FADGPTAIRDVASWRVKETE 362
EP G +LK + V + +P + L +VAL FA+G T +R+ R KE++
Sbjct: 268 -EPIGTVRVETSPNLKGVVPEHLVLMIDELPLVALLGVFAEGETVVRNAEELRKKESD 326
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421

R+ + +LG +EE D I + + ++D DHRMAM FS+A +E V
Sbjct: 327 RIRVLVENFKRLGVEIEEFKDGFKIVGKQSIKGGSVDPGEGDHRMAMLFISIAGLVSEEGVD 386

Query: 422 IRDPGCTRKTFPDYFDVLSTFV 443
++D C +FP++++L V

Sbjct: 387 VKDHECVAVSFPNFIYELLERVV 408

>ref|ZP_05853789.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blautia hansenii DSM 20583]

gb|EEX22710.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Blautia hansenii DSM 20583]

Length = 426

Score = 118 bits (296), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 120/433 (27%), Positives = 198/433 (45%), Gaps = 35/433 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++L AL++GTT V N L D + +G+ +E +
Sbjct: 9 LRGLAVPGDKSISHRAVMLGALAKGTTSTVNFLLKGADCLSTISCFEKMGIIE--QLPS 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G +A E + L GN+G R L+ + AG L G +++RP+
Sbjct: 67 EILIHGKG--LHGLNAPETI-LDAGNSGTTTLLSGIL--AGQAFCTTLTGDAISIQKRP 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK-LSGSISSQYLSALLMAAPLA 193
++ L Q+G ++ C P+++ G P + LS S+Q S +L+A A
Sbjct: 122 TRIITPLSQMGKIESLSDNGCAPLKITG---HPLKPIHYLSPVSSAQVKSCVLLAGMYA 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D ++ + +S + E+ LR FG + G +N V GD
Sbjct: 179 --DGITKVTEPYLSRNHSELMRL---SFGADVISEGTTAAIT---GNPVLEGQNVIVPGD 230

Query: 254 ASSASYFLA-GAAITGGTVTVEGCGTSTSLQGDVKAFAVLEMMGAKVTWTETSVTVTGPPR 312
SSA+YF+A G I G + ++ G + + +V MGA + +
Sbjct: 231 ISSAAYFIAAGLLIPGSEILIKDVGINPTRDGI--LKVCADMGADIQLLNKREY----GK 284

Query: 313 EPFGR---KH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
EP KH LKA + +P D LAV+A FA G T IRD +VKE+ R+
Sbjct: 285 EPVADILVKHSELKATVIEGALIPTLIDELPMLAVMAAFAQGTTVIRDAQELKVKESNRL 344

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAA-CAEVPVTIR 423
I L+ +GA + D I + L +D+Y DHR+AM+F++A A+ I
Sbjct: 345 DIIVQHLISAMGADIIPTEGMEIHGGKPLKGAVLDSYMDHRIAMSAFVAGMAADGETEIL 404

Query: 424 DPGCTRKTFPDYF 436

+ C ++P+++

Sbjct: 405 NASCVDISYPEFY 417

>ref|YP_002530500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Q1]

gb|ACM13211.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus Q1]
Length = 399

Score = 118 bits (295), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 118/427 (27%), Positives = 196/427 (45%), Gaps = 43/427 (10%)

Query: 33 LLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKE 92
+ A++EG T + L D + + +G+ + + VVG G +E +E
Sbjct: 1 MFGAIAEGKTTIKGFLPGADCLSTISCFKEMGVDIVQN--GDEVTVVGKG----LEGLQE 54

Query: 93 -EVQLFLGNAGIAMRSLTAAVTAAGGNATYV--LDGVPRMRERPIGDLVVGLKQLGADV 149
+ L +GN+G +R ++ + N + + G + +RP+ + LKQ+GA++D
Sbjct: 55 PKAVLDVGNSTGTTIRLMSGIL----ANTPFFSCVQGDASIARPMKRVTNPLKQMGANID 110

Query: 150 CFLGTDCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALLMAAPLALGDVEIEIIDKL 205
P+ + G G +K S S+Q SA+L+A A G +
Sbjct: 111 GREEGTFTPLTIRG-----GDLKAIEYTSPPVASAQVKSAILLAGLRAEGVTAV----- 158

Query: 206 ISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL-A 262
+ P++ + T R++E FGVK + + GGQK + + V GD SSA++FL A

Sbjct: 159 -TEPHISRDRHTERMLEAFGVKVTREGKTVK--LAGGQKL-TATDVQVPGDVSSAAFFLVA 214

Query: 263 GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLK 321
GA I + ++ G + + +VLE M A T + + P LK

Sbjct: 215 GAIIPNSKLVQLQNVGMNPTRTGI--IDVLEKMDATFTVEPINEGASEPAANITITETSSLK 272

Query: 322 AIDVNMNMKMPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
I++ + +P + + V+AL A +G T I+D +VKET R+ + ELTKLGA +

Sbjct: 273 GIEIGGDIIPRLIDEIPVIALAATQAEGITVIKDAHELKVKETNRIDTVVAELTKLGARI 332

Query: 379 EEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFD 437
E D II L +++Y DHR+ M ++A C AE TI D ++P +F+

Sbjct: 333 EATDDGMIYIGKSALKGNTVNSYGDHRIGMMLAIAGCLAEGKTTIEDAEAVGVSYPTFFE 392

Query: 438 VLSTFVK 444
L K

Sbjct: 393 ELQRLTK 399

>ref|ZP_06392147.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dethiosulfovibrio
peptidovorans DSM 11002]
gb|EFC91088.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dethiosulfovibrio
peptidovorans DSM 11002]
Length = 427

Score = 118 bits (295), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 132/442 (29%), Positives = 197/442 (44%), Gaps = 44/442 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ I+G +++PG KS+S+R+ +L ALS V N + D L + LG SVE +

Sbjct: 3 RSINGRIEVPDGKSIHRVGILGALSSRGIEVTNFSGADCASTLDCVEKLGCSVE--RH 60

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R V G A+ L GN+G R L + G + VL G ++ R

Sbjct: 61 GDRVKVARGEI-----AEASRTLDAGNSGTARLLCGLLAGVPPTFS-VLTGDDSLQRR 114

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L+ LGA +D G P+ + G L GG+ L + S+Q SALL+A

Sbjct: 115 PMSRIVDPLRVLGARIDGRDGGKRLPLSIRGTR-LTGGQYVLPMA-SAQVKSALLLAGLS 172

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY----IKGGQKYKSPKNA 248
A G V + + +P + T ++E GV Y + GG ++ P

Sbjct: 173 AQGSVTV-----VEPLPTRDHTIEIMLEHLGVPIRRDGDVSVTVYPFDLPGG-SWRVP--- 223

Query: 249 YVEGDASSASYFLAGAAI-TGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
GD SSA++++ AAI + +V + G G + EVL MG + S

Sbjct: 224 ---GDFSSAAFVIAAAICSDSSVRLSGVGLNPTR--TGLLEVLRSMGLDCSVENESAQG 278

Query: 308 TGPPREPF-----RKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRV 358
EP G R D+ + M D LAV A A+G T IR RV

Sbjct: 279 G---EPVGDILVRSSSLRSVSVGSDM-VPSMVDELPLLAVAATQAEGTTEIRGAGELRV 333

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAE 417
KE +R+ A+ L +GA + E D I +KL +D+ DHR+AMA ++A A+

Sbjct: 334 KECRIAABAEGLRAMGADITEHDDGWITPGSQKLRGARVDSRGDHRIAMAMAVAGLAAD 393

Query: 418 VPVTIRDPGCTRKTFPDYFDVL 439
PV I C ++P++F L

Sbjct: 394 GPVEILGSDCVSISYPEFFSQL 415

>ref|ZP_02142005.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter litoralis
Och 149]
gb|EDQ16389.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter litoralis
Och 149]
Length = 441

Score = 118 bits (295), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 130/434 (29%), Positives = 200/434 (46%), Gaps = 30/434 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

Sbjct: 9 ++G ++PG KS+S+R L+L ALS G T + LL +DV A+R G +V +
LTGEARVPGDKSISHRSLILGALS SVGETRISGLLEGQDVLDTAKAMRAFGATVTDHGGGE 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ + + GN+G +R + A+ + +AT+ D + RP

Sbjct: 69 WSVYGVGVGGF-----AEPDGVIDCGNSGTGVRLIMGAMATSPISATFTGDA--SLNGRP 121

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L GA G P V +P V + + S+Q SA+L+A

Sbjct: 122 MARVTDPLALFQAQSHGRQGGRLPMTLVGAADVPV---VTYTVPVPSAQVKSALLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+ + + E R++ FG + D+ + R GQ P+ V

Sbjct: 179 APG--QTVVIEAEATR DHE---RMLAGFGAEISVEDTDEGRVITLTGQPELKPKQIDVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V V G G + L MGA +T+ V P

Sbjct: 234 RDPSSAAFPVCAALIVPGSDVLVPGIGLNPTR--AGLFTTLREMGADLT YENERVEGGE 291

Query: 311 PREPFGR--KHLKAIDV---NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ R L I+V M D L+VVA FA G T +R V RVKE++R+

Sbjct: 292 VADLRARFSPDLTGIEVPPARAASMI DEYPVLSVVASFARGDTVMRGVKELRVKESDRID 351

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDT---YDDHRMAMAF-SLAACAEVPVT 421
A+ + L G +VE+GPD+ I+T NV T + DHR+AM+F L + PV

Sbjct: 352 AMASGLRANGVAVEDGPDWIVITGQGHNVAGGATCASFLDHRIAMSFLVLGMATQKPKV 411

Query: 422 IRDPGCTRKTFPDY 435
+ D G +FP +

Sbjct: 412 VDDAGPIATSFPIF 425

>ref|ZP_07946765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eggerthella sp.
1_3_56FAA]
gb|EFV34237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eggerthella sp.
1_3_56FAA]
Length = 442

Score = 117 bits (294), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 124/449 (27%), Positives = 204/449 (45%), Gaps = 35/449 (7%)

Query: 4 AEEIVLQPI-KEISGTVKLPGSKSLNRILL AALSEGTTVDNLLNSEDVHYMLGALRT 62
A V+ P+ + G+ +PG KS+S+R +L AA++EGT+ + +L+SEDV + A+

Sbjct: 5 ANATVVNPLPAPLRGSASVPGDKSISHRAVLFAAMAE GTSRLSGVLDSE D VRSSIRAVGQ 64

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
LG V +K ++ G G ++ E + GN+G +R L + A +

Sbjct: 65 LGAQVSLKQPDGSLAGGVTGWGAAGPSQPEAPIDCGNSGTTVRLLMGV L--APWSVRVE 122

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G ++ RP+ + L ++GA + G + P+ V G GL + S+Q

Sbjct: 123 LTGDDSLQRRPMRRITAPLMKMGARFEPE-GRETLP LTVCGSEGLRAITYD-APMASAQL 180

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+A+L+A A G + P T ++ FGV + + DR G

Sbjct: 181 KTAVLLAGVYARGTTTLNPS-----PSRNHTEMLPEFGVT---TTAADRTASVTGPAA 232

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
V GD SSA++ + A + ++ VE + + + F LE MGA ++

Sbjct: 233 LRACEVQVPGDPSSAFLVCAAVLKP DSSIQVENVSLNTAR--IGFTRTLERMGADISVR 290

Query: 302 ETSVTVTGPPREPF G-----RKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD 352
T +EP+G +L +V +K+ D LA+VA A G T R+

Sbjct: 291 HTGAA----GKEPYGIVSACYTPNLHGCEVPADKIATIVDEV PVLALVA AHARGVTVFRE 346

Query: 353 VASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLN V---TAIDTYDDHRMAM 408
V+ RVKET+R+ AI L LG +G D + P L V A D+ +DHR+AM

Sbjct: 347 VSELRVKETDR LAAIVEGLETLGVD AWDGNDLFVEGQP-GLQVPVGA AFDSKNDHRLAM 405

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++LA C PV + + + ++P +

Sbjct: 406 TWALAGLCGNAPVEVENFDSVKISYPQFL 434

>ref|ZP_04783741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Weissella
paramesenteroides ATCC 33313]
gb|EER74176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Weissella
paramesenteroides ATCC 33313]
Length = 430

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 123/450 (27%), Positives = 211/450 (46%), Gaps = 48/450 (10%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ GT+ +PG KS+S+R ++L +++ G T V +LL+SEDV + A+ LG++ +
Sbjct: 11 KQLRGTLTMPGDKSISHRAVMLGSIASGDTRVQHLLDSEDVRRRTVTAMSNLGVTFSTENH 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA-----AVTAAGGNATYVLDG 125
+ GK E + + L +GN+G R L A+T G N+
Sbjct: 71 D-----LIIHGKSLNELVEPKQMLDMGNSGTTARLLMGLLANQPFATFRGDNS----- 119

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP ++ L+ +G V D PV G L G +L + S+Q SA
Sbjct: 120 ---LSKRPFARVIKPLRAMG--VSYVSKNDHLPVTKLGTRYLEGLVYELPVA-SAQVKSA 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+++AA A + II+ + + + E R++ FGV + + + Q +
Sbjct: 174 IILAALQA--KSQTTIEPIATRDHTE--RMLAAFVGMVKREGNQIKI---APQTHLKA 225

Query: 246 KNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
V GD SSA+++L AG + +T++ G + + +L+ MGA+ + S
Sbjct: 226 TTIRVPGDISSAAFVLVAGLLVPNSQLTLKQVGINPRTGI--LTILQRMGAQFIYQNES 283

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNMKMPDV-AMT-----LAVVALFADGPTAIRDVASWRV 358
G P + H ++++ + DV AM + +VA A G T I D + V
Sbjct: 284 --SDGEPMAI-QVHSQSLNSTIITATDVPAMIDEIPLIVLVATQAQGDITIISDASELHV 340

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTADITYDDHRMAMAFSLAAC 415
KE++R+ + T+L KLGA++E D I TP T ID+ DHR+ M ++AA
Sbjct: 341 KESDRIATVTTQLNKLGANIEPREDGFYIHGGTPLHVDQPTTIDSCGDHRVGMMLTIAAL 400

Query: 416 AEV-PVTIRDPGCTRKTFPDYFDVLSTFVK 444
V++ + ++PD+F L+ VK
Sbjct: 401 ITTGEVSLANAEAVNISYPDFFRDLNEVVK 430

>ref|ZP_04583050.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
winhamensis ATCC BAA-430]
gb|EEO26150.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
winhamensis ATCC BAA-430]
Length = 434

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 123/452 (27%), Positives = 205/452 (45%), Gaps = 62/452 (13%)

Query: 18 TVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
T K+ KS+S+R + A LS+ + V N L ED L + LGLSVE
Sbjct: 15 TDKIASDKSISHRCAMFALLSDKPSFVKNYLEGEDTLDTLEIAKKLGLSVEK----- 66

Query: 78 VVCGGKGF---PVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
C G P ++ +E L+ GNAG AMR ++A N +VL G + +RP
Sbjct: 67 ---CHGGLLLTTPKNIQEPNTILYCGNAGTAMRLYLGLLSAQ--NGIFVLSGDMYLNKRP 121

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+ +GA++ + P+ + G L S S+Q SA+L++A A
Sbjct: 122 MKRIVEPLRSIGAEILGRSSGEFAPLVIKGNPKLESF-FYTSKIPSAQIKSAMLALSALFA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-----FYIKGGQKYKSPKNA 248
G+ + + +S + E L+ G+ AE + D+ IK + P N
Sbjct: 181 KGESVYQ--EPELSRDHSEKMLK-----GMGAEIESAIDKNGAVEIKIKPLKSKLEPLNL 233

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA--EVLEMMGAKVTWTETSVT 306


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      + D SSA +F      AIT +      G      L      +      VLE MG +T+ ETS T
Sbjct: 234 EIPADPSSAFFFAVAVAITPNS---RGILRNVLNKNTRIEAFSVLEKMGVTITYKETS 290

Query: 307 -----VTGPPREPFGGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRD 352
      + P      + LKA++++      +++P +A+ +A      A G + +++
Sbjct: 291 YESIGDIIINAP-----ESLKAVELSEKISWLIDEIPALAIAMAC----AKGKSVVKN 339

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
      RVKET+R+ A+      L      G      +E D I      L      +D++ DHR+AM+F++
Sbjct: 340 AKELRVKETDRKAVVENLRACGIEAQELDDGFYIVGG-MLKKACVDSFGDHRIAMSAFV 398

Query: 413 AACAEVPTTIRDPGCTRKTTPDYFDVLSTFVK 444
      A      +      + I + C      +FP++ ++L + K
Sbjct: 399 AGL-KSGMEIENAEICINVSFPNFLEILQSLTK 429

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>emb|CAN61775.1| hypothetical protein VITISV_024881 [Vitis vinifera]
Length = 424

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 58/75 (77%), Positives = 64/75 (85%)

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Query: 100 NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPV 159
      NAG MR L AAVTAAGG+A+YV+DGV RMRE IGDLV GLKQLGADV+ FLGT+C PV
Sbjct: 327 NAGTVMRPLIAAVTAAGGDASYVIDGVLRMRETSIGDLVTGLKQLGADVNGFLGTNCSPV 386

Query: 160 RVNGIGGLPGGKVKL 174
      RVNG GGLPGGK+KL
Sbjct: 387 RVNGNGGLPGGKMKL 401

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>ref|YP_003810268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium
HdN1]
emb|CBL44611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [gamma proteobacterium
HdN1]
Length = 739

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 124/437 (28%), Positives = 203/437 (46%), Gaps = 33/437 (7%)

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Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLNSSEVDHYMLGALRTLGLSVE 68
      +QP ++GT+++PG KS+S+R ++L AL++G T V L ED L R +G+ +E
Sbjct: 309 VQPGGSMNGTLRVPGDKSISHRSIMLGALADGITEVSGFLEGEDSLATLQTFRDMGVVIE 368

Query: 69 ADKAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      + R VG G A L+LGN+G +MR L+ + ++T L G
Sbjct: 369 GPNEGRVRFVGLRGLRAAPGA-----LYLNSGTSMRLLSGLLAGQAFDST--LTGDE 421

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      + RP+G + L Q+GA V + PP+R+ G L G + + S+Q S +L
Sbjct: 422 SLSHRPMGRVAKPLLQMGGA-VIATEPSGTPPIRITGRQRLRGIHYDMPMA-SAQVKSCVL 479

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
      +A A G+ + P + T R++ FG VK E S + GG K+
Sbjct: 480 LAGLYAEGETSVT-----EPAPTRDHTERMLRGFGYTVKTEGST----ISLTGGGSLKAT 530

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + V D SSA++F+ A+I G +T++ G + + +L MG + +
Sbjct: 531 Q-IDVPADISSAAFFMVAASICPGADITLQHVGINPTR--IGVINILRAMGNGNIELSNER 587

Query: 305 VTVTGPPEPFGGRKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
      V G P + LK I + +++P D L + A A G T + RVK
Sbjct: 588 -EVGGEPPVADIRVCYAALKGIHIPEDQVPLAIDEFPALFIAAACAQGETVLTGAEEELRVK 646

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEV 418
      E++R+ + L LG + PD II + + ++ DHR+AM+F++AA A
Sbjct: 647 ESDRIQVMADGLNTLGVDAKPTPDGIIIR-GGIIGGGEVYSHSDHRIAMSFTIAALRAND 705

Query: 419 PVTIRDPGCTRKTTPDY 435
      + I+D +FP +
Sbjct: 706 VIVIQDCANVMTSFPTF 722

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>ref|ZP_01870816.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caminibacter
    mediatlanticus TB-2]
gb|EDM24149.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Caminibacter
    mediatlanticus TB-2]
Length = 431

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 124/451 (27%), Positives = 210/451 (46%), Gaps = 54/451 (11%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K+ + + KS+S+R + + L+ G ++ N L +ED L + LG +E +
Sbjct: 9 KQFNEEFVLVDADKSIHRCAIFSLLTNGENIKNYLRAEDTLNSLEIAKKLGAKIEDNGD 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
      + V P + + + L+ GN+G +R + + AG + +VL G +R+R
Sbjct: 69 VIKIVA-----PKKIKEADDVLYCGNSGTTIRIYSGLL--AGVDGFFVLTGDEYLRKR 119

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL----SGSISQYLSALLM 188
      P+ + L +GA +D + P+ + G GK+K S S+Q SA+++
Sbjct: 120 PMKRISAPLISIGAKIDGRETANLAPLSIRG-----GKLKSFNYESKIASAQVKSAMIL 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGGQKYKSP 245
      AA L D+ ++ +S + E R+++ G E + W R I ++ +P
Sbjct: 174 AA-LNTNDIST-YVEPFLSRDHTE---RMLKGMGADIECKMENGKW-RVNIAPLKEKLN 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      N V D SSA +F AAI T ++ T Q ++ +VLE MGA + +
Sbjct: 228 LNITVPNDPSSAFFFAVAAAIINSTAIKN--VTLNQTRIEAYKVLEKMGATIEYI---- 281

Query: 306 TVTGPPREPFGFR-----KHLKAIDVNMN-----KMPDVAMTLAVVALFADGPTAIRDVA 354
      + EP G LKA++V+ N ++P +AM +AV ADG + +R
Sbjct: 282 -LKEDKYEPIGDIIIVKGNKLKAVEVSENIPWLIDELPALAMVMAV----ADGKSIVRGAK 336

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLA 413
      RVKE++R+ A+ L K G +E D Y II K ID++ DHR+AM+F++
Sbjct: 337 ELRVKESDRIKAVVENLKKCGVEAKEFEDGYEIIIGGDVK--SALIDSFGDHRAMSF 394

Query: 414 ACAEVPVTIRDPGCTRTKTFPDYFDVLSTFVK 444
      + I+ C +FP++F +LS K
Sbjct: 395 GILS-GMKIQQAECINTSFPNFFKLLSKVTK 424

>ref|ZP_01445538.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelagibaca
    bermudensis HTCC2601]
gb|EAU44250.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseovarius sp.
    HTCC2601]
Length = 447

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 133/446 (29%), Positives = 201/446 (45%), Gaps = 45/446 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      +SG +PG KS+S+R L+L A++ G T V LL +DV A+R G VE
Sbjct: 18 LSGEAHVPGDKSISHRSLILGAMAVGETRVTGLLEGQDVLDTAKAMRAFGAEVEKRGDTW 77

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      VG GG A+ E + GN+G +R + A+ AT+ D + +RP+
Sbjct: 78 HVNGVGVGGF-----AEPEQVIDCGNSGTGVRLIMGAMATTPITATFTGDA--SLNKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLA 193
      + L GA G P V LP V+ + + S+Q SA+L+A A
Sbjct: 131 ARVTDPLALFGAQAVGREGRLPMTIIVGARDPLP---VRYATPVPSAQVKSAVLLAGLNA 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
      G E +I++ + + E R++ FG K ++ + R GQ P+ V
Sbjct: 188 PG--ETVVIEREATRDSHSE---RMLTGFGAKVVTEETEGRVITLTGQPELKPQVIVVPR 242

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
      D SSA++ + A IT G+ V V G + + F L+ MGA +T+ P
```

Sbjct: 243 DPSSAAFPVCAALITEGSDVLPNIGLNPTAGLFF--TLQEMGADLTFFEN-----P 292

Query: 312 REPFGR-----KHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRV 358
RE G LK I+V + M D L+VVA FA+G T + V RV

Sbjct: 293 REEGGEPVADLRARFSPDLKGI EVP AERAASMI DEYPVLSVVASFAEGKTHMPGVKELRV 352

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A---IDTYDDHRMAMAFSLAAC 415
KE++R+ A+ T L G V+EG D+ + NV ++ DHR+AM+F +

Sbjct: 353 KESDRIDAMATGLRANGVEVEDEGEDWWT VHG RGHGNVPGGAETASHLDHRIAMSFLVMGL 412

Query: 416 AEV-PVTIRDPGCTRKTFPDYFDVLS 440
A PV + D G +FP + ++S

Sbjct: 413 ATTEPVRVDDGGPIATSFPIFEPLMS 438

>emb|CAM75693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Magnetospirillum
gryphiswaldense MSR-1]
Length = 446

Score = 117 bits (294), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 134/412 (32%), Positives = 190/412 (46%), Gaps = 38/412 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+SG+ K+PG KS+S+R L+ AL+ G + V+ LL +DV A+R LG VE D +

Sbjct: 13 LSGSAKVPGDKSVSHRALMFGALAVGESRVEGLLEGDDVLR TAAAMRALGAEVERLDDGS 72

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R G GG K P EEV L LGN+G R + V A T V G +R R

Sbjct: 73 WRLYGRGVGGLKEP-----EEV-LDLGNSGTGARLMMGLV--ATHPFTTVFTGDASLRSR 124

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
P+ + + L Q+GA F G D P+ V G G +L + S+Q SA+L+A

Sbjct: 125 PMKRVSPLPSQMG AQ---FFGRDGGRLPMTVVG TGNPLPITYELPVA-SAQVKSAILLAG 180

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
G + +I++ + + E+ LR FG V EH D R G + ++

Sbjct: 181 LNTPG--QTTVIEREATRDHTELMRL---NFGAQVDVEHGDQGR IITVTGFPELTGRHV 235

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++ A IT G+ + + G G L+ + L MGA + + E

Sbjct: 236 IVPADPSSAAFP AVAAIITPGSDIVLTGVGMNPLR--TGLYQTLREMGADLAF-ENQRED 292

Query: 308 TGPPREFPFGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G +H L +DV + P D LAV A FA G T + ++ RVKE++

Sbjct: 293 GGEQVADLRVRHSALMGVDVPAERAPSMIDEYPILAVAAAFATGTT RMFGLSELRVKESD 352

Query: 363 RMVAIRTELTKLGASVEEGPDYCI I---TPPEKLNVT AIDTYDDHRMAMAF 410
R A L G VEE D I+ PP A++ DHR+AMAF

Sbjct: 353 RFAATLRGLLACGVQEEDGDTLIVHSGKPPMGGATI AVNL--DHRIAMAF 402

>ref|YP_001633700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus
aurantiacus J-10-fl]
ref|YP_002567831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus sp.
Y-400-fl]
sp|A9WBA4.1|AROA_CHLAA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B9LFL8.1|AROA_CHLSY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABY33311.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus
aurantiacus J-10-fl]
gb|ACM51506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroflexus sp.
Y-400-fl]
Length = 435

Score = 117 bits (293), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 129/447 (28%), Positives = 215/447 (48%), Gaps = 34/447 (7%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRIILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66

Sbjct: 4 I L K + G +++PG KS+S+R +L A++ G+ + + L D + +R LG++
ITLTAPKRLRGVIEVPGDKSISHRSVLFNAIATGSAHITHFLPGADCLSTVACIRALGVT 63

Query: 67 VEADKAAKRAVV---VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE + A+R ++ VG GG D L GN+G +R L + VL

Sbjct: 64 VE--QAERELIVHGVGLGGLREPADV-----LDCGNSGTTLRLLAGLLAGH--PFFSVL 114

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G +R RP +VV L+ +GA +D D P+ + G L GG +L SI+S +

Sbjct: 115 TGDASLRSRPQRRIVVPLRAMGAQIDGRDDGDRAPLAIRG-NRLRGGHYEL--SIASAQV 171

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ L+ A + + + ++ S + E R++ G+ E + + D+ I+ +

Sbjct: 172 KSALLLA-ALNAEQPLTLTGRIDSRDHE---RMLAAMGL--EITVTADQITIQQPSEAT 225

Query: 244 SPK--NAYVEGDASSASYFLAGAAIT--GGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+P + V GD SSA+++ AAI VT C + G + EVL+ MGA +T

Sbjct: 226 APTALSLRVPGDPSSAAFVWAAAIHPDAELVTPGVCLNPTRIGAI---EVLQAMGADLT 282

Query: 300 WTETSVTVTGPPREPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
+ + P + R L+ + +P D LAV A A G T IRD

Sbjct: 283 VMNERLEGSEPVGDVVVRSSSLRGTTIAGTLIPRLIDEIPVLAVAAACASGETVIRDAQE 342

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R KET+R+ + L+ +GA VE D I+ P +L T ++++ DHR+AMAF+++AA

Sbjct: 343 LRAKETDRIATVAAGLSAMGAVVEPTADGMVIVGQPGQLQGTTLNSFHDHRLAMAWAIAA 402

Query: 415 -CAEVPVTIRDPGCTRKTFPDYFDVLS 440
A TI +P ++P+++ L+

Sbjct: 403 MVARGETTILEPAAAVSYPEFWQTLA 429

>ref|YP_741773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkalilimnicola
ehrichii MLHE-1]
sp|Q0AA54.1|AROA_ALHEH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI56283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkalilimnicola
ehrichii MLHE-1]
Length = 446

Score = 117 bits (293), Expect = 3e-24, Method: Compositional matrix adjust.
Identities = 124/445 (27%), Positives = 199/445 (44%), Gaps = 36/445 (8%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
E ++P + G +++PG KS+S+R ++L AL+EG T + L D L R +G+

Sbjct: 2 EFHVRPGGALRGRLRVPGDKSISHRAIMLGALAEGETRISGFLEGADALATLRTFRAMGV 61

Query: 66 SVEADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
++ + V VG G + P + L LGN+G +MR L + AG + L

Sbjct: 62 DIDGPHQGRVTVQGVGLHGLRAP-----DGPLDLGNSGTSMLLCCGLL--AGQSFDTTL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RP+ ++ L +GA ++ G P+ V G L G +L S+Q

Sbjct: 114 TGDASLSRRPMRRVIDPLTAMGAVIESGQGGTA-PLTVRGGQPLHGIDYELP-VASAQVK 171

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL+A A G + P + T R++ FG R G

Sbjct: 172 SALLLAGLYARRTCCTV-----EPAPTRDHTERMLAGFGYPVQE---GRRVCIEGGGRL 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
V D SSA++FL GA+I G+ +T+E G + V ++L +MGA + +

Sbjct: 224 RGGEIDVPADISSAAFVVGASIAEGSDITLEHVGMNPTRTGV--VDILRLMGADI-QVQ 280

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLA-----VVALFADGPTAIRDVA 354
V G EP +++ + +P+ + LA V A A+G T +

Sbjct: 281 NEREVG---EPVADLRVRSAPLKGVAIPEALVPLAIDEFPVLFVAAACAEGETLLTGAE 337

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
RVKE++R+ + LT LG + E PD I + ++ DHR+AMAF+++AA

Sbjct: 338 ELRVKESDRIAVMAEGLTTLGVTAEPQPDGMRIVGQPDWGGGRVHSHGDHRIAMAFMAA 397

Query: 415 C-AEVPVTIRDPGCTRKTFPDYFDV 438
A P+ I D +FP + ++
Sbjct: 398 TRAREPIEIEDCANVNTSFPGFVEL 422

>ref|YP_003060729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hirschia baltica ATCC 49814]
gb|ACT60032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hirschia baltica ATCC 49814]
Length = 438

Score = 117 bits (293), Expect = 4e-24, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 205/442 (46%), Gaps = 37/442 (8%)

Query: 10 QPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
+PI + G ++ PG KS S+R L+ A L+EGT+ ++ LL EDV A+ G VE
Sbjct: 6 KPISRLDGALRAPGDKSCSHRALMFAGLAEGTSFIEGLLEGEDVKDTAKAMAACGADVE- 64

Query: 70 DKAACKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ +R V G G +++ K L +GN+G R + V AT+ DG +
Sbjct: 65 RISLRWKVTGVGAA-GLKNPKN--ILDMGNSGTGARLMMGLVAGQKLKATF--DGDVSL 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RP+G ++ L ++GA + G P+ + G P ++ + +S + + +M
Sbjct: 120 RSRPMGRVLDPLAEMGAKNESNGGK--LPLTLEGA---PLSAIEYTPPHASQVKSCVML 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247
A LG + I+++ + T R++ FG V E D R ++GGQ+ + N
Sbjct: 175 A--GLGAIGTTIVNE--PRKTRDHTERMLRAFGVTVDVEEKDGGCRISLEGQQLTA-TN 229

Query: 248 AYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS-- 304
+ GD SSA++ + AG + G+V+V + + + A + MGA + +T
Sbjct: 230 VDIPGDPSSATFLWAAGLLVQEGSVSVLNMENNTDGLVHAA--KAMGANLNVVKTGEA 287

Query: 305 -----VTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
T+T P L + +++ P V+A FADG T + RV
Sbjct: 288 GGEVITITITSIPSSLNAATPELAIVPAMIDEFP----LFGVLAADFADGDTLVGTAEELRV 343

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAAA--IDTYDDHRMAMAFSLAAC 415
KE++R+ A L G EE PD I+ + V ++ DHR+AM+ + C
Sbjct: 344 KESDRITATVNMLKANGVHAERPDGFIIVRGCGRGVPGGGIVEACHDHRIAMSALVMGC 403

Query: 416 -AEVPVTIRDPGCTRKTFPDYF 436
A+ PV++ + ++PD+F
Sbjct: 404 AAKAPVSVDNVSAIATSYPDFF 425

>ref|YP_003149651.1| 5-enolpyruvylshikimate-3-phosphate synthase [Kytococcus sedentarius DSM 20547]
gb|ACV06886.1| 5-enolpyruvylshikimate-3-phosphate synthase [Kytococcus sedentarius DSM 20547]
Length = 348

Score = 117 bits (292), Expect = 4e-24, Method: Compositional matrix adjust.
Identities = 91/270 (33%), Positives = 138/270 (51%), Gaps = 17/270 (6%)

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-- 229
V++ S SSQ++SALL+A + + + S P+++MT +++ GV AE D
Sbjct: 85 VEVDAASSQFVSALLLAGCTVHSGLTVRATGTVPSRPHIDMTCHALQQVGVAEQRDET 144

Query: 230 SWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAE 289
SW +++G K P VE D SSA+ F A AA+ GGTVT+ G ++ Q +
Sbjct: 145 SW---WVEG--KRPDPFEVTVPEPDLSSAAVFAAAAAGGTVTLPGWPRSTTQAGDTIRD 199

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTA 349
+L MGA+ TE + VTG L I+ +++ ++ +A A AD P+
Sbjct: 200 LLTRMGARCELTEAGLRVTG-----GELHGIEADLSAAGELTPVVAATAALADSPSR 251

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAAIDTYDDHRMAMA 409
+ + R ET+R+ A+ TE+ LG V E PD IT P L+ + TY DHR+AMA

Sbjct: 252 LTGIGHLRGHETDRLAALATEINALGGEVRELPDGLEIT-PRPLHGGSFATYHDHRLAMA 310

Query: 410 FSLAACAEVPTIRDPGCTRKTFPDYFDVL 439

+L + ++D T KT P FD L

Sbjct: 311 GALLGLRVPGEVQDIATTAKTVPG-FDHL 339

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 20/47 (42%), Positives = 29/47 (61%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61

+ TV +PGSKS +NR L LAAL+ G + + + L++ D M AL

Sbjct: 30 LDATVHVPGSKSWTNRWLALAALASGPSTLHSPLDARDTRLMASALH 76

>gb|ACS75029.1| AroA [Methylophilus methylotrophus]
Length = 126

Score = 117 bits (292), Expect = 5e-24, Method: Composition-based stats.
Identities = 67/132 (50%), Positives = 85/132 (64%), Gaps = 7/132 (5%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E++ L + GT+ LPGSKS+SNR LLLAAL++G T++ +LL S+D ML AL +LG

Sbjct: 2 EQLHLPAAHQAQGTITLPGSKSISNRTLLAALADGVTTIIRDLLASDDTARMLEALTSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

L +E + V GCGG FP ++ LFLGNAG A R LTAA+ + G Y L

Sbjct: 62 LQLE-NIGENAWRVGTGCGGNFP----NKQADLFLGNAGTAFRPLTAALAFSEGE--YHLH 114

Query: 125 GVPRMRERPIGD 136

GVPRM ERPIGD

Sbjct: 115 GVPRMHERPIGD 126

>ref|NP_930003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Photorhabdus
luminescens subsp. laumondii TT01]
emb|CAE15143.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii
TT01]
Length = 451

Score = 117 bits (292), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 119/448 (26%), Positives = 205/448 (45%), Gaps = 31/448 (6%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66

I + K ++G++ LP SKS S R +L A+L+EGT+ ++N+ + + M LG S

Sbjct: 12 IEINKTKSLNGSITLPASKSSSTRAILTASLTGTSKINNMAAGNNNTTAMKLNC SRLGAS 71

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126

+D +V G + +++ GN+G+ +R L V + ++ +

Sbjct: 72 FNSDITG--TIVEG----IDIRQIDKKIIFNPGNSGVVLR-LLMGVAGYLPDTEFITEYS 124

Query: 127 PRMRERPIGDLVVGLKQLGADVDCF-LGTDC-PPVRVNGIGGLPGGKVKLSGSISSQYLS 184

+ R ++V LK L ++ C +G D P+ + + G ++S SSQ+LS

Sbjct: 125 YSLGTRSQLEMVNALKSL--NIQCTAVGPDSSLPISMKSDKNI-GNYTEISCRKSSQFLS 181

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

LL ++ D++I++ID + + V T+ + + G+ E+ D + F+ G ++

Sbjct: 182 GLLYLGAISERLDQIKVIDTITAPSMVHTTINLRKAGINIEYDDKFRNFFTTGKSRFI- 240

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET- 303

P V D +S + LA A VT+ G L G+ L G K+++

Sbjct: 241 PSEFSVGADPASTAAILALCASLNSDVTNLNGFFEEEL-GNGAVVNYLINSGTKISFIRDD 299

Query: 304 --SVTVTGPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361

++ G LKA D + + PD LA +A FA+G + ++ R KE+

Sbjct: 300 CLNIRSGGT-----LKAQDFDGLAPDAVPALAAALAFANGKSVFYNIEHIRYKES 350

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMAFSLAA--CAE 417

+R+ R EL K+G EE D II P +D + DH + MA + C E

Sbjct: 351 DRISDFRRELDKIGIRSEERLDQLIYGNPYGYKGGVIVDGHYDHGLIMALTITIGLHCD 410

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
P+ I +P +T+P+YF +ST N
Sbjct: 411 -PLIIEEPYHVQGQTYPEYFAEISTLGN 437

>ref|YP_003291767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodothermus marinus
DSM 4252]
gb|ACY49379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodothermus marinus
DSM 4252]
Length = 434

Score = 117 bits (292), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 129/434 (29%), Positives = 201/434 (46%), Gaps = 28/434 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V+LP KS+++R LLAAL++GT+ + N + D L LR LG+ + D+
Sbjct: 12 RSLGLVVELPPDKSIAHRAALLAALADGTSRLVNYSAPADPQSTLSCLRQLGVPIYEDE- 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFNLGAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
++V G A + L GN+G MR L + AG VL G + R
Sbjct: 71 --HGILVVEGRGLEGLQAPDR-PLDCGNSGTMRLLAGIL--AGQPFDSVLVGDAASLSRR 125

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+Q+GA++ G P+ + G L G +L S+Q S +L+A
Sbjct: 126 PMERIATPLRQMGAEFLTLDGH--APIHIRGGRTLRGITYRLPVP-SAQVKSCVLLAGLF 182

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ + + IP + T R++ G+ + ++GG + + + +
Sbjct: 183 AEGETT-----IEIPSRDHTERML---GLSVVELNGERYLTVRGGMRIIPA-RTWTIPR 233

Query: 253 DASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D S+A++FL AG + + + G G + +VL MGA +T E + G P
Sbjct: 234 DFSAAAFVLVAGTIVPDSEIRLPGVGLNPSRS--ALLDVLRAMGADIT-VENERSYGGEP 290

Query: 312 REPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ L + V +P D L V A A G T IRD A RVKET+R+ A
Sbjct: 291 IADLVRSSTLHGVQVGGAIIIPNLIDEIPVLTVAAACATGRTEIRDAEELRVKETDRIAA 350

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDP 425
+ L LGA VE D I +L T + ++DDHR+AMA +A AE I
Sbjct: 351 MAENLQALGARVEVFDDGLAIEGGHRLRGTTVRSFDDHRIAMAMGVAGLVAEGETIIEGA 410

Query: 426 GCTRKTFPDYFDVL 439
C R +FP +++VL
Sbjct: 411 ECARISFPGFWEVL 424

>ref|YP_001431593.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseiflexus
castenholzii DSM 13941]
sp|A7NJA5.1|AROAROSCS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABU57575.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseiflexus
castenholzii DSM 13941]
Length = 431

Score = 116 bits (291), Expect = 5e-24, Method: Compositional matrix adjust.
Identities = 125/440 (28%), Positives = 200/440 (45%), Gaps = 35/440 (7%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G + LPG KS+S+R +LL A++ G V N L D + ++ LG+ VE +
Sbjct: 9 RRLRGIIDLPGDKSISHRAVLLNAIATGAAEVANFLTGDCLSTIACVQALGVRVERHED 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATY-VLDGVPRMR 130
R V G G + +E V + GN+G +R LT + AG + VL G +R
Sbjct: 69 TVR--VFGAG----LRSLREPVDVLDGNSGTTLRLLTGML--AGQEGIFAVLTGDASLR 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP +V L+ LGA +D + P+ V G L GG L + S+Q SALL+AA
Sbjct: 121 SRPQQRIVAPLALGATLDGRDRGNRAPLVVRG-AYLHGGAYDLPIA-SAQVKSALLLAA 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
GD + + + + E R++ G R + P + V
Sbjct: 179 --LFGDGLTLTLGRTDGRDHTE---RMLAAMGATITVDGQTIRLTPPDRSEALHPLSLRV 233

Query: 251 EGDASSASYFLAGAAIT-GGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
GD SSA+++ AA+ +T G C + G + + L MGA++ V
Sbjct: 234 PGDPSSATFWWVAAALHPDAELTTTGVLNPTRTGAL---DALRAMGAQIDVANQRVE-- 288

Query: 309 GPPREPFGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
EP G +++ ++ + ++ D LA+ A A+G T IRD RVKE
Sbjct: 289 --GGEFVGDTVVRSSSLHGIVIEGALIPRLIDELPVLALAAACAEGETIIRDAQELRVKE 346

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-P 419
T+R+ + LT LGA VE D II L ++++ DHR+AM +++A
Sbjct: 347 TDRIATVVAGLTALGAVVEPTEDGMIIAGGGLRGATLESHGDHRLAMTWAIAGLVGAGE 406

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
T+ ++P++++VL
Sbjct: 407 TTLHGAEAVDVSYPEFWNVL 426

>ref|ZP_07376339.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ahrensia sp. R2A130]
gb|EFL88233.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ahrensia sp. R2A130]
Length = 453

Score = 116 bits (291), Expect = 6e-24, Method: Compositional matrix adjust.
Identities = 129/440 (29%), Positives = 198/440 (45%), Gaps = 28/440 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTVK+PG KS+S+R L+L +++G T V++LL ++DV A++ LG ++E K
Sbjct: 25 LSGTVKVPDGKSIHSRLILGTIADGHTTVESLLEADDVMTAKSAMQALGATIE--KRGD 82

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G G +E + L GNAG R V T++ G P + RP+
Sbjct: 83 TWHIDGVNGALLEPRE---PLDFGNAGTGSRLTMGLVAGYDFPVTFI--GDPSLSSRPM 137

Query: 135 GDLVVGLKQLGADVDCFL---GTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
G ++ L++ G V G D P+ V+G LP S+Q SA+L+A
Sbjct: 138 GRVLNPLRETGLQVKSTTTENGPDRLPLTVHG-APLPVPVTVRVPVASAQVKSALLAGL 196

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G +I+ + + + E R++ FG V D R GQ P++
Sbjct: 197 NIAGTT--TVIEPVFTRDHTE---RMLAGFGANVSVTDDDGVRTITVEGQTPLKPQDIT 251

Query: 250 VEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
V GD SSAS+ +AG + G VTV+ + + L MGA +T E T
Sbjct: 252 VPGDPSSASFAIVAGLVVPGSDVTVKDVLNPNTR--TGLFDTLVEMGANLTI-ENRRTTG 308

Query: 309 GPPREPFGRKH--LKIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G +H LK + V + P D LAV A FA G T + + RVKE +R
Sbjct: 309 GEEIGDIRVRHSTLKGVSVPATRAPSMIDEYPVLAVAASFAQGETVMNGLDELVRVKECDR 368

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV-PVTI 422
+ A L G EG D + + ++T+ DHR+AMAF + A E PV +
Sbjct: 369 LAATARGLEANGVDCTEGEDTLTVRGGPVVGGGDVETHLDHRIAMAFVLMGLASEKPVVRV 428

Query: 423 RDPGCTRKTFPDYFDVLSTF 442
D +F ++ ++ +
Sbjct: 429 DDTFMIATSFREFRPLMESL 448

>ref|YP_798445.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
borgpetersenii serovar Hardjo-bovis L550]
ref|YP_800336.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
borgpetersenii serovar Hardjo-bovis JB197]
sp|Q04U42.1|AROALPEBJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q04Z13.1|AROALPEBL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ79512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
borgpetersenii serovar Hardjo-bovis L550]
gb|ABJ75578.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
borgpetersenii serovar Hardjo-bovis JB197]
Length = 440

Score = 116 bits (291), Expect = 6e-24, Method: Compositional matrix adjust.
Identities = 123/471 (26%), Positives = 201/471 (42%), Gaps = 71/471 (15%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
++L+ +K SG + +PG KSL+R +L AAL +G + V L +ED + A LGL
Sbjct: 1 MILKNVKLKSGETITVPGDKSLSHRSVLFALCKGKSKVTGFLEADPLNTMSAFTKLGLK 60

Query: 67 V-----EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V E + KR + V L GNAG +R L+A +
Sbjct: 61 VRKVKPGYEYEFESPGKRGFI-----SPNVLDLDFGNAGTGIR-LSAGLLCGLPG 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK---LS 175
VL G +++RP+G ++ L +GA + + P++V G K+K
Sbjct: 108 VNAVLTDGSLKKRPMGRIIKPLTAMGASILGLGEKETAPLKVE-----GKKLSFRYE 161

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW---- 231
I+S + + LM A +A + ++E + ++S + E R + G K E +
Sbjct: 162 SPIASQIKSKCLMLAAIA-SETDLEYSNLSRDHTENMFRFL---GNKIEQISPFHFKI 217

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEV 290
+ Y+ G ++K P GD SSA++FL G G + V G + + + +
Sbjct: 218 EPPYVLNGGEFKVP-----GDISSAAFFVLGVLAKEGNLLVRNIGLNPAR--IGILKA 269

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP-----DVAMTLAVVAL 342
LE+MGAK+ + EP G +N +P D L+V L
Sbjct: 270 LELMGAKIEIRNQRMECG---EPVGLDKTYPILNKTNIKSLIPSIIIDEIPILSVAGL 325

Query: 343 FADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLVN----- 395
FA G IR R KE++R+ + + LG VEE PD T P+ L +
Sbjct: 326 FAKGGFEIRHAEELRAKESDRIHTMVSNFRALGIEVEEYPDGYAFDGTSPQSLEIWKFLA 385

Query: 396 ----TAIDTYDDHRMAMAFSL-AACAEVPVTIRDPGCTRKTFFPDYFDVLST 441
+I ++ DHR+ M+F + + + I + +FP + +L +
Sbjct: 386 SGKKISILSHMDHRITMSFLIFKTLSGFNLHIDETSWIETSFPGFEEKLLES 436

>emb|CAH19218.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida]
Length = 431

Score = 116 bits (291), Expect = 6e-24, Method: Compositional matrix adjust.
Identities = 119/441 (26%), Positives = 200/441 (45%), Gaps = 28/441 (6%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
++ +QP +++G ++ P SKS R A +++G + + N +S D + LG
Sbjct: 2 KVTIQP-GDLTGIIQSPASKSSMQRACAAALVAKGISEIINPGHSNDDKAARDIVSRLGA 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D+ + G K PV + G +G+++R T V + T + G
Sbjct: 61 RLE-DQPDGSLQITSEGVK-PVAPFID-----CGESGLSIRMFTPIVALSKEEVT--IKG 111

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ L LG V G P+ + G L V + GS+SSQ+L+
Sbjct: 112 SGLSVTRPMDFFDEILPHLGKVKSNQGK--LPLVIQG--PLKPADVTVDGSLSSQFLTG 167

Query: 186 LLMAAPLAL-GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LL+A A DV I++ + L S PY+++TL +M+RFG+K + +++ FY K G Y
Sbjct: 168 LLLAYAAADASDVAIKVTN-LKSRPYIDLTLDMVKRFGKLTPENRNYEEFYKAGNVYDE 226

Query: 245 PK--NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
K VEGD S ++ L AI G +TV G S Q D + L A +
Sbjct: 227 TKMQRYTVEGDWSSGAFLLVAGAIAG-PITVRGLDIASQTADKAIVQALMSANAGIAIDA 285

Query: 303 TSVTVTGPPREPFGKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P + L A + + PD+ L +A + G T I+ V+ KE++

Sbjct: 286 KEIKLH--PAD-----LNAFEFDATDCPDLPPLVALASYCKGETKIKGVSRLAHKESD 337

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV-PVT 421
R + ++ E K+G + D + + + + + DHR+AMA ++AA V T

Sbjct: 338 RGLTLQDEFGKMGVEIHLEGLMRVIGGKGVKGAEVSSRHDHRIAMACAVAALKAVGETT 397

Query: 422 IRDPGCTRKTFFPDYFDVLSTF 442
I K++PD++ L

Sbjct: 398 IEHAEAVNKSYPDFYSDLKQL 418

>ref|YP_001002153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorhodospira
halophila SL1]
sp|A1WUI9.1|AROA_HALHL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABM61351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halorhodospira
halophila SL1]
Length = 444

Score = 116 bits (291), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 130/446 (29%), Positives = 209/446 (46%), Gaps = 34/446 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E + P + G ++PG KS+S+R ++L AL++GTT + +L DV + R LG

Sbjct: 4 ENNRVAPGGALHGEARVPGDKSISHRAVMLGALADGTTTRITGMLEGADVLATIDVFRALG 63

Query: 65 LSVEA-DKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+++E ++ A VG G P A+E L +GN+G +MR L + + VL

Sbjct: 64 VAIEGPEQGAVTVHGVGWEGLRP--PARE---LDVGNSGTSMRLLAGLLAGLPFDT--VL 116

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RP+ + L ++GA + P+R++G L G L + S+Q

Sbjct: 117 TGDASLNRRRPMRRVTEPLAEMGARITTS-DAGTAPLRIHGGSPLAGIDYTL PVA-SAQVK 174

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SALL+A A G + P + T R+++ FG S ++GG++

Sbjct: 175 SALLLAGMRAEGHTCV-----TEPAPTRDHTERMLQGFYGPV--SRDLATVCLEGGRRLY 227

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
V D SSA++ L A+I G+ +T+ G + V E+L MGA +

Sbjct: 228 G-TGVDVPADISSAAFLLVAAASIAPGSDLTLRHVGWNPTRTGV--VEILRRMGADIEVLS 284

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAV---VALF-----ADGPTAIRDVA 354
T V G EP +++ + +P+ + LA+ ALF A+G T + A

Sbjct: 285 TD-EVGG---EPVADLRVRSAAALRGIAIPEELVPLAIDEFPALFIAAACAEGETQLTGAA 340

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
RVKE++R+ + L LG +VE D I L + ++ DHR+AMAF++AA

Sbjct: 341 ELRVKESDRIAVMAEGLQTLGVTVEPREDGVRIVGQPVLGGRVHSHTDHRIAMAFAVAA 400

Query: 415 C-AEVPVTIRDPGCTRKTFFPDYFDVL 439
AE PV I R +FP + ++L

Sbjct: 401 LRAEAPVEIEACENVRTSFPGFVELL 426

>ref|YP_391465.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiomicrospira
crunogena XCL-2]
sp|Q31GD2.1|AROA_THICR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB41791.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thiomicrospira
crunogena XCL-2]
Length = 445

Score = 116 bits (290), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 128/460 (27%), Positives = 216/460 (46%), Gaps = 36/460 (7%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGAL 60
M+ + +QP I G +++PG KS+S+R ++L +++EG T V L +D L A

Sbjct: 1 MSNNIQFKVQGGTIKGRIRVPGDKSISHRSIMLGSIAEGVTQVTGFLGDDSLATLKAF 60

Query: 61 RTLGSLVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
+ +G+ +E + VG G K + L +GN+G AMR + + AG +
Sbjct: 61 QAMGVEIEGPNQGNVTIHGVLKGL-----KKPDHPLDMGNSGTAMRLMAGIL--AGQDF 113

Query: 120 TYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
L G + +RP+ + L +GA +D G PP++++ L G L + S
Sbjct: 114 ECELIGDASLSKRPMKRVTSPLADMGARIDTAEGGK-PPLKIHPSSDLKGIDYTLPLMA-S 171

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWD-RFYI 236
+Q S +L+A A G+ + + P + T R++ FG V++E D + +
Sbjct: 172 AQVKSCVLLAGLYAEGETTV-----IEPAPTRDHTERMLNGFGYPVQSEKLEDMQTKVTL 226

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
GG K + KN V D SSA++F+ AA+ + +E G + V ++L++MG
Sbjct: 227 AGGGKLTAKNIDVPSDISSAAFFMVAEEADLVIEHVGINPTRTGV--IDILKLMG 283

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLA-----VVALFADGP 347
A +T E TV G EP +K+ + K+P+ + LA V A A+G
Sbjct: 284 ADITL-ENEATVGG---EPVADVRIKSSKLKGIKIPALVPLAIDEFPVLFVAAASAEQG 339

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP-EKLNVTIDTYDDHRM 406
T + RVKE +R+ + L +G + D II +K I ++ DHR+
Sbjct: 340 TILSGAEELRVKECDRIQVMADALVAVGIDAQPTEDGMIINGGLQKAQSAEIQSHHDHRI 399

Query: 407 AMAFSLAACAEVP-VTIRDPGCTRKTFPDYFDVLSTFVK 445
+MA ++A V +TI D R +FP + ++ +T N
Sbjct: 400 SMAMTIAGLNAVSEITIDDCANVRTSFPTFIELANTVGLN 439

>ref|NP_767378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium japonicum USDA 110]
sp|Q89WF2.1|AROABRAJA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAC46003.1| aroA [Bradyrhizobium japonicum USDA 110]
Length = 469

Score = 116 bits (290), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 130/456 (28%), Positives = 202/456 (44%), Gaps = 61/456 (13%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
++G V++PG KS+S+R L+L AL+ G T + LL EDV +++ LG SVE A
Sbjct: 42 LTGKVRVPGDKSISHRALILGALAVGETRISGLLEGEDVLNTAKSMQALGASVERTGDFA 101

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ VG G A+ + L GN+G R + AV AG + V DG +R RP
Sbjct: 102 WKVQGVGVAGF-----AQPKAALDFGNSGTGCLRLVMGAV--AGCPISAVFDGDASLSRP 154

Query: 134 IGDVLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS-----IS 179
+ ++ L+++GA V + G GG++ L+ S
Sbjct: 155 MRRILDPLEKMGARV-----VSGGEGGRLPLTLQGARDPLPITYKTPVAS 199

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIK 237
+Q SA+L+A A G +I+ S + E+ L+ FG + + R
Sbjct: 200 AQIKSAVLLAGLAAPGTT--TVIESEASRDHTEMLK--HFGADITSTKEGQHGRRITL 254

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
GQ N V D SSA++ + A I G+ V + T L+ L MGA
Sbjct: 255 VGQPELHGANVVVPADPSSAAFPVVAALIAEGSDVVLSDVMTNPLR--TGLFTTLREMG 312

Query: 297 KVTWTETSVTVTGPPREPFGFGR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPT 348
+ +E V G EP + L+ ++V + P D + LAV A FA+G T
Sbjct: 313 SIEESE---VRGDAGEPMAQLRVVRASKLRGVEVPPERAPSMIDEYLVLAASFAEGTT 368

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTIDTYDDHRMA 407
+R + RVKE++R+ A L G VE G D + + T+ DHR+A
Sbjct: 369 IMRGLQELRVKESDRLEATAEMLRVNGVKVEVSGDDLVLVQGRGHVPGGGTVATHMDHRIA 428

Query: 408 MAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
M+ + CA + PVT+ D +FPD+ ++ +

Sbjct: 429 MSALVMGCASDQPVTVDATAFIATSFDPDFIPMMRSL 464

>ref|YP_423626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Magnetospirillum
magneticum AMB-1]
sp|Q2VZA8.1|AROAMAGMM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE53067.1| 5-enolpyruvylshikimate-3-phosphate synthase [Magnetospirillum
magneticum AMB-1]
Length = 446

Score = 116 bits (290), Expect = 7e-24, Method: Compositional matrix adjust.
Identities = 124/439 (28%), Positives = 200/439 (45%), Gaps = 31/439 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
++G+ +PG KS+S+R L+L AL+ G +VV LL +DV +R LG VE D +
Sbjct: 15 LAGSAPVPGDKSISHRALMLGALAVGESVVTGLLEGDDVLRTAACMRALGAEVERRDDGS 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R G GG D L +GN+G R L V + DG +R RP
Sbjct: 75 WRLFGRGVGGLMEPADV-----LDMGNSGTGARLLMGLVATHPFTCFFTGDG--SLRSRP 127

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ ++ L ++GA F+ D P+ V G +L + S+Q SA+++A
Sbjct: 128 MRRVIDPLSRMGAR---FVSRDGGRLPLAVTGTAQPTPITYELPVA-SAQVKSAILLAGL 183

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G E +I++ + + E+ LR FG V+ E ++ R G + +
Sbjct: 184 NTAG--ETTVEREATRDHTEMLR---NFGATVRVEDAEGGGRITVVGFPPELTGRPVV 238

Query: 250 VEGDASSASY-FLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D SSA++ +A + G + + GT L+ + L MGA + +
Sbjct: 239 VPADPSSAAFPVVAALLVEGSEIRLPNVGTNPLR--TGlyQLLEMGADIRFDHPRDQAG 296

Query: 309 GPPREPFGK-KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + R LK +DV + P D LAV A FA+G T +R + RVKE++R+
Sbjct: 297 EPVADLVVRSSRLKGVDPAPERAPSMIDEYPILAVAAFAEGTTRMRGLGELRVKESDRL 356

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAEV-PVT 421
A+ L G +VEE D I+ ++ + T+ DHR+AM+F + A PV
Sbjct: 357 AAMARGLAACGVAVEEEKDALIVHGTGRIPDGDATVTTHFDHRIAMSFLVMGMASARPVA 416

Query: 422 IRDPGCTRKTFFPDYFDVLS 440
+ D +FP + ++++
Sbjct: 417 VDDSEADTSFPAPFVELMN 435

>ref|ZP_01305930.1| hypothetical protein RED65_00130 [Oceanobacter sp. RED65]
gb|EAT13120.1| hypothetical protein RED65_00130 [Oceanobacter sp. RED65]
Length = 744

Score = 116 bits (290), Expect = 8e-24, Method: Compositional matrix adjust.
Identities = 118/443 (26%), Positives = 207/443 (46%), Gaps = 33/443 (7%)

Query: 8 VLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV 67
+ P + G+ ++PG KS+S+R ++L +++ GTT V+ L ED L A R +G+ +
Sbjct: 311 IATPGASVRGSFRVPGDKSISHRSIMLGSATGTTEVEGFLEGEDSLATLQAFRDMGVVI 370

Query: 68 EADKAAKRAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
E + + VG G + P L+LGN+G +MR L + AG + + G
Sbjct: 371 EGPHRGRVTIHVGVLHGLQSPN-----TLYLGNSTSMRLLAGLM--AGQSFDVEMTG 422

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+ + L+++GA ++ PP+ + G L G L + S+Q S
Sbjct: 423 DESLSKRPMNRVANPLREMGATITET-AAEGRPPLLIKGGDALTGIDYTLMA-SAQVKSC 480

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G + + P + T R+++ FG S + I+ G + K+
Sbjct: 481 VLLAGLYAKGTTTSV----VEPAPTRDHTERMLQGFYGPV--SVEGSKVTIESGHELKAT 533

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K V D SSA++F+ A+I + +T++ G + + +L MGA + +
Sbjct: 534 K-IDVPSDISSAAFFMVAASIAPDSITLQHVGINPTR--IGVINILRAMGANIELSNEK 590

Query: 305 VTVTGPFPREPFGGRK--HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V G P + LK I++ +++P D + + A A+G T + RVK
Sbjct: 591 -EVGGEFVADIRVRSACLKGINIPEDQVPLAIDFPAIFIAAACAEKKTVLTGAEEELRVK 649

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAAC- 415
E++R+ A+ L LG E D II+ I T+ DHR+AM+F++A+
Sbjct: 650 ESDRIQAMVDGLKILGVEAEGTEDGAIISGFGAQGAFGGGEIVTHHDHRIAMSFTVASLR 709

Query: 416 AEVPVTIRDPGCTRKTFFPDYFDV 438
AE + + D +FP + D+
Sbjct: 710 AEKQIKVLDCANVATSFPGFVDL 732

>ref|NP_970228.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase), EPSP
synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Bdellovibrio bacteriovorus HD100]
emb|CAE78287.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase), EPSP
synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
[Bdellovibrio bacteriovorus HD100]
Length = 394

Score = 116 bits (290), Expect = 8e-24, Method: Compositional matrix adjust.
Identities = 95/356 (26%), Positives = 170/356 (47%), Gaps = 19/356 (5%)

Query: 87 VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGA 146
+++ +E ++ G G R + A+ A+ + L+ PR+ +RP L+ L QLG
Sbjct: 51 LKEIRERSRIDCGEGGTTFRFM--ALRASRMRGVHTLEATPRLLQRPQKGLLDLSQLGV 108

Query: 147 DVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLI 206
+ V+ P +K++ S SSQY SAL++ L D+E E++ +
Sbjct: 109 QTQI---KNREMFVVSEGWKRPRTPLKVNTSESSQYASALILNCWLLDFDLEFELVGDKV 165

Query: 207 SIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAI 266
S Y ++T+++++ G++ + +++ I GQ+ S VE D SSA + A+
Sbjct: 166 SESYFQLTVQMLKELGMRMQVQG--NKYLIPAGQRI-SKLEYRVESDLSSAFTMASAGAL 222

Query: 267 TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPFPREPFGRKHLKAIDVN 326
GG + S Q D F E+ + M + E ++ V +P L+A++ +
Sbjct: 223 VGGAKLL-NYPVKSSQPDGIFVEIFQMNIEITEMVEGALCV-----KPCA--GLRAVNWD 274

Query: 327 MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 386
+ + PD+ LAV+ +A+G + + + KE+ R+ I +LG S E PD I
Sbjct: 275 LYQSPDLFPVLAVLCSWANGSSKLYNAPHLAAKESNRIAKIADLFERLGISHEVLDPGMI 334

Query: 387 I--TPPEKLVN-TAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFFPDYFDVL 439
I P + L D+ DHRM MA +L +TI +P K+FP+++D++
Sbjct: 335 IHGNPQQSLKKGITFSDQDHRMVMAATLMKLGHDITIENPEAINKSFPEFWDI 390

>ref|YP_001435871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ignicoccus hospitalis
KIN4/I]
gb|ABU82464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ignicoccus hospitalis
KIN4/I]
Length = 443

Score = 116 bits (290), Expect = 9e-24, Method: Compositional matrix adjust.
Identities = 122/431 (28%), Positives = 203/431 (47%), Gaps = 31/431 (7%)

Query: 17 GTVKLPGSKSLSNRIILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G+V+ P SKS + R LA L+EG + + S+DV L A+R G VEA
Sbjct: 29 GSVEAPPSKSWQRAAFLALLAEGRSSFRVPESDDVLASLEAVRAFGAKVEAK----- 82

Query: 77 VVVGCGGKFPVEDAKEEVQ---LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
GG+ +E + +V + + +G R A T V+ G +R RP
Sbjct: 83 -----GGEVAIEGGEVKVPEDVINMRSGTGARIAIAVGTLPVKFGFVVVTGNASLRRRP 137

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193

+ +V + LGA+V G P V GGLPGG+ ++ GS++SQ+++A L+A+ +
Sbjct: 138 MTPVVEVMNALGAEEVSLRGGLLP---VVSFGGLPGGEAEVDGSVTSQHVTAALIASTKS 194
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+I + +S Y+ +T R+M FG K + + ++ + K+ ++ V GD
Sbjct: 195 ERGAKI--TVKNAVSRGYIALTERVMRLFGAKVKCDAKYSYCEVEPSE-LKAVRSE-VPGD 251
Query: 254 ASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
+ A++ A A ++GG V V S GD + + L G +V++++ + V G R
Sbjct: 252 YALAAFPAALAVVSGGEVKVGPLPPPESGPGDHRLLVDYLRKFGVEVSYSYDGYLRVEGSRV 311
Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
K VN+ PD+A+ LA VA + G + + ++ KE+ R+ I L
Sbjct: 312 P-----KGTRVNLKDEPDALPLAAVAASVKGESVLAGLSHLVYKESNRIETILQTLK 364
Query: 373 KLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKT 431
G S +GP ++ E L + DDHR+AM ++ A V I C K+
Sbjct: 365 CFGVSARVDGPSIRVLG-TESLRPCRLKCPDDHRIAMLA AVLGSAGAV-IESAECVNKS 422
Query: 432 FPDYFDVLSTF 442
+P ++D LS+
Sbjct: 423 WPGFWDALSSL 433

>ref|YP_001878489.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Akkermansia
muciniphila ATCC BAA-835]
sp|B2UN97.1|AROA_AKKM8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD05708.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Akkermansia
muciniphila ATCC BAA-835]
Length = 435

Score = 115 bits (289), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 126/455 (27%), Positives = 199/455 (43%), Gaps = 50/455 (10%)

Query: 12 IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADK 71
I + G + +PG KS+S+R +L L+EG T VDN L SED L A+ LG V+ +
Sbjct: 8 ISSLQGALTVPDGKSI SHRAAILGGLAEGVTEVDNFLCSEDCNLTLRAMEQLGAKVDVLE 67
Query: 72 AAK-----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ R V K P E + GN+G MR L + A ++ D
Sbjct: 68 ERQGYGPVRFRITGVAMSPKAP-----ERPIDCGNSGTGMRLLAGMLAACPFDSMFMD 121
Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVK-LSGSI---S 179
+ RP+G ++ L+Q+GA ++ C P+ ++G G+V +S ++ S
Sbjct: 122 A--SLSSRPMGRIMQPLEQMGARIEARGAKPGCAPLSIHG-----GRVHPISYTLPMAS 173
Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYI- 236
+Q SA+L+A A G + P V + T RL FGV + D +
Sbjct: 174 AQVKSAILLAGMFADGTTTVRQ-----PAVTRDHTERLFRHFGVPC----TVDGLTVG 222
Query: 237 KGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMG 295
G + V D SSA++++ A A+ G +T+ G + V A L+ MG
Sbjct: 223 TCGPALPVAHDLTVPADISSAAFWMVAASRPGSRLTLRQVGLNKTRNAVISA--LQRMG 280
Query: 296 AKVTWTETSVTVTGPPR---EPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTA 349
A++ TS G P +G L + ++P D LAV G
Sbjct: 281 ARMDIVPTSPEDAGEPYGDITVYGSDSLHGTSLLPPEIPNLIDEIPI LAVAGALGRGDFI 340
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
+R+ RVKET+R+ L +G VEE D ++ L T + +Y DHR+AM+
Sbjct: 341 VRNARELRVKETDRIATTAANLRLMGVDVEEFDGDMVVHGGTPLKGTLSYGDHRIAMS 400
Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFFPDYFDVLSTFV 443
F +A A+ + D C ++P + L+ F+
Sbjct: 401 FLVAGLSAQGETVVVTDACINTSYPGFERDLAQFL 435

>ref|YP_496604.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Novosphingobium
aromaticivorans DSM 12444]

sp|Q2G8Q3.1|AROA_NOVAD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABD25770.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Novosphingobium
aromaticivorans DSM 12444]
Length = 441

Score = 115 bits (289), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 131/448 (29%), Positives = 208/448 (46%), Gaps = 37/448 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R ++L AL+ G T V LL EDV A+R +G ++E D
Sbjct: 12 LKGRIGVPGDKSISHRSIMLGALAVGETRVTGLLEGEDVLSTAAAMRAMGATIERDADGM 71

Query: 75 RAVV-VGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V VG GG + A L +GN+G + R L V AT+V D + +RP
Sbjct: 72 WHVHGVGVGGLLQPQQA-----LDMGNSGTSTRLLMGLVATHPITATFVGDA--SLSKRP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G ++ L +GA+ G P + +GI P ++ + S+Q SA+L+A
Sbjct: 125 MGRVIDPLSTMGAEFTASPGGRL-PLTLRGIS--PAVPIEYRLPVASAQVKSALLAGLN 181

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEE--HSDSWDRFYIKGGQYKSPKNAY 249
G + + IP + + R++ FG + +D ++G + K P++
Sbjct: 182 TPG-----VTTVIEPIPTRDHSEMRGRGAEELTVDAADGARVIRVRGEAELEK-PQDIA 235

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A + G+ + VE G + +VL +MG + +A V
Sbjct: 236 VPGDPSSAAFFVVAALLVEGSDLVVENVGLNPTR--AALFDVLRMLGGSIEELNRR-EVG 292

Query: 309 GPPREPFGGRKH--LKAIIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P +H L IDV+ +P D L V A A G T + RVKE++R
Sbjct: 293 GEPVADLRVRHSLLTGIDVDPVAVPSMVDEFVLFVAAALAKGRTVTTGLEELRVKESDR 352

Query: 364 MVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT-----IDTYDDHRMAMAFSLAACAE 417
+ A+R L GA+V E D II T + L TA + T+ DHR+AM+ ++A A
Sbjct: 353 ISAMRAALELAGATVTETEDGLIIDGTGGDPLPGTAEGASVVTHLDHRIAMSMAIAGIAS 412

Query: 418 VP-VTIRDPGCTRKTFPDYFDVLSTFVK 444
V + D +FP + +L + +
Sbjct: 413 RNGVEVDDTRPIATSFVPVFESLLESATR 440

>ref|ZP_08081145.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus ruminis
ATCC 25644]
gb|EFZ34308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus ruminis
ATCC 25644]
Length = 437

Score = 115 bits (289), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 130/458 (28%), Positives = 211/458 (46%), Gaps = 45/458 (9%)

Query: 8 VLQ--PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+LQ P + G + +PG KS+S+R L++ A+SEG TV+++ L ED + AL+ LG+
Sbjct: 4 ILQKAPKNGHLHGNLTVPGDKSISHRALMIGAISEGKTVIEHFLCGEDCLSTMKALQDLGV 63

Query: 66 SVEADKAAKRAVVVG-CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + VG G K P E L +GN+G R + + AG N ++
Sbjct: 64 KIVRNGNHVEVEGVGQTGFQKQ-----EKPLDMGNSGTTTTRLMGGLL--AGQNLDKAME 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + LK+ GA V+ P + V+G L +K+ + S+Q S
Sbjct: 116 GDSSLKRPKMRVSEPLKRFKAKVELSDQGTLPAL-VHG-KKLHEATIKMDVA-SAQVKS 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-----G 239
AL+ AA A G I++KL + + E+ LR FG + ++ + G G
Sbjct: 173 ALIFAALYADGTS--TIVEKLPTRDHTEIMLRA---FGADVKTAEADVGTISVSGKPRKLG 227

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVT 299
+K P + +A+ + G+ T V++ T L VL MG V+
Sbjct: 228 RKVVVPSDISAAFFIAAAALIPGSETTFENVSLNPRTTGILH-----VLCKMGNGVS 280

Query: 300 WT---ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDV 353
S +G R + L+AI++ +P + L +VA+ ADG + I
Sbjct: 281 IVPDPNESGEQSGTIRVKYAP--LRAIELTEDVPSIIDELPLVAMLAASADGTSKITGA 338

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAFS 411
A RVKET+R+ EL K G +EE D II E NV +D++ DHR+ M +
Sbjct: 339 AELRVKETDRIAVTAQELRKFGVEIEELEDGMIKGRNWNVQTQKLDHSHGDHRIGMMDA 398

Query: 412 LAAC-AEVPVTIRDPGCTRKTFFPDYFDVLSTF---VKN 445
+AA A+ + + + ++P +F L+ VKN
Sbjct: 399 IAALKADCEMELENEAAIDISYPTFFSDLAKITGGVKN 436

>ref|ZP_02187665.1| 5-enolpyruvylshikimate-3-phosphate synthase [alpha proteobacterium
BAL199]
gb|EDP65319.1| 5-enolpyruvylshikimate-3-phosphate synthase [alpha proteobacterium
BAL199]
Length = 447

Score = 115 bits (287), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 131/443 (29%), Positives = 198/443 (44%), Gaps = 35/443 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++GT+++PG KS+S+R L+ LS G T ++ LL ED+ GA+R G VE K
Sbjct: 11 RPLTGTLRIPGDKSISHRSLIFGGLSVGETTIEGLEGEDILATAGAMRAFGCEVERGKD 70

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R V G G V E + GNAG R L AA T + G +R
Sbjct: 71 G-RWHVHGRG----VSGLDEPADVIDCGNAGTGARLLMG--VAAQQPITTIPTGDGSLRR 123

Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLM 188
RP+G ++ L Q+G G P + P + + ++ S+Q SA+L+
Sbjct: 124 RPMGRVMTPLSQMGVRFATRQGGRLPGAIVG-----PETLIPIEYTLPMASAQVKSAILL 178

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A G + + P + T ++ FG V+ E R GQ + +
Sbjct: 179 AGLGAAGHTTV----IEPKPTRDHTETMLRHFGADVVRVEDMPGGGRRITLVGQPELTGR 233

Query: 247 NAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V D SSA++ +A + G +T+ G GT L+ E L MGA +T T
Sbjct: 234 KVVVPADPSSAFAVAALLVEGSEITLPGVGTNPLR--FGLFETLIEMGADITLTNRR- 290

Query: 306 TVTGPPREPFGGRKH--LKAIIDVNMNKMMP--DVAMTLAVVALFADGPTAIRDVASWRVKE 360
T G P +H L+ I+V + P D LAV A A+G T +R + RVKE
Sbjct: 291 TEAGEPVADLIIRHGPLRGIEVPPERAPTMIIDEYPILAVAASVAEGTVMRGGLEELRVKE 350

Query: 361 TERMVAIRTELTKLGASVE-EGPDYCIITPPEKL-NVTAIDTYDDHRMAMAF-SLAACAE 417
++R+ A+ LT G V+ +G D + + T I DHR+AM+F L +E
Sbjct: 351 SDRLGAMAQGLTACGVRVDVDGDDLTVRGASNGVAGRTTIPVDLDHRIAMSFLVLGMVSE 410

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLS 440
V I D +FP + D+++
Sbjct: 411 EFVAIDDAAAIATSFPGFADLMN 433

>ref|YP_001939700.1| 5-enolpyruvylshikimate-3-phosphate synthase and cytidylate kinase
[Methylobacterium thermophilum V4]
gb|ACD83102.1| 5-enolpyruvylshikimate-3-phosphate synthase and cytidylate kinase
[Methylobacterium thermophilum V4]
Length = 695

Score = 114 bits (286), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 130/457 (28%), Positives = 215/457 (47%), Gaps = 44/457 (9%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
++++P I G + +PG KS+S+R ++LA+L+ G + + + L S D L A +G+
Sbjct: 8 LIVEPCPLIKGEISVPGDKSISHRAVMLASLARGRSKIRHFLPSADCLCTLRAFEAMGVR 67

Query: 67 VEADKAAKRAVVV-GCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE K K +++ G GG+ P E + GN+G MR + ++A + +

Sbjct: 68 VE--KEGKTTLLIEGKGGQLDPPFE-----AIDCGNSGTMRLMAGILSAQPFYSKLIG 119

Query: 124 DGVPFRMRERPIGDLVVLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
D + RP+ ++ L+ +GA + + PP+ + L G +L S+Q

Sbjct: 120 DR--SLSRPMPNRIIEPLRLMGAKIRAEGKENTPPLFIEP-STLKGIDYRLPIP-SAQVK 175

Query: 184 SALLMAAPLALGDVEIEIIDKLIS-IPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
S +L A A G I ++I +P + T RL E+FGV+ ++ + GG K

Sbjct: 176 SCILFAGLFAPG-----ITRIIEPVPSPRDHTEFLFEQFGVRTLREEN-GCIVLHGGMKL 228

Query: 243 KSPKNAYVEGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
++ + V GD SSA++++ AA + + V G + ++L MGA +

Sbjct: 229 EA-SDVDVPGDFSAAFWIGAAAALPNSSELVRSVGLNPTR--TGLLKILLRMGAHI--- 282

Query: 302 ETSVTVTGPPPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
E SV + EP G LK + +++ D LAV+ A+G T IR+

Sbjct: 283 EESVE-SHARGEPIGSLWIRGNKLKGTVIQGDIVGVIDELPILAVIGALAEGITEIRNA 341

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFS-L 412
RVKE++R+ AI T L G VEE D I E + ++++ DHR+AMAFS L

Sbjct: 342 QELRVKESDRIKAIVTNLRAFGEVEELVDGMRIQGMESVQPARVESFGDHRIAMAFSIL 401

Query: 413 AACAEVPTTIRDPGCTRKTFP---DYFDVLSTFVKN 445
A A I D C ++P D + + +F K

Sbjct: 402 ALKANKASRIEDVDCIATSYPGFEQDLYALTQSFSKE 438

>ref|YP_003756447.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hyphomicrobium
denitrificans ATCC 51888]
gb|ADJ24126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hyphomicrobium
denitrificans ATCC 51888]
Length = 446

Score = 114 bits (286), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 127/437 (29%), Positives = 198/437 (45%), Gaps = 26/437 (5%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V+LPG KS+S+R L+ AL+ GTT + LL SEDV A+ LG E K

Sbjct: 17 LKGRVRLPGDKSISHRALIFGALATGTTRIRGLLESEDVVNTARAVSALGAHAE-----K 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V G+ P + L GN+G R + + AG T + G + RP+

Sbjct: 72 RGDVWEVKGRGPGLRQPTEPLDFGNSGTGARLMMGVI--AGHPITVQMTGDASLSRRPM 129

Query: 135 GDLVVLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L Q+G +V G + P+ + G L L S+Q SA+L+A +

Sbjct: 130 RRVLGPLMQMGLEV-IETGRETLPLTLRGTSSELIPVYPLP-VPSAQVKSALLAGLHSA 187

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G E +I+ + + E R++ FG V+ + I+G + ++ V G

Sbjct: 188 G--ETTIEHEATRDETE---RMLRHFGANVRIMDKEGGRAITIRGDAELTG-RDILVPG 241

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++ +A A I G+ VT+EG + L+ MG VT P

Sbjct: 242 DPSSAAFLVAAALIVPGSDVTIEGVLINPTR--TGLYTTLQEMGGDVTLNQRREEGGEPI 299

Query: 312 REPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ R LK + V + P D LA ++ FA G T + +A +VKE++R+ A

Sbjct: 300 ADIRVRASELKGVRVPAERAPSMIDYEPVLAASAFAGTTQMDGLAELKVKESDRLQAT 359

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAACA-EVPVTIRDP 425
T L G + D I+ ++L + T+ DHR+AMAF A A E P+T+ D

Sbjct: 360 ATGLEVNGVTARIDGSLIVEGKQRLKGGGLVATHLDHRIAMAFSLTAGLASEKPITVDDT 419

Query: 426 GCTRKTFPDYFDVLSTF 442
+FP++ ++ T

Sbjct: 420 TMIATSFPEFRGLMETL 436

>ref|ZP_07965739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Segniliparus rugosus
ATCC BAA-974]

gb|EFV13033.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Segniliparus rugosus
ATCC BAA-974]
Length = 377

Score = 114 bits (286), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 103/302 (34%), Positives = 147/302 (48%), Gaps = 30/302 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ TV LPGSKS++NR L+LAAL+ + + L S D ML ALR +G V +
Sbjct: 56 LDATVGLPGSKSITNRLVLAAALASSPSRIVGTLRSRDTDLMLDALRRMGAGVRIHD-DQ 114

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + G P+ +A +V L AG MR L A A G ++ DG + R RP+
Sbjct: 115 TTVDIEPG---PLREASVDVGL----AGTVMRFLPPAAALATGAVSF--DGDEQARARPL 165

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLA 193
++ L+ LG VD D P V G G + GG+V + S SSQ++S LL++ A
Sbjct: 166 DTILNALRDLGVAVDG---DSLPFVVRGQGRVGRGEVAVDASASSQFVSGLLLSGARYD 221

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP-----KN 247
G + L S P++EMT+++E GV+ E + ++ P +
Sbjct: 222 EGLTVRVVGGPLPSAPHIEMTVQMLEDSGVRVEQPEQ-----HVWRIPPSPIAGRE 272

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
VE D S+AS FLA AA GG V V TT+ Q +L MGA V + +TV
Sbjct: 273 WLVEPDLSNASPFLAAAAAAGEVVRVPRWPTTTTQAGDAIRHILARMGATVRLQDGWLTV 332

Query: 308 TG 309
G
Sbjct: 333 QG 334

>ref|YP_001318531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkaliphilus
metalliredigens QYMF]
sp|A6TL04.1|AROA_ALKMQ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABR46872.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alkaliphilus
metalliredigens QYMF]
Length = 425

Score = 114 bits (285), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 120/453 (26%), Positives = 227/453 (50%), Gaps = 44/453 (9%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+V ++++ G + +PG KS+S+R ++L+++S+GT+ V L ED + R LG+
Sbjct: 2 LVTNKVEKLEGKMTVPGDKSISHRAIMLSSISKGTSRVKGFRLGEDCLSTISCFRDLGID 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E D+ + ++ G G + E + + GN+G +R ++ + AG ++ G
Sbjct: 62 IE-DRGTE-IIIQKKG---LHGLSEPLNVLDAGNSGTTIRLISGIL--AGQKFLTIVTG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLS 184
+R+RP+ + L+++GA ++ + P+ + G G L G + + +SS Q S
Sbjct: 114 DASLRKRPMERIATPLRKMGAFIGRDIYGNLAPLVIRG-GNLKG--MDYASPVSSAQVKS 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+A GD + +K+ S + E L+ G+ A + S D+ + G+
Sbjct: 171 AILLAGLYGEGDTIVR--EKITSRDHTEKMLK-----GLGA--NISTDQGVTRLGKSELY 221

Query: 245 PKNAYVEGDASSASYFLAGAA-ITGGTVTVEGCGTT-----SLQGDVKFAEVLE 292
++ V GD SSA++F+AGAA + G + EG G + GD++ + +
Sbjct: 222 GQSIIEVPGDISAFAFFMAGAAALPGSFLITEGVGLNPTRTGIIDVLRDMGGDIEIHNLRQ 281

Query: 293 MMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRD 352
G ++ + + G ++ +G + K I + ++ D LA++A A+G T I
Sbjct: 282 SGGEEIG---DIMIRG--KKLYGTEIGKEI---IPRLIDEIPVLAIIAATAEGKTIITG 332

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
+VKE+ R+ A+ TE+ K+G V E PD I + + +++Y DHR+AMA ++
Sbjct: 333 AEELKVKESNRITAMVTEMQKVGIKVTETLPDGMEIEGGQVITGGRVESYGDHRIAMAMAI 392

Query: 413 AAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
A+ P+ I D C +FP++ + L V+
Sbjct: 393 CGLFAQEPIKINDSQCIDISFPNFEEKLKAVVR 425

>ref|YP_916014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paracoccus
denitrificans PD1222]
sp|A1B474.1|ARO_A_PARDP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABL70318.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Paracoccus
denitrificans PD1222]
Length = 443

Score = 114 bits (285), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 128/437 (29%), Positives = 205/437 (46%), Gaps = 31/437 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
++G ++PG KS+S+R L+L ALS G T + LL +DV A+R G VE +
Sbjct: 18 LTGEAQVPGDKSISHRALILGALSVDGTHITGLLEGQDVLDTAAMRAFGAQVERLGE 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG A+ E + GN+G +R + A+ AT+ D + RP
Sbjct: 78 WRVNGVGVGGF----AEPEGVIDCGNSGTGVRILMGAMATTPITATFTGDA--SLSRRP 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L+ G +V G P +P V+ + S+Q SA+L+A
Sbjct: 131 MGRVTDPLELFGCEVTAREGKRLPLTIKGASEPVP---VRYKTPVASAQIKSAVLLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G+ + + + P + T R++ FG + E + +KG + K P+ V
Sbjct: 188 APGETVV-----IEAEPTRDHTERMLAGFGAAITTTETAEGHVIIKGRPELK-PQPVA 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVWTWTETSVTVTG 309
D SSA++ +A A I G+ + V G + D + +LE MGA + + E G
Sbjct: 242 PRDPSSAAFPVAAAALIVPGSEIRVPGVSRNPTR-DGLYVTLLE-MGADIRF-ENQREEGG 298

Query: 310 PPREFPGRKH--LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P +H LK + V + M D L+V+A FA+G T ++ V RVKE++R+
Sbjct: 299 EPVADLVVRHGLKGVTVPAERAASMIDEFPILSVIACFAEGTTVMQGVHELVRVKESDRI 358

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-DTYDDHRMAMAFSLAACA-EVPVTI 422
A+ L GA V + D + L+ A T+ DHR+AM+F +A A P+++
Sbjct: 359 DAMAVGLRANGAEVVDQTDMTVHKGGLDGGATCATHLDHRIAMSFLVAGLASHQPISV 418

Query: 423 RDPGCTRKTFPDYFDVL 439
D G +FPD+ ++
Sbjct: 419 DDGGPIATSFPDFLPLM 435

>ref|YP_912693.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
phaeobacteroides DSM 266]
sp|A1BIP2.1|ARO_A_CHLPD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABL66269.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
phaeobacteroides DSM 266]
Length = 434

Score = 114 bits (285), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 119/445 (26%), Positives = 211/445 (47%), Gaps = 46/445 (10%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK----- 74
LP KS+S+R L+ ALS+GTT + N D L L+ G+++ ++ A
Sbjct: 11 LPPDKSISHRAALIGALSDGTTEIVNFSGGFDNQSTLAVLQASGIALIQEECAGSYGRRI 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + + L N+G MR + A + VL+G + +RP+
Sbjct: 71 RRVVIESRGLWSF--LAPQAPLMCNNSGSTMRFAGILAAQPFES--VLEGDSSLMKRPM 126

Query: 135 GDLVVGLKQLGADVD-CFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+Q+GA V+ F GT P+R+ G L + +L +SS + +L+ A L
Sbjct: 127 NRVADPLRQMGAVELSFSGT--APIRIQGTKDLHSLEYRL--PVSSAQVKSLVAFALH 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
D + II+ + S + E+ L G++ + +R I G+K K Y+ D
Sbjct: 183 -ADGQTRIIEPIRSRDHTEMLML-----GLETIDQPNGERVIIIVPGRKRIESKPFYIPAD 235

Query: 254 ASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
S+A + +A A + G+ + + C + G + +L GA ++ E S + G
Sbjct: 236 PSAACFIVALALLAKGSDIIRDLCLNPTRTG--YLAILAGAGAGIS-VENSRVIGG-- 289

Query: 312 REPFQ-----RKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
E G L ++ ++ N + ++ M LAV++ F+ G + A R KE
Sbjct: 290 -EAIGDVLVHSEGELNSLVISDPHEVANVIDEIPM-LAVLSAFSSGRFELHHAELRTKE 347

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAACAE- 417
++R+ A+ L +LG E+ PD + + V +I+++DDHR+AM+F+++A A
Sbjct: 348 SDRIDALVVNLERLGFQCEQYPDGFKVNGRIAMPKGVVSIESFDDHRIAMSFAIAGKATG 407

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
V + I D G +FP++F+++ +
Sbjct: 408 VDLAISDIGVGVVSFPNFFFEIESL 432

>ref|YP_001280145.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Psychrobacter sp. PRwf-1]
gb|ABQ94195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychrobacter sp.
PRwf-1]
Length = 770

Score = 114 bits (284), Expect = 3e-23, Method: Compositional matrix adjust.
Identities = 121/446 (27%), Positives = 203/446 (45%), Gaps = 36/446 (8%)

Query: 8 VLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
++ P I+GT+ +PG KS+S+R ++ +L+EG T V L ED L A R +G+++
Sbjct: 327 IITPSSSTINGTIAVPGDKSISHRSIMFGSLAEGVTRVSGFLEGEDALATLQAFRDMGVTI 386

Query: 68 EADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E + + VG G P L++GN+G MR L+ + A ++ VL G
Sbjct: 387 EGPENGNNVVIHGVINGLKP-----SRTPLYMGNSGTTMRLLSGILAAQSFS--VLTGD 439

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYL 183
+ +RP+ + L+++GA + P+ + G G S+Q
Sbjct: 440 ASLSKRPMERVAKPLREMGATLQTTGERGTAPISITGSDKRGSKLHGITYDMPVASAQVK 499

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
S L++A A G + +I IS + E R++ FG E + ++GG K
Sbjct: 500 SCLILAGLWAE--KTTVIQPEISRHDTE---RMLSAFGYDVE--VEGNTISVEGGGKLT 552

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ A V D SSA++F+ A+I + +T+ G + + ++L++MGA ++ +
Sbjct: 553 ACDIA-VPADISSAAFFMVAASIAKDSQITITQVGMNPTRTGI--IDILKLMGADISLSN 609

Query: 303 TSVTVTGPPPREPFGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
+ V G P K LK I + +P D L V A A G T + R
Sbjct: 610 ETF-VGGEPVADITIKSAQLKGITPEALVPLAIDEFPVLFVAASCAQQQT VLTGAKELR 668

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAF 410
VKE++R+ + LT+LG D II + I ++ DHR+AM+F
Sbjct: 669 VKESDRIAVMADLTQLGVDCAVTDGIIIEGKGDGQSHQAVFGGGEIYSHHDHRIAMSF 728

Query: 411 SLAAC-AEVPVTIRDPGCTRKTFPDY 435
S+A+ A +TI+ +FP +
Sbjct: 729 SVASLRATDTITIQGVETVNTSFPGF 754

>ref|YP_002298688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodospirillum
centenum SW]
gb|ACI99875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodospirillum
centenum SW]

Length = 448

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 127/471 (26%), Positives = 203/471 (43%), Gaps = 69/471 (14%)

```
Query: 2   AGAEEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
          AG  ++ +  ++GTV +PG KS+S+R L+  ALS G T ++ LL  +DV  ALR
Sbjct: 6   AGPRPLLSRRSGALAGTVPDGSISHRALMFGALSLGETRIEGLLEGDDVLRATAALR 65

Query: 62  TLGLSVEADKAAKRAVVV---GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
          LG  EA++  +  G GG  A+  L +GN+G A R L  +  A
Sbjct: 66  ALG--AEAERLPDGTWITRGRGVGGL-----AEPAQVLDMGNSGTARLLMGLL--ATHP 116

Query: 119  ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
          T V+ G  + +RP+  +  L+ +GA  G  G LPG  +  +
Sbjct: 117  FTSVMTGDASLTGRPMARVTTPLETMGARFALRSG-----GRLPGAVIGTDRPV 165

Query: 179  -----SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD 229
          S+Q  SA+L+A  A G  +  +  P  + T R++  FG++  +
Sbjct: 166  PIAYRLPVASQVKSAILLAGLNAPGRRTTV-----IEPEPTRDHTERMLRHFGIEVTVEE 220

Query: 230  SWDRFYIK--GGQKYKSPKNAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVK 286
          + D  GQ  + ++ V  D SSA++  A I G  +++ G GT  +
Sbjct: 221  AGDGALAATVTGQELTARDLRVPADPSSAAFPAAVALIRPGSALSPLPGVGTNPRR--TG 278

Query: 287  FAEVLEMMGAKVTTWETSVTVTGPPPREPFGR-----KHLKAIDVNMNKMP---DVA 334
          E L  MGA  + +  PRE  G  L+ ++V  + P  D
Sbjct: 279  LFETLRAMGADIAYAN-----PREEGGEPVADLLVRASGLRGVEVPPEAPSMIDEY 330

Query: 335  MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TTP 390
          L + A  A+GPT +R +  RVKE++R+  +  L  G +VE G D+ ++  PP
Sbjct: 331  PVLICIAAACAEGPTVMRGIGELRVKESDRLAMMADGLAACGVTVEAGEDWMVVHGRGRPP 390

Query: 391  EKLNVTAIDTYDDHRMAMAF--SLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
          + T  DHR+AM+F  L  E PV + D  +FP +  +++
Sbjct: 391  A--GGATVATAMDHRIAMSFLVLGMATEQPVRVDDGAFIDTSFPGFVALMN 439
```

```
>ref|YP_828529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Solibacter
          usitatus Ellin6076]
sp|Q01Q26.1|AROASOLUE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
          AltName: Full=5-enolpyruvylshikimate-3-phosphate
          synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ88244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Solibacter
          usitatus Ellin6076]
Length = 426
```

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 117/453 (25%), Positives = 205/453 (45%), Gaps = 58/453 (12%)

```
Query: 9   LQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
          + P  I+G + LPG KS+S+R ++++++EG + + N  D H  LG +R LG+ +
Sbjct: 5   ISPAAAITGAILTPGDKSISHRYAMISSIAEGDSRILNYSTGADCHSTLGCMRALGIEIT 64

Query: 69  ADKAAKRAVVVGC---GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
          +  VV G  G + P D  L  GN+G +R L+  + AA  T + G
Sbjct: 65  GE--GTEFVVHGKGLDGLRAPAGD-----LDAGNSGSTIRMLS-GILAAQPFTTRIF-G 114

Query: 126  VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQ 181
          +  RP+ ++  L Q+GA++  PP+ ++  GGK++  S+Q
Sbjct: 115  DESLSRRPMQRIMKPLAQMGAEIRA-REEKFPPLEIH-----GGKLRAIDYTLVPVPSAQ 167

Query: 182  YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
          + +L A  A G  E  + + + S  +E+ LR  FG AE + +  + G  +
Sbjct: 168  VKTCVLFAGLFAEG--ETTVTEPVRSRDHTETIALR---EFG--AELTAAGKITLTGRPR 220

Query: 242  YKSPKNAYVEGDASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
          + ++ V  D SSA++F+  A  + G ++ + G G  +  ++L  MGAk+
Sbjct: 221  L-TGRDLIVPSDISSAAFFIVAALLVRGSSLVIRGVGLNPSRS--ALLDLLIGMGAKIRI 277

Query: 301  TETSVTVTGPPPREPFGRKHLKAIDVNMNKMP-----DVAMTLAVVALFADGP 347
```

```

          P E      + + I V + +          D LAV+      +
Sbjct: 278 -----PQLESQNGELIGEIQVEHSALQGGVIEGGLTAAVIDEIPVLAVLGAATEEG 328

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMA 407
          I+D   RVKET+R+  +  L +LG + EE PD +I  +K      D++ DHR+A
Sbjct: 329 LTIKDAGELRVKETDRIATVVENLRRLGVTAEETPDGLVIPGRQKFRAAEFDSFGDHRIA 388

Query: 408 MAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVL 439
          MAF++AA  +      I++      +FP+++ L
Sbjct: 389 MAFAVAALRGDGESVIQNADAASVSFPEFWSTL 421

```

```

>ref|YP_684057.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter
denitrificans OCh 114]
sp|Q161H2.1|AROA_ROSDO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG33371.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter
denitrificans OCh 114]
Length = 450

```

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 131/435 (30%), Positives = 203/435 (46%), Gaps = 32/435 (7%)

```

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
          ++G ++PG KS+S+R L+L ALS G T + LL +DV A+R G +V +
Sbjct: 18 LTGEARVPGDKSISHRSLILGALSVGETRISGLLEGQDVLDTAKAMRAFGATVTDHGGGE 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
          +V VG GG A+ + + GN+G +R + A+ + +AT+ D + RP
Sbjct: 78 WSVHGVGVGGF-----AEPDGVIDCGNSGTGVRLIMGAMATSPISATFTGDA--SLNGRP 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
          + + L GA G P V +P V + + S+Q SA+L+A
Sbjct: 131 MARVTDPLALFGAQSYGRQGRLPMTVVGAAEPVP---VTYTVPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
          A G + +I+ + + E R++ FG + E +D + G + KS K V
Sbjct: 188 APG--QTVVIEAEATR DHTE---RMLAGFGAEISVEDADEGRVITLTGQPELKSQK-IDV 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
          D SSA++ + A I G+ V V G G + L MGA +T+ V
Sbjct: 242 PRDPSSAAFPVCAALIVPGSDVLVPGI GLNPTR--AGLFTTLREMGADLT YENERVEGGE 299

Query: 310 PPREFPGR--KHLKAIDV---NMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          P + R L I+V M D L+VVA FA G T +R V RVKE++R+
Sbjct: 300 PVADLRARFSPDLTGIEVPPARAASMIDEYPVLSVVASFARGDTVMRGVKELRVKESDRI 359

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADT---YDDHRMAMAFSLAACAEVVPV 420
          A+ + L G +VE+GPD+ ++T NV T + DHR+AM+F + A + PV
Sbjct: 360 DAMASGLRANGVAVEDGPDWWVVTGRGHGNVAGGATCASFLDHRIAMSFLVMGMATQKPV 419

Query: 421 TIRDPGCTRKTFPDY 435
          T+ D G +FP +
Sbjct: 420 TVDDAGPIATSFPIF 434

```

```

>ref|YP_253363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
haemolyticus JCSC1435]
sp|Q4L6G8.1|AROA_STA HJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE04757.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
haemolyticus JCSC1435]
Length = 432

```

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 111/432 (25%), Positives = 203/432 (46%), Gaps = 36/432 (8%)

```

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
          G +++PG KS+++R ++LA+L+ G + + L ED + + LG+++E A+

```

Sbjct: 15 GEIEVPGDKSMTHRAIMLASLATGQSTIYKPLLGEDCLRTIEIFKLLGVNIEL---AEEK 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
++V G + + L+ GN+G R L + +G N VL G + +RP+

Sbjct: 72 IIVDSPGYNKFKTPHQ--TLYTGNSGTTTLLAGLL--SGLNLCVLSGDASIGKRPMDR 127

Query: 137 LVVGLKQLGADV----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
++ L+ +GA++ D F P +NGI K++++ S+Q SALL A+

Sbjct: 128 VMKPLRLMGANITGIDDNFTPLIKPASINGITY---KMEVA---SAQVKSALLFASLF 180

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ +I +D +S + E + E+F + S + K+ K+ YV G

Sbjct: 181 SNDSSKITELD--VSRNHT---TMFEQFNIPISISGKEITTQPNAEHIKA-KDFYVPG 234

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F+ A IT G+ +T+ G + + +++++ M + ++T T P

Sbjct: 235 DISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMEGNIECL--NITDTSEP 290

Query: 312 REPFGRKH--LKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMV 365
K+ LK + + + +P L ++AL A G + I+D +VKET R+

Sbjct: 291 TASIRVKYTPNLKPVLEIGDIVPKAIDELPIALLCTQASGTSIIKDAEELKVKETNRID 350

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVTIRD 424
L LG ++ D II P E +D+ DHR+ M ++A+ ++ P+ IR

Sbjct: 351 TTADMLGGLGFELQPTDDGLIHPSEFKKSATVDSLTDHRIGMMLAIASLLSDKPLNIRQ 410

Query: 425 PGCTRKTFFPDYF 436
+FP +

Sbjct: 411 FDAVNVSFPGFL 422

>ref|YP_003627046.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moraxella catarrhalis
RH4]
gb|ADG61153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Moraxella catarrhalis
RH4]
Length = 767

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 121/442 (27%), Positives = 209/442 (47%), Gaps = 35/442 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P ISG + +PG KS+S+R ++ AL++G T V L ED L A +G+ +E

Sbjct: 332 IRPQNAISGVISVPGDKSISHRSIMFGALADGVTHVTGFLQGEDALATLQAFADMGVKIE 391

Query: 69 --ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+DK V + G K P + L++GN+G +MR L ++A ++ V+ G

Sbjct: 392 RNSDKVTIHGVGID-GLKAP-----KTPLYMGNSGTSMLLAGILSAQAFDS--VMTGD 442

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +RP+ + V L+ +GA + P+ + G L + +L + S+Q S L

Sbjct: 443 VLSLQRPMEVAVPLRNMGAQISTGKKGTAPLSITGSQTLNAIEYQLPVA-SAQIKSCL 501

Query: 187 LMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++A+ A G II+ +S + E R++ FG + + + GG + +

Sbjct: 502 ILASLWAKGTT--TIEPEVSRDHTE---RMLNAGYPVQVDGC--KISVTGGGRL-TAT 553

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++F+ AI GG +T+E G + V ++L +MGA +T +V

Sbjct: 554 DIIVPADISSAAFFMVLGAIGGGEGLTIEKVMNPTRTGV--IDILTMGADITVMNEAV 611

Query: 306 TVTGPPREPFGFR-KHLKAIDVNMNKMMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
P + R L ID+ + +P D L + A A G T + RVKE+

Sbjct: 612 VGGPIADITVRPSDLHGIDIPHEHLVPLAIDEFPILFIAASCAYGVTKLTGAKELRVKES 671

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIIT----PPEKLNVT---IDTYDDHRMAMAFSLAA 414
+R+ + L LG + D II EK + I+++ DHR+AM+F+++A+

Sbjct: 672 DRIQVMADGLATLGIDSKVLEDGIIIQGKGIQGEKNAIFGGGVIESHHDHRIAMSFAS 731

Query: 415 C-AEVPVTIRDPGCTRKTFFDY 435
A + I+ +FP++

Sbjct: 732 SRATDDIIIGTETVNTSFPNF 753

>gb|AAM75972.1|AF481102_8 5-enolpyruvylshikimate-3-phosphate synthase [Candidatus Tremblaya princeps]
Length = 432

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 124/435 (28%), Positives = 185/435 (42%), Gaps = 31/435 (7%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALS-EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
+ G +P SKS SNR + A +S + T + L+S+D +L A + G+ E
Sbjct: 14 RHRRGLALVPTSKSASNREVACAFVSLKATQLSGRTLHSDDTAVLLNAAHSFGILAEQHG 73

Query: 72 AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R C V +L++GN+G R + A+ +A ++ G PRM
Sbjct: 74 RTLRLGPERCKHGLLV-----AELYVGNSTTARLVCASACRRPRHA--LVHGDPDRMHR 125

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPG-GKVKLSGSISSQYL-SALLMA 189
RP L VGL LGA V F PV + L L S SSQ++ SA+L +
Sbjct: 126 RPALALTVGLASLAKVLHFAVQGSLLPVAIGPTCNLKNFAPMPLPMSESSQFITS AVLAS 185

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF-YIKGGQKYKSPKNA 248
+ D I S YV T+ +M FG+ +E W R+ + + P +
Sbjct: 186 HGIVHKDTPICQGLTSSRLYVASTIDIMGLFGMCSE-GHGWQRYAHAPASMDCEYPGS- 243

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D +SASY A + G + CG + Q D A+ + MG + +
Sbjct: 244 -TDFDMTSASYPTALGCMGMGMWRML-CGVDHASQSDATMADAMSSMGAMWQCRDGNAM 301

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
R H + PD AMT ++L G + V SWR KET+R++A+
Sbjct: 302 WRAAR-----HAPTPRLLCCSAPDGAMTAMTISLALAGASDAVGVLVSWRYKETDRVLAM 355

Query: 368 RTELTKLGLASVEEGPD-----YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
EL ++G + + G C +T + +V+ TY DHR+AM SL A V
Sbjct: 356 ALELRMRGVAADCGMGSMACLSCSLTWHGRADVS---TYRDHRIAMCCSLMHAAGCGVRT 412

Query: 423 RDPGCTRKTFPDYFD 437
P C KT+PDY
Sbjct: 413 SGPQCVCCKTYPDY LH 427

>ref|YP_001154310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum arsenaticum DSM 13514]
gb|ABP51658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum arsenaticum DSM 13514]
Length = 398

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 122/432 (28%), Positives = 198/432 (45%), Gaps = 51/432 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ G LP SK S R+LL +AL+EG TVV L S+DV M+ A++ + +++ AD A
Sbjct: 8 RLEGRFPLPPSKPYSQRLLLASALAEGETVVRGLELSDDVVMVRAIQPIASITLRADTA 67

Query: 73 --AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+KR + + + +G +R+ A G +R
Sbjct: 68 VVSKR-----EPDKYRAFNVMESGFTLRTAVAVYAGIPGLTAVYFGGT--LR 112

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNG--IGGLPGGKVKLSGSISSQYLSALLM 188
RPI +LV L+L V G V ++G +G +V++ +SSQY+S L+
Sbjct: 113 GRPIDELVEVLRLR-VSVSKLPGA---VVIDGRRRLGRF---RVEIRADVSSQYISGLMF 164

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A G V + ++ S +VE T ++ FG + D ++GG +SP
Sbjct: 165 LAAAGDGGVVVPKGERK-SWSFVEATADVLRFLGAEVSMGDE--VVVEGG--LRSPGTV 218

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD S AS+ L + TGG V +EG T + D ++ + MGA + + + V
Sbjct: 219 DVPGLDSLASFLLVASLATGGKVRLEGAVT---KLDVVLDIFKFMGADIAYGDGYVEAR 275

Query: 309 GPPREPFRKHLKAIDVNMNKMPLDAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G K +DV++ PD+ M +A+ A + +AIR V R KE++R+ +
Sbjct: 276 G-----GFTKGVDVLDGPNPDLVMPVALAAAMVEEQSAIRGVEHLRFKESDRVATVL 327

Query: 369 TELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
L +LG EG I PP++ +V + DHR+ + ++AA V + D
Sbjct: 328 DVLWRLGVDARYEGGVLYIKPPKRRDVR-FSSSGDHRIGL-MAMAAAKAVGGCVDDISP 385

Query: 428 TRKTFPD---YF 436
K++P YF
Sbjct: 386 VAKSWPSAILYF 397

>ref|ZP_01916521.1| prephenate dehydrogenase, putative/3-phosphoshikimate
1-carboxyvinyltransferase AroA [Limnobacter sp. MED105]
gb|EDM82249.1| prephenate dehydrogenase, putative/3-phosphoshikimate
1-carboxyvinyltransferase AroA [Limnobacter sp. MED105]
Length = 447

Score = 114 bits (284), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 125/437 (28%), Positives = 210/437 (48%), Gaps = 39/437 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEA-DKAA 73
+SG+ ++PG KS+S+R +++ ++EG T V+ L ED + A R LG+ +E D+
Sbjct: 17 MSGSARVPGDKSISHRSIMMGSAIEGITEVEGFLEGEDALATMNAFRALGVQIEGPDGRK 76

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ VG G K P + L GN+G +MR ++ + AG + +L G + +R
Sbjct: 77 VKVHGVGMHGLKAPRQ-----VLDCGNSGTSMRLMSGLL--AGQDFDCMLTGDSSSLGKR 128

Query: 133 PIGDLVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L +GA ++ G PP+ ++G L L + S+Q S +L+A
Sbjct: 129 PMKRVIDPLVLMGARIEAQEGGR-PPLHIHGRTTLKAIDYVLPMA-SAQVKSCVLLAGLY 186

Query: 193 ALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G ++ P V + T R++ FGV E + + +KGGQ K+ K V
Sbjct: 187 ADGTTT-----VTEPAVTRDHTERMLRGFGV--EVITNGAKASVKGQTLKATK-IDV 236

Query: 251 EGDASSASYFLAGAAIT-GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++F+ A+I +T++ G + V ++L++MGA + + + V G
Sbjct: 237 PSDISSAAFFMVAASIAPQADITLKHVGLNPTRTGV--IDILKLMGANIELSNHA-EVGG 293

Query: 310 PPREPFRGRK--LKAIDVNMNKMPL--DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + LK I++ + +P D L V A A G T + RVKE++R+
Sbjct: 294 EPVADVVRSAALKGIEIPEHLVPLAIDEFPVLFVAAANATGRTILTGAELRVKESDRI 353

Query: 365 VAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVTATIDTYDDHRMAMAFSLAAC-AEV 418
+ L K G E D II + T+I++ DHR+AM+FS+AA AE
Sbjct: 354 AVMAHGLQKCGIDAEPTEGMIQGLGHIGGTRYKATSIESQGDHRIAMSFSVAAIRAEG 413

Query: 419 PVTIRDPGCTRKTFPDY 435
+ I +FP +
Sbjct: 414 TMVIHGAQTVDTSFPGF 430

>ref|YP_003186595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-01]
dbj|BAH98215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-01]
dbj|BAI01266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-03]
dbj|BAI04314.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-07]
dbj|BAI07361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-22]
dbj|BAI10409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-26]
dbj|BAI13457.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-32]
dbj|BAI16503.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter
pasteurianus IFO 3283-01-42C]

dbj|BAI19487.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetobacter pasteurianus IFO 3283-12]
Length = 466

Score = 113 bits (283), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 130/444 (29%), Positives = 208/444 (46%), Gaps = 37/444 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAA 73
+SG++++PG KS+S+R L+ A+L++GTT + LL EDV A+R LG +V+
Sbjct: 38 LSGSIRVPKDKSISHRALMFASLAKGTTTHISGLLEGEDVLCTAAAMRALGADAVQEGPGQ 97

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R G G + + + L +GN+G A R L+ + + G T V+ G +R RP
Sbjct: 98 WRVSGPGVG-----QLKEPDNVLDMGNSGTAAARLLSGILASHG--MTSVMTGDASLRRRP 150

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ ++ L GA FL + P+ + G+ +L S+Q SA+L+A
Sbjct: 151 MKRVMDPLAGTGA---TFLAREGGRLPMAIRGLADPKPLDYRLP-VASAQVKSALLAGL 206

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
A+G+ +E + + + + E LR FG V E + R G+ ++
Sbjct: 207 NAVGETRVE--EPVATRDHTENMLR---HFGAEVSVKTPDGGRRIIRLQGRPNLVARDVA 261

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV----TWTETS 304
V GD SSA++ L A + G+ +T+ G G L+ L+ MGA++ TE
Sbjct: 262 VPGDPSSAAFFLVAALLVAGSDITIFVGVLNPLR--TGLFTTLQEMGAQLEILNARTEGG 319

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+V G R LK ++V + P D LAV A +A G + V RVKE+
Sbjct: 320 ESV-GDLR--VRASALKGEVPPERAPSMIDEYPVLAVAAAYASGVSRCFVGEELRVKES 376

Query: 362 ERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFS-LAACAEV 418
+R+ A L G EG D + T ++T+ DHR+AM+ S + AE
Sbjct: 377 DRLAATVALLENNGVRTAVEGNDMVVYGTAGHIPGGGKVVETHMDHRLAMSASVMGLVAEK 436

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
PV I D +FP Y D++++
Sbjct: 437 PVEIDTFSFIETSFPPQYLDLMNSI 460

>ref|ZP_05705366.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cardiobacterium hominis ATCC 15826]
gb|EEV88510.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cardiobacterium hominis ATCC 15826]
Length = 436

Score = 113 bits (283), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 130/439 (29%), Positives = 201/439 (45%), Gaps = 39/439 (8%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P+ + GTV++PG KS+S+R ++L AL+EGTT V L ED + A + +G+ +
Sbjct: 9 PVDVVRGTGVRVPKDKSISHRAIMLGALAEGTTEVSGFLEGEDCLATMRAFQAMGVEI-VH 67

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A R + G G A L +GN+G +MR L + AG VL G +
Sbjct: 68 HGAGRVTIHGAGLHGLRAPAA---PLDVGNSTGSMRLLAGVL--AGQPFDAVLVGDAASLM 122

Query: 131 ERPIGDLVVGLKQLGAD-VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+RP+ + L +GA+ V +GT P+ ++G L G L + S+Q SALL+A
Sbjct: 123 KRPMRRVTEPLALMGAEIVTSDVGT--APLVIHG-RPLHGMDYTLTPVA-SAQLKSALLLA 178

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G I + +S + E R++ FGV E + I+GGQ+ S
Sbjct: 179 GLFAEGTT--RITETGVS RDHSE--RMLRGFVSVKEDGAT--LAIRGGQRL-SACEVV 230

Query: 250 VEGDASSASYFLAGAAITG-GTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A I G + +E G + V E+L MG +
Sbjct: 231 VPGDVSSAAFFIVAALIAREGALLLENVGMNPTRAAV--VEILRAMGGDIEILHAR-EAG 287

Query: 309 GPP----REPFGGRKHLKAID-----VNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
G P R + H AID + +++ P L + A A+G T + RVK

Sbjct: 288 GEPVADLRVRPSQLHGIAIDEALVPPIAIDFPP---ILFIAAACAEGETRATALHELVRK 343

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAF-SLAACA 416
E++R+ + L LG G D I T +++++ DHR+AM+F + A A

Sbjct: 344 ESDRLATMEAGLRALGVDCVAGADSMITIRGKAGTAFTGGTVESHGDHRIAMSFATAALRA 403

Query: 417 EVPVTIRDPGCTRKTFPDY 435
P+ +RD +FP +

Sbjct: 404 AAPIVVRDCANVATSFPSF 422

>ref|ZP_02154867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanibulbus
indolifex HEL-45]
gb|EDQ03614.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanibulbus
indolifex HEL-45]
Length = 441

Score = 113 bits (283), Expect = 5e-23, Method: Compositional matrix adjust.
Identities = 130/443 (29%), Positives = 205/443 (46%), Gaps = 34/443 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT ++PG KS+S+R L+L A++ G T + LL +DV A+R G V D

Sbjct: 9 LSGTAEPVPGDKSISHRSLILGAMAVGETTITGLLEGQDVLDATAMRAFGAEV-IDHGGG 67

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V G G G F A+ + + GN+G +R L A+ + + T+ D + RP

Sbjct: 68 SYSVHGVGVGGF---AEPDNVIDCGNSGTGVRLLMGAMATSPISVTFTGDA--SLNSRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V +P V+ + + S+Q SA+L+A

Sbjct: 122 MARVTDPLALFGTQSVGRTGGRLPMTLVGAEPVP---VRYTVPVPSAQVKSALLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+ + + E R++ FG + D+ + R GQ P++ V

Sbjct: 179 APG--KTVVIEAEATRDHTE---RMLAGFGAEITVEDTEEGRVITLTGQPELKPHIDVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKAFAVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V V G G + L MGA +T+ E T G

Sbjct: 234 RDPSSAAFPVCAALIVPGSDVLVPGIGLNPT--AGLFTTLREMGADLT--ENERTEGGE 290

Query: 311 P----REPFGKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F +L I+V + M D L+VVA A G T +R V RVKE++R

Sbjct: 291 PVADLRKAF-SPNLHGIEVPPERAASMIDEYPVLSVVAACATGDTLMRGVKELRVKESDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLN---TAIDTYDDHRMAMAF-SLAACAEVP 419
+ A+ + L G VE+GPD+ I+ N+ ++ DHR+AM+F L A+ P

Sbjct: 350 IEAMASGLRANGIEVEDGPDWIVKGLGHGNIPGGATCQSHLDHRIAMSFLLIGMVAQQP 409

Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
V + D G +FP + +++++

Sbjct: 410 VQVDDGGPIATSFPIFEPLMASL 432

>ref|YP_001356132.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitratiruptor sp.
SB155-2]
sp|A6Q2R6.1|AROA_NITSB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAF69775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitratiruptor sp.
SB155-2]
Length = 433

Score = 113 bits (282), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 125/437 (28%), Positives = 208/437 (47%), Gaps = 48/437 (10%)

Query: 25 KSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + LS+ + ++N L +ED L ++ LG VE ++ ++ ++ K

Sbjct: 23 KSISHRSAMFSLLSDEPSQIENFLRAEDTLNLTLEIVKALGAQVE--ESDEKILI-----K 75

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQL 144
P + + + L GN+G MR + AG N +VL G +RERP+ + L+ +

Sbjct: 76 PPKQIQEPKDVLDGNSGTGMRLFCGLL--AGINGFFVLTGDKYLREPRMARVAKPLRSI 133

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA +D + P+ + G L + S S+Q SAL++AA A G+ I

Sbjct: 134 GAKIDGRDNGNKAPLALRGNTDLEPFDYE-SPIASAQVKSALILAAALRAKGECSI----- 187

Query: 205 LISIPYV--EMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKSPKNAYVEGDASSASYF 260
S P + + T R+++ G + S R+ + K P + D SSA +F

Sbjct: 188 --SEPELSRDHTERMQLQGMGANIDTHWSHGRYRVDVPLTKPLEPLKIRIPADPSSAFFF 245

Query: 261 LAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG--- 316
AAI V +E + ++ +VL+ MGA V + E EP G

Sbjct: 246 AVAAAIAPRSKVLENITLNPTR--IEAFKVLQKMGADVVFLEKENKY-----EPIGDII 298

Query: 317 --RKHLKAIDVNMN-----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
L ++V+ N ++P +A+ +AV ADG + +R+ RVKE++R+ +

Sbjct: 299 VTHNSLHGVEVSENIPWLIDELPALAIAMAV---ADGRSIVRNAKELRVKESDRITCVV 354

Query: 369 TELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRDPGC 427
L K G +E D Y II +L+ AID+ DHR+AM+F +A + +RD C

Sbjct: 355 ENLKKCGIQAQEFEDGYEIIIG--ELHSAIDSCGDHRIAMSFLIAGLVS-GMEVRDIEC 411

Query: 428 TRKTFPDYFDVLSTFVK 444
+ +FP++ D+LS VK

Sbjct: 412 IKTSFPNFLDLLSQIVK 428

>ref|ZP_07056514.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus SJ1]
gb|EF164543.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cereus SJ1]
Length = 394

Score = 113 bits (282), Expect = 6e-23, Method: Compositional matrix adjust.
Identities = 106/363 (29%), Positives = 170/363 (46%), Gaps = 36/363 (9%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYV--LDGVPRMRERPIGDLVVGLKQLGADVDCFLG 153
L +GN+G +R ++ + N + + G + +RP+ + LKQ+GA++D

Sbjct: 54 LDVGNSGTTIRLMSGIL----ANTPFFSCVQGDASIAKRPKRVTNPLKQMGANIDGREE 109

Query: 154 TDCPPVRVNGIGGLPGGKVK----LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIP 209
P+ + G G +K S S+Q SA+L+A A G + + P

Sbjct: 110 GTFTPLTIRG-----GDLKAIEYTPVASAQVKSAILLAGLRAEGVTAV-----TEP 156

Query: 210 YV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAI 266
++ + T R++E FGK + + GGQK + + V GD SSA++FL AGA I

Sbjct: 157 HISRDHTERMLEAFGVKV--TREGTKVKLAGGQKL-TATDVQVPGDVSSAAFFLVAGAI 213

Query: 267 TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDV 325
+ +E G + + +VLE MGA T + + P LK I++

Sbjct: 214 PNSKLVLENVGMNPTRTGI--IDVLEKMGATFTVEPINEGASEPAANITITETSSLKGIEI 271

Query: 326 NMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGP 382
+ +P + + V+AL A +G T I+D +VKET R+ + ELTKLGA +E

Sbjct: 272 GGDIIPLRLIDEIPVIALAATQAEGITVIKDAHELVKETNRIDTVVAELTKLGARIEATD 331

Query: 383 DYCIIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLST 441
D II L +++Y DHR+ M ++A C AE I D ++P +F+ L

Sbjct: 332 DGMIIYGKSALKGNTVNSYGDHRIGMMLAIAGCIAEGKTIIEDAEAVGVSYPTFFFEELQK 391

Query: 442 FVK 444
K

Sbjct: 392 LAK 394

>ref|ZP_04677860.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
warneri L37603]
gb|EEQ80033.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
warneri L37603]
Length = 433

Score = 113 bits (282), Expect = 7e-23, Method: Compositional matrix adjust.
Identities = 120/460 (26%), Positives = 208/460 (45%), Gaps = 62/460 (13%)

Query: 1 MAGAEEIVLQ-PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGA 59
M+ AE I + P+K G +++PG KS+++R ++LA+L+ G T + L ED +
Sbjct: 2 MSTAETIQINGPLK---GEIEVPGDKSMTHRAIMLASLATGQTQIHKPLLGEDCKRTMNI 58

Query: 60 LRTLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGN 118
R LG+S+ ++ R +V G + K Q L+ GN+G R L ++ G
Sbjct: 59 FRLLGVSITEEE--DRLIVDSPG----YQHFKTPHQVLYTGNSGTTTLLAGLLSGIGIE 112

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGP-PVRVNGIGGLPGGKVKLSGS 177
+ VL G + +RP+ ++ L ++ A++ G P ++ + I G+
Sbjct: 113 S--VLSGDVSGKRPMDRVLPKLLKMNANICGVEGNYTPLIIPSDIKGM----TYTMEV 166

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYI 236
S+Q SA+L A+ + I ID V H+++ ++ F I
Sbjct: 167 ASAQVKSAILFASIFSNESSSITEID-----VSRNHTETMFNHFNI 207

Query: 237 K---GGQ-----KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQG 283
G+ K+ P + YV GD SSA++F+ A IT G+ VT+ G +
Sbjct: 208 PIIVNGKTIVTEPLAVKHKPHDFYVPGDISSAFFIVAALITPGSDVTIHNVGINPTRS 267

Query: 284 DVKFAEVLEMMGAKVTVTETSVTVTGPPREPFGGRKH---LK AIDVNMNKMMPDVAMTLAVV 340
+ ++++ MG ++ T+VT P ++ LK I ++ +P L V+
Sbjct: 268 GI--IDIVQQMGGRIEL--TNVTKEAAPTASIRVQYTPNLKPIQIHGELVPRADIELPVI 323

Query: 341 ALF---ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 397
AL A G + I+D +VKET R+ L +LG ++ D II P E
Sbjct: 324 ALLCTQASGTSVIKDAEELKVKETNRIDTTADMLNQLGFELQPTNDGLIHPSEFKTSVT 383

Query: 398 IDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
+D+ DHR+ M ++A+ + P+TI +FP +
Sbjct: 384 VDSQTDHRIGMMLAIASLLSSEPLTIEQFDAVNVSPFGFL 423

>ref|YP_003321851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobaculum
terrenum ATCC BAA-798]
gb|ACZ41029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermobaculum
terrenum ATCC BAA-798]
Length = 439

Score = 113 bits (282), Expect = 7e-23, Method: Compositional matrix adjust.
Identities = 123/454 (27%), Positives = 197/454 (43%), Gaps = 48/454 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I + P + + G + PG KS+S+R + AL++GTT + N + D L L +LG
Sbjct: 2 DITISPARSVHGNIMP PGDKSISHRAAIFGALAAGTTDIYNYSPARDCQSTLECLLSLGT 61

Query: 66 SVEADKAAKRAVVVG-CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ D R VG G K P E L GN+G MR L A+ A + D
Sbjct: 62 GIRRDGNYIRVEGVGDTGFKEP-----ESILDCGNSGTTMRLIGALAPMDLYAVLIGD 115

Query: 125 GVPRMRE-----RPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSIS 179
R +P+GD+ GL+ + D + PPV + G G + G + + S
Sbjct: 116 KSLTKRPMDRVLPKPLGDM--GLRYYARNKDRY-----PPVSIRG-GKIQQIHYQ-TPVAS 166

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-- 237
+Q SA+L+A A G E + + S + E R+++ G + + + R
Sbjct: 167 AQVKSAILLAGLRAEG--ETVVTEPAKSRDHTE---RMLKAMGAQIQSDGTTVRLVASRL 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVDFAEVLEMMGAK 297
+ P + +A+ + + +T + + + F VLE MGA
Sbjct: 222 SATTFHVPADPSSAAFILAAALIVPESKVTTSNICLNPT-----RIGFLNVLERMGAN 274

Query: 298 VTWTETSVTVTGPPREPFG-----RKHLK AIDVNMNKMMP---DVAMTLAVVALFADGPTA 349
+ + EP G L I++ ++P D LAV+A A G T
Sbjct: 275 IEIHNERESSG---EPIGDIEASTSELNGIEIGGTEIPTLIDEIPILAVLATQAKGRTV 330

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMA 409
IRD R+KET+R+ + L ++GA + E D I P KL +D DHR+AMA
Sbjct: 331 IRDAEELRIKETDRISVLCRALQQMGADIREMRDGFIEHGPCKLKGAQVDPDHDHRIAMA 390

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
 ++A+ AE TI C ++P+++D LS+
 Sbjct: 391 LAVASLIAEDKTTILGAECASISYPNFWHDHLSL 424

>ref|ZP_01437294.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fulvimarina pelagi
 HTCC2506]
 gb|EAU42291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Fulvimarina pelagi
 HTCC2506]
 Length = 429

Score = 113 bits (282), Expect = 7e-23, Method: Compositional matrix adjust.
 Identities = 123/435 (28%), Positives = 198/435 (45%), Gaps = 36/435 (8%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
 +PG KS+S+R L L+ GTT V LL EDV A+ +G + K + VV G
 Sbjct: 1 MPGDKSISHRAFLFGGLASGTTTRVTGLLEGEDVLATGRAMIAMGALIR--KEGQTFVVDG 58

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
 G +E E L GNAG R V A +T+V D + +RP+G ++
 Sbjct: 59 VNGCCLLE---PEEPLDFGNAGTGARLTMGVLGAYHFGSTFVGDA--SLSKRPMGRVLDP 113

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAPLALGDV 197
 L+++G V D P+ ++G P + + S+Q SA+L A G
 Sbjct: 114 LREMGVQV-VARSKDRLPLSIHG---PKATAPIEYRVPMASQVKSAVLFAGLNTPGVT 168

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAEE---HSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
 + I+ +++ + E +++E FG E D +++G + + + V GD
 Sbjct: 169 TV--IEPVMTRDHE---KMLEGFGANIEVETKPDGSRHIHLQGGELRGLSDFQVPGDP 223

Query: 255 SSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPRE 313
 SSA++ +AG + G VT+E + + E L MG + + T G
 Sbjct: 224 SSAAFPIVAGLVVPGSDVTIENVLMNPT--IGLIETLREMGGSEILDAR-TEGGEDVA 280

Query: 314 PFGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
 +H L +++V + P D LAV A FA G T +R + RVKE++R+ A+
 Sbjct: 281 DLRIHSELTSVEVTAERAPSMIDEYPVLAVAAFAKGRVTMRGLDELRVKESDRLSAVA 340

Query: 369 TELTKLGASVEEGPDYCIIT-PPEKLVN--TAIDTYDDHRMAMAF-SLAACAEVPVTIRD 424
 L EEG D+ ++ PE ++ T+ DHR+AM+F L + PVTI D
 Sbjct: 341 AGLAANNVRHEEGADWLVEGDPEGRGYGGGSVVTHLDHR IAMSFLVLGLASGKPVITDD 400

Query: 425 PGCTRKTFPDYFDVL 439
 +FP++ D++
 Sbjct: 401 GRMIATSFPEFEDLM 415

>ref|YP_755334.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Maricaulis maris
 MCS10]
 sp|Q0ATJ1.1|AROAMARMM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABI64396.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Maricaulis maris
 MCS10]
 Length = 447

Score = 112 bits (281), Expect = 8e-23, Method: Compositional matrix adjust.
 Identities = 133/447 (29%), Positives = 201/447 (44%), Gaps = 36/447 (8%)

Query: 10 QPIKEISGTVKLPKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
 +P +SGT+K PG KS+S+R +L L+G T V LL S+DV A LG VE
 Sbjct: 15 RPAPALSGTIKAPGDKSISHRAFILGLGAKGVTEVTGLLESDDVINSGRAAAALGAKVE- 73

Query: 70 DKAACKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
 + GCGG++ A L GNAG +R + AV G +A ++ D +
 Sbjct: 74 HLGPGHWRIDGCGGQWTPSAP----LDFGNAGTGVRLLMGAVAGTGTSAFIGD--ESL 127

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLM 188
 RP+ + L ++GA G P ++G G L G + + I S+Q SA+L+
 Sbjct: 128 SSRPMRRVTDPLGEMGARFTTTGGRL--PAHLDG-GPLAG--IHYTPPIASQVKSAVLL 182

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGV--KAEHSDSWDRFYIKGGQKY-KSP 245
AA A G + + I+ + E LR FGV E + + G Q P
Sbjct: 183 AALGATGTTVVH--EPQITRDHTETMLRA---FGVTLTVERDGAAATVTLTGPQTLIACP 237

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SS+++ + A I+ G+ +T+EG + E L+ MGA +T T
Sbjct: 238 VD--VPGDPSSSAFAIVAALISPGSDITLEGVMDNPAR--TGLIETLKEMGADITLTP-G 292

Query: 305 VTVTGPFPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ G KH L I V + P D L V A +ADG T + + R K
Sbjct: 293 PDMAGEKTMHIHVKSQHLHGITVPATRAPSMIDEYPVLCVAAAYADGITHMPGLEELRAK 352

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATID---TYDDHRMAMA-FSLAAC 415
E++R+ L G VEEG D +T V T+ DHR+AM+ +
Sbjct: 353 ESDRLAGSAAMLRAVGPVEEGEDSLAVTGMGIGGVPGGGRVTVTHDHRMLAMSGLVIGLG 412

Query: 416 A EVPVTIRDPGCTRKTFPDYFDVLSTF 442
A+ ++ D ++PD+FD ++T
Sbjct: 413 AKAASSVDDIAMIAISYPDFDHIATL 439

>ref|YP_003263214.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halothiobacillus
neapolitanus c2]
gb|ACX96167.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Halothiobacillus
neapolitanus c2]
Length = 456

Score = 112 bits (281), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 126/453 (27%), Positives = 203/453 (44%), Gaps = 49/453 (10%)

Query: 8 VLQPIK-EISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ QP + +I G++++PG KS+S+R ++L AL++GTT + L ED L R +G+
Sbjct: 15 ITQPGRAKIQGSIRVPGDKSISHRSIMLGALADGTTEITGFLQGEDSLNLTLCFRAMGVE 74

Query: 67 V-EADKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ E + R VG G K P L++GN+G +MR + + AG + VL+
Sbjct: 75 ITEPVEGRVRVNGVGLHGLKAPAH-----PLYVGNSGTSMLMAGIL--AQQSFDTVLE 126

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ ++ L Q+GA ++ G P+ + G L + L + S+Q S
Sbjct: 127 GDESLSRRPMKRVIDPLTQMGAVIESAEGGRS-PLTIRGGQRLRAIEYTLPLMA-SAQVKS 184

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L+A A G + P + T R++ FG D GGQ
Sbjct: 185 CVLLAGLYAEGKTCVT-----EPAPTRDHTERMLTGFYGPVAR-DGSTACLDGGGQLIA- 237

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ V D SSA++F+ A+I +T+E G + V ++L++MGA +T
Sbjct: 238 -RQIDVPADISSAAFFMVAASIAPEADITLHVGMNPTRTGV--IDILKLMGADITLHN- 293

Query: 304 SVTVTGPFPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIR 351
PRE G L+ ID+ +P D L V A A+G T +
Sbjct: 294 -----PREVGGEADVADVKIRSAKLRGIDPEALVPLAIDEFPALFVAAACAEGRTVLT 346

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTATIDTYDDHRMA 407
RVKE++R+ + L KLG PD II + I + DHR+A
Sbjct: 347 GAEELRVKESDRIAMADGLNKLGVATATPDGMIQKGKANSQSFGSAEISQGDHRIA 406

Query: 408 MAFSLAACAEV-PVTIRDPGCTRKTFPDYFDVL 439
M+F++A V +TI + +FP + D+
Sbjct: 407 MSFAVAGLRVGTITIHNCEVFVTSFPGFADLF 439

>emb|CBK78945.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium cf.
saccharolyticum K10]
Length = 427

Score = 112 bits (281), Expect = 9e-23, Method: Compositional matrix adjust.
Identities = 119/432 (27%), Positives = 197/432 (45%), Gaps = 33/432 (7%)

Query: 15 ISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

Sbjct: 10 + G V +PG KS+S+R ++ A+++G T +D L D + +G+S+E +
LRGEVTVPGDKSISHRSVMFGAIAKGLTEIDGFLQGADCLSTISCFERMGSIE--NRGE 67

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R +V G G + KE + L GN+G R L+ ++A T L G +R+RP

Sbjct: 68 RVLVFGNG----MHGLKEPDGVLDCGNSGTTTLLSGLLSAQPFVCT--LTGDESIRKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L Q+GA + C P+ + G L G + S S+Q SA+L+A A

Sbjct: 122 MKRIITPLSQMGASIKSVNNGCAPLFIEG-QRLHGISYQ-SPVASAQVKSAVLLAGLYA 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIK-GGQKYKSPKNAYV 250
G E ++ +S + E+ ++ FG V+ E + + R + GQK P +

Sbjct: 180 EG--ETRVTEPYLSRNHSEL---MLAHFGADVTEGTTAVLRPARELFGQKISVPGDISS 234

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+A+ + G+ + + G + + V MGA + S +G

Sbjct: 235 AAFFIAAALMVPGSELL-----IRNVGINPTRDGI--LTVCRSMGADIEILNPSAG-SGE 286

Query: 311 PREPFGKRK--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P +H L ++ +P D +A +A ADG T IRD A +VKE+ R+

Sbjct: 287 PVADLLVRHSSLHGTEIGGAVIPTLIDELPVIAAMACLADGKTVIRDAAELKVKESNRIA 346

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT-IRD 424
+ L+ +GA VEE D II L+ ID+ DHR+AM F++ A A T I D

Sbjct: 347 VMTEGLSAMGARVEETADGMIHGGSPHLGAVIDSRKDHRIAMTFAVTALAASGQTEILD 406

Query: 425 PGCTRKTFPDYF 436
C ++P ++

Sbjct: 407 ADCVSIISYPGFY 418

>ref|YP_003772576.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
gasicomitatum LMG 18811]
emb|CBL91757.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leuconostoc
gasicomitatum LMG 18811]
Length = 434

Score = 112 bits (281), Expect = 9e-23, Method: Compositional matrix adjust.
Identities = 119/445 (26%), Positives = 206/445 (46%), Gaps = 32/445 (7%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G + +PG KS+S+R L+ A++ G T +DN L S+DV + R LG+++ +

Sbjct: 8 PKSGLHGEITVPGDKSISHRALMFGAIATGETRIDNFLMSDDVMRTMTVFRELGVAI--N 65

Query: 71 KAAKRAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ + V+G G F K + L +GN+G + R L ++ + ++ G +

Sbjct: 66 QVGSQIKVIGKGLDSF----TKPKHALNMGNSGTSTRLLMGLLSKQPFDLSTFF--GDESL 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+ + L + A D P +R N L G ++ + S+Q SA+L+

Sbjct: 120 SSRPLRRVAEPLSLMNAQFDLTADNFLPGTIRAN--NRLQGMTYEMPVA-SAQVKSAILL 176

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A A G E II+K+ S + E R++ +FG ++ I+ + + ++

Sbjct: 177 AGIQAEG--ETIIIEKVTSRDHTE---RMLRQFGGIITNNGV--ITIQQPQLRG-QHV 228

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++F+ IT +T++ G + V ++LE MGA +

Sbjct: 229 LVPSDISAAFFMAGLITPNSEITLKKVGNPTR--VGVIKLLERMGANIKQEPFISDG 286

Query: 308 TGPPREPFGKRHLKAIDVNMNKMPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERM 364
+ L I++ + +P L ++AL A G T I A RVKET+R+

Sbjct: 287 EALADIVIKSQLHGINIMADDIPSAVDELPIALAAATQALGDTVISGAELRVKETDRI 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT----IDTYDDHRMAMAFSLAA-CAEVP 419
+ +ELTKLGA +EE D II L+V +D++ DHR+ M ++AA E

Sbjct: 347 ATVISELTKLGADIEEKQDGMIIHGGTPLHVMQDSVLLDSHGDHRIGMMNAVALITEGN 406

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVK 444
V + ++P + L+ ++

Sbjct: 407 VILTGEDAMSVSYPGFLADLTAIMR 431

>ref|YP_002360949.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylocella
silvestris BL2]
gb|ACK49587.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylocella
silvestris BL2]
Length = 443

Score = 112 bits (280), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 136/442 (30%), Positives = 192/442 (43%), Gaps = 47/442 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G +K PG KS+S+R L+L LS GTT + LL EDV + LG VE A
Sbjct: 16 LAGRIKPPGDKSISHRALILGLLSVGTTEITGLLEGEDVIHTAKVCGALGARVE-RLAPG 74

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R V GCG G + E L GN+G MR + V AG T LDG +R RP
Sbjct: 75 RWRVEGCGIGSL---LQPEETLDFGNSGTGMRLMMGVV--AGHPITATLDGDASLRTRP 128

Query: 134 IGDVLVGLKQLGAD-VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ ++ L +GA + G CP + +P V S S+Q SA+L+A
Sbjct: 129 MRRVLDPLMMMAQAQTLTSAEGGRCPIILKGTAEPIP--IVYKSPVASAQIKSAVLLAGLN 186

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+ G E +I+ S + E LR FG +K E R G+ P V
Sbjct: 187 SPG--ETSVIEPEASRDHTEKMLRY---FGAALKVEPFGENGRKITLQGRPELKPAVAV 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGC-----GTTSLQGDVKFAEVLEMMGAKV 298
GD SSA++ L A I + + +E + D++ + E G +V
Sbjct: 242 PGDPSSAAALVAATIVENSIVIESMMMNPLRTGLLTTLLEMGADIEIIDRREEGGEEV 301

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
+ V G LK +DV + P D LAV A FA G T +R +
Sbjct: 302 ----ADLRVRG-----AALKGVDPVPAARAPSMIDEYPILAVAASFARGQTRMRGLGE 349

Query: 356 WRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTIAIDTYDDHRMAMAF-SLA 413
RVKE++R+ A+ L G + G D + E + T+ DHR+AM+F L
Sbjct: 350 LRVKESDRLEAVAAGLRACGVDPQIIGDDLIVEGGAEVSGGLVATHLDHRIAMSFILIG 409

Query: 414 ACAEVPVTIRDPGCTRKTFPDY 435
A+ PV I D G +FPD+
Sbjct: 410 LAAQKPVAIDDVGMIAISFPDF 431

>ref|XP_001392796.2| shikimate dehydrogenase [Aspergillus niger CBS 513.88]
Length = 1270

Score = 112 bits (280), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 82/210 (39%), Positives = 112/210 (53%), Gaps = 15/210 (7%)

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA-EVLEMMGAKVT 299
+Y +P VE DASSA+Y LA AAITG T TV G+ SLQGD +FA +VL MG V
Sbjct: 315 RYVNPAYEYMVEDASSATYPLAIAAITGTTCTVPNIGSKSLQGDARFAVDVLRPMGCTVE 374

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADG-----PTAIRDVA 354
T++S TVTG P G +V+M M D +T +V+A A G T I +A
Sbjct: 375 QTDSSSTVTGAP---GGVLRPLPNVDMPEMTDAFLTASVLAAVARGDGSNHTTRIYGIA 430

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT----AIDTYDDHRMAMAF 410
+ RVKE R+ A++ EL K G E D I ++ ++ + YDDHR+A +F
Sbjct: 431 NQRVKECNRIKAMKDELAKFGVVCREHDDGIEIDGIDRTSLRQPAGGVFCYDDHRVAFSF 490

Query: 411 S-LAACAEVPVTIRDPGCTRKTFPDYFDVL 439
S L+ I + C KT+P ++D L
Sbjct: 491 SVLSLVTPQSTLILERECEVGKTWPGWWDLSL 520

>gb|AAQ75178.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Alvinella pompejana
epibiont 7G3]
Length = 431

Score = 112 bits (280), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 123/436 (28%), Positives = 199/436 (45%), Gaps = 59/436 (13%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + LS+ T+ ++N L +ED L ++ LG ++ + GG
Sbjct: 24 KSISHRCAIFSLSDKTSKIENFLLAEDTLASLSIVKQLGANITQN-----GGD 72

Query: 85 F---PVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P + KE E L GNAG A+R ++ G ++L G +R RP+ ++
Sbjct: 73 IBITPPDTLKEPEEVLDCGNAGTAIRLFIGFLSGVDG--LFILTGDKYLVRPMSRVIEP 130

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSGSISSQYLSALLMAAPLALGD 196
L+++GA VD + P+ + G GK+K S S+Q SAL++A+ A
Sbjct: 131 LREIGARVDGRDRGNLAPIVIRG-----GKLPFRYNPINSQAQVKSALILASLRAYSK 184

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ ++S + E L M E+ W I +K P N V D SS
Sbjct: 185 SYR--ESILSRDHTERILSGMGAGVTTLENG--W--IEITPLKKPLEPLNIRVPADPSS 238

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSL-QGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
+F AI + T+ SL + V+ VL+ MGA + + E EP
Sbjct: 239 GFFFAVATAIIPNSKTI--IKDVSLNKTRVEAYRVLQDMGADIEFIEKESY----EPI 291

Query: 316 G-----RKHLKAIDVNMN-----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G LK+I V+ N ++P +++ +AV ADG + + + RVKE++R
Sbjct: 292 GDIIIKYNGKLKSIRVDKNIAWLIDELPALSIA MAV---ADGISVVENAKELRVKESDR 347

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I L + G +E D I E L T I++Y DHR+AM+F++A + I
Sbjct: 348 ISTILEGLNRCGIETKEFSDGYEIVGGE-LKSTTINSYGDHRVAMSFAIAGVV-ASIKIE 405

Query: 424 DPGCTRKTFPDYFDVL 439
D C +FP++FD+L
Sbjct: 406 DIECINTSFNPFDDIL 421

>ref|YP_001543746.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Herpetosiphon
aurantiacus ATCC 23779]
sp|A9AZ72.1|AROA_HERA2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABX03618.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Herpetosiphon
aurantiacus ATCC 23779]
Length = 431

Score = 112 bits (280), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 124/438 (28%), Positives = 196/438 (44%), Gaps = 38/438 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G + +PG KS+S+R +L AL+EG + L D + LR +G+ +E
Sbjct: 9 KRLRG AISVPKDKSISHRSVLFNALAEGNAEITGFLPGADCLSSIACLRQMGVEIEHSDD 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R G G D L GN+G +R L + VL G +R R
Sbjct: 69 KVRVFGRLRGLREPSDV-----LDCGNSGTTLRLLAGLLAQ--PFLSVLTGDASLRSR 121

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P +V L+QLGA +D + P+ + G + GG +L + S+Q SALL+A
Sbjct: 122 PQKRIVEPLRQLGAKLDGRDNGNRAPLVIRGTT-IHGGNYELPIA-SAQVKSALLLAG-- 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
GD + + K++S + E R++ G+ D Y + P + +V G
Sbjct: 178 LTGDAPMRLSGKIVSRDHTE---RMLIAMGIDLTVKDDEIVLYPPSHPVFPYPLSLHVP 234

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----- 303
D SSA+++ AAI +T G G + +VL+ MGA +T +
Sbjct: 235 DPSSATFWWVAAIHPDAEITTLGVGLNPSR--TGALDVLKAMGADITISNERNEGAEPV 292

Query: 304 -SVTVTGPPREPFPGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
VTV G L+ ++ + +P D LAV A A G T + D R K

Sbjct: 293 GDVTVRG-----GGLRGTRIDGDLIPRLIDEIPVLAVAAACAVGETTVVADAEELRAK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEV 418
ET+R+ + +ELT +GA++E PD II +L + ++ DHR+AMA ++A AE

Sbjct: 345 ETRVATVVELTAMGATLEATPDGMIAGGELQGAHVQSHGDHRIAMALAVAGLVAEG 404

Query: 419 PVTIRDPGCTRKTFPDYF 436
I + ++P ++

Sbjct: 405 ETIIDEAEAVTVSYPTFW 422

>ref|ZP_06347541.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp.
M62/1]
gb|EFE11336.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium sp.
M62/1]
Length = 427

Score = 112 bits (279), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 119/432 (27%), Positives = 197/432 (45%), Gaps = 33/432 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V +PG KS+S+R ++ A+++G T +D L D + +G+S+E +
Sbjct: 10 LRGEVTVPGDKSISHRSVMFGAIAKGLTEIDGFLQGADCLSTISCFERMGVSI--NRGE 67

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R +V G G + KE + L GN+G R L+ ++A T L G +R+RP
Sbjct: 68 RVLVFGNG---MHGLKEPDGVLDCGNSGTTTLLSGLLSAQPFVCVT--LTGDESIRKRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L Q+GA + C P+ + G L G + S S+Q SA+L+A A
Sbjct: 122 MKRIITPLSQMGASIKSVNNNGCAPLFIEG-QRLHGISYQ-SPVASAQVKSALLAGLYA 179

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKG-GQKYKSPKNAYV 250
G E + + +S + E+ ++ FG V+ E + + R + GQK P +
Sbjct: 180 EG--ETRVTEPYLSRNHSEL---MLAHFGADVTEGTTAVLRPARELLGQKISVPGDISS 234

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+A+ + G+ + + G + + V MGA + S +G
Sbjct: 235 AAFFIAAALMVPGSELL-----IRNVGINPTRDGI--LTVCRSMGADIEILNPSAG-SGE 286

Query: 311 PREPFGKRH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P +H L ++ +P D +A +A ADG T IRD A +VKE+ R+
Sbjct: 287 PVADLLVRHSSLHGTEIGGAVIPTLIDELPVIAAMACLAGDKTVIRDAAELVKVESNRIA 346

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT-IRD 424
+ L+ +GA VEE D II L+ ID+ DHR+AM F++ A A T I D
Sbjct: 347 VMTEGLSAMGARVEETADGMIHGGSPHGAVIDSRKDHRIAMTFAVATALAASGQTEILD 406

Query: 425 PGCTRKTFPDYF 436
C ++P ++
Sbjct: 407 ADCVSISYPGFY 418

>ref|ZP_04455105.1| hypothetical protein GCWU000342_01121 [Shuttleworthia satelles DSM
14600]
gb|EEP28313.1| hypothetical protein GCWU000342_01121 [Shuttleworthia satelles DSM
14600]
Length = 422

Score = 112 bits (279), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 118/444 (26%), Positives = 206/444 (46%), Gaps = 39/444 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G +++PG KS+S+R ++L +++ G T + L+ D + R LG+ + D
Sbjct: 3 QSLHGRIRIPGDKSISHRGIMLSIARGMTELFGLDGADCRSSIA CFRQLGVDIIQDGD 62

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R ++G GG ++ KE L +GN+G R ++ + AG + L G ++ R
Sbjct: 63 HIR--ILG-GGLHGLQQPKE--ILNVGNSGTTARLMSGIL--AGQSFPSLTGDASIQR 115

Query: 133 PIGDLVGLKQLGADVDCFLGTDCPPVRV--NGIGGLPGGKVKLSGSISSQYLSALLMAA 190

P+ ++ L +GA + C P+ + + + G+ LS S+Q S++L+A
Sbjct: 116 PMTRIIDPLHAMGARIRSRDDGCAPLDIEPSALRGID----YLSPLASAQVKSSVLLAG 171
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLR-----LMEFVGKAEHSDSWDRFYIKGGQKYKSP 245
A G + + + S + E LR L+E G+ S + D GQK
Sbjct: 172 LYAQG--KTSVTEPAKSRDHSEMRMLRAFGADLIED-GLTVSISPNDLT----GQKI--- 221
Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+V GD SSA+Y++A A+I G+ + +E + + + MGA +
Sbjct: 222 ---HVPGDISSAAYWIAAASIIPGSEIIENVNINPTRDGI--LHIARAMGADIEEINPH 276
Query: 305 VTVTGPPEPFGGRK-HLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKE 360
P + F R L V+ +P + + V+AL A +G T I D RVKE
Sbjct: 277 TVSQEPVADLFVRSaelhgtrVDGPIIPRLIDEIPVIALMACAEGETTIADAHELRVKE 336
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVP 419
++R+ ++ L+ +G SV D +I L I T DHR+AM F++A+ A+ P
Sbjct: 337 SDRIESMVKNLSAMGVSVTGTDDGMVICGGASLRGADIVTCHDHRIAMTFVASLLADGP 396
Query: 420 VTIRDPGCTRKTFPDYFDVLSTFV 443
V + DP C ++P ++ L +
Sbjct: 397 VHLDDPDCVSVSYPGFYRSLQLLL 420

>ref|ZP_01551129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stappia aggregata IAM
12614]
gb|EAV40333.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stappia aggregata IAM
12614]
Length = 451

Score = 112 bits (279), Expect = 1e-22, Method: Compositional matrix adjust.
Identities = 129/451 (28%), Positives = 204/451 (45%), Gaps = 55/451 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+++PG KS+S+R L+ AL+ G T V LL SEDV A+R +G ++ +
Sbjct: 18 LTGTIRVPGDKSISHRSLMFGALAVGRTTVKGLLESEDVLATADAMRAVGATITKLEDGS 77
Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V +G G + E + GNAG +R + AT+V D + +RP
Sbjct: 78 YTVDGIGLGLSL-----EPEHVIDFGNAGTGVRLTMGIFGSHNIAATFVGDA--SLSKRP 130
Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+ +G +V G D P + G P + ++ + S+Q SA+L+A
Sbjct: 131 MGRVLNPLRDMGTNVIARDG-DRLPASIRG----PEQALPITYRVPMPSAQVKSAVLLAG 185
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G E +I+ IP + T +++ FG + +++ +R GQ P++
Sbjct: 186 LNAAG--ETTVIEP---IPTRDHTEKMLKGFADISVTLNEAGERVIKLGQPELKPQDI 240
Query: 249 YVEGDASSASYFLAGAAITGGT-VTVE-----GCGTTSLQ--GDVKFAEVLEMMGA 296
V GD SSA++ L A I G+ V +E G TT ++ GD+ E G
Sbjct: 241 DVPGDPSAAPFLVAALIVPGSDVVIENVLLNEHRTGLITTLIEMGGDISILNRRETGGE 300
Query: 297 KVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDV 353
+V + LK I V + P D LAV A FA+G T + +
Sbjct: 301 EVGDLHVKA-----KLKGITVPAERAPSMIDEYPVLAVAAAAFAEGETFMPGL 348
Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ADITYDDHRMAMAF-S 411
RVKE++R+ A+ L G E D +T + T+ DHR+AM+F
Sbjct: 349 EELRVKESDRLLAAVARGLEANGIPCETEDTLTVTGGADGIGGMVTHLDHRIAMSFLV 408
Query: 412 LAACAEVPVTIRDPGCTRKTFPDY---FDVL 439
L A PVT+ D +FP + FD L
Sbjct: 409 LGMAAHNPVTVDGAVIATSFPFTTSLFDGL 439

>ref|NP_559639.1| 3-phosphoshikimate 1-carboxyvinyltransferase (aroA) [Pyrobaculum
aerophilum str. IM2]
gb|AAL63821.1| 3-phosphoshikimate 1-carboxyvinyltransferase (aroA) [Pyrobaculum
aerophilum str. IM2]
Length = 400

Score = 111 bits (277), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 113/424 (26%), Positives = 188/424 (44%), Gaps = 46/424 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G + P SK +S R LL AAL+EG T + + S+DV A++ + + ++ D
Sbjct: 9 LEGRFQSPSPKPMSSQRYLLAALAEGETEITRIEWSDDVVATARAVQPISSILIKGD--- 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF----LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
RAVV ++ E + +G +G +R+ + G G +
Sbjct: 66 -RAVV-----SRREPDFYRAFNVGESGFTLRATAVSVYAGIPGLTAVYFGGT--L 111

Query: 130 RERPIGLDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
R RPI +L+ L++L V ++ +G L +V++ ISSQY+S L+
Sbjct: 112 RGRPIDELIEVLRLKLEVVKL---PGAVIIKKGELGRL--EVEIRADISSQYISGLMFL 165

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A + G V I+ + + S +VE T ++ F + + + YI+ G + KSP
Sbjct: 166 AAVGSGGV-IKPLGERKSWSFVEATAEVLRAFRAEVKLGE-----YIEVGGRMKSPGKLA 219

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V GD S +++ + TGG V + G + + D + MG +T E V G
Sbjct: 220 VPGDFSLSAFLVVAGVATGGEVEIRGPLS---KLDEPLVNAFKAMGVDITTGEGWVRAGK 276

Query: 310 PPREFPGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ IDVN++ PD+ M A+ A + + IR V + R KE+ R+ +
Sbjct: 277 -----GFYRGIDVNLSDNPDVLMPTALAAGMVEEESTIRGVETLRYKESNRIATVID 328

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
L +LG V D I P K A ++ DHR+ + +LAA V + D
Sbjct: 329 VLERLVGVQRHEKDAIYIKGPPKRRDVAFSSHGDRIGL-MALAASKIVGGCVDDISPVA 387

Query: 430 KTFP 433
K++P
Sbjct: 388 KSWP 391

>ref|ZP_04389819.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas
endodontalis ATCC 35406]
gb|EEN82904.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas
endodontalis ATCC 35406]
Length = 431

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 122/447 (27%), Positives = 196/447 (43%), Gaps = 62/447 (13%)

Query: 20 KLPKSKSLSNRILLLAALS-EGTTVVDNLLNS-----EDVHYMLGALRTLGLSVEADK 71
LP +KS +NR+L++A L+ E V + LL+ +DV M L+ +G + A+
Sbjct: 7 HLPPIAKSNANRLVLMAYLAGEFPRVRETLSSQGDWEDCPDDVRIMCRVLQEMGATSGAET 66

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
++ + L +G AG +R +TA + A G + G R++
Sbjct: 67 SSDTPFTL-----LDVGAAGTVLRFVTA-LAAVGTERPLQITGTTRLKN 109

Query: 132 RPIGLDVLVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLS-GSISSQY 182
RP+ L+ LK LGAD+ T PP R L GG + + SSQ+
Sbjct: 110 RPLRPLDELKALGADIRGEWSEENAHDLTIYPPSR-----PLRGGTLSSFTDRQSSQF 164

Query: 183 LSALLMAAPLALGDVEI-EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+SALLM AP I E+ + S PY+++TL +M G ++++ G
Sbjct: 165 ISALLMIAPYFSAPFTIPELPRRGNSYPYIDLTLAMMREAGADWSYTETGVVVKPGGYSG 224

Query: 242 YKSPKNAYV-EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + A V E D S+ASY +A+ V + + QGD + +G + +
Sbjct: 225 DRLLMARVPEDWWSAASYAFGWSAVHRPVFLPSLRASDRQGDKAIVGFMRPLGVEARF 284

Query: 301 TE---TSVTVTGPFR-----EPFGRKHLKAIDVNMNMPDVAAMLAVVALFADGPTAIRDV 353
E + T PR P G +N++PD+ TL V AL P ++ V
Sbjct: 285 LEGGGVELIPTDVPRACYTPEG-----LNEVPDLVPTLVVTALMRRQPFLMKGV 334

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYC----IITPPEKLNVTIAIDTYDDHRMAMA 409

AS R+KE++R+ + G + E D +P E +DT +DHRMAMA
Sbjct: 335 ASLRKESDRLRQLVETAALFGFRLHESDDALAWDGTFSPEAQRTILVDTAEDHRMAMA 394

Query: 410 FSLAACAEVPTIRDPGCTRKTFFPDYF 436
+S+A+ V D K++P ++
Sbjct: 395 WSIASILYPQVQYTDASVVSKSYPGFW 421

>ref|YP_004059748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfuricurvum
kujiense DSM 16994]
gb|ADR33548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfuricurvum
kujiense DSM 16994]
Length = 425

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 116/425 (27%), Positives = 196/425 (46%), Gaps = 30/425 (7%)

Query: 25 KSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGK 84
KS+S+R + A L+EG + V+N L +ED L + LG + D + + G
Sbjct: 23 KSISHRCAMFVLAEGESRVENFLRAEDTLNLTIVGHLGAQIHDDG--EVITIRSNG- 78

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
+++ E L GN+G MR +++A G+ +VL G ++ RP+ + L+ +
Sbjct: 79 --IQETSE--ILDGSGTGMRLFCGLLSAEGH--FVLTGDEYLRKRRPMKRVTQPLRSI 132

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA +D D P+ + G V S S+Q SA+++AA + G +
Sbjct: 133 GAKLDGRNNGDLAPLSIRGASLKAFDYV--SPIASAQVKSAMMLAALRSDGVCTFR--EP 188

Query: 205 LISIPYVEMTLRLM-ERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAG 263
+S + E LR M R + + W + P N V D SSA +F
Sbjct: 189 ELSRDHTERMRLRGMGARVEINGLETKIWPL-----EAPLKPLNIRVPADPSSAFFFAVA 242

Query: 264 AAITGGTVT-VEGCGTSLQGDVKFAEVLEMMGAKVTWT--ETSVTVTGPPREPFGRKHL 320
AAIT + T +EG + ++ +VLE MGAK+T+T + G R H
Sbjct: 243 AAITPNSSTLIEGVTLNPTNTR--IEAFKVLERMGAKITYTLNDERYEPIGTIRVEHAPLHA 300

Query: 321 KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
++ N+ + D L++ A+G + I++ RVKE++R+ + L G EE
Sbjct: 301 VTVEENIAWLIDELPALSIAMACAEKSGSIKNAEELRVKESDRIKTVVDNLLNLCGIETEE 360

Query: 381 GPD-YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYFDVL 439
PD Y +I +L +++++ DHR+AM+F L + + + D C +FP++F++L
Sbjct: 361 YPDGYAVIGG--ELKSARVNSFGDHRIAMSF-LIGGLKCGMEVEDIECINTSFPNFFELL 417

Query: 440 STFVK 444
K
Sbjct: 418 EMCTK 422

>ref|YP_003516068.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter mustelae
12198]
emb|CBG39320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter mustelae
12198]
Length = 424

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 119/448 (26%), Positives = 207/448 (46%), Gaps = 45/448 (10%)

Query: 11 PIKEISGTVK-LPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
P + G V+ + KS+S+R + + L++G V N L + D L + LGL V
Sbjct: 6 PATSLKGVVENIASDKSISHRCAMFSLAKGACEVQNFLQASDTLDTLKIAQHLGLEVIQ 65

Query: 70 DKAARAVVVGCGGKFPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ +++ P ++ +E + L GNAG AMR T + AG +VL G
Sbjct: 66 KNSNTLSLI-----PPKNGIKEPNVLLDCGNAGTAMRLYTGLL--AGVKGYFVLCGDK 116

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ ++ L+ +GA + G P ++ IG G S S+Q SA+L
Sbjct: 117 YLHARPMQRVIAPLQSIGARIFAREGGYAP---LSIIGAKLQGFAYASPIASQVKSAML 173

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
 ++ A E + +S + E R++++ G K + S + ++ Q P +
 Sbjct: 174 LSGLF--SSSRFSEPELSRDHTE---RMLKKMGAKI--TKSANTIELEPLQGPLDPFS 226

Query: 248 AYVEGDASSASYF-LAGAAITGGTVTVEGC--GTTSLQGDVKFAEVLEMMGAKVTWTETS 304
 + D SSA +F LAG + G + ++ T +Q EVL+ MGAK+++
 Sbjct: 227 ITIPSDPSSAFFFALAGVIVPGSHLVKLVNLPTRIQ----YEVLLKMGAKISYENKK 282

Query: 305 VTVTGPPEPFGGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRV 358
 + L AI+V+ ++++P +A+ +AV A G + +++ RV
 Sbjct: 283 EQIETGDIIESSDLCAIEVSEHIAWLIDELPALAIAMAV---AKGKSVVKNAKELRV 338

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CA 416
 KE++R+ A+ + L K+G E D I E L +D+Y DHR+AM+F++A C
 Sbjct: 339 KESDRKAVVSNLQKMGIVATEREDGFEILGGE-LKPARVDSYGDHRIAMSFVAMLLCG 397

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
 I D C +FP++ ++L K
 Sbjct: 398 G---EIEDFSCVNISFPNFLEILEQIKK 422

>ref|YP_003860414.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ignisphaera aggregans
 DSM 17230]
 gb|ADM28534.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ignisphaera aggregans
 DSM 17230]
 Length = 411

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
 Identities = 119/437 (27%), Positives = 204/437 (46%), Gaps = 46/437 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALASEGTTVDNLLNSEDVHYMLGALRTLGL 65
 IV++ K ISG+++ P SKS + R++ + +++ +DNL+ S DV L A+ LG+
 Sbjct: 2 RIVIEKSK-ISGSIEAPQSKSYAIRLIFASIITD--VELDNLILSRDVKAAALNAVEALGI 58

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
 S E + +R V K+ V + G + +R L V+ GG T +DG
 Sbjct: 59 SYENGRFIRRDV-----RIVKDYVNV--GESATVLRMLPIVSVIGGRIT--IDG 105

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSA 185
 +R RP+ +V L G + D P+ + G L +++ G SSQY+S
 Sbjct: 106 DESLRRRPLKAVVEALTDRGVKIYG---DRLPITIEG--RLRDQYIEIRGDESSQYISG 159

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
 + A ++ G I I + S Y+ +T ++ GV+ + S +R ++ + +P
 Sbjct: 160 FMYAFTISGGGT-IVIKPPISSKSYIYLTDDILRSIGVEVKFSG--NRIDVEPTEDI-TP 215

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGT-TSLQGDVKFAEVLEMMGA-----KVT 299
 V GD +S+++A A +TGG + V G + GD E+ MGA T
 Sbjct: 216 YRGRVPGDYLLSSFYVASALLTGRIYVYGLPQPANYFGDHSIVEIYRSMGALSIFYSNNT 275

Query: 300 WTETSVTVTGPPEPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
 W +V ++ID++++ PD+A ++A +A A+G + IR V R+K
 Sbjct: 276 WFAEAVDT-----YRSIDIDIDAPDLAPSIATIANGISVIRGVRRRLRIK 323

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
 E++R++ I + L G V D I E ++I +DHR+AM + A V
 Sbjct: 324 ESDRVMTISSALKSFGIDVNISIDTIEIYGGEFQR-SSIQCPNDHRIAMMVTPLAL-RVG 381

Query: 420 VTIRDPGCTRKTFPDYF 436
 I C K+ P+++
 Sbjct: 382 GVDAEACVDKSNPNFW 398

>ref|ZP_01818831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
 pneumoniae SP3-BS71]
 gb|EDK73280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
 pneumoniae SP3-BS71]
 Length = 396

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
 Identities = 110/413 (26%), Positives = 190/413 (46%), Gaps = 25/413 (6%)

Query: 37 LSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAKRAVVVCGGKFPVEDAKEEVQL 96
++EG T V ++L EDV + R LG+ +E VG G ++A L
Sbjct: 1 MAEGETKVYDILRGEDVLSTMQVFRDLGVEIEDKDG VITVQQVGMAGLKAPQNA-----L 55

Query: 97 FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDC 156
+GN+G ++R ++ + AG + + G + +RP+ + + LK++G + D
Sbjct: 56 NMGNSGTSIRLISGVL--AGADFEVEMFGDDSLSKRPMDRVTLPLKKMGVSISGQTERDL 113

Query: 157 PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLR 216
PP+R+ G L +L + S+Q SAL+ AA A G E II+K + + E
Sbjct: 114 PPLRLKGTKNLRPIHYELPIA-SAQVKSALMFAALQAKG--ESVIEKEYTRNHTD---D 167

Query: 217 LMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEG 275
++++FG S + ++G QK K V GD SSA+++L AG + ++
Sbjct: 168 MLQQFG--GHLSVDGKKITVQGPQKLTGQK-VVVPGLDISSAFLVAGLIAPNSRLVLQN 224

Query: 276 CGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPPDAM 335
G + + +V+ MG K+ TE V LK ++ +P +
Sbjct: 225 VGINETRTGI--IDVIRAMGGKLEITEID-PVAKSATLIVESDDLKGTEICGALIPRLID 281

Query: 336 TLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK 392
L ++AL A G T I+D +VKET+R+ + L +GA + D II
Sbjct: 282 ELPIIALLATQAQGVTVIKDAEELKVKETDRIQVVADALNSMGADITPTADGMIKGSKA 341

Query: 393 LNVTAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
L+ ++T+ DHR+ M ++AA A+ V + ++P +FD L + +
Sbjct: 342 LHGARVNTFGDHRIGMMAIAALLVADGEVELDRAEAINTSYPSFFDDLES LI 394

>ref|ZP_01386111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
ferrooxidans DSM 13031]
gb|EAT59036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
ferrooxidans DSM 13031]
Length = 433

Score = 110 bits (276), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 115/442 (26%), Positives = 202/442 (45%), Gaps = 41/442 (9%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLS-----VEADKAAK 74
LP KS+S+R L+ ALSEGTT + N D L L+ G++ V+ + +
Sbjct: 11 LPPDKSISHRAALIGALSEGTTETNFSGGFDNQSTLSVLQRAGIALSQEEIVQLNGRTQ 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + + E L N+G MR + A + + D + +RP+
Sbjct: 71 RRVVIKSRGLWSFQPPAEP--LMCNNSGSTMRFAGILAAQPFRSELIGDS--SLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GAD++ + P+ +NG L +L + S + +L+ A L
Sbjct: 127 KRVADPLRLMGADIE-LSSSGTAPILINGTKALKPIAYRL--PVPSAQVKS LVAFAALH- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D E II+++ S + E+ L L E F E R + G+K + Y+ D
Sbjct: 183 ADGESRIIEQVRSRDHTEVMLGL-ESFDQNGE-----RVIVVPGRKQIEARPFYIPADP 235

Query: 255 SSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLMMGA-----KVTWTET--S 304
S+A + +A G G + + + F ++L GA +V E+
Sbjct: 236 SAACFIVALGLLARGSEIMIRDVCLNPTRA--AFLDILMAAGAGLHIENLRVIGGESIGD 293

Query: 305 VTVTGPPR-EPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ V+ R EP + I + ++++P LAV++ FA G + + A R KE++R
Sbjct: 294 ILVSSASRIEPLCISDPQLIAIAIDEIP----MLAVLSAFATGCFELHNAELRTKESDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAMAFSLAACAE-VPV 420
+ A+ L +LG E+ PD ++T ++ +D++DDHR+AM+F++A A
Sbjct: 350 IAALVNLRLERLGFVCEQYPDGFVVTGRKQAPSGTVVLDSDHRIAMSFAIAGRATGGSF 409

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I D +FP++F++L +
Sbjct: 410 DITDIDVGVSPFNFFELDSL 431

>ref|YP_001996267.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroherpeton
thalassium ATCC 35110]
sp|B3QZC7.1|AROA_CHLT3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF13820.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chloroherpeton
thalassium ATCC 35110]
Length = 435

Score = 110 bits (275), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 117/454 (25%), Positives = 205/454 (45%), Gaps = 41/454 (9%)

Query: 12 IKEISGTV-KLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA- 69
+K +GT LP KS+S+R L+ ALS G T + N D L L++LG+ ++
Sbjct: 1 MKTFNGTFFNLPPDKSISHTALIGALSNGITEITNYSAGLDNQTTLSVLQSLGVDIQQE 60

Query: 70 -----DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
D +R VV+ G + + +K E L N+G +R L+ + A T V
Sbjct: 61 SFLTNDGYEQRKVVVKSGLWSLSRSKRE--LMCNNSGSTIRMLSGILAAQPFRTTLV-- 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L Q+GA + T PP+ + G P ++ I S +
Sbjct: 117 GDHSLMKRPMRRVAEPLTQMGASIK-LSETGAPPIEIE--GKKPLSPIQFYQKIPSAQVK 173

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L++ A L + EII+ + + + E+ L G++ E R + GQK
Sbjct: 174 SLVIFAALHADGIS-EIIEPIQTRNHTLML-----GLEPELQPDGSRKIVIEGQKNIE 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTSSLQGDVKFAEVLEMMGAKVTWTET 303
K V D S A + +A ++G + + ++ G + + +L GAK+ TE
Sbjct: 227 AKPFTVPADPSGACFLVALGLLSGKSDIRLKNVGLNHTRAG--YLSLLREAGAKLP-TEN 283

Query: 304 SVTVTGP-----PREPFGRKHLKAIDVNM-NKMPDVAMTLAVVALFADGPTAIRDVASW 356
+ T+ G + K L+ D + + + D LAV++ A G + A
Sbjct: 284 NRTIGGELLGDIISNDYITKPLRINDAQIVSDIIDEIPMLAVLSAMATGEFELHHAEL 343

Query: 357 RVKETERMVAIRTELTKLGASVEEGPD-YCII----TPPEKLNVTADITYDDHRMAMAFS 411
R KE++R+ A+ L +LG EE D +C+ P + +T T+ DHR+AM+F+
Sbjct: 344 RAKESDRIHALVMNQLRGLGFVCEEYKDGFCVTGRTHNPTGTIEIT---TFYDHRAMSF 400

Query: 412 LAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
+A + + + D +FP++F ++ + K
Sbjct: 401 IAGHFSNAEIQLDDNSSIAVSFPNFFSLIDSMQK 434

>ref|YP_003695752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Starkeya novella DSM
506]
gb|ADH91133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Starkeya novella DSM
506]
Length = 453

Score = 110 bits (275), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 131/437 (29%), Positives = 195/437 (44%), Gaps = 35/437 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+ GTV++PG KS+S+R L+ L+ G T + LL EDV A LG +VE +
Sbjct: 19 LKGTVRVPGDKSVSHRSLIFGTAVGETRISGLLEGEDVLNTAKACAALGATVERLGE 78

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
R VG GG + P E L GNAG R + V AG DG +R+R
Sbjct: 79 WRVEGVGVGGLRVP-----EGVLDGFGNAGTGSRLMMGVV--AGNPVATFDGDASLRKR 130

Query: 133 PIGDLVVGLKQLGAD-VDCFLGTDGPPVRVNGIGGLPGGKVKL---SGSISSQYLSALLM 188
P+ ++ L+++G VD G P+ + G P V + S S+Q SA+L+
Sbjct: 131 PMRRILDPLEKMGVQVVDAAEGGRL-PLTLKG---PQELVPIIYESPVASQAQIKSAVLL 185

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A G E +I+K S + E R++ FG V E + R G+ P
Sbjct: 186 AGLGAPG--ETTIVIEKEASRDHTE---RMLTHFGAQVSVEPYGAHGRKVTCLKRPELKPA 240

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V D SSA++ L A I G+ V +EG T L+ + L+ MGA + + V
Sbjct: 241 PIRVPADPSSAAFPPLVAALIVPGSEVVIEGVTNPLRTGLFI--TLKEMGADIAFENERV 298

Query: 306 TVTGPPREPFGGRKH-LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ R L +DV + P D LAV A FA G T + ++ RVKE+
Sbjct: 299 EGGESVADIRVRASALHGVDPVAERAPSMIDEYPVLAVAAAFASGTTTRMNGLSELRVKES 358

Query: 362 ERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE-EVP 419
+R+ A+ L G + EG D + + T+ DHR+AM+F + A + P
Sbjct: 359 DRLAAVADGLKAAGVAHRIEGDDLLEGAAGAAGGGTVATHMDHRIAMSFLVMGLATDTP 418

Query: 420 VTIRDPGCTRKTFPDYF 436
+ + D +FP +
Sbjct: 419 LKVDDISFIATSFPTFL 435

>ref|YP_002019329.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelodictyon
phaeoclathratiforme BU-1]
sp|B4SFD3.1|AROA_PELPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF44712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pelodictyon
phaeoclathratiforme BU-1]
Length = 433

Score = 110 bits (275), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 118/445 (26%), Positives = 200/445 (44%), Gaps = 47/445 (10%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE-----ADKAAK 74
LP KS+S+R L+ ALSEGTT + N D LG L+ G+++ AD
Sbjct: 11 LPPDKSISHRAALIGALSEGTTAIMNFSGGFDNQSTLGVLDAGITLRQELLELEGADGRTV 70

Query: 75 RAVVVGCGGKFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V++ G + + L N+G MR + A + AA A+ ++ G + +RP+
Sbjct: 71 RQVIESKGLWSFQ--PPSAPLMCNNSGSTMR-MFAGILAAQPFASELI-GDSSLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+Q+GAD+ + P+ + G L +L + S + +L+ A L
Sbjct: 127 KRVADPLRQMGADLQ-LSPSGTAPICIKGSKELKPINRYL--PVPSAQVKSLSLVAFAALH- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D E II+ + S + E+ L G+ + D +R + G+K + K Y+ D
Sbjct: 183 ADGESRIIESVRSRDHTEVML-----GLDSFEQDG-ERVIVVPGRKTVAAKPFYIPADP 235

Query: 255 SSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV----- 305
S+A + +A G G + + + F +L GA +T V
Sbjct: 236 SAACFIVALGLLARGSEIIIRDVCLNPTRA--AFLNILTDAGACLTENQVRVIGGETIGD 293

Query: 306 --TVTGPPREPFGGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
EP + + ++++P LAV++ FA G + + A R KE++R
Sbjct: 294 ILVENHAALEPLLITDPQLVAFIIDEIP---MLAVLSAFASGRFELHNAELRTKESDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAE- 417
+ A+ L +LG E+ PD + ITP ID++DHR+AM+F++A A
Sbjct: 350 IDALVVNLQRLGFDCEQYPDGFVVKGRITPS---GTVVIDSFDDHRIAMSFAIAGKATG 406

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
P+ + D +FP++FD+L +
Sbjct: 407 CPIDLSIDVVGVSFPNFFDLDSL 431

>ref|YP_903843.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Ruthia
magnifica str. Cm (Calyptogenia magnifica)]
sp|A1AWR5.1|AROA_RUTMC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABL02372.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus Ruthia
magnifica str. Cm (Calyptogenia magnifica)]
Length = 435

Score = 110 bits (275), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 114/459 (24%), Positives = 223/459 (48%), Gaps = 65/459 (14%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ V++P +SG +K+PG KS+S+R ++L +L+ G T + L ED L A + +G+
Sbjct: 3 KFFVVKPTNSLSGCLKVPKDKSISHRSIMLGSLANGVTKISGFLEGEDTLSTLKAFQDMGV 62

Query: 66 SVEADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + VG G K P+ L LGN+G ++R ++ + A ++ L
Sbjct: 63 KIEYNGDNVTIYGVGLNGLKKPL-----TPLDLGNSGTSIRLISGILAAQKFDSE--LC 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+G ++ L ++GA ++ G P+++ G L G L + S+Q S
Sbjct: 115 GDESLSKRPMGRVINPLTKMGAMIESNNGK--LPLKIKGGQALNGIHYDLLVA-SAQVKS 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+L+A A G+ I+ + P + T R+++ FG K + + ++ + GG +
Sbjct: 172 CVLLAGLYAKGETCIKEL-----APTRDHTERMLKGFYKIDVKN--NKICLIGGTQL-- 222

Query: 245 PKNAY---VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
NA+ V D SSA++F+ A+I +T+ G + + ++L++MGA ++
Sbjct: 223 --NAFAIQVPSDISAFAFFMVAASIAPKADITLTGVNINPTR--IGVIDILKLMGANLSL 278

Query: 301 T---ETSVTVTGPPREPFGKHLKADVNMNKMPPDVAMTLA-----VVALFADGPTA 349
+ E + R + LK I ++P+ ++LA + A A G T
Sbjct: 279 SNEREIGGELLADIR--IQSEQLKGI-----RIPEELVSLAIDELPVIFIAASCAKGETI 331

Query: 350 IRDVASWRVKETER-----MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADIT 400
+ D RVKE++R ++ I+ E+ + G ++ G + + P I++
Sbjct: 332 LTDAKELRVKESDRIQVMADGLSILGKNEVEDGKIQGG---VFSKPG---IVIES 383

Query: 401 YDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDV 438
+ DHR++M+F++A+ + + I D + +FP++ ++
Sbjct: 384 HHDHRISMSFAIASLRQYIIEIEDVDNVKTSFPNFVEL 422

>ref|ZP_07572580.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobium
chlorophenolicum L-1]
gb|EFN12016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobium
chlorophenolicum L-1]
Length = 446

Score = 110 bits (274), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 122/450 (27%), Positives = 201/450 (44%), Gaps = 48/450 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+ +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R +G + D
Sbjct: 19 LSGTITVPGDKSISHRSLMLSALAVGESHVEGLLEGEDVLSTAAAMRAMGADISKDADGV 78

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ VG GG A L +GN+G + R L V + AT+V D + +RP
Sbjct: 79 WHIHGVGVGGLLQPTSA-----LDMGNSGTSTRLLMGLVASHAITATFVGDA--SLSKRP 131

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L ++GA G P + G P + + S+Q SA+L+A
Sbjct: 132 MARVTEPLSRMGASFTTSPGDRLP---LTMRGACPAVPLDYRLPVASAQVKSAILLAGLN 188

Query: 193 ALGDVEIEIIDKLIS-IPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G I +++ IP + + R+++ FG + E R G+ P++
Sbjct: 189 APG-----ITRVVEPIPTRDHSERMLKGFADLHVETEADGTRIITLRGEAELRPQSIT 242

Query: 250 VEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++ +A + G VT+ G + + ++L MG +
Sbjct: 243 VPGDPSSAAFPMAALLVPGSKVTIANVGLNATR--AGLIDLREMGGDIAIKN----- 294

Query: 309 GPPR---EPFG-----RKHLKADVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASW 356
PR EP G LK ++ + + P D + A FA+G + R +
Sbjct: 295 --PREVGGEFVGDLVITASALKGVPEDPARAPSMIDEYPVAFIAAFAEGRSTFRGLEEL 352

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAFSLA 413
RVKE++R+ + L +G +VEE D +I I T DHR+AM+F+++

Sbjct: 353 RVKESDRIATMAAGLRAIGVTVEELEDGIVIEGSGGALLPGGGPIATSLDHRIAMSFAIS 412

Query: 414 AC-AEVPVTIRDPGCTRKTTPDYFDVLSTF 442

++ VTI D +FP + +L +

Sbjct: 413 GLMSKKGVTTIDMRPVATSFPGFTGLLRSL 442

>ref|ZP_05046551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanobium sp. PCC 7001]

gb|EDY39860.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Cyanobium sp. PCC 7001]

Length = 441

Score = 110 bits (274), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 126/408 (30%), Positives = 194/408 (47%), Gaps = 24/408 (5%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G V++PG KS+S+R LL A++ G T ++ LL +ED LR +G+ V A

Sbjct: 19 LRGRVQVPGDKSISRALLFGAIACGETRIEGLLPAEDPLSTAACLAMGVEVSPIAAGA 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133

V G G ++ +E + GN+G MR + + G +VL G +R RP

Sbjct: 79 VVRVQVG---LDGLQEPGDVLDGNSGTTMLMLGLLAGRAGR-HFVLSGDASLRGRP 133

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193

+ + L ++GA V + P+ V G L G V+ + S+Q SALL+AA A

Sbjct: 134 MRRVGAPLARMGAVVHGRKDNFAPLAVLQA-LRGTTVR-TPVASAQVKSALLLAALTA 191

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKNAYVEG 252

G + I+ S + E R++ FG + ++ G + ++ V G

Sbjct: 192 EGPTTV--IEPSQSRDHSE---RMLRAFGASLVVDGPGNTCVTVQPGAPLQG-QSVVVP 245

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311

D SSA+++L AIT G +TVE G + EVLE MGA++T V G P

Sbjct: 246 DISSAAFVLVAGAITPGADLTVENVGLNPSR--TGILEVLEQMGARLTVLNRR-DVAGEP 302

Query: 312 REPFGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366

+H L+A + +P D LAV A A+G + I D A RVKET+R+

Sbjct: 303 VGDLRVQHGPLQAFSIGGELIPRLVDEIPVLAVAACCAEGTSRIHDAAELRVKETDRLAV 362

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414

+ +L +GA +EE D + L +D+ DHR+AM+ ++AA

Sbjct: 363 MARQLGAMGARIEEYEDGMAVEGAGALRGAELDSETDHRVAMSLAVAA 410

>ref|YP_003551577.1| 5-enolpyruvylshikimate-3-phosphate synthase [Candidatus Puniceispirillum marinum IMCC1322]

gb|ADE39493.1| 5-enolpyruvylshikimate-3-phosphate synthase [Candidatus Puniceispirillum marinum IMCC1322]

Length = 446

Score = 110 bits (274), Expect = 6e-22, Method: Compositional matrix adjust.
Identities = 128/453 (28%), Positives = 194/453 (42%), Gaps = 41/453 (9%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69

Q ++G + +PG KS+S+R L+L +L+ GTT V LL DV A+R LG+ +

Sbjct: 12 QRTDNLGAIIDVPGDKSMSHRSILGSLAIGTTKVTGLLEGADVLTADAMRALGVDITR 71

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129

V+VG G V E L LGN+G +R L V AT+ D +

Sbjct: 72 HDDGTW-VIVGQGLHGLV---APETALDLGNSGTGVRLLMGVVAGQAITATFTGDA--SL 125

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189

RP+ + L+Q+G V G PV + G P S S+Q SA+L+A

Sbjct: 126 SVRPMARITDPLQMGTHVASRDG-GLLPVTITG-QSEPMAISYESPVASAQIKSAILLA 183

Query: 190 APLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

A GD E+I+ S + E LR FG E + D + GG + +

Sbjct: 184 GLTARGDT--EVIEPHASRDHTESMLR---HFGATVEQTVRDDGTHVQLHGGAQLIAAD 238

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305

A V D SSA++ + A +T G+ +T+ G L+ L MG ++
Sbjct: 239 IA-VRPDSSAAAFPMVAALLTKGSDITLPSIGMNPLR--TGLITTLIEMGGDISILN--- 292
Query: 306 TVTGPPR----EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDV 353
PR EP ++ D++ +P D L+V A A G T + V
Sbjct: 293 -----PRDEGGEPVADLRVRHSDLHGGINIPAERAASMIDEFILSVAATQAYGTTIMNGV 347
Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAF-SL 412
A RVKET+R+ + L GA V D +T +++ DHR+AM+F +L
Sbjct: 348 AELRVKETDRIKVMADGLIAAGAIVSYDDDTMTVTGGPIAGGMTVNSQHDHRIAMSFLT 407
Query: 413 AACAEVPTTIRDPGCTRKTFPDYFDVLSTFVK 445
+ PV++ +FPD+ ++ N
Sbjct: 408 GLISNAPVSVEGCETIHTSFDPFAKIMQNAGAN 440

>ref|ZP_06949694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MN8]
gb|EFH94658.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MN8]
Length = 435

Score = 109 bits (273), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 121/448 (27%), Positives = 207/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALR 61
E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62
Query: 62 TLGLSV EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D + +VV G + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVDIKED---EDKLVVNSPG-YKAFKTPHQV-LYTGNSGTTTTRLLAGLLSGLGIES-- 115
Query: 122 VLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI K++++
Sbjct: 116 VLSGDVSIKRPMDRVLRLPKSMNANIEGIEDNYTPLIIPSVIKGI----NYKMEVA-- 169
Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L E II +L +S + E R F + E ++ I
Sbjct: 170 -SAQVKSAILFA---SLFSKEATIIKELDVSRNHTETMFR---HFNIPIE-AEGLSITTI 221
Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG
Sbjct: 222 PEAIRYIKPADPHVPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMG 279
Query: 296 AKVTWTETSVTVTGPPREPFRGRKH---LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +
Sbjct: 280 GNIQLFNQ--TTGAAPTASIRIQYTPMLQPIKIEGELVPKAIDELPIALLCTQAVGTST 337
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M
Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMM 397
Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++A+ + PV I+ +FP +
Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

>ref|YP_003817722.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevundimonas
subvibrioides ATCC 15264]
gb|ADL00099.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brevundimonas
subvibrioides ATCC 15264]
Length = 438

Score = 109 bits (272), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 138/454 (30%), Positives = 204/454 (44%), Gaps = 46/454 (10%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 63
A + +P + GTV+ PG KS+S+R ++L A++ G T +D LL +DV A
Sbjct: 5 APHLTARPGHPLRGTVRAPGDKSISHRSMILGAMASGVTEIDGLLEGDDVLATARAAEAF 64

Query: 64 GLSVEADKAAKRAVVVCGCG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G VE R V G GG + P + GNAG +R L A AAG
Sbjct: 65 GAKVE-RLGGGRWRVTGRGGFQTPTG-----VIDCGNAGTGVRLMGA--AAGYPIAAT 115

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLP----GGKVKLSGSI 178
DG +R RP+G + L ++GA F + P G LP GG + +
Sbjct: 116 FDGDASLRGRPMGRVTDHLTRMGA---TFAWSGKP-----GLLPATLTGGALHAIDHV 165

Query: 179 ----SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
S+Q SA+L+A A G + +K + T R++ FG + D + +
Sbjct: 166 QTVASAQVKSAILLAGLNASGTTTSVSEPEK-----SRDHTERMLRAFGAVVDVEDQGEGW 220

Query: 235 YI--KGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVL 291
I +GGQ V GD SSA++ L AG + G VTVEG L+ + F L
Sbjct: 221 VIRLRGGQPLTG-TTVSVPGDPSSAAFPLAAGLIVPGSEVTVEGVMLNPLRTGL-FDTWL 278

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGRKH--LKAIDVNMNK---MPDVAMTLAVVALFADG 346
E MGA +T V+ G +H L+ + V ++ M D LA A FA G
Sbjct: 279 E-MGADLTIANRRVS-GGEDVGDITARHSPLQGVVVPESRAASMIDEYPILAATAAFVAVG 336

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406
T +R V RVKE++R+ + L G V+E P+ I+T + T DHR+
Sbjct: 337 ATVMRGVGEEMRVKESDRIRLMVDGLRACGVGVDEEPEGFIVTGGAVPGGATVHTAHDHRI 396

Query: 407 AMA-FSLAACAEVPTVIRDPGCTRKTFPDYFDVL 439
AM+ L A P+T+ +P +FP + +++
Sbjct: 397 AMSHLVLGLAAAPITVDEPDMIATSFPGFVEMM 430

>ref|YP_254900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus
acidocaldarius DSM 639]
gb|AA79607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfolobus
acidocaldarius DSM 639]
Length = 358

Score = 109 bits (272), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 97/347 (27%), Positives = 166/347 (47%), Gaps = 25/347 (7%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTD 155
L G + +R + ++ GG VLDG +R RPI +V L ++
Sbjct: 27 LNFGGSATTLRMMIPILSVLGGEV--VLDGNESLRRRPITAIVEALAG-----QIRFSSN 79

Query: 156 CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL 215
PV + G L V++ G SSQY+S + A L G +IEII L S Y+ MT+
Sbjct: 80 YLPVTMTG--KLKENYVRIRGDESSQYISGFIYAFSLVNGG-DIEIIPPLSSKSYIHMTI 136

Query: 216 RLMEFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
L+ G + + +R ++ G+ ++ + V GD + AS++ +AITGG + ++G
Sbjct: 137 DLINALGGSVKFTG--NRIRVERGE-FRDFRGD-VPGDYALASFYAIASAITGGEIQIKG 192

Query: 276 CGTTSLSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVA 334
+ GD ++++ MG S V+G +K I V+++ MPD+A
Sbjct: 193 LYSPPYDGDHSIVKIIKNMGVDSRVEGNSWIVSG-----NGIIGKIKVDVDDMPDLA 245

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
++A +A FA T I + R+KE++R+ I++ L +V D+ I P KL
Sbjct: 246 PSIACIAPFATSETETIGIKRLRIKESDRVSTIKSTLEAFSGNVVVDTFIKIF-PSKLT 304

Query: 395 VTAIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFPDYF-DVLS 440
+I +DHR+AM + + T+ + C K+ P ++ D++S
Sbjct: 305 EGSIIICPNDHRIAMMAGVISL-RTGGTVENACVKNKSNPSFWLDLIS 350

>ref|ZP_05038951.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. PCC
7335]
gb|EDX87686.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. PCC
7335]
Length = 409

Score = 108 bits (271), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 119/424 (28%), Positives = 187/424 (44%), Gaps = 32/424 (7%)

Query: 33 LLAALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE 92
+L A+++GTT + LL ED +G + +D A+ V G GG D
Sbjct: 1 MLGAIAQGTTTRIKGLLLGEDPRSTAACFTAMGAKI-SDLEAEWVTVEGTGGDLQEPDDV- 58

Query: 93 EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFL 152
L GN+G +R + + A G + + G +R RP+ ++ L +GA +
Sbjct: 59 ---LDAGNSGTTLRMLGLLAAQPGK-FFAVTGDDSLRSRPMKRVIAPLTSMGATIFGKA 114

Query: 153 GTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV- 211
P+ V G P I+S + + L+ A LA+ I D I+ P +
Sbjct: 115 DHTLAPLGVIGQSLQP---FHYHSPIASAQVKSCLLLAGLAI-----IGDTTITEPSLS 165

Query: 212 -EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT-GG 269
+ + R+++ FG + I G K + V GD SSA+++L AAIT G
Sbjct: 166 RDHSERMLKAFGASLSIDSATHSVTIHGPAKLTG-QTVIVPGDISSAFWLVAAAITPGS 224

Query: 270 TVTVEGCGTTSLQGDKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMN- 328
+ +E G + V + L M A +T E VTG P KH + I ++
Sbjct: 225 NLLIENVGINPRTGV--LDALAAMNADITL-ENERDVTGEPVADLRVKHSELIGCHIGG 281

Query: 329 ----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL--GASVE--E 380
++ D LAV ALFA G T I D A RVKE++R+ + + L K+ G+ E E
Sbjct: 282 DLIPRLIDEVPIAALFAVGTITTDAAELRVKESDRLAVMASALNKMAPGSITEQTE 341

Query: 381 GPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTTFPDYFDVL 439
G + +L T +D++ DHR+AMA ++AA A I+ ++P + L
Sbjct: 342 GMEIKGTGADTQLTATLDSHSDHRIAMALTIAATRARGQTAIQRAEAAAI SYPTFVSTL 401

Query: 440 STFV 443
T V
Sbjct: 402 ETAV 405

>ref|ZP_02468029.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia
thailandensis MSMB43]
Length = 409

Score = 108 bits (271), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 99/404 (24%), Positives = 177/404 (43%), Gaps = 31/404 (7%)

Query: 46 NLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVE---DAKEEVQLFLGNA 101
N L + M A R LG ++ D+ + G GG+F + DAK +
Sbjct: 3 NDLRCIETETMKAACRKLGATI--DETPDTLTITGIGGRFSTDVHVIDAK-----GS 52

Query: 102 GIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCCPPVRV 161
G+ R++ A + G +L G +R R + L L LGA+ +LG D +
Sbjct: 53 GLVFRMTMALSSMRG--IPTILTGDATLRRRVMKPLFDALHALGANF-TYLGDDGKAPVI 109

Query: 162 NGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVENTLRLMERF 221
N L G L+G ISSQ+++ALLM PL V+I I ++S Y++ TL M
Sbjct: 110 NWGKALDGSHTLAGDISSQFVTALLMTTPLGQRGVDIRITPPVLSQSYIDQTLDFMRLA 169

Query: 222 GVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
G+ + S + + + G Y++ + ++ D +S SY L A+ G + G +L
Sbjct: 170 GIDVQASPDYATYRVSPG-GYRA-FDTHINADFTSLSYLLMACALFPGVYRIAGIQEKT 227

Query: 282 QGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVA 341
QG+ F +++E +G ++ + + + +++ P++ TL ++
Sbjct: 228 QGERLFVDIVEALGVRLRYASGHMLDVDSSNADLEGN---FEFDVSSGPNIPTLVALS 283

Query: 342 LFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE--EGPD----YCIITPPEKLN 394
LF G +R + R ++ R+ ++ E+ KLGA +E PD +
Sbjct: 284 LFVKGLLTVRGGSVTRFHKSRIESMVGEVRKLGADIEIIRHPDGHTDGFVTRGRDRYAG 343

Query: 395 VTAIDTYDDHRMAMAFSLAAC-EVPVTIRDPGCTRKTTFPDYFD 437
++ + DHR M+ +AA + ++ +FPD+ D
Sbjct: 344 GVSLSNGDHRNFMSLFVAALRFDNACSLDGYADVSCSFDFID 387

>ref|ZP_00958039.1| EPSP synthase, 3-phosphoshikimate 1-carboxyvinyltransferase

[Oceanicaulis alexandrii HTCC2633]
gb|EAP88755.1| EPSP synthase, 3-phosphoshikimate 1-carboxyvinyltransferase
[Oceanicaulis alexandrii HTCC2633]
Length = 471

Score = 108 bits (271), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 124/462 (26%), Positives = 206/462 (44%), Gaps = 65/462 (14%)

Query: 10 QPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+P+ + G ++ KS S+R ++ +AL++G + ++ LL SEDV A+ LG VE
Sbjct: 41 RPNVNLKGRLLQAAADKSCSHRAVIFSALADGESRIEGLLESEDVLATARAVAALGAQVER 100

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ A + +V P E L LGN+G +R L A + A +V D +
Sbjct: 101 EGAGRSVVTGRGQWTSPE-----PLDLGNSGTGVRLLMGAASRFDLTAEFVGD--ESL 152

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ ++ L ++G G P V L GS S L+A+
Sbjct: 153 SSRPMARVLDPLSRMGVKSQSSDGGRLP-----VTLRGSSS---LNAIDYT 195

Query: 190 APLALGDVEIEII-----DKLISIPYV--EMTLRLMERFG--VKAHSDSWDRFYIK 237
P+A V+ I+ + ++ P+ + T + +G + E + ++
Sbjct: 196 PPVASAQVKSAILLAGLGAKGETIVREPHATRDHTEVMAVYGADLSVERQAGLIARVR 255

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
GG+ SP N + GD SSA++ +A A +T + +TV G T S + EVL+MMGA
Sbjct: 256 GGRTL-SPANVSIPGDPSSAAPPVAAALVTRDSEITVTGVMTNSAR--FGLYEVLMKMMGA 312

Query: 297 KVTWTETSVTVTGPPREPFGGRK-----HLKAIDVNMNKMP---DVAMTLAVVALFA 344
+ T P E G + L ++V + P D L+V+A FA
Sbjct: 313 DLEMT-----PAGERCGEQLVDITVRSGALHGVEVPASIAPSMIDEYPILSVIAAFA 364

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTY 401
DG T ++ +A R KE++R+ A L G +E G D + + V + T+
Sbjct: 365 DGVTVMKGLAELRAKESDRLAASAALLQANGVEIELGEDSLTVHGCQDGVPGGGMVKTH 424

Query: 402 DDHRMAM-AFSLAACAEVPTIRDPGCTRKTFFPDYFDVLSTF 442
DHR+AM A + A+ PV++ D G ++PD+F ++
Sbjct: 425 HDHRLAMSALIMGLGAQAPVSVDDVGMIAATSYPDFFGHMAAL 466

>ref|YP_003825018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosediminibacter
oecani DSM 16646]
gb|ADL07395.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermosediminibacter
oecani DSM 16646]
Length = 428

Score = 108 bits (271), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 128/449 (28%), Positives = 218/449 (48%), Gaps = 40/449 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ ++ + + G + P KS+S+R ++L A++EG T V+ L ++D + + +G+
Sbjct: 2 DVTVEGKRRLRGEIFAPPDKSISHRSVMLGAVAEGITRVERFLTADDCLRTVDCFKKMGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + A + ++ G G + K + L+ GN+G +R L+ + G AT + G
Sbjct: 62 DILFE-APDKVIINGRGLRGL---KKPDGPLYAGNSGTTIRLLSGILAGQGFEAT--ITG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+G +V L +GA ++ G P+ + G G L G + +L + S+Q SA
Sbjct: 116 DESILKRPMPGRVVEPLTMMGAVIEGAGGGRYAPLTIRG-GRLLKIRYELPVA-SAQVKSA 173

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G E +I+K + + E+ ++ FG + SD R S
Sbjct: 174 ILLAGLYAEG--ETTVIEKHKTRDHTTEI---MLAHFGGRISTSDGEVRLT---PVDKLSA 225

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVT----- 299
+ V GD SSA++F+A AA+T G+ + + G + + +VL MG +
Sbjct: 226 ERVTVPGDISAFAFFMAAAVTEGSELLIRDVGINPRTGI--IDVIREMGCNKIYDER 283

Query: 300 -WTETSVT---VTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352

W V V G + L+ I + +P D +AV A FA+G T IRD
Sbjct: 284 IWNGEKVADVLVKG-----EGLRGITIKGEIIPRLIDEIPVIAVAAFAEGETIIRD 335

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
A RVKE++R+ AI L + G V E D II L +++ DHR+AMA ++
Sbjct: 336 AAELRVKESDRKAIKAVNLRFRGTEVTELEDGMIIRGGGFLKPAEFESFGDHRIAMAMAV 395

Query: 413 AACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
AA A P I++ C + +FP +F+ L
Sbjct: 396 AALAIPGPSRIKNAECVKISFPGFFETLE 424

>ref|YP_530294.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB18]
gb|ABD85975.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB18]
Length = 467

Score = 108 bits (270), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 137/440 (31%), Positives = 201/440 (45%), Gaps = 35/440 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
++G V++PG KS+S+R L+L AL+ G T + LL EDV A+R LG SVE A
Sbjct: 40 LTGRVRVPGDKSISHRALILGALAVGETRISGLLEGEDVLNTAKAMRALGASVERTGDFA 99

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG A+ L GN+G R + AV AG T DG +R RP
Sbjct: 100 WRIHGVGVGGF-----AQPAAALDFGNSGTGCRLLVMGAV--AGCPITATFDGDASLRSRP 152

Query: 134 IGDVLVVLKQLGADV-DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ +V L+ +GA V D G P LP + + S+Q SA+L+A
Sbjct: 153 MRRIVDPLELMGARVIDSREGGRLPLTLQGARDPLP--ILYRTPVASAQIKSAVLLAGLA 210

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +I++ S + E+ ++ FG + +E + R GQ V
Sbjct: 211 APGIT--TVIEQEASRDHTEL---MLSHFGAQIVSEPEGAGHGRKISLTGQPELRGAPVVV 265

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ + A I G+ + + T L+ + L MG + +E V G
Sbjct: 266 PADPSSAAFPIVAALIVPGSDIVLTVMTNPLR--TGLFKTLREMGGSIIESE----VRG 319

Query: 310 PPPEPFGR-----KHLKAIDVNMNMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKET 361
EP + LK ++V + P D + LAV A FA+G T +R + RVKE+
Sbjct: 320 DAGEPMAQFRVRASQLKGVEVPPERAPSMIDEYLVLAFAAFAEGTTRMRGLKELRVKES 379

Query: 362 ERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAM-AFSLAACAEVP 419
+R+ A L G SVE +G D + + T DHR+AM A + A+ P
Sbjct: 380 DRLEATAAMLRLNGVSVEIDGDDLIVEGRGHVPGGGLVATEMDHRIAMSALVMGLAADQP 439

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
VTI D G +FPD+ ++
Sbjct: 440 VTIDDTGFIATSFPDFIPMM 459

>gb|ADQ77202.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TCH60]
Length = 435

Score = 108 bits (270), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 121/448 (27%), Positives = 206/448 (45%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALR 61
E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62

Query: 62 TLGLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ + K + +VV G + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVDI---KEYEDKLVVNSPG-YKAFKTPHQV-LYTGNSGTTTLLAGLLSGLGIES-- 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI K++++

Sbjct: 116 VLSGDSVIGKRPMDRVLRLPLKSMNANIEGIEDNYTPLIIKPSVIKGINY----KMEVA-- 169

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A+ L E II +L +S + E R F + E ++ I

Sbjct: 170 -SAQVKSAILFAS---LFSKEATIIKELDVSRNHTETMFR---HFNIPIE-AEGLSITTI 221

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG

Sbjct: 222 PEAIRYIKPADFHVPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGGRKH---LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +

Sbjct: 280 GNIQLFNQ--TTGAAPTASIRIQYTPMLQPIKIEGELVPKAIDELPVIALLCQAVGTST 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M

Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFFPDYF 436
++A+ + PV I+ +FP +

Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

>ref|ZP_04580452.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter bilis
ATCC 43879]
gb|EEO24774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter bilis
ATCC 43879]
Length = 443

Score = 108 bits (270), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 121/446 (27%), Positives = 198/446 (44%), Gaps = 45/446 (10%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
L KSLS+R+ + + ++ T V + L +ED L + LGL + +K

Sbjct: 19 LASDKSLSHRVCMSLFLADSTCRVKHFLRAEDTQRSLTIAQNGLKAKFEK----- 69

Query: 81 CGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIG 135
G + K+ +Q L+ GN+G +MR T + AG N VL G + RP+G

Sbjct: 70 -NGDLLLTPPKKGLQTPNDILYCGNSGTSMLFTGLL--AGANLYAVLCGDIYLHARPMG 126

Query: 136 DLVVGLKQLGADVDC-FLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALLM 188
++ L+ +GA++ + T V + +P K KL G S+Q SAL++

Sbjct: 127 RILKPLRSIGANITSRIIKTKDGVKEVAPLCVIP-SKNKLQGFTYHSQIASAQVKSALIL 185

Query: 189 AAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDS-----WDRFYIKGGQKY 242
A AL E I + +S + E L +++ + D + F +K K

Sbjct: 186 A---ALQGSEKSIIFSECELSRDHTENMLYALQKNPYLQKDDKLHITPFGAFDMKN--KL 240

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + D SSA +F A I T +T+ + ++ ++LE MGAK+ +

Sbjct: 241 LKAFDISIPNDPSSAFFFAVLACIMPETSITLRRVMMNKTR--IEAFKILEKMGAKIRYE 298

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDV--NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
LKA+D+ N+ + D L++ A G + IR+ A RVK

Sbjct: 299 NERNDFEKIADITISSAELKAVDITENIAWLIDEIPALSIACSVAKGTSRIRNAAELRVK 358

Query: 360 ETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
E++R+ + L G E D + II L +D+ DHR+AM+F++AAC

Sbjct: 359 ESDRISVVAQGLKSFGIQCVEYDDGFDIIGGT--LQKGVVDSKGDHRIAMSFAIAACM-C 415

Query: 419 PVTIRDPGCTRKTFFPDYFDVLSTFVK 444
I D C + +FP++ D+LS F K

Sbjct: 416 GKGILDTECIQTSFPNFDLLSYFAK 441

>ref|ZP_07822573.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Peptoniphilus harei ACS-146-V-Sch2b]
gb|EFR32487.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Peptoniphilus harei ACS-146-V-Sch2b]
Length = 412

Score = 108 bits (270), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 110/441 (24%), Positives = 199/441 (45%), Gaps = 55/441 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALAESEGTTV--VDNLLNSEVDHYMLGALRTLGLSVEAD 70
K++ G + SKS ++R + AAL+ G ++ +DNL S+D+ L + +LG+ + +
Sbjct: 9 KKLDGKISGITSKSYAHRAIFCAALARGESILEIDNL--SKDIEASLNVVESLGVKISRE 66

Query: 71 KAAKRAVVVGCGGKFPVEDAKE---EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
G K +E +E + + +G +G +R + + A G A + G
Sbjct: 67 -----GSKIHIIEAPQEFNKKSLIDVGESGSTLRFILPILGALGIEAEVIRRGSL 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
R + L + ++ + + + G L +L G+ISSQ+++ LL
Sbjct: 116 VTRTNSV-----YFDLFPNHGVYITEEGEKILIRG--KLTYNFELPGNISSQFVTGLL 167

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS---DSWDRFYIKGGQKYK 243
+AA D I++ + S PY++MT+ +M++FGVK S RF GQ Y
Sbjct: 168 LAAGGIGQDCTIKLTETESKPYIDMTIDVMDKFGVKVLEDKNIYSSKGRFI---GQDY- 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
VE D S+A +FLA V V G S+QGD + +G +
Sbjct: 224 -----IVEKDWSNALFFLASG-----VEVIGLNKLSIQGDKEALRYFNEGLLE----- 266

Query: 304 SVTVTGPPREPFGKRLK-AIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
++ + R K I ++ +PD L+V+ + ++ ++KE++
Sbjct: 267 --NISENSYKFIKRNDAKEKIIDAKNIPDTIPILSVLCGLYGKEIEVINIERLKLKESD 324

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ + L +LG V D K N I+++DHR+AM+ S+AA A+ P+
Sbjct: 325 RVESTIEMLERLGKVKVSLKGDSSFSFRGVGKFNCKINSFNDHRIAMSASIAAGFAKGPIE 384

Query: 422 IRDPGCTRKTTFPDYFDVLSTF 442
I D C K++ +++ L++
Sbjct: 385 IVDSECVEKSYREFYKDLASL 405

>ref|YP_040877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MRSA252]
ref|ZP_05601955.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 55/2053]
ref|ZP_05604587.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 65-1322]
ref|ZP_05607201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 68-397]
ref|ZP_05609935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus E1410]
ref|ZP_05612466.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M876]
ref|ZP_06311935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C160]
ref|ZP_06313667.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Btn1260]
ref|ZP_06316600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus WW2703/97]
ref|ZP_06322042.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M899]
ref|ZP_06326913.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C427]
ref|ZP_06332036.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C101]
ref|ZP_06375680.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus A017934/97]
ref|ZP_06667132.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 58-424]
ref|ZP_06668950.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M809]
ref|ZP_06671521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M1015]
ref|ZP_06820606.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus EMRSA16]
sp|Q6GGU5.1|ARO_STAAR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;

AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAG40473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MRSA252]
gb|EEV04125.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 55/2053]
gb|EEV06517.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 65-1322]
gb|EEV09566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 68-397]
gb|EEV11807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus E1410]
gb|EEV14821.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M876]
gb|EFB44142.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C101]
gb|EFB47362.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C427]
gb|EFB52647.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M899]
gb|EFB57341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus WW2703/97]
gb|EFB60618.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Btn1260]
gb|EFC00629.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus C160]
gb|EFC29195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus A017934/97]
gb|EFD97459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M1015]
gb|EFE26547.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 58-424]
gb|EFF09704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus M809]
gb|EFG57966.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus EMRSA16]
gb|EFU25749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus CGS00]
Length = 432

Score = 108 bits (270), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 115/435 (26%), Positives = 200/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPGSKSLNRIILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVDIKED---E 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VV G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 DKLVVNSPG-YKAFKTPHQV-LYTGNSGTTTRLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVLGKQLGADVDCFLGTDGP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI K++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIKPSVIKGI----NYKMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E R F + E ++ I +Y P + +
Sbjct: 178 --SLFSKEATIIKELDVSRNHTETMFR--HFNIPIE-AEGLSITTIPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISSAFAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGRKH---LKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPIKIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDVNVVSFPGFL 422

>ref|YP_002542836.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium
radiobacter K84]
gb|ACM24911.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Agrobacterium
radiobacter K84]
Length = 454

Score = 108 bits (270), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 125/444 (28%), Positives = 204/444 (45%), Gaps = 39/444 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+++PG KS+S+R + L+ G T + LL EDV A+R +G +E KA
Sbjct: 18 LSGTIRVPGDKSISHRAFMFGGLASGETRITGLLEGEDVLNTGKAMRAMGAKIE--KAGD 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G + E L GNAG R V +T++ D + +RP+
Sbjct: 76 EWIIKGVNGALL---APEAPLDFGNAGTGSRLTMGLVGVYHFESTFIGDA--SLSKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+Q+G V G D PV ++G P ++ + S+Q SA+L+A
Sbjct: 131 GRILDPLRQMGVQVKSSEG-DRLPVTLHG----PETANPITYRVPMAAQVKSALLAGL 185

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIK---GGQKYKSPKN 247
A G +I+ +++ + E +++ FG AE S DR ++ GQ +
Sbjct: 186 NAPGIT--SVIEPVMTRDTE---KMLAGFG--AELSVETDRDGVRIIRLQGGKLFQGT 238

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVWTETSVT 306
V GD SS ++ L A I G+ +T+ + + L+ MGA + + +
Sbjct: 239 IDVPGDPSSTAFLVAALIVAGSDITIRNVLMNPTRTGLIL--TLQEMGADIEILDKRLA 296

Query: 307 VTGPPREPFGRKH-LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ R LK + V + P D LAV A FA+G T + + RVKE++
Sbjct: 297 GGEDVADLRVRSSALKGVTVPAERAPSMIDEYPVLAVAAFAEGTTVMLGLEELRVKESD 356

Query: 363 RMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT---IDTYDDHRMAMAFSLAACA- 416
R+ A+ LT G EG + P K A + T+ DHR+AM+F + A
Sbjct: 357 RLSAVAEGLTLNGVDCTEGEASLTVRGRPDGKGLGNAGGEVKTDLHDHRIAMSFLVMGLAS 416

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLS 440
E PV + D +FP++FD+++
Sbjct: 417 EHPVKVDDSAMIAISFPEFFDLMA 440

>ref|YP_508650.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Jannaschia sp. CCS1]
sp|Q28UI7.1|AROA_JANSC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABD53625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Jannaschia sp. CCS1]
Length = 450

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 128/442 (28%), Positives = 197/442 (44%), Gaps = 46/442 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT ++PG KS+S+R L+ A++ G T V LL +DV A+R G V +
Sbjct: 18 LTGTAEVPGDKSISHRSLIFGAMAVGETRVTGLLEGQDVLDTASAMRAFGAEVAREDDGT 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ VG GG +D L GN+G +R L A+ + T+ D +R RP
Sbjct: 78 WSIHGVGVGGFVEPDDV-----LDCNGSGTGVRLLMGAMATTPISVFTGDA--SLRSRP 130

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+ + L G P V +P V+ + + S+Q SA+L+A
Sbjct: 131 MARVTDPLALFGTRAYGRAQGRPLMTLVGAEPMP---VRYATPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G E +I+ + + E R++ FG + + + R GQ +P+ V

Sbjct: 188 APG--ETVVIEAEATRDHSE---RMLAGFGAQISTEVTQEGRVITLTGQPELTPQVIAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A IT G+ V V G + E L MGA +T+

Sbjct: 243 RDPSSAAFPVCAAIITEGSDVLVPNIGLNPTR--AGLFETLRDMGADLTyen----- 292

Query: 311 PREPFGRK-----HLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWR 357
PRE G +K I+V + M D L+VVA A+G T +R V R

Sbjct: 293 PREEGGEFVADLRKAFSPDMKGIEVPPERAASMIDEYPILSVVAANAEGTTVMRGVKELR 352

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTaidTYDDHRMAMAFSLAA 414
VKE++R+ A+ L G VE+GPD+ I+ P + T+ DHR+AM+F A

Sbjct: 353 VKESDRIAAMADGLRLNGIEVEDGPDWWIVHGRGPGMGAGGATVATHLDHRIAMSFLCAG 412

Query: 415 CA-EVPVTIRDPGCTRKTFPDY 435
A + +TI D G +FP +

Sbjct: 413 FASQQGITIDDSGPIATSFPIF 434

>ref|ZP_05842095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter sp. SW2]
gb|EEW26847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter sp. SW2]
Length = 449

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 129/436 (29%), Positives = 201/436 (46%), Gaps = 35/436 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G ++PG KS+S+R L+ A++ G T + LL +DV A+R G V A

Sbjct: 18 LRGVAEVPKDKSISHRALIFGAMAVGETRISGLLEGQDVLDLTARAMRAFGAQVVQHGAGS 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG D + GN+G +R + + AT+ D +R+RP

Sbjct: 78 WSVHGVGVGGFAEPADVID----CGNSGTGVRLIMGCMATHAMTATFTGDA--SLRKR 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+G + L GA G P V +P V+ + + S+Q SA+L+A

Sbjct: 131 MGRVTEPLALFGARSYGRKGGRLPMTVVGAAQVPV---VRYTTPVPSAQVKSALLLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I++ P + + R++ FG + DS + R GQ P+ V

Sbjct: 188 APG--QTVVIERE---PTRDHSEMRLLGFGAELFVEDSAEGRVITLTGQPELRPQVAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A + G+ + V G + +L + F ++EM GA + + + + G

Sbjct: 243 RDPSSAAFPVCAALVVEGSDIFVPGV-SQNLTRNGLFLTLEM-GADIAF-QNPRSEGGE 299

Query: 311 P----REPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R FG L+ I+V + P D LAVVA FA+G T +R V RVKE++R

Sbjct: 300 PVADLRVRFG--PLRGIEVPPERAPSMIDEYPILAVVAFAEGRVTMRGVKELRVKESDR 357

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTaidT---YDDHRMAMAF-SLAACAEVP 419
+ A+ L G VEE D I+ V T + DHR+AM+F L A+ P

Sbjct: 358 IDAMARGLEACVRVEEDEDTLIVHGMGAGGVPGGATCAVHLDHRIAMSFLVLGMAAKAP 417

Query: 420 VTIRDPGCTRKTFPDY 435
VT+ D +FP +

Sbjct: 418 VTVDASPIATSFVPV 433

>ref|YP_631714.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Myxococcus
xanthus DK 1622]
gb|ABF86828.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Myxococcus
xanthus DK 1622]
Length = 430

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 128/450 (28%), Positives = 195/450 (43%), Gaps = 44/450 (9%)

Query: 2 AGAEIEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
A A IV+ P + + P SKS + R L+L L+ G+ + ++ +E + +R

Sbjct: 4 AKASRIVVDPSALHAAPLTPVSKSDAQRALVLGHLT-GSWPLPSV-QAEADEDLPADVR 61

Query: 62 TLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
L VEA + DA ++ G A + + AAVT G A +
Sbjct: 62 VLRQGVREALRLPP-----DAVRDIDCADGGAPFRILATQAAVTP-GAQAARF 106

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGK--VKLSGSI 178
G PR+ ERP G L L++ + L P PV + ++ G+
Sbjct: 107 T--GTPRLGERPHGPLFTSLREALGPMGLTLEGTGWPVELRAPRDTSNATPVFRVPGAQ 164

Query: 179 SSQYLSALLMA-APLALGD---VEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRF 234
SSQY S+LL+ A L L + +EI L S Y+E+TL + RFG S S +
Sbjct: 165 SSQYASSLLGCAALYLRERRPWRVEIDGPLTSAGYLELTTLWLSRFGFDILRSPS--SY 222

Query: 235 YIKGGQKYKSPKN-AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
+ G Y +P + GD SS Y L A TGGTV G S D ++E
Sbjct: 223 TVAG---YAAPPVPTLPGDWSSLGVLVAVKTGGTVVRADTG--SAHPDDAIVRLIEQ 277

Query: 294 MGAKVTWTETSVTVTGPPREPFGFRKHLKA-IDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+G + GPP L + + + PD+ TLA +A P+ + +
Sbjct: 278 VGLRAV-----PAGPPFTLKVEGQLSGGLRASGECPDLLPTLAALACVLPAPSTLTE 330

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM-AF 410
V RVKE++R+ IRT + G + E + +I PP + + DHR+AM A
Sbjct: 331 VGILRVKESDRLEGIRTLVKAFGGTTTELQGEQLLIQPPRTTPAGFEMSSEGDHRLAMTAA 390

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+L + P+T+ P C K+FP ++ LS
Sbjct: 391 TLCVLSTPLTLTGPECVEKSFPGFWRQLS 420

>ref|YP_003891978.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurimonas
autotrophica DSM 16294]
gb|ADN08966.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurimonas
autotrophica DSM 16294]
Length = 426

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 119/449 (26%), Positives = 205/449 (45%), Gaps = 39/449 (8%)

Query: 6 EIVLQPIKEISGTV-KLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++V+ P + S + ++ KS+S+R ++ A LS G ++N L +ED L ++ LG
Sbjct: 3 KVVVLPAQNFSNLNISEIAPDKSISHRSVMFAMLSNGVNEIENFLRAEDTINSLEIVKNLG 62

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE D + G F + D GN+G MR +++A G+ +VL
Sbjct: 63 AKVEDDGKIIKISSSGIQEPFEILD-----GNSGTGMRLFCGLLSSAEGH--FVLT 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G +R RP+ + L +GA +D D P+ + G L + S S+Q S
Sbjct: 113 GDKYLRRRPMKRVTPAPLISIGAKLDGRKNGDLAPLSIRG-ASLKAFDYE-SKIASAQVKS 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+++AA A D I+ +S + E L+ G+ A+ + + + S
Sbjct: 171 AMILAALRA--DGVCTYIEPELSRDHTERM LK-----GMGADIKVEGLKTTVTPLKNLLS 223

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P V D SSA +F AAI VT+EG + ++ + LE MGA +++
Sbjct: 224 PLKIRVPADPSSAFFFAVAAAIMPDSHVTLEGVTLNPTR--IEAFKALERMGADISY--- 278

Query: 304 SVTVTGPPREPFGFRKHLK-----AIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
+ EP G H+K I+ N++ + D L++ A+G + +++
Sbjct: 279 --ELRDDKYEPVGNIHVKYAPLHGIVIEENISWLIDELPALSIAMACANGESLVKNABEEL 336

Query: 357 RVKETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC 415
RVKE++R+ + L V+E D Y II KL +D+ DHR+AM+F +A
Sbjct: 337 RVKESDRISTVVEGLRACNIEVDEYEDGYKIIG--SKLQKAQVDSGDHRIAMSFIIAGL 394

Query: 416 AEPVVTIRDPGCTRKTFPDYFDVLSFVK 444
+ + + D C +FP++F++L +
Sbjct: 395 -KCGMEVTDLECINTSFPNFFELLQKITQ 422

>ref|ZP_01465782.1| probable 3-phosphoshikimate 1-carboxyvinyltransferase, putative
[Stigmatella aurantiaca DW4/3-1]
gb|EAU63463.1| probable 3-phosphoshikimate 1-carboxyvinyltransferase, putative
[Stigmatella aurantiaca DW4/3-1]
Length = 434

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 125/445 (28%), Positives = 195/445 (43%), Gaps = 53/445 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ + P + + P SKS + R L+LA L+ H+ L +L++
Sbjct: 17 QLHIDPSHLTAARLTPPVSKSDAQRALVLAHLTG-----HWPLSSLQS--- 59

Query: 66 SVEADKAA-----KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
EAD A KR V P+ D V G A + AAVT A
Sbjct: 60 EPEADLPADVRVLKRGVEALRLPPGPLRD---VDCADGGAPFRILVTQAAVTP---GAR 112

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDGP-PVRVNGIGGLPGGKVKLSGSIS 179
G PR+ ERP G L L++ L P PV ++ G ++ G S
Sbjct: 113 VRFTGTPTLGERPHGALFTSLREALGPKGLALTEGKPPVELHAPEGTQNPVFRVPGDQS 172

Query: 180 SQYLSALLM-AAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
SQY S+LL+ +A L L + +EI L S Y+E+TL + RFG E S S RF
Sbjct: 173 SQYASSLLLSAALFLREKRPWSVEIQGTLSAGYLELTTLTLRFRFGFTVEESAS--RFT 230

Query: 236 IKGGQKYKSPKNA-YVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
+ Y+ P+NA + GD SS Y L A TGG+V E + D +++
Sbjct: 231 VTA---YQPPQNAPALPGDWSSSLGYLLLIARWTGGSV--ERADPANAHDPQAILRLVQPA 285

Query: 295 G-AKVTWTETSVTVTGPPEPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDV 353
G VT + + + + G K + + + PD+ TLA + P+ + DV
Sbjct: 286 GLTPVTGPDLTMRLEG-----KARAGLVASGKECPDLLPTLAALGCVLPAPSTLTDV 337

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM-AFS 411
RVKE++R+ IRT + G + +TPP +++++ DHR+AM + +
Sbjct: 338 GILRVKESDRLEGIRTLVAAYGGRTTLEGETLTLTPPSAPPAHFMSNSHGDHRLAMVSAT 397

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYF 436
L+ + +T+ P C K+FP ++
Sbjct: 398 LSVLSGARLTLTGPECVEKSFPGFW 422

>ref|YP_004050170.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Calditerrivibrio
nitroreducens DSM 19672]
gb|ADR18007.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Calditerrivibrio
nitroreducens DSM 19672]
Length = 428

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 119/450 (26%), Positives = 205/450 (45%), Gaps = 48/450 (10%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
+ I+ + G+V +P KS+++R + ++++EG +VV N L S D + A++ +G+
Sbjct: 2 VTFDRIETLKGSVTVPPDKSITHRAFIFSSMAEGRSVVLNPLMSRDTIATMNAMKAVGVE 61

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V G G +D + N+G R +T +G VL G
Sbjct: 62 FIKLDNGFEIVSKGYRGFNEPQDV-----INCENSGTTARLITGLFAPSG--RYVVLTDG 114

Query: 127 PRMRERPIGDLVVGLKQLGADV----DCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQY 182
+R RP+ + L+ +GAD+ D FL P +++ + +SS
Sbjct: 115 NSLRRRPMDRVKRPLQTMGADIRLSRDRFLPMTVLP SKMH-----PADIMA EVSSAQ 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+ + + + L L D +K I+ + E LR FG A+ + ++G K
Sbjct: 167 VKSAVILSGLQL-DGYTSYTEKEITRNHTETMLR---DFG--ADIMVEGKKITVRG-VKN 219

Query: 243 KSPKNAYVEGDASSASYFLAGAAIT--GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTW 300
P+ V GD SSA++F+ GAAI G + + G + VL MG ++
Sbjct: 220 LIPQKTTVPDGFSSAAFFI-GAAIMFEGAEIKIRSVGLNPTR--TGLLTVL RDMGVQI-- 274

Query: 301 TETSVTVTGPPREPFGRKHLK-----AIDVNMNKMPPDVAMTLAVVALFADGPTAIR 351
ET +T + EP G ++K ++ N + ++ M LAV+ LFA+ P IR
Sbjct: 275 -ETELTSSSA--EPMGDIYIKHGRLKGGKICGEIIPNIIDEIPM-LAVLGLFAESPLEIR 330

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI--DTYDDHRMAMA 409
RVKE++R+ ++ ++ LG VEE PD + P +KL I ++DHR+AM
Sbjct: 331 GAEELRVKESDRIKSVVENISALGGEVEEYPDGLKVYPLKKLKDKKEILLKSFDDHRIAMV 390

Query: 410 FSLAACAEVPTIRDPGCTRKTFPDYFDVL 439
L + ++I + +FPD+ + L
Sbjct: 391 NILLSKRFGNISIDEISAIDVSFPDFLEKL 420

>ref|YP_001603691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
ref|YP_002277261.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
emb|CAP57405.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
gb|ACI52646.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
Length = 449

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 128/445 (28%), Positives = 196/445 (44%), Gaps = 43/445 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V +PG KS+S+R L+ AAL+ G T + LL EDV A+R LG V +
Sbjct: 21 LSGSVAVPGDKSISHRALMFALARGETRISGLLEGEDVLRATADAMRALGAVVT--RTGP 78

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
A V G +++ + L +GN+G A R L+ + + G V+ G +R RP+
Sbjct: 79 GAWHVTGRGLGTLQEPAD--VLDMGNSGTAARLLSGILASHG--IFSVMTGDASLRGRPM 134

Query: 135 GDLVVLKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L GA G P+ +NG+ +L + S+Q SA+L+A A
Sbjct: 135 KRVTDLAATGATFLSRAGRL-PLAINGVADPAPLSYRLPVA-SAQVKSALLLAGLNAA 192

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYSKPNAYVEG 252
G +E + + + + E LR FG V E + R G+ ++ V G
Sbjct: 193 GTTRVE--EPVATRDHTENMLR---HFGAEVTVEALGAGGRITITLVGRPDVARDVVVPG 247

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV----- 305
D SSA++ L A + G +VTV G G L+ L MG + + V
Sbjct: 248 DPSSAAFVLVAALLVPGSSVTVRGVGLNPLR--TGLFTTLREMGDLRLSNERVEGGEVP 305

Query: 306 ----TVTGPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V GP L +DV ++ P D LAV A A G + R + RV
Sbjct: 306 GDLTAVAGP-----LHGVDVPADRAPSMIDEYPLAVAAAHAATGRSRFRGLEELRV 356

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI--IDTYDDHRMAMAFS-LAAC 415
KE++R+ A L + G VE D I+T ++T DHR+AM+ + L
Sbjct: 357 KESDRLAATVALLQRNGVEVEVVGDDMIVTGTGGAIPGGGVVETRMHRLAMSATVLGLA 416

Query: 416 AEVPTIRDPGCTRKTFPDYFDVLS 440
A PV + D +FP + D+++
Sbjct: 417 ARTPVGVDDTAFIDTSFPGFIDLMN 441

>ref|YP_003953653.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
gb|ADO71826.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
Length = 420

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 125/445 (28%), Positives = 195/445 (43%), Gaps = 53/445 (11%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++ + P + + P SKS + R L+LA L+ H+ L +L++

Sbjct: 3 QLHIDPSHLTAARLTPPVSKSDAQRALVLAHLTG-----HWPLSSLQS--- 45

Query: 66 SVEADKAA-----KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
EAD A KR V P+ D V G A + AAVT A

Sbjct: 46 EPEADLPADVRLKRGVEALRLPPGPLRD---VDCADGGAPFRILVTQAAVTP---GAR 98

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCP-PVRVNGIGGLPGGKVKLSGSIS 179
G PR+ ERP G L L++ L P PV ++ G ++ G S

Sbjct: 99 VRFTGTGPRLGERPHGALFTSLREALGPKGLALTEGKPPVELHAPEGTQNPVFRVPGDQS 158

Query: 180 SQYLSALLM-AAPLALGD---VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
SQY S+LL+ +A L L + +EI L S Y+E+TL + RFG E S S RF

Sbjct: 159 SQYASSLLLGSAALFLREKRPWSVEIQGTLSAGYLELTTLWLRRTFGFTVEESAS--RFT 216

Query: 236 IKGGQKYKSPKNA-YVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
+ Y+ P+NA + GD SS Y L A TGG+V E + D +++

Sbjct: 217 VTA---YQPPQNAPALPGDWSSLGYYLLIAWRTGGSV--ERADPANAHDPQAILRLVQPA 271

Query: 295 G-AKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPPDAMTLAVVALFADGPTAIRDV 353
G VT + + + G K + + + PD+ TLA + P+ + DV

Sbjct: 272 GLTPVTGPDLTMRLEG-----KARAGLVASGKECPDLLPTLAALGCVLPAPSTLTDV 323

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM-AFS 411
RVKE++R+ IRT + G + +TPP +++++ DHR+AM + +

Sbjct: 324 GILRVKESDRLEGIRTLVAAYGGRTTLEGETLTLPSPAPPAHFSMNSHGDHRLAMVSAT 383

Query: 412 LAACAEPVPTIRDPGCTRKTFPDYF 436
L+ + +T+ P C K+FP ++

Sbjct: 384 LSVLSGARLTTLTGPECVEKSFPGFW 408

>gb|ADX76594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
pseudintermedius ED99]
Length = 429

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 110/438 (25%), Positives = 197/438 (44%), Gaps = 36/438 (8%)

Query: 17 GTVKLPGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +PG KS+++R ++LA+L++G +V+ + L ED LG+ ++ A

Sbjct: 12 GEASVPGDKSMTHRAIMLASLAQGHSHVIHPLLGEDCLRTAKIFEKLGVKMDI---TDEA 68

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ + G + + L+ GN+G R + A G VL G + +RP+

Sbjct: 69 ITIDSPGYAHFQTPHQ--TLYTGNSGTTTTRLM--AGLLGGLGIQSVLSGDASIGKRPMDR 124

Query: 137 LVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
++ L+Q+ ++ P + G + G ++ + S+Q SA+L A+ A

Sbjct: 125 VLQPLRQMNVNISGVEDNYTP--LIIGSSKVKGIHYEMPVA-SAQVKSAILFASLFAQNT 181

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQKYKSPKNAYVEGDAS 255
I ID +S + E + +G+ + D + G G + P++ V GD S

Sbjct: 182 TTIREID--LSRNHTET---MFAHYGIPVQTQDLT--VTLPGEGIHIIQPRDFDVPDIS 234

Query: 256 SASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA + + A IT G+ +T+ G + + E++E MG K++ + + GP EP

Sbjct: 235 SAVFLIVAALITPGSDITLHNVGINPTRDGI--IEIVERMGGKISLSNQT---NGP--EP 287

Query: 315 FGR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
LK I++ + +P D T+A++ A G + I+D +VKET R+

Sbjct: 288 TATIRVQYTTDDLKGIEIGGSLIPRCIDELPTIALLCTQAHGSSIIKDAEELKVKETNRID 347

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRD 424
EL KLG +E D II P + +D+++DHR+ M ++A+ P+ I

Sbjct: 348 TTANELGKLGLKLEPTDDGLIIPSTISQIQPVDSHNDHRIGMMLAVASLMTPEPIEIAQ 407

Query: 425 PGCTRKTFPDYFDVLSTF 442
+FP + +L

Sbjct: 408 FESVNVSFPGFLPLLKQL 425

>ref|ZP_04060728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
hominis SK119]
ref|ZP_07843748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
hominis subsp. hominis C80]
gb|EEK11323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
hominis SK119]
gb|EFS18765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
hominis subsp. hominis C80]
Length = 432

Score = 108 bits (269), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 108/448 (24%), Positives = 205/448 (45%), Gaps = 64/448 (14%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++L++L++G +++ L ED + + LG+ +E ++
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLSSLAKGKSIIIEQPLLGEDCLRTIEIFKLLGVEIEIE--H 70

Query: 75 RAVVVGCGGK-FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R +V G + F + L+ GN+G R L ++ G VL G + +RP
Sbjct: 71 RLIVNSPGYQHFNIHQQT----LYTGNSGTTTLLLAGLLSGLGIEC--VLSGDTSIGKRP 124

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
+ ++ LK + A+++ P P +NGI +++++ S+Q SA+L A
Sbjct: 125 MDRILKPLKLMNANINGIENNYTPLIKPSAINGINY----QMEVA---SAQVKSAILFA 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY---IKGGQKYKS-- 244
+ + +I +D + H+++ + Y I+ QK +
Sbjct: 178 SLFSKEASQITELD-----ISRNHTETMFKHYPQIPIQVQKVVITS 218

Query: 245 -----PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
PKN V GD SSA++F+ A I+ G+ +T+ G + + +++E M
Sbjct: 219 PYAISNIQPKNFVPGDISSAAFFIVAALISPGSDITIHNVGINPTRSGI--IDIVEQMN 276

Query: 296 AKVTWTETSVTVTGPPREPFGKRH---LKAIDVNMNKMPPDVAMTLAVVALF---ADGPTA 349
+ +VT + P ++ LK I + + +P L ++AL A G +
Sbjct: 277 GNIELF--NVTESSEPTASIRVQYTNNLKPTIEGDLIPKAIDELPIIALCTQASGTSM 334

Query: 350 IRDVASVRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M
Sbjct: 335 IKDAEELKVKETNRIDTTADMLNLLGFKLQATEDGLIHPSELTRNAIVDSLTDHRIGMM 394

Query: 410 FSLAAC-AEVPVTIRDPGCTRTKTFPDYF 436
++A+ ++ P+TIR +FP +
Sbjct: 395 LAVASILSDSPLTIRQFDVNVVSFPGFL 422

>ref|YP_001411431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parvibaculum
lavamentivorans DS-1]
sp|A7HPE1.1|ARO_A_ParL1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS61774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Parvibaculum
lavamentivorans DS-1]
Length = 451

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 125/456 (27%), Positives = 196/456 (42%), Gaps = 45/456 (9%)

Query: 4 AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 63
A + +P + G++ +PG KS+S+R L+ AL+ G T + LL EDV +R L
Sbjct: 9 ASSLTAEPSGALLGSITVPGDKSISHRALIFGALAVGETRIGGLLEGEDVLATAETMRRL 68

Query: 64 GLSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATY 121
G VE +V VG GG KE Q L GN+G R + V AT+
Sbjct: 69 GAEVERHADGTWSVHGVGVGG-----LKEPDQPLDFGNSGTGARLVMGLVAGHPITATF 122

Query: 122 VLDGVPRMRERPIGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ D + RP+G ++ L + GA G P+ + G G +L + S+Q
Sbjct: 123 IGDA--SLSRREMGRVIAPLTETGATFHAREGGRL-PLTLTGAGRALPITYRLPVA-SAQ 178

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI--KGG 239

```

      SA+L+A  A G      +  +  P  + T R++ FG  E D      +  G
Sbjct: 179 VKSAVLLAGLNAPG-----VTTVIEETPTRDHTERMLRAFGAHIEVEDGPRGLIVIRLTG 233

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      +  P  V GD SSA++ + A +T G+ +TV G      +  +  + ++EM G
Sbjct: 234 EPELKPCRISVPGDPSSAAFPVVAALLTPGSEITVTGITLNPFRAGL-YTTLMEMGGDIE 292

Query: 299 TWTETSVTVTGPPEPFGR-----KHLKAIDV---NMNKMPDVAMTLAVVALFADG 346
      +  RE G      LK I+V      M D      LA+ A FA+G
Sbjct: 293 VMNQ-----REEGGEVADLRVRASRLKGIEVPPARAASMIDEYPVLAIAAAFAEG 343

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDH 404
      T + +  RVKE++R+ A + L G V E D ++      + T+ DH
Sbjct: 344 ETRMLGIHELVRKESDRIAATASGLRANGVKVHESDDGMVVEGRSGEVGGGHVATHIDH 403

Query: 405 RMAMAF-SLAACAEVPTIRDPGCTRKTFFPDYFDVL 439
      R+AM+F +  A+ PVT+ D      +FP++ ++
Sbjct: 404 RIAMSFLVMGLAAQKPVTVDDAAMIATSFPNFTGLM 439

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>ref|ZP_05110808.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
drancourtii LLAP12]
gb|EET11488.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
drancourtii LLAP12]
Length = 438

```

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 112/445 (25%), Positives = 206/445 (46%), Gaps = 44/445 (9%)

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Query: 6  EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      ++ +P  + G + +PG KS+S+R ++  A+++GTTV++  L+ ED  L A + +G+
Sbjct: 5  NLISKPSPSLKGEMSVPGDKSISHRSIIFGAIAKGTTVINGFLDGEDCMATLRAFQAMGV 64

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      +E  ++ VV+  GK  ++  K E +  GN+G +MR L  + A  ++  L G
Sbjct: 65 LIEGPD--EQQVVIYGVGKHGLK--KPEQIIDCGNSGTSMRLLAGLLAAQSFDSQ--LTG 118

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      + +RP+  +  L Q+GAD+  G  PP+ + G  L G  +  + S+Q S
Sbjct: 119 DESLLKRPMRLRISKPLTQMGADISTVDGK--PPISIKGGEKLHGIHYVMPEA-SAQVKSC 175

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      +L+A  A G  E  +  + +S + E+  ++E F      S+  +  I  +  +
Sbjct: 176 ILLAGLYAQG--ETSVTETGVSРННТЕV---MLESFSYPVRRSE--NTITINSASECLAT 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVT----- 299
      + +V GD SSA++F+  A I  G+ +  +  G  +  +  +L MGA +T
Sbjct: 229 E-IFVPGDISSAAFFIVAATIVPGSDILIRHVGINPTRTGI--VHILLEMGAADITLLNQR 285

Query: 300 -----WTETSVTVTGPPEPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPPTAIR 351
      W  P  L  I+++  +P  D  +  + A  A G T +
Sbjct: 286 QQGEWVADLHVRYP-----LTGINISPELVPLAIDEFPFIIFIAAACARGQTILH 336

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFS 411
      R KE++R+ A+  L +LG +  +  D +I  L  +D+ DHR+AM+F+
Sbjct: 337 GAKELRFKESDRIAMVNGLRQLGINAQALDDGALID-GGALQGGTVDSLGDHRIAMSFA 395

Query: 412 LA-ACAEVPTIRDPGCTRKTFFPDY 435
      +A A A P+ +++  +FP +
Sbjct: 396 IAGAVASGPPIIVKNCANVATSFPLF 420

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>ref|YP_001219416.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Vesicomysocius okutanii HA]
sp|A5CWH5.1|AROAVESOH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAF61692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Vesicomysocius okutanii HA]
Length = 435

```

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 108/445 (24%), Positives = 210/445 (47%), Gaps = 37/445 (8%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+ ++ P + G +K+PG KS+S+R ++L +L+ G T + L +DV L + +G+
Sbjct: 3 KFIINPSNSMYGNLKIPGDKSISHRSIMLGSLANGVTKISGFLEGKDVLSLTKGFQNMGV 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+E + VG G K V L GN+G ++R ++ + A ++ L G
Sbjct: 63 KIERNSDNVIYGVGLNGL-----KKSILVPLNFGNSGTSIRLISGILAAQTFDSE--LYG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP+G ++ L Q+GA ++ G P+++ G L G L + S+Q S
Sbjct: 116 DESLSKRPMGRVINPLVQMGLIESNDGK--LPIKIKGGQTLKGINYDLPVA-SAQVKSC 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G+ I+ SI + T R+++ G + + + ++ + GG + +
Sbjct: 173 ILLAGLYAQGETCIK-----ESILTRDHTERMLKGLGYRLD--TNKNKICLTGGAQLNAA 225

Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N V D SSA++F+ A+I +T+ G + + ++L++MGA ++ +
Sbjct: 226 -NIQVPSDISSAAFFIVAASIAPQADITLIGVNVNPTRTGI--IDILKLMGANLSLSNEC 282

Query: 305 VVTGTGP--PREPFRKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V + G LK I + + +P D + + A A G T + + RVK
Sbjct: 283 V-IGGELLANIRIQSAQLKGRIPKDLVPLAIDEFFAIFIAASCAKGETILTNAKELRVK 341

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
E++R+ + L+ LG E D + + P + I ++ DHR++M+F++A+
Sbjct: 342 ESDRIQVMADGLSILGIENEVFEDGKIKGGVFSKPS----STIKSHHDHRISMSFAIAS 397

Query: 415 C-AEVPVTIRDPGCTRTKTFPDYFDV 438
+ I D + +FP++ ++
Sbjct: 398 LRCHYAIEIEDVDNVQTSFPNFVEL 422

>ref|ZP_05780873.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citreicella sp. SE45]
gb|EEX14637.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Citreicella sp. SE45]
Length = 442

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 128/440 (29%), Positives = 200/440 (45%), Gaps = 33/440 (7%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L A++ G T V LL +DV A+R G VE
Sbjct: 9 LRGEAHVPGDKSISHRSLILGAMAVGETRVTGLLEGQDVLDTAKAMRAFGAEVEKRGDTW 68

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG A+ E + GN+G +R + A+ AT+ D + +RP+
Sbjct: 69 HVQGVGVGGF----AEPEQVIDCGNSGTGVRILIMGAMATTPITATFTGDA--SLNKRPM 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLA 193
+ L GA G P V LP V+ + + S+Q SA+L+A A
Sbjct: 122 ARVTDPLALFGARAYGREGRLPMTIVGARDPLP---VRYATPVPSAQVKSAVLLAGLNA 178

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G E +I++ + + E R++ FG + + + + R GQ P+ V
Sbjct: 179 PG--ETVVIEREATRHSSE---RMLAGFGAQVSTETTAEGRVITLTGQPELRPQVIVVPR 233

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++ + A IT G+ V V G + + F L+ MGA +T+ E G P
Sbjct: 234 DPSSAAFPVCAALITEGSDVLVPNIGLNPTRAGLFF--TLQDMGADLTF-ENEREEGGEP 290

Query: 312 ----REPFRKHLKAIDVNMNMP---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
R F L+ I+V + M D L+VVA FA G T + V RVKE++R+
Sbjct: 291 VADLRARFS-PDLRGIEVPAERAASMIDEYPVLSVVAATGKTHMPGVREL RVKESDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACA-EVPV 420
A+ L G +V+EG D+ + NV ++ DHR+AM+F + A P+
Sbjct: 350 DAMAVGLRAAGVTVEGEDWTVHGLGHGNVPGGVVTASHLDHRIAMSFLVMGLATHSPM 409

Query: 421 TIRDPGCTRKTFFPDYFDVLS 440
+ D G +FP + +++
Sbjct: 410 RVDDGGPIATSFPIFEGLMT 429

>ref|YP_002520696.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides KD131]
gb|ACM03623.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides KD131]
Length = 436

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 126/438 (28%), Positives = 203/438 (46%), Gaps = 31/438 (7%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G ++PG KS+S+R L+L A++ G T + LL +DV A+R G V + A
Sbjct: 9 LKGRAEIPGDKSISHRALILGAMAVGETQITGLLEGQDVLDTAKAMRAFGAEVIQHGPGA 68

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VG GG P E + GN+G +R + A+ + AT+ D +R+R
Sbjct: 69 WSVHGVGVGGFTEPAE-----VIDCGNSGTGVRLVMGAMATSPLTATFTGDA--SLRKR 120

Query: 133 PIGDLVVLGKLQGLADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAP 191
P+G + L G G P V +P V+ + + S+Q SA+L+A
Sbjct: 121 PMGRVTDPLALFGTRAYGRKGGRLPMTLVGAADPVP---VRYTVPMPSAQVKSALLAGL 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + +I++ + + E R++ FG + + + GQ P+ V
Sbjct: 178 NAPG--QTVVIEREATRDHSE---RMLRGFGAALSJETGPEGQIITLTGQPELRPQTAV 232

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ + A I G+ + V G + D + +LE MGA + + E G
Sbjct: 233 PRDPSSAAFPVCAALIVEGSEILVPGVSRNPTR-DGLYVTLE-MGADIAF-ENEREEGG 289

Query: 310 PPREFPGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASVRVKETERM 364
P + LK ++V + P D L+VVA FA+G T +R V RVKE++R+
Sbjct: 290 EPVADLRVRASALKGVEVPPERAPSMIDEYPILSVVAAFAEGSTVMRGVKELRVKESDRI 349

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-DTYDDHRMAMAF-SLAACAEVPVTI 422
A+ L G +EE D I+ +++ A T+ DHR+AM+F L AE PVT+
Sbjct: 350 DAMARGLEACGVRIEEDDTLIVHGMDRVPGGATCATHLDHRIAMSFLVLGMAAEAPVTV 409

Query: 423 RDPGCTRKTFFPDYFDVLS 440
D +FP + D+++
Sbjct: 410 DDGSPPIATSFPAFTDLMT 427

>ref|YP_004149331.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Staphylococcus
pseudintermedius HKU10-03]
gb|ADV05695.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Staphylococcus
pseudintermedius HKU10-03]
Length = 429

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 110/438 (25%), Positives = 196/438 (44%), Gaps = 36/438 (8%)

Query: 17 GTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRA 76
G +PG KS+++R ++LA+L++G +V+ L ED LG+ ++ A
Sbjct: 12 GEASVPGDKSMTHRAIMLASLAQGHSVIHQPLLGEDCLRTAKIFEKLGVKMDI---TDEA 68

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ + G + + L+ GN+G R + A G VL G + +RP+
Sbjct: 69 ITIDSPGYAHFQTPHQ--TLYTGNSTGTTTSLM--AGLLGGLGIQSVLSGDASIGKRPMDR 124

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
++ L+Q+ ++ P + G + G ++ + S+Q SA+L A+ A
Sbjct: 125 VLQPLRQMNVNISGVEDNYTP--LIIGSSKVKGIHYEMPVA-SAQVKSAILFASLFAQNT 181

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQKYKSPKNAYVEGDAS 255
I ID +S + E + +G+ + D + G G + P++ V GD S
Sbjct: 182 TTIREID--LSRNHTET---MFAHYGIPVQTQDLT--VTLPGEGIHIIQPRDFDVPGLDIS 234

Query: 256 SASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SA + + A IT G+ +T+ G + + E++E MG K++ + + GP EP
Sbjct: 235 SAVFLIVAALITPGSDITLHNVGINPTRDGI--IEIVERMGGKISLSNQT---NGP--EP 287

Query: 315 FGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
LK I++ + +P D T+A++ A G + I+D +VKET R+
Sbjct: 288 TATIRVQYTDDLKGIEIGGSLIPRCIDELPTIALLCTQAHGSSIIKDAEELKVKETNRID 347

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRD 424
EL KLG +E D II P + +D+++DHR+ M ++A+ P+ I
Sbjct: 348 TTANELGKLGLKLEPTDDGLIIPSTISQIQPVDSHNDHRIGMMLAVASLMTPEPIEIAQ 407

Query: 425 PGCTRKTFFPDYFDVLSTF 442
+FP + +L
Sbjct: 408 FESVNVSFPGFLPLLKQL 425

>ref|ZP_07359438.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces viscosus
C505]
Length = 491

Score = 107 bits (268), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 134/441 (30%), Positives = 204/441 (46%), Gaps = 26/441 (5%)

Query: 19 VKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAAKRAV 77
V+LPGSKSLS R LLLAA+++ T + LL S D ML AL LG E D+ R
Sbjct: 40 VELPGSKSLSARALLAAIADAPTTLTGLLRSDRTEMLAALSVLGARFEDLDETGTRLR 99

Query: 78 VVGCGGKFPVEDAKEEV-QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
V + + +G AG MR + A A +A V DG R RP+
Sbjct: 100 VTPAPLPLHVQTGPGGAGRIDVGLAGTVMRFPALAAALA--DAPVVFDDGEAARHRPMPAP 157

Query: 137 LVVGLKQLGADVDCFLGTDCCPVRVN-GIGGL---PGGKVKLSGSISSQYLSALLMAAPL 192
L+ L LGA+V P RV G G L G +V + GS SSQ++SALL+ +
Sbjct: 158 LLGALAALGAEVTHLGEPLPFRVGPBGDALLRTEGARVAVDGSASSQFVSALLLLGAI 217

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHE-----SDSWDRFYIKGGQKYKSPKN 247
G +E+ + S+ +V MT+ + G+ + D + + G+
Sbjct: 218 LPGGLELTPTGPVPSLTHVGMTVATLRERGIADVDEPAPGAGDGERTWRVHPGRPRGG--E 275

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+E D S+A FLA A + GG V+V + Q + +L +G +VT T+ +T
Sbjct: 276 VAIEPDLSNAGPFLLAALVAGGRVSVPHWPAATTQAGNAWRVLLPRLGGEVTLTDGLLTA 335

Query: 308 TGPPREPFPGRKHLKAIDVNMNKM---VAMTLAVVALFADGPTA-IRDVASWRVKETERM 364
G R L I +++ + + + A G T+ + +A R ET+R+
Sbjct: 336 HGTGR-----LTGIHADLSDVGEAPLPTVAALALAGAQTSTLTGIAHLRGHETDRL 388

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRD 424
A+ T++ LG EE D II P L+ A+ +Y DHRMA ++ + V++ D
Sbjct: 389 AALATQIRLLGGDAESDDGLIIR-PAPLHGAALRSYADHRMATFAAIIGLSVDGVSLDD 447

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
CT KT P + D+ + +
Sbjct: 448 VECTSKTLPGFDTLWAAMLAT 468

>ref|YP_002378.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
interrogans serovar Copenhageni str. Fiocruz L1-130]
sp|Q72PM1.1|AROAL_EPIC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAS71015.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
interrogans serovar Copenhageni str. Fiocruz L1-130]
Length = 440

Score = 107 bits (267), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 121/456 (26%), Positives = 202/456 (44%), Gaps = 55/456 (12%)

Query: 16 SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75

S +++PG KSLs+R +L AALS+G + V L +ED + A LGL V+ K +
Sbjct: 10 SREIEVPGDKSLSHRSVLF AALS+G+SKGSKVTGFLEAEDPLNTMSAFAKLGLKVQKVKPGEY 69

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVLDGVPRMRERP 133
K V L GNAG +R L+A + G NAT L G +++RP
Sbjct: 70 EFESPGKNKL----VSPNVLDLDFGNAGTGIR-LSAGLICGLPGINAT--LTGDNSLKKRP 122

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G ++ L +GA + + P+++ G L G + I+S + + LM A ++
Sbjct: 123 MGRIIKPLSSMGASIVGLGEKETAPLKIEG-KKLKG--FRYESPIASAQVKSCMLMLAAIS 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYKSPKNA 248
+ ++E + ++S + E R + G K E F IK G +++ P
Sbjct: 180 -SETDLEYSENILSRDHTENMFRFL---GNKIEQISPL-HFKIKPPYVLNGGEFRVP--- 231

Query: 249 YVEGDASSASYFLA-GAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
GD SSA++FL G G + ++ G + + A L+ MGAK+ +
Sbjct: 232 ---GDISAFAFLVLGVLAKEGNLLIKNIGLNPARTGILTA--LQSMGAKIEIQNKRIEC 286

Query: 308 TGPPREPFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
EP G +LK ++ + +P D L+V FA+G IR R K
Sbjct: 287 G----EPVGD LKTPSNLKKSNIPESLIPSIIDEIPILSVAGFFAEGGF EIRHAEELRAK 342

Query: 360 ETERMVAIRTELTKLGASVEEGPD-YCIITPEK-----LNVTAIDTYDDHRMAM 408
E++R+ + + +LG VEE D Y +K + I +Y DHR+AM
Sbjct: 343 ESDRIHTMVSNFRELGIEVEEYTDGYSFDTGSKKSSEVWTRLSTVKKIPIQSYMDHRIAM 402

Query: 409 AFSL-AACAEPVPTIRDPGCTRKTFPDYFDVLSTFV 443
+F + + + + I + +FP + +L + +
Sbjct: 403 SFLIFKTL SGLDLQIDETSWIETSFPGFEKLESCI 438

>ref|YP_003395528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Conexibacter woesei
DSM 14684]
gb|ADB52153.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Conexibacter woesei
DSM 14684]
Length = 446

Score = 107 bits (267), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 117/417 (28%), Positives = 191/417 (45%), Gaps = 32/417 (7%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G+++P KS+S+R L AA++ V N L++ D + L A+ +G V+
Sbjct: 21 PASGLRGLSLRVPPDKSISHRAALFAAMTPEPVSVTNYLDAADTNSTLAAVEQIGALVQR- 79

Query: 71 KAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ A ++ GCG + DA E + + +GNAG MR L + G ++ DG +
Sbjct: 80 RGAGELLIRGCG---LRDAHESDGPIDVGNAGTLMRLLPGLWATQPGR-SWTFDGDSSI 134

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
R RPI + L+ +GA +D TD PP ++G L G + + + S+Q S +L
Sbjct: 135 RRRPIDRIADPLRLMGARIDA---TDERFPPFTLHG-ADLTGIEYMPVA-SAQVKSCVL 189

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A G + + P + T R++ G E +R ++ +
Sbjct: 190 IAGMTTAGGTTV-----IEPAPSRDHTERMLAAAGAPVERDG--NRVTVRHVDELGLDAI 242

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKV--TWTETS 304
A V GD SSA++++A A + G+ + +E + F ++E MG V E
Sbjct: 243 A-VPGDLSSAAFVWAAAVLVPGSRIVLEDVNVNWTR--TGFLRIVERMGGIVLGDLEEHG 299

Query: 305 VTVTGPPEPFRGRKH--LKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRVK 359
G P H L A V ++P L +VAL FADG T +R A RVK
Sbjct: 300 AFTPGEPISELDVAHGPLSATTVEAEVPLAIDELPLVALLGCFADGETTVRGAAELRVK 359

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACA 416
E++R+ + L LGA +E D ++ L I ++ DHR+AM ++A A
Sbjct: 360 ESDRIQTVVDGLNGLGADIEGTDGDFVVRGGTGLRGGRISSHGDHRLAMLGAVAGLA 416

>ref|YP_745846.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Granulibacter

bethesdensis CGDNIH1]
 sp|Q0BQH9.1|AROA_GRABC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABI62923.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Granulibacter
 bethesdensis CGDNIH1]
 Length = 454

Score = 107 bits (267), Expect = 4e-21, Method: Compositional matrix adjust.
 Identities = 129/438 (29%), Positives = 192/438 (43%), Gaps = 36/438 (8%)

Query: 19 VKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK-RAV 77
 V +PG KS+S+R L++ AL+ G T + LL EDV A+R LG V D R
 Sbjct: 28 VHVPGDKSISHRALMIGALAVGETRISGLLEGEDVLRATAAMRALGAEVVRDAPGSRVA 87
 Query: 78 VVCGGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
 G GG D L +GN+G A R LT + A + V+ G +R+RP+ +
 Sbjct: 88 GRGIGGLTEPADV-----LDMGNSGTAAARLLTGVL--ASHDLFAVMTGDASLRKRPMPRV 140
 Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
 L GA G P+ V G G +L + S+Q SA+L+A A G+
 Sbjct: 141 TDPLAACGAGFHTSRSGRL-PMVVRGTGEALPLHYRLPVA-SAQVKSAILLAGLNARGET 198
 Query: 198 EIEIIDLKISIPYVEMTLRLMERFVGKAEHSDSWD---RFYIKGGQKYKSPKNAYVEGDA 254
 +E + + + E LR FG + + D R GQ + V D
 Sbjct: 199 VVE--EPHATRDHSENMLR---HFGATVQVEPTGDGAGRIVRLQGQPELRAADIVVPADP 253
 Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
 SSA++ L A + G+ +T+ G G L+ + L MGA +T + E
 Sbjct: 254 SSAAFPLVAALLVPGSEITLAGVGLNPLR--TGLFDTLVEMGAALTIANRRIEGG----E 307
 Query: 314 PFGRKHLKAIDVNMNKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
 P G ++A ++ ++P D L+V A A G T +R +A RVKE++R+
 Sbjct: 308 PVGDITVRASLTGHVEVPPERAPSMDIEFPILSVAAVASGTTRMRGLAELRVKESDRLA 367
 Query: 366 AIRTELTKLGASVE-EGPDYCIITPPEKLNVT-ADTYDDHRMAM-AFSLAACAEVPVTI 422
 A L+ G VE EG D +I + TY DHR+AM A L + PVT
 Sbjct: 368 ATAALLSVNGVQVEIEGDDLIVIGCGGPPPGGLVTITYMDHRLAMSALVGLTTQAPVTA 427
 Query: 423 RDPGCTRKTFPDYFDVLS 440
 D +FP + +++
 Sbjct: 428 DDAAFIDTSFPGFATLMT 445

>gb|EGA97254.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
 011]
 Length = 432

Score = 107 bits (267), Expect = 4e-21, Method: Compositional matrix adjust.
 Identities = 114/435 (26%), Positives = 200/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
 Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVEIKEDD--E 70
 Query: 75 RAVVVGCGGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
 + VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
 Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSTTTTRLLAGLLSGLGIES--VLSGDVSIKGRPM 125
 Query: 135 GDLVVGKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
 ++ LK + A+++ P P + GI K++++ S+Q SA+L A
 Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIKPSVIKGI---NYKMEVA---SAQVKSAILFA- 177
 Query: 191 PLALGDVEIEIIDLK-ISPYPVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY 249
 +L E II +L +S + E R F + E ++ +Y P + +
 Sbjct: 178 --SLFSKEATIIKELDVSRNHTETMFR--HFNIPIE-AEGLSITTTPEAIRYIKPADFH 231
 Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
 V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
 Sbjct: 232 VPGDISAFAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGKRKH---LKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVASLLSREPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDAVNVSFPGFL 422

>ref|YP_416804.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
RF122]
ref|ZP_05685412.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9635]
sp|Q2YY90.1|AROAA_STAAB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAI81017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
RF122]
gb|EEV71267.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9635]
gb|ADI97977.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ED133]
gb|ADL23268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus JKD6159]
gb|EGA99859.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
O46]
Length = 432

Score = 107 bits (267), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 114/435 (26%), Positives = 200/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRITMDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSGTTTRLLAGLLSGLGIES--VLSGDVVSIGKRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDGCP---PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI K++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIKPSVIKGI---NYKMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E R F + E ++ +Y P + +
Sbjct: 178 --SLFSKEATIIKELDVSRNHTETMFR---HFNIPIE-AEGLSITTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISSAFFIVAALITPGSDVTIHNNGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGKRKH---LKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDAVNVSFPGFL 422

>ref|YP_003545597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobium japonicum
UT26S]
dbj|BAI96985.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingobium japonicum

UT26S]
Length = 450

Score = 107 bits (267), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 122/460 (26%), Positives = 204/460 (44%), Gaps = 40/460 (8%)

Query: 1 MAGAEIEVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M A+ +SG++ +PG KS+S+R L+L+AL+ G + V+ LL EDV A+
Sbjct: 9 MPQAQPATFTTAASALSGSIAVPGDKSISHRSLMLSALAVGESRVEGLLEGEDVLATAAAM 68

Query: 61 RTLGLSVEADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
R +G + D + VG GG E A L +GN+G + R L + + A
Sbjct: 69 RAMGADIRRDADGIWHIHGVGVGGLLPESA-----LDMGNSGTSTRLLMGLIASHAITA 123

Query: 120 TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI- 178
T+V D + +RP+ + L ++GA G P + G P + +
Sbjct: 124 TFGVDA--SLSKRPMARVTEPLSRMGASFTTSPGDRLP---LTMRGACPAVPLDYRLPVA 178

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLIS-IPYVEMTLRLMERFG--VKAHSDSWDRFY 235
S+Q SA+L+A A G I +++ IP + + R+++ FG + E R
Sbjct: 179 SAQVKSAILLAGLNAPG-----ITRVVEPIPTRDHSERMLKGFADLHVEVEGDGTRIV 232

Query: 236 IKGGQKYKSPKNAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
G+ P++ V GD SSA++ +A + G V + G + + ++L M
Sbjct: 233 TLRGEAELRPQSITVPGDPSSAAFPMAALLVPGSKVAIANVGLNATR--AGLIDLLREM 290

Query: 295 GAKVTWTETSVTVTGPPREPFG-----RKHLKAIDVNMNKM---DVAMTLAVVALFADG 346
G + E V G EP G L+ ++ + + P D + A A+G
Sbjct: 291 GGDI-LVENPREVG---EPVGDLVITASTLQGVPEPDPARAPSMIDEYPVAFIAAALAE 346

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLVNTAIDTYDD 403
+ R + RVKE++R+ + L +G +VEE D +I I T D
Sbjct: 347 RSTFRGLEELRVKESDRIATMAAGLRAIGVTVEELEDGIVIEGSGGALLPGGGPIATKLD 406

Query: 404 HRMAMAFSLAA-CAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
HR+AM+F++A ++ VTI D +FP + +L +
Sbjct: 407 HRIAMSFAGVAGLVSKKGVTTIDMRPVATSFPGFTALLRSL 446

>ref|ZP_06896114.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseomonas cervicalis
ATCC 49957]
gb|EFH12190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseomonas cervicalis
ATCC 49957]
Length = 446

Score = 107 bits (266), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 137/442 (30%), Positives = 197/442 (44%), Gaps = 38/442 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
+P + ++G + + G KS+S+R L+ AL+ G T + LL EDV A+R LG +VE
Sbjct: 5 RPHQGLAGRLTVAGDKSISHRALMFGALAVGRDITGLLEGEDVLRTAAAMRALGATVER 64

Query: 70 -DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ A + G GG ED L +GN+G A R + + AG VL G
Sbjct: 65 LGEGAWQVSGRGVGGVLEPEDV-----LDMGNSGTARLICGLL--AGHPVFAVLTDGAS 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSA 185
+R+RP+ + L GA G P+ V G + L ++ S+Q SA
Sbjct: 118 LRKRPMRRVTDPLAASGARFSSRAGGRL-PLAVQGA---AEPMPLDYTLPMASAQVKS 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKS 244
+L+A A G +++ + + E LR FG ++ R I+ GQ
Sbjct: 173 VLLAGLCARG--VTRVVEPEATRDHTENMLR---HFGATVRVAEDGPRRVIELEGQPELV 227

Query: 245 PKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
V GD SSA++ L A I G +TVE G L+ L MGA++T
Sbjct: 228 AAPVAVPGDPSSAAFPVLAALIVPGSALTVEHVGLNPLR--TGLFTTLREMGAELTVENE 285

Query: 304 SVTVTGPPREPFG-RHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V P + R L+A+DV ++P D LAV A A G + R +A RVK
Sbjct: 286 RVEGGEPVGDLTARFGALRAVDVPAARVPSMVDEYPIAFAAACATGTSRFRGLAELRVK 345

Query: 360 ETERMVAIRTELTKLGASVE-EGPDY----CIITPPEKLNVTADITYDDHRMAM-AFSLA 413
E++R+ A L G VE EG D C PP NV T+ DHR+AM A L
Sbjct: 346 ESDRVAATAALLAANGIKVEIEGDDMLVHGCAGNPPGGGNV---THMDHRIAMSALILG 402

Query: 414 ACAEVPVTIRDPGCTRKTFPDY 435
E PV++ D +FP +
Sbjct: 403 LATEQPVSVDSSFIDTSFPGF 424

>ref|ZP_06318845.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus WBG10049]
gb|EFB55048.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus WBG10049]
Length = 432

Score = 107 bits (266), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 115/435 (26%), Positives = 199/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ + K +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRMTDIFRLLGVDI---KEYE 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VV G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 DKLVVNSPG-YKAFKTPHQV-LYTGNSGTTTRLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVLKQLGADVDCFLGTDGP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI K++++ S+Q SA+L A+
Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIHKPSVIKGINY----KMEVA---SAQVKSAILFAS 178

Query: 191 PLALGDVEIEIIDLK-ISISYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
L E II +L +S + E R F + E ++ I +Y P + +
Sbjct: 179 ---LFSKEATIIEKELDVSRNHTETMFR---HFNIPIE-AEGLSITTIPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTWTSTVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISAFAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGNIQLFNQ--TTG 287

Query: 309 GPPREPFGKRK---LKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPIKIEGELVPKAIDELPVIALLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDAVNVSPFGFL 422

>ref|YP_001406072.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter hominis
ATCC BAA-381]
sp|A7I0N1.1|ARO_ACAMHC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS51320.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter hominis
ATCC BAA-381]
Length = 424

Score = 107 bits (266), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 120/423 (28%), Positives = 192/423 (45%), Gaps = 24/423 (5%)

Query: 25 KSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R ++ + LS GT ++N L +ED + L R LG AD K +V K
Sbjct: 21 KSISHRAVIFSLSSGNTKIEFNFLFAEDTEHSLEIARKLG----ADIEIKEGIVFIDAPK 76

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQL 144
VE + L GN+G +MR + + G +VL G + ERP+ + L ++
Sbjct: 77 KIVEP---DCILECGNSGTSMLRFMGLLASVEG--FFVLSGDEYLNERPMPKRVGEPLCKV 131

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + L D P+ + G G L K K S S+Q +AL++A AL E +
Sbjct: 132 GAKIYGRILDGDKAPLCIQG-GKLDFFKFK-SKIASAQVKTALILA---ALNSQGCEYSEP 186

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E +++++ G E S +K K P ++ D SSA Y+ A
Sbjct: 187 ELSRDHSE---KMLKKMGADIEISGL--NLKVKPLTKPLDPLEIFIPNDPSSAFYYAVAA 241

Query: 265 AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAID 324
I G+ + + + ++ EVL MGA + +T S LKA++
Sbjct: 242 TIIPGSKIILKNMLLN-KTRIEAYEVLRLKMGANIKFTPKSEIYEQIGDIEISYAPLKAVE 300

Query: 325 V--NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGP 382
V N++ + D A LA+ A G + +R+ RVKE++R+ I L G +V E
Sbjct: 301 VSENIWLIIDEAPALAIACAKGTSVLRNAKELRVKESDRKIVICEGLKCCGINVTELE 360

Query: 383 DYCIIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
D IT E I Y DHR+AM+F++ + + I + C +FP++ +L
Sbjct: 361 DGFKITGGEA-EPAIITPYGDHRIAMSFAILG-LKCGMIIENSECIATSFNFGKILKQI 418

Query: 443 VKN 445
N
Sbjct: 419 GAN 421

>ref|ZP_01750762.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp. CCS2]
gb|EBA12436.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp. CCS2]
Length = 441

Score = 107 bits (266), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 130/446 (29%), Positives = 200/446 (44%), Gaps = 34/446 (7%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEA 69
+P +SG +PG KS+S+R L+L A+ G T + LL EDV A+ G +V
Sbjct: 4 RPCGPLSGEAAHVPDGKSIHRSILIGAMCVGQTRITGLLEGEDVLDTGRAEAFGATVTN 63

Query: 70 DKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V VG GG A+ E + GN+G +R + A+ T+ D
Sbjct: 64 HGDGEWTVTGVGVGGF-----AEPEQVIDCGNSGTGVRLIMGAMATCPITVFTGDA--S 116

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+G + L G G P V + + + S+Q SA+L+
Sbjct: 117 LNRPMPGRVTDPLALFGTQAVGRQGRLPMTLVGAVDPV--PVRYVVPVPSAQVKSALL 174

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A G + +I+K + + E R+++ FG + E +D R GQ +P+
Sbjct: 175 AGLNAPG--QTVVIEKEATRDHTE---RMLQGFGATLTVEQTDE-GRVITLDGQPELTPQ 228

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V D SSA++ + A IT G+ V V G + L+ MGA + + E
Sbjct: 229 TIVVPRDPSSAAFPVCAAIITPGSDVLVPNIGLNPTN--AGLFTTLQDMGADLVY-ENMR 285

Query: 306 TVTGPP---REPFGRKHLKAIDV---NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
G P R F LK I V M D L+VVA FA G T ++ V RV
Sbjct: 286 EEGGEPVADLRKF-SPDLKGIAVPPARAASMIDEYPVLSVVAALFALGVTDMDQGVKELRV 344

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN---TAIDTYDDHRMAMAFSLAAC 415
KE++R+ A+ L G SV+EGPD+ +T NV + + DHR+AMAF +
Sbjct: 345 KESDRIDAMAKGLRAAGVSVDEGPDWWKVTGLGHGNVPGGATVASQLDHRIAMAFVMVMGM 404

Query: 416 A-EVPVTIRDPGCTRKTFPDYFDVLS 440
A + P+++ D +FP + D+++
Sbjct: 405 ATQKPMVDDGSPFIATSFPIFEDLMA 430

>ref|YP_001045145.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides ATCC 17029]
sp|A3PPV7.1|AROA_RHOS1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ABN78373.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides ATCC 17029]
Length = 445

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 125/437 (28%), Positives = 203/437 (46%), Gaps = 29/437 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G ++PG KS+S+R L+L A++ G T + LL +DV A+R G V + A
Sbjct: 18 LKGRAEIPGDKSISHRALILGAMAVGETQITGLLEGQDVLDTAKAMRAFGAEVIQHGPGA 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG GG A+ + GN+G +R + A+ + AT+ D +R+RP
Sbjct: 78 WSVHGVGVGGF-----AEPAEVIDCGNSGTGVRLVMGAMATSPLTATFTGDA--SLRKRK 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L G G P V +P V+ + + S+Q SA+L+A
Sbjct: 131 MGRVTDPLALFTRAYGRKGGRLPMTLVGAADVPV---VRYTVPMPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G + +I++ + + E R++ FG + + + + GQ P+ V
Sbjct: 188 APG--QTVVIEREATRDHSE---RMLRGFGAELSVETGPEGQIITLTGQPELRPQTVAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ + V G + D + +LE MGA + + E G
Sbjct: 243 RDPSSAAFPVCAALIVEGSEILVPGVSRNPTR-DGLYVTLL-EGADIAF-ENEREEGGE 299

Query: 311 PREPFGRK--HLKAIDVMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P + LK ++V + P D L+VVA FA+G T +R V RVKE++R+
Sbjct: 300 PVADLRVRASALKGVEVPPERAPSMIDEYPILSVVAFAEGSTIMRGVKELRVKESDRID 359

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-DTYDDHRMAMAF-SLAACAEVPTIR 423
A+ L G +EE D I+ ++ A T+ DHR+AM+F L AE PVT+
Sbjct: 360 AMARGLEACGVRIEEDTLIVHGMGRVPGGATCATHLDHRIAMSFLVLGMAAEAPVTVD 419

Query: 424 DPGCTRKTFPDYFDVLS 440
D +FP + D+++
Sbjct: 420 DGSPIATSFPAPTDLMT 436

>ref|ZP_06324490.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus D139]
ref|ZP_06343429.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus H19]
gb|EFB49571.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus D139]
gb|EFC07774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus H19]
Length = 432

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 114/435 (26%), Positives = 200/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI K++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIIPSVIKGI---NYKMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDLK-ISISYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E R F + E ++ +Y P + +
Sbjct: 178 --SLFSKESTIIKELDVSRNHTETMFR--HFNIPIE-AEGLSITTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T

Sbjct: 232 VPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGRRKH---LKAIDVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET

Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV

Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +

Sbjct: 408 IKQFDAVNVSFPGFL 422

>ref|ZP_07658197.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseibium sp.
TrichSKD4]
gb|EFO32864.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseibium sp.
TrichSKD4]
Length = 451

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 123/443 (27%), Positives = 195/443 (44%), Gaps = 50/443 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+ GTV +PG KS+S+R L+ AL+ G T LL SEDV A+R +G +E D

Sbjct: 18 LRGTVTVPDGKSIHRALMFGALAVGRTTATGLLESEDVLATADAMRVVGAVIEKTDNGT 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+G G + E + GNAG +R AT+V D + +RP

Sbjct: 78 YTIDGIGLGSLL----EPESVIDFGNAGTGVRLTMGIFGTHDIAATFVGDA--SLSKRP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPL 192
+G ++ L+ +G +V G P LP +V ++ S+Q SA+L+A

Sbjct: 131 MGRVLDPLRDMGTNVVARSGDRLPASIRGAKNPLPLTYRVPVA---SAQVKSALLLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +I+ + + + E ++++ FG + + +D +R GQ P+ V

Sbjct: 188 APGTT--TVIEPIATRDHTE---KMLKGFGADISVKLNDDGERVITLQGQPELKPQAIEV 242

Query: 251 EGDASSASYFLAGAAITGGT-VTVE-----GCGTTSLQ--GDVKFAEVLEMMGAKV 298
D SSA++ + A I G+ VT+E G TT ++ GD++ E G ++

Sbjct: 243 PADPSSAAFAIVAALIVPGSDVTIEKVLLNEHRIGLITTLIEMGGDIEIVNRRETGGEEI 302

Query: 299 TWTETSVTVTGPPEPFGRRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVAS 355
+ LK I V + P D LA+ A FA+G T + +

Sbjct: 303 GDVRVKAS-----QLKGITVPAKRAPSMIDEYPVLAIAASFAEGDTHMPGLDE 350

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAF-SL 412
RVKE++R+ A+ L EG D C+ N+ + T+ DHR+AMAF L

Sbjct: 351 LRVKESDRLAAVARGLEANNVPCVEGED-CLVTGTGAANIGGGTVVTHLDHRIAMAFVLV 409

Query: 413 AACAEVPVTIRDPGCTRKTFPDY 435
+ PVT+ D +FP +

Sbjct: 410 GMASHSPVTVDDGAVIATSFPF 432

>ref|ZP_05124567.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacteraceae
bacterium KLH11]
gb|EEE39199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacteraceae
bacterium KLH11]
Length = 448

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 129/451 (28%), Positives = 206/451 (45%), Gaps = 34/451 (7%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++ P ++GT ++PG KS+S+R L+L A++ G T + LL EDV A+R G

Sbjct: 10 MISHPCGPLTGTAEVPGDKSIHRSLILGAMAVGETRISGLLEGEDVLDTAKAMRAFGAE 69

Query: 67 VEADKAAKRAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125

Sbjct: 70 V D V G G G F A+ + + GN+G +R + A+ + AT+ D
V-TDHGKGEWTVHGVGVGGF----AEPDQVIDCGNSGTGVRLIMGAMATSPITATFTGDA 124

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLS 184
+ +RP+ + L G G P V P V+ + S+Q S

Sbjct: 125 --SLNKRPMARVTDPLALFGTQSVGRAGGRLPMTIVGAADPTP---VRYEVPVPSAQVKS 179

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY 242
A+L+A A G + +I+K + + E R++ FG + E +D + G +

Sbjct: 180 AVLLAGLNAPG--KTVVIEKEATRDHSE---RMLAGFGAEITVEDTDEGRVITLTGRPEL 234

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K P+ V D SSA++ + A +T G+ V V G G + L MGA +T+

Sbjct: 235 K-PQVIAVPRDPSSAAFPVCAALVTPGSDVLVPGIGLNPTR--AGLFTTLREMGADLTY- 290

Query: 302 ETSVTVTGPPREPFGRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVAS 355
E G P K+ +K I+V + M D L+VVA A G T + V

Sbjct: 291 ENEREEGGEPVADLRKAYSPNMKGIEVPPERAASMIDEYPVLSVVAANATGKTMMAGVKE 350

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFS- 411
RVKE++R+ A+ L G +VEEG D+ + NV +++ DHR+AM+F

Sbjct: 351 LRVKESDRIDAMARGLRANGVTVEEGDDWWSVDGLGIGNVPGGGTCESFLDHRIAMSFMV 410

Query: 412 LAACAEVPVTIRDPGCTRKTFFDYFDVLSTF 442
+ A PV++ D G +FP + +++T

Sbjct: 411 MGMGARTPVSVDDGGPIATSFPIFEPLMATL 441

>ref|ZP_07327822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetivibrio
cellulolyticus CD2]
gb|EFL60899.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acetivibrio
cellulolyticus CD2]
Length = 424

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 117/447 (26%), Positives = 200/447 (44%), Gaps = 50/447 (11%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R +LL +L++GTT +D L ED + R + +S+E +K

Sbjct: 9 LRGEITVPGDKSISHRAILLGSLAKGTTEIDGFLMGEDCLSTIDCFRKMHVSIIEILANSK 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ G G P A L G +G A+R L + + N+ D +P

Sbjct: 69 IKIQNGLYGLKPPSSA-----LNAGRSGTALRLLGLVLAQPFPNSVLTRD--ESSVRKP 121

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL-----SALL 187
IG +V L+ +GA ++ + P+ + P KL G + L S LL

Sbjct: 122 IGKVVKPLRDMGAIINGRDDGNLCPLTI-----FPS---KLKGQTHNLSLRDTHIKSPLL 173

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-----HSDSWDRFYIKGGQK 241
+A A GD ++ ++ + S + E+ ++ FG + S + Y

Sbjct: 174 LAGLYAQGDTKV--VEAVKSRDHTL---MLNYFGADISVNGLEVTAHSVENLY----- 222

Query: 242 YKSPKNAYVEGDASSASYFL-AGAAITGGT VTVEGCGTTSLQGDVKFAEVLEMMGAKV-T 299
+N V GD S ASYF+ AG + + ++ G + + +V MGA+

Sbjct: 223 ---AQNIEVPGDISIASYFITAGLIVPNSDIVIKNVGVNPTRTGI--IDVYRSMGAKIEI 277

Query: 300 WTETSVTVTGPPEPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
E +V+ LKA+ + + +P D +AV A+ A G T I ++ +

Sbjct: 278 LNERTVSNEKVADIRVVSSPLKAVTIEGDLIPRLIDEIPVIAVAAIMASGKTIINNLKGF 337

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-C 415
++K++ ++ + TEL+KLGASV+E D II KL T ++ Y+ + MA +A

Sbjct: 338 KIKDSGKLKMLSTELSKLGASVQETEDGMIIEGGRKLTGTIVEGYNYPATMALCVAGLV 397

Query: 416 AEVPVTIRDPGCTRKTFFDYFDVLSTF 442
A+ IR +P++ VL+

Sbjct: 398 ADGETMIRKTQVLDIAYPEFISVLNRL 424

>emb|CAQ49888.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus

subsp. aureus ST398]
Length = 432

Score = 107 bits (266), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 114/435 (26%), Positives = 200/435 (45%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPKPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSGTTTTRLLAGLLSGLGIES--VLSGDVSIKRP 125

Query: 135 GDLVVLGKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI K++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKSMNANIEGIEDNYTPLIIKPSVIKGI---NYKMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDLK-ISPYPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E R F + E ++ +Y P + +
Sbjct: 178 --SLFSKEPTIIEKLDVSRNHTETMFR--HFNIPIE-AEGLSITTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISAFAFFIVAALITPGSDVTIHNNGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGGRKH---LKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFFDYF 436
I+ +FP +
Sbjct: 408 IKQFDVAVNVSPGFL 422

>ref|ZP_01447705.1| EPSP synthase, 3-phosphoshikimate 1-carboxyvinyltransferase [alpha
proteobacterium HTCC2255]
gb|EAU51887.1| EPSP synthase, 3-phosphoshikimate 1-carboxyvinyltransferase [alpha
proteobacterium HTCC2255]
Length = 445

Score = 106 bits (265), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 126/442 (28%), Positives = 203/442 (45%), Gaps = 28/442 (6%)

Query: 10 QPIKEISGTVKLPKPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
Q + GT +PG KS+S+R L+L ALS G T + LL +DV A+ G V
Sbjct: 13 QSAGPLKGTAVIPGDKSVSHRSLILGALSVEGETKISGLLLGQDVLDTARAMAAFGARVID 72

Query: 70 DKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+V VG GG ED + GNAG +R + A++ + NAT+ D
Sbjct: 73 HGEWNVSNGVGVGGFSEPEIDIID----CGNAGTGVRLIMGAMSTSPINATFTGDA--S 125

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL-SGSISSQYLSALL 187
+R RP+G + L+ GA G + + +G + S S+Q SA+L
Sbjct: 126 LRSRPMGRITDPLELFGAKS---YGRSKGFLPLTMVGARDAHGINYTSPHPSAQIKSAIL 182

Query: 188 MAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPK 246
+A +LG E +I+ + + E R++ FG E ++ + F I G+ +
Sbjct: 183 LAGLNSLG--ETTLIEPEKTRDHSE---RMLRGFGANIETVETKNGFEITLGRPELIAQ 237

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSV 305
N V D SSA++ + A I G+ + + G + + F ++EM GA + + +
Sbjct: 238 NIAVPCDPSSAFAFPVCAALIVEGSEIFLPNIGLNPTRSGL-FTTLVEM-GADIVFENNRL 295

Query: 306 TVTGPPREPFGGR-KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
P + R L I+V ++ P D L+VVA FA G T +R + RVKE
Sbjct: 296 EGGEPVADLRVRASSLDGIEVPSDRAPSMIDEYPILSVVAFAFGSKTIMRGIKELRVKEC 355

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPP--EKLNVTAIDTYDDHRMAMAF-SLAACAEV 418
+R+ A+ L +G +EEG DY I+ E T+ DHR+AM+F + ++
Sbjct: 356 DRIDAMARGLEAMGVKIEEGEDYLIVHGQNGEVEGGGIAQTHLDHRIAMSFLCMGLASKK 415

Query: 419 PVTIRDPGCTRKTFPDYFDVLS 440
V + D +FP + +++S
Sbjct: 416 SVKVDDGHAIATSFPIFTNLMS 437

>ref|YP_355096.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides 2.4.1]
sp|Q3IW89.1|AROARHOS4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABA81195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
sphaeroides 2.4.1]
Length = 445

Score = 106 bits (265), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 126/438 (28%), Positives = 203/438 (46%), Gaps = 31/438 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G ++PG KS+S+R L+L A++ G T + LL +DV A+R G V + A
Sbjct: 18 LKGRAEIPGDKSISHRALILGAMAVGETRITGLLEGQDVLDATAMRAFGAEVIQHGPGA 77

Query: 74 KRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VG GG P E + GN+G +R + A+ + AT+ D +R+R
Sbjct: 78 WSVHGVGVGGFTEPAE-----VIDCGNSGTGVRLVMGAMATSPLTATFTGDA--SLRKR 129

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAP 191
P+G + L G G P V +P V+ + + S+Q SA+L+A
Sbjct: 130 PMGRVTDPLALFGTRAYGRKGGRLPMTLVGAADPVP---VRYTVPVPSAQVKSAVLLAGL 186

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + +I++ + + E R++ FG + + + + GQ P+ V
Sbjct: 187 NAPG--QTVVIEREATRDHSE---RMLRGFGAELSVETGPEGQVITLTGQPELRPQTVAV 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ + A I G+ + V G + D + +LE MGA + + E G
Sbjct: 242 PRDPSSAAFPVCAALIVEGSEILVPGVSRNPTR-DGLYVTLLE-MGADIAF-ENEREEGG 298

Query: 310 PPREFPGRK--HLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P + LK ++V + P D L+VVA FA+G T +R V RVKE++R+
Sbjct: 299 EPVADLRVRASALKGVEVPPERAPSMIDEYPILSVVAAFAEGLTIMRGVKELRVKESDRI 358

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-DTYDDHRMAMAF-SLAACAEVPVTI 422
A+ L G +EE D I+ ++ A T+ DHR+AM+F L AE PVT+
Sbjct: 359 DAMARGLEACGVRIEEDDTLIVHGMGRVPGGATCATHLDHRIAMSFLVLGMAAEAPVTV 418

Query: 423 RDPGCTRKTFPDYFDVLS 440
D +FP + D+++
Sbjct: 419 DDGSPAIATSFPAFIDLMA 436

>ref|YP_002887359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Exiguobacterium sp.
ATlb]
gb|ACQ71914.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Exiguobacterium sp.
ATlb]
Length = 416

Score = 106 bits (265), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 115/406 (28%), Positives = 188/406 (46%), Gaps = 32/406 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAK 74
++G++++P KS+++R LL ++ GTT V N L D + A+R+LG AD +
Sbjct: 3 LNGSIRVPSDKSITHRALLFGMMANGTTHVRNPLLGDRCSTIEAIRSLG----ADVTEQ 58

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ ++ G + P +L GN+G MR L + +G N ++ L G + RP+
Sbjct: 59 QDELIIGIESP-----RSARLDCGNSGTTMRLILGLL--SGYNGSFELVGDESLSRRPM 111

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA V D P+ + G L L + S+Q SA+L+A A
Sbjct: 112 RRVTEPLRNMGAHVGTG---DMAPLVIEGTT-LQSIDYTLPA-SAQVKSALLAGLRAS 165

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + + ++S + E R++ FG K + I+ + V D
Sbjct: 166 GTTVVR--EPMLSRDHTE---RMLPLFGAKLSIVNEEGLRVIRVEPSTLTGCTVDVPADP 220

Query: 255 SSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWT-ETSVTVTGPP 311
SSA++F AGAA+ + T + C + G F LE MGA V + E SV
Sbjct: 221 SSAAFFWAGAAAMVANSVTTTVDCLNETRIG---FLRTLERMGANVVISNERSVGEERVG 277

Query: 312 REPFGKRHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
L V + +P D A+VA A+ P+ ++D A RVKET+R+ +
Sbjct: 278 DVTVTTSLSGTVEKDFIPSQIDELPLFALVASQANSPSIVKDAEELRVKETDRIDVVV 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTAIIDYDDHRMAMAFSLAA 414
+EL KLG + G + I P +L+ + TY DHR++M +A+
Sbjct: 338 SELRKLGVDI-VGTEDGFIVQPSRLHGGDVSTYGDHRLSMMLQVAS 382

>ref|YP_612194.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria sp. TM1040]
sp|Q1GK84.1|AROA_SILST RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF62932.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria sp. TM1040]
Length = 450

Score = 106 bits (265), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 127/435 (29%), Positives = 204/435 (46%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L A++ G T + LL EDV A++ G V +
Sbjct: 18 LKGEAHVPGDKSISHRSLILGAMAVGETKISGLLEGEDVLDTAKAMQAFGAEEVNVHGGGE 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ E + GN+G +R + A+ + AT+ D + +RP
Sbjct: 78 WSVFVGVGVG---AEPENVIDCGNSGTGVRLIMGAMATSPITATFTGDA--SLNKR 130

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+ + L GA G P V +P V+ + S+Q SA+L+A
Sbjct: 131 MARVTDPLALFGAQSVGREGGRLPMTIVGAAEPVP---VRYEVPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I++ + + E R++ FG + D+ + R GQ P+ V
Sbjct: 188 APG--KTVVIEREATRDHSE---RMLAGFGAEITVEDTKEGRVITLTGQPELKPVIAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ + A IT G+ V V G G + + + L+ MGA +T+ E T G
Sbjct: 243 RDPSSAAFPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF-ENPRTEGGE 299

Query: 311 PREPFGKRH---LKAIDVNMNMK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P K+ +K I+V + M D L+VVA FA G T + V RVKE++R+
Sbjct: 300 PVADLRKAYSPDMKGIEVPPERAASMIDEYPVLSVVSASFATGTTMMAGVKELRVKESDRI 359

Query: 365 VAIRTELTKLGASVEEGPDYCI--TPPEKLNVTAI-DTYDDHRMAMAFS-LAACAEVPV 420
A+ L G +VEEG D+ + PE + +++ DHR+AM+F + A+ PV
Sbjct: 360 DAMAKGLRANGVTVEEGEDWWSVEGCGPEGVKGGGTAESFLDHRIAMSFVMGMGAQNPV 419

Query: 421 TIRDPGCTRKTFPDY 435
++ D +FP +
Sbjct: 420 SVDDGSPATSFPIF 434

>ref|ZP_01037287.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseovarius sp. 217]
gb|EAQ24222.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseovarius sp. 217]
Length = 439

Score = 106 bits (265), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 130/448 (29%), Positives = 199/448 (44%), Gaps = 48/448 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +PG KS+S+R L+L ALS G TV+ LL EDV A+R G V D+
Sbjct: 9 LSGVADVPGDKSISHRSLILGALSVEGTITGLLEGEDVLDTAKAMRAFGAEVTRDETGS 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
V VG GG A+ + + GN+G +R + A+ + AT+ D + +RP
Sbjct: 69 WHVHGVGVGGF-----AEPDHVIDCGNSGTGVRLIMGAMATSPITATFTGDA--SLNKR 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ + L G G P PV + + +P +VK SA
Sbjct: 122 MARVTDPLALFGRSVGRAGRLPMTIVGAADPVPIRYVVPVPSAQVK-----SA 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKS 244
+L+A A G + +I++ + + E R++ FG + ++ + R GQ
Sbjct: 172 VLLAGLNAPG--QTVVIEREATRDHTE---RMLAGFGAEIVTEETAEGRVITLTGQPELR 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
+ V D SSA++ + A I G+ V V G + L MGA + + E
Sbjct: 227 AQTIVVPRDPSSAAFPVCAALIVPGSDVLVPNIGLNPTN--AGLFTTLREMGADLEY-EN 283

Query: 304 SVTVTGPP----REPFGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASW 356
G P R F LK I+V + M D L+VVA FA G T +R V
Sbjct: 284 LREEGGEFVADLRARFS-PDLKGIEVPPERAASMIDEYPVLSVVASFATGETVMRGVKEL 342

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAITD---YDDHRMAMAFSLA 413
RVKE++R+ A+ L G VE+GPD+ I+ NV T + DHR+AM+F +
Sbjct: 343 RVKESDRIEAMAAGLRAGGVEVEDGPDWWIVHGRGHGNVLGGQTCASHLDHRIAMSFVM 402

Query: 414 ACAEV-PVTIRDPGCTRKTFPDYFDVLS 440
A PV++ D +FP + +++
Sbjct: 403 GMATTAPVSVDDASPIATSFPIFEHLMA 430

>ref|NP_105914.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium loti
MAFF303099]
sp|Q98CC1.1|AROARHILO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB51700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium loti
MAFF303099]
Length = 452

Score = 106 bits (264), Expect = 7e-21, Method: Compositional matrix adjust.
Identities = 120/457 (26%), Positives = 199/457 (43%), Gaps = 56/457 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ +SGT ++PG KS+S+R + L+ G T + LL EDV A++ +G +E K
Sbjct: 16 QALSGTARVPGDKSISHRSMFGGLASGETRITGLLEGEDVMRTGAAMKAMGAHIE--KR 73

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V+ G G ++ E L GNAG R V T++ D + R
Sbjct: 74 GAEWVIRGTGNALLQ---PEGPLDFGNAGTGSRLTMGLVGTYDMETTFIGDA--SLSGR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMA 189
P+G ++ L+Q+G V D P+ ++G P ++ + S+Q SA+L+A
Sbjct: 129 PMGRVLEPLRQMGVQVLKATPGDRMPITLHG---PKHAAPITYRVPMSAQVKSAVLLA 184

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247
G +I+ +++ + E +++++ FG + E + R GQ + +
Sbjct: 185 GLNTPGIT--TVIEPVMTRDHT---KMLKGFGANLSVETDERGVRHIFIEGQGRITGQT 239

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVT 306
V GD SSA + L A I G+ +T+E + + L+ MG ++
Sbjct: 240 IAVPGDPSSAGFPLVAALIVPGSDITIENVLMNPTRTGLLL--TLQEMGGQIDILN---- 293

Query: 307 VTGPPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
PR G LK + V + P D LAV A FA+G T ++ +
Sbjct: 294 ----PRNAGGEDVADLRVRYSELKGVAVPPERAPSMIDEYPVLAASFAEGETLMQGLE 349

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTAITDYDDH 404

RVKE++R+ A+ L G EG + P L+ T + T+ DH
Sbjct: 350 ELRVKESDRLSAVANGLKLNGVDCTEGEASLAVRGRPGGKGLGGHPNGLD TT-VQTHLDH 408

Query: 405 RMAMAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
R+AM+F + A E PVTI D +FP++ +++

Sbjct: 409 RIAMSFLVMGLATEKPV TIDDQAMIATSFPEFMGLMT 445

>ref|ZP_05084505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudovibrio sp.
JE062]
gb|EEA95441.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudovibrio sp.
JE062]
Length = 442

Score = 106 bits (264), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 123/438 (28%), Positives = 198/438 (45%), Gaps = 32/438 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS-VEADKAA 73
++G +K+PG KS+S+R L+ AL+ G T + LL SEDV A+ +G V +
Sbjct: 9 LNGQIKVPGDKSISHRSLMFGALALGKTTISGLLESEDVIGTANAMNAVGA KCVRQEDGT 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG G + E + GNAG +R L + A+ A + G + RP
Sbjct: 69 WTVDGVLGSL L-----EPEAPIDFGNAGTGVR-LAMGIFASHPIA-VTMTGDASLSGRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPL 192
+G ++ L+++G V G P +P +V ++ S+Q SA+L+A
Sbjct: 122 MGRVLNPLREMGVQVVARNGDRLPASIRGSDNPIPIITYRVPMA---SAQVKSALLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G +I+ + + + E +++ FG + E ++S +R GQ P++ V
Sbjct: 179 TAGTT--TVIEPVATRDHTE---KMLVGFAGELNVEINESGERVITLQGQPKLQPDITV 233

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWT--ETSVT 306
GD SSA++ + A IT G+ VTVEG + + L MGA +T + E+
Sbjct: 234 PGDPSSAAFPIVAALITPGSDVTVEGVLLNEHR--IGLITSLLEMGADITISNERESGGE 291

Query: 307 VTGPPREFFGRKHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G R + + LK I V + P D L+V A FA G T + + RVKE++R
Sbjct: 292 KIGDIRAKYSK--LKGITVPAGRAPSMIDEYPILSVAAAFAGGETVMLGLEELRVKESDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT-PPEKLNVT AIDTYDDHRMAMAF-SLAACAEVPT 421
+ A+ L G E D +T + + T+ DHR+AM+F L A PV
Sbjct: 350 LAAVARGLEANGIPCVEKQDSLTVTGGANNIGGGTVATHLDHRIAMSFLILGLAAHKPVQ 409

Query: 422 IRDPGCTRKTFPDYFDVL 439
+ D +FP + +
Sbjct: 410 VDAAPIATSFPTFLSMF 427

>ref|ZP_05076700.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
bacterium HTCC2083]
gb|EDZ44360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacteraceae
bacterium HTCC2083]
Length = 441

Score = 106 bits (264), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 125/439 (28%), Positives = 199/439 (45%), Gaps = 30/439 (6%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +PG KS+S+R L+L A++ G T + LL EDV A+R+ G V + +
Sbjct: 11 GRADVPGDKSISHRALILGAMAVGETCITGLLEGEDVLD TGRAMRSFGAEVTDHGDGEWS 70

Query: 77 VV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP I G 135
V VG GG A+ E + GN+G +R + A+ + T G + RP+
Sbjct: 71 VHGVGVGGF-----AEPENVIDCGNSGTGVRLIMGAMATT--DITAAFTGDASLSNRPMA 123

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLAL 194
+ L G +G D + + +G V+ + + S+Q SA+L+A A
Sbjct: 124 RVTDPLALFGTKA---VGRDGGRLPMTIVGAKEPVVRYTTHVPSAQVKSALLAGLNAP 180

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPKNAYVEGD 253
G + +I+K + + E R+++ FG + D+ + I GQ P+ V D
Sbjct: 181 G--QTVVIEKEATRDHTE---RMLQGFGAELTVEDTDEGHVITLTGQPELVPQVITVPRD 235

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++ + A IT G+ V V G + E L MGA +++ + P
Sbjct: 236 PSSAAFPVCAALITEGSDVLVPNIGLNPTR--AGLFETLREMGADLSYENERIEGGEFMA 293

Query: 313 EPFGR--KHLKAIDV---NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ R +K I+V M D L+VVA A GPT +R V RVKE++R+ A+
Sbjct: 294 DLRARFSPDMKIEVPPARAASMIDEYPVLSVVAANASGPTVMRGVKELRVKESDRIEAM 353

Query: 368 RTELTKLGLASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAF-SLAACAEVPTIR 423
L G VE+G D+ I+ NV ++ DHR+AM+F L A PV +
Sbjct: 354 AVGLRANGVEVEDGSDWWIVQCGMGNVQGAECASHLDHRIAMSFLVLGMSAIKPVRVD 413

Query: 424 DPGCTRKTFPDYFDVLSTF 442
D G +FP + +++
Sbjct: 414 DAGPIATSFPIFEPLMAAL 432

>ref|ZP_05051528.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Octadecabacter
antarcticus 307]
gb|EDY77794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Octadecabacter
antarcticus 307]
Length = 469

Score = 106 bits (264), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 128/435 (29%), Positives = 196/435 (45%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L AL+ G T + LL +DV A+ G V +
Sbjct: 37 LRGEAYVPGDKSISHRALILGALAVGETKITGLLEGQDVLDTGRAMEAFGAEVINHGGGE 96

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ E + GN+G +R + A+ + T G + RP
Sbjct: 97 WSVHGVGVGGF-----AEPENVIDCGNSGTGVRLIMGAMATC--DITVTFTGDASLNGRP 149

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L G G P V P V+ + S+Q SA+L+A
Sbjct: 150 MGRVTDPLALFGTQAVGREGGRLPMTIVGAKHATP---VRYMVPVPSAQVKSALLAGLN 206

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G E +I+K + + E R++ FG D+ + R GQ P+ V
Sbjct: 207 APG--ETVVIEKEATRDHTE---RMLVGFGADLTVEDTDEGRVITLVGQPELKPQTIIVP 261

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 310
D SSA++ + A + G+ V V G + + + L+ MGA +T+ E T G
Sbjct: 262 RDPSSAAFPVCAALLAEGSDVLVPNIGLNPTRAGLFY--TLQDMGADLTF-ENMRTEGGE 318

Query: 311 PREPFGRKH---LKAIDV---NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P ++ + I+V M D L+VVA FA G T +R V RVKE++R+
Sbjct: 319 PVADLRARYSPNMHGIEVPPARAASMIDEYPVLSVVAAFASGQTVMRGVREL RVKESDRI 378

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD---DHRMAMAFSLAACA-EVPV 420
A+ T L G +V+EGPD+ I+T NV T DHR+AM+F + A P+
Sbjct: 379 DAMATGLRAAGVTVDEGPDWWIVTGLGFGNVAGGITAQSRLDHRIAMSFLVMGLATNAPM 438

Query: 421 TIRDPGCTRKTFPDY 435
++ D G +FP +
Sbjct: 439 SVDDGGPIATSFPIF 453

>ref|ZP_05275017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-064]
Length = 390

Score = 106 bits (264), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 98/357 (27%), Positives = 174/357 (48%), Gaps = 22/357 (6%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP IGDLVVGLKQLGADVDCFLGTD 155

Sbjct: 48 L +GN+G +R + + AG + V + +RP+ +++ L+Q+GA + G++
LDIGNSGTTIRLMMGIL--AGRDFDTVXXXXESIAKRPMNRVMLPLQQMGAKMHGKDGSE 105

Query: 156 CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTL 215
P+ +NG L + + + S+Q SA++ AA A G+ I +K + T

Sbjct: 106 FAPITINGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEGETIIHEKEK-----TRDHTE 159

Query: 216 RLMEFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVE 274
++ +FG + E R +KGGQ + + + V GD SSA++F+ IT G + +

Sbjct: 160 HMIRQFGEIEMDGLTIR--VKGQTF-TGQEMTVPGDVSSAAFFIVAGLITPGSEIELT 216

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRK--HLKAIDVNMNMKMPD 332
G + + +V+E MG + ++S + TG K LK ++ + +P

Sbjct: 217 HVGLNPTRTGI--FDVVEQMGGSLVVKDSSRS-TGKLAGTVVVKTSCLKGTEIGGDIIPR 273

Query: 333 VAMTLAVVALFA--DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITP 389
+ + V+AL A +G T I+D A +VKET R+ A+ TEL K+GA + D II

Sbjct: 274 LIDEIPVIALLAQAEGTTIIKDAAELKVKETNRIDAVATELNKMGADITPTEDGLIIRG 333

Query: 390 PEKLNVTIAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
L+ + +Y DHR+ M +AA E V + P ++P +F+ + + +K

Sbjct: 334 KTPLHAANVTSYGDHRIGMMLQIAALLVEEGDVELERPEAVSVSYPTFFEDIRSLK 390

>ref|ZP_02146464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeobacter
gallaeciensis BS107]
gb|EDQ12212.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeobacter
gallaeciensis BS107]
Length = 440

Score = 106 bits (264), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 128/442 (28%), Positives = 206/442 (46%), Gaps = 32/442 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G ++PG KS+S+R L+L AL+ G T + LL EDV A++ +G V

Sbjct: 9 LTGIAEVPGDKSIHRSLILGALAVGETKISGLLEGEDVLDTAKAMQAMGAEVINHGGGN 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERP 133
+V VG GG A+ E + GN+G +R + + + T+ D + +RP

Sbjct: 69 WSVHGVGVGGL-----AEPEQVIDCGSGTGVRLIMGVMATSPITVFTTGDA--SLNKR 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V P V+ + + S+Q SA+L+A

Sbjct: 122 MARVTDPLALFGTQSVGRSGGRLPMTIVGAAEPTP---VRYTVPVPSAQVKSAVLLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+K + + E R++ FG + D+ + R GQ P+ V

Sbjct: 179 APG--QTVVIEKEATRDHSE---RMLAGFGAETIVEDTDEGRVITLTGQPELKPQVIAVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ + A IT G+ V V G G + + + L+ MGA +T+ E G

Sbjct: 234 RDPSSAAFPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF-ENMREEGGE 290

Query: 311 PREPFGRKH---LKAIDVNMNK--MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P ++ +K IDV + M D L+VVA FA G T + V RVKE++R+

Sbjct: 291 PVADLRARYSPDMKIDVPPERAASMIDEYPVLSVVSFATGKTMGTGVKELRVKESDRI 350

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKL-NVTAIDTYDDHRMAMAFS-LAACAEVPV 420
A+ L G VEEG D+ +T PE + +++ DHR+AM+F + A+ PV

Sbjct: 351 DAMARGLRANGVMVEEGDDWAVTGLGPEGVPGGGTCEFLDHRIAMSFVMGMGAQKPV 410

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
T+ D +FP + +++T

Sbjct: 411 TVDDGTPIATSFPIFTPLMTTL 432

>ref|YP_164847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria pomeroyi
DSS-3]
gb|AAV97156.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria pomeroyi
DSS-3]
Length = 448

Score = 106 bits (264), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 129/444 (29%), Positives = 203/444 (45%), Gaps = 40/444 (9%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P +SG ++PG KS+S+R L+L A++ G T + LL EDV A+R G V
Sbjct: 13 HPCGPLSGVAEVPDGSISHRALILGAMAVGETRITGLLEGEDVLDTAKAMRAFGAEVTR 72

Query: 70 DKAACKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+V VG GG A+ E + GN+G +R + A+ + +AT+ D
Sbjct: 73 HADGSWSVHGVGVGGF-----AEPEQVIDCGNSGTGVRLIMGAMATSPISATFTGDA--S 125

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALL 187
+ +RP+ + L GA G P V +P V+ + S+Q SA+L
Sbjct: 126 LNKRPMAVTDPLALFGAQAVGREGGRLPMTIVGAADPVP---VRYEVPVPSAQVKSAYL 182

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G + +I+K + + E R++ FG V E +D + G + K P
Sbjct: 183 LAGLNAPG--QTVVIEKEATRDHSE---RMLAGFGAETVETDDEGRVITLTGRPELK-P 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V D SSA++ + A IT G+ V V G G + L MGA +T+ E
Sbjct: 237 QVIAVPRDPSSAAPPVCAALITPGSDVLPVIGLNPTR--AGLFTTLREMGADLTY-ENE 293

Query: 305 VVTGTGPPREPFGGRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRV 358
T G P ++ +K I V + M D L+VVA A G T + V RV
Sbjct: 294 RTEGGEPVADLRARYSPDMKGITVPPERAASMIDEYPVLSVVAANAQGVMTMMGGVKELRV 353

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTAI-----DTYDDHRMAMAFS- 411
KE++R+ A+ L G +VEEG D+ + L + + +++ DHR+AM+F
Sbjct: 354 KESDRIDAMARGLRANGVTVEEGDDWAV---HGLGIGKVPGGGTCEFLDHRIAMSFMV 410

Query: 412 LAACAEVPVTIRDPGCTRKTFPDY 435
+ A+ PV++ D +FP +
Sbjct: 411 MGMGAQAPVSVNDGSPISATSFPIF 434

>ref|YP_001960561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
phaeobacteroides BS1]
sp|B3ENJ1.1|ARO_A_CHLPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACE05080.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
phaeobacteroides BS1]
Length = 435

Score = 106 bits (264), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 114/444 (25%), Positives = 201/444 (45%), Gaps = 43/444 (9%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA-----K 74
LP KS+++R L+ A+++GTT + N D LG L+ G++V +K
Sbjct: 11 LPPDKSIAHRAALIGAVADGTTEISNFSGGFDNQSTLGVLQACGIAVHQEKLKGPNGNIS 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + + ++ E L N+G MR + A + L G + +RP+
Sbjct: 71 RNVVIHAQGFWSL--SRPEKDLMCNNSGSTMRMFAGILAAQPFESR--LAGDSSLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GADV + PV + G L +L S+Q S + +AA A
Sbjct: 127 QRVAHPLRLMGADV-ALSSDNTAPVAIRGTTHLRPIDYELPVP-SAQVKSVALAALHAE 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G E +I+ L S + E+ L G+K E I G+K K ++ GD
Sbjct: 185 G--ESRVIETLPSRNHTEML-----GLKVEALSDGRSAVIIPGRKTVPAKPFHIPGDP 236

Query: 255 SSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS----- 304
S+A + +A ++ G+ V + C + G + VL GA+++
Sbjct: 237 SAACFIIALGLLSAGSEIVVRDVLNPTRTG---YMGVLLGAGAEISMENIRFAGGEKIG 293

Query: 305 --VVTGTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P +P + +++++P LAV++ A G + + A R KE++

Sbjct: 294 DVLVRHSPSMKPLSISDPAVVANSIDEIP----MLAVLSACATGAFELYNAAELRAKESD 349
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---AIDTYDDHRMAMAFSLA-ACAEV 418
R+ A+ L ++G +E D +T + + T AID+YDDHR+AM+F++A +
Sbjct: 350 RISAVVDNLERIGFVCDEYADGFAVTGRKDVPTGKVAIDSYDDHRIAMSFAIADRVVPM 409
Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
+ I D +FPD+F+++ +
Sbjct: 410 ELDISDAKVIGVSFPDFFEIIESL 433

>ref|YP_003505660.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Denitrovibrio
acetiphilus DSM 12809]
gb|ADD69704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Denitrovibrio
acetiphilus DSM 12809]
Length = 426

Score = 106 bits (264), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 122/442 (27%), Positives = 202/442 (45%), Gaps = 45/442 (10%)

Query: 17 GTVKLPGSKSLSNRILLALAALSEGTTVVNDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
GTV++P KS+S+R +L ++++G V+D LL S D + A+R +G+ E
Sbjct: 12 GTVRVP SDKSISHSFMLSMAKGRGRVIDPLL-SADTKATMAAMRAVGQFEE---TVN 67
Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
V+ G ++ + + N+G + R LT A N YVL G MR+RP+
Sbjct: 68 GFVITSDGYQNFKEPSDVIDCM--NSGTSARLLTGVF--APTNYVLTGDNMSMRKRPMD 123
Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPG--GKVKLSGSI-SSQYLSALLMAAPL 192
+++ L ++GA P+ + LP V+L+ S S+Q SA+L+A
Sbjct: 124 RVILPLTEMGAKFAARDNGSKLPLTI-----LPSVTNPVELTASTKSAQVKSAILLAGVQ 178
Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G +K ++ + E+ L + A + + ++G +S + V G
Sbjct: 179 TEG--VTYTEKAVTRNHEIMLS-----ALGANLTVDGLKISVEGAADLRSI-DVVVPG 230
Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FL G + + + +E G + + VL MG K E G
Sbjct: 231 DFSSAAFFLGGLTLMFDNSELILENVGLNPTRSGM--LNVLTQMGVKY---EIDSERGGA- 284
Query: 312 REPFGKHLKAI-----DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
E G +K+ D+ N + ++ M +A + LFA+ P IR+ RVKE++
Sbjct: 285 -EKLGDICIKSQSFEGCTIDGDIVANMIDELPM-VATLGLFANSPTIRNAKELRVKESD 342
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM-AFSLAACAEVPV 420
R+ A L +LGA VEE D + P + +N A + +DDHRMAM A LA +
Sbjct: 343 RIEATLYNLRLQGAEEVEYEDGMKVYPIKSVNDKAEKAFDDHRMAMIAIMLAKRFGGNI 402
Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
T+ D C +FP + + +
Sbjct: 403 TVDDMQCVDVSFPTFIETFESL 424

>ref|ZP_04866271.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_TCH959]
gb|EES92882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_TCH959]
Length = 435

Score = 105 bits (263), Expect = 9e-21, Method: Compositional matrix adjust.
Identities = 119/448 (26%), Positives = 207/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLSNRILLALAALSEGTTVVNDNLLNSEDVHYMLGALR 61
E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62
Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D ++ VV G + + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVEIKEDD--EKLVTSPG--YQSFNTPHQV-LYTGNSGTTTLLAGLLSGLGIES-- 115
Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCP----PVRVNGIGGLPGGKVKLSGS 177

VL G + +RP+ ++ LK + A+++ P P + GI K++++
Sbjct: 116 VLSGDSVIGKRPMDRVLRLPKSMNANIEGIEDNYTPLIIKPSVIKGI----NYKMEVA-- 169
Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L E II +L +S + E + F + E ++
Sbjct: 170 -SAQVKSAILFA---SLFSKEPTIIKELDVSRNHTET---MFSHFNIPIE-AEGLSINTT 221
Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG
Sbjct: 222 PEAIRYIKPADFHVPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMG 279
Query: 296 AKVTWTETSVTVTGPPREPFGGRKH---LKAIDVNMNKMMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +
Sbjct: 280 GNIQLFNQ--TTGAETASIRIQYTPLQPIITIEGELVPKAIDELPVIALLCQAVGTST 337
Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M
Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMM 397
Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++A+ + PV I+ +FP +
Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

>ref|ZP_01224478.1| prephenate [marine gamma proteobacterium HTCC2207]
gb|EAS46974.1| prephenate [marine gamma proteobacterium HTCC2207]
Length = 749

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 118/439 (26%), Positives = 200/439 (45%), Gaps = 47/439 (10%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +++PG KS+S+R ++L +++EG T V L ED L A R +G+ +E R
Sbjct: 326 GDIRVPGDKSMHSRISIMLGSIAEGMTEVTGFLEGEDSLATLQAFRGMGVIIIEGPDQG-RV 384
Query: 77 VVVGCG---GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V+ G G K P + L+LGN+G +MR L+ + AG L G + RP
Sbjct: 385 VIHGVGLHGLKAPT-----PLYLGNSGTSMRLLSGLL--AGQTFDVELTGDESLSGRP 436
Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMA 189
+ + L ++GA ++ G PP+ + G G K+K + S+Q S +L+A
Sbjct: 437 MARVADPLAEMGAVIETAPGGR-PPMLIKG-----GNKLPIDYVLPMAAQAQVKSVCVLLA 490
Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G+ + P + + R++ FG S + + GG + +
Sbjct: 491 GLYAEGETS-----TIEPAPTRDHSEMRGRGFGYSVVS DGS--KASLSGGGSLTATR-ID 542
Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D SSA++F+ AAIT G+ +T+ G + V +L MG + + V
Sbjct: 543 VPADISSAAFFMVAAAITPGSDITLRHVGNPTR--VGVINILRQMGTSLIELSNEK-EVG 599
Query: 309 GPPREPFGGRKHLKAIDVNMNKMMPDVAMTLA-----VVALFADGPTAIRDVASWRVKE 360
G EP ++ ++N +P+ + LA V A A G T + RVKE
Sbjct: 600 G---EPVADIRIRYAEIENGIVIPEDQVPLAIDFPPVLFVAAACATGETVLTGAEELRVKE 656
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAAC-AEVP 419
++R+ ++ L LG + D I + L + ++DDHR+AMAF++A ++
Sbjct: 657 SDRIQSMADGLVTLGIDAQSTADGIRIQGGQ-LGSGTVHSHDDHRIAMAFIAGLRSQGE 715
Query: 420 VTIRDPGCTRKTFPDYFDV 438
+ I + +FP + D+
Sbjct: 716 IEIIECNNIATSFPGFVDL 734

>ref|ZP_05739280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Silicibacter sp.
TrichCH4B]
gb|EEW60351.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Silicibacter sp.
TrichCH4B]
Length = 450

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.

Identities = 126/435 (28%), Positives = 204/435 (46%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L A++ G T + LL EDV A++ G V +
Sbjct: 18 LKGEAHVPGDKSISHRSLILGAMAVGETKISGLLEGEDVLDTAKAMQAFGAEVINHGGGE 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ E + GN+G +R + A+ + AT+ D + +RP
Sbjct: 78 WSVFVGVGVGGF-----AEPENVIDCGNSGTGVRLIMGAMATSPITATFTGDA--SLNKR 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L GA G P V +P V+ + S+Q SA+L+A
Sbjct: 131 MARVTDPLALFQAQSVGREGGRLPMTIVGAAEPVP---VRYEVPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I++ + + E R++ FG + D+ + R GQ P+ V
Sbjct: 188 APG--KTVVIEREATRDHSE---RMLAGFGAEITVEDTEEGRVITLTGQPELKPQVIAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A +T G+ V V G G + + + L+ MGA +T+ E T G
Sbjct: 243 RDPSSAAFPVCAALVTPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF-ENPRTEGGE 299

Query: 311 PREPFGRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P K+ +K I+V + M D L+VVA FA G T + V RVKE++R+
Sbjct: 300 PVADLRKAYSPDMKGIEVPPERAASMIDEYPVLSVVSFATGTTMMAGVKELRVKESDRI 359

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTAI-DTYDDHRMAMAFS-LAACAEVPV 420
A+ L G +VEEG D+ + PE + +++ DHR+AM+F + A+ PV
Sbjct: 360 DAMAKGLRANGVTVEEGEDWWSVEGCGPEGVKGGGTAEFLDHRIAMSFMVMGMGAQNPV 419

Query: 421 TIRDPGCTRKTFFPDY 435
++ D +FP +
Sbjct: 420 SVDDGSPIATSFPIF 434

>ref|YP_002121647.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenobaculum sp.
Y04AAS1]
gb|ACG57669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hydrogenobaculum sp.
Y04AAS1]
Length = 427

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 122/445 (27%), Positives = 207/445 (46%), Gaps = 38/445 (8%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++++ ++I ++P KS+S+R ++ AL+ GT+ + N L +ED L R LG++
Sbjct: 1 MIIKKVEKIEKELRVPSDKSISHRSVMFGALASGTSYIKNWLVAEDTLATLDIFRKLGIN 60

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + ++ GGK E KE E L N+G R +T+ + A G N VL G
Sbjct: 61 IRRENN---ILEIKGGK---EYFKEPEDILDAKNSGTTAR-ITSGILA-GFNFFSVLTG 111

Query: 126 VPRMRERPIGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+++RP+ + L +GA + P+ + G G L GG + + S+Q S
Sbjct: 112 DESLKKRPMKRVTRPLSLMGATIIGREDASLLPIAIG-GDLIGGSFE-NKEASAQVKSC 169

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAH-SDSWDRFYIKGGQKYKS 244
+L+A LA + E+I+ S + E R++ G S++ IK G +
Sbjct: 170 ILLAGFLAKENTITEVIEPYTSRDHTE---RMLSSMGADINIISNNKHIVIKSGGVL-N 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE-- 302
P N V D SSA++ A A +T + V + D F + +M GA + +
Sbjct: 226 PINIDVPADPSSAAFIALLTKDSYVVLKDVLINPTRDGFRRKAKDM-GANINYINKR 284

Query: 303 -----TSVTVTGPPREPFGKRHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
+ V P +LKA I ++ +P D L+V+ FA+G + ++
Sbjct: 285 HQNGEDIADIEVRYSP-----NLKAISIDEKDVPSLIDEIPILSVLMCFEAGISLVKG 337

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIPTYDDHRMAMAFS- 411
R KE++R+ AI L GA +EE D I P KL + I ++ DHR+AM+ S
Sbjct: 338 AKELRKESDRIRAIYVNLKNAGAIIEEFEDGFSIKGPCKLKLKEIKSFKDHRIAMSMSI 397

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYF 436
L + DP C ++P++F
Sbjct: 398 LGMVLGTEAELDDPECVSISYPNFF 422

>ref|YP_580471.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Psychrobacter
cryohalolentis K5]
gb|ABE74987.1| prephenate dehydrogenase / 3-phosphoshikimate
1-carboxyvinyltransferase [Psychrobacter cryohalolentis
K5]
Length = 780

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 118/457 (25%), Positives = 209/457 (45%), Gaps = 54/457 (11%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P +SGT+ +PG KS+S+R ++L +L+ G T V L ED L A R +G+++E
Sbjct: 332 ITPSNTVSGTIAIPGDKSISHRSIMLGLSLATGVTKVTGFLEGEDALATLQAFRDMGVITIE 391

Query: 69 ADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VG G P + L++GN+G +MR L+ + A ++ VL G
Sbjct: 392 GPDNGNLTIHVGVMNGLKP-----SKTPLYMGNSGTSMRLLSGILAAQAFDS--VLTGDT 444

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG--GLPGGKVKLSGSI--SSQYLS 184
+ +RP+ + L+++GA + P+ + G G P V+ + S+Q S
Sbjct: 445 SLNKRPMERVAAPLREMGAVIQSTGQGTAPLSITGRDSVGKPLQGEYDMPVASAQIKS 504

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LL+A A G ++ P V + T R++ FG + +R ++GG
Sbjct: 505 CLLLAGLWAEAGTTT-----VTQPEVSRDHTERMLSAFGYPV--TVDGNRISVEGGGAL 555

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
N V D SSA++F+ AAI+ G+ +T++ G + + ++L++M A ++ +
Sbjct: 556 TG-GNIAVPADISSAAFFMVA AISQGSELTALKQVGINPTRTGI--IDILKLMQADISLS 612

Query: 302 -ETSVTVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLA-----VVALFADGPTAIRD 352
ET V EP +++ ++ ++P+ + LA + A A G T +
Sbjct: 613 NETHVG-----GEPVADITIRSSNLVGIEIPEYLVPLAIDEFPVLFAASCAQGRVTLTG 667

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVT-----ID 399
RVKE++R+ + L LG D II +N + I
Sbjct: 668 AKELRVKESDRIAVMAEGLQTLGVDCTVTEDGLIIEGKGVVGQSNVNNNSQSVFGGGHIV 727

Query: 400 TYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDY 435
++ DHR+AM+F++A+ A +TI +FP +
Sbjct: 728 SHHDHRIAMSAFVASLRASKQITIEGVETVNTSFPGF 764

>ref|YP_002575765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter lari
RM2100]
gb|ACM64514.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter lari
RM2100]
Length = 428

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 117/438 (26%), Positives = 202/438 (46%), Gaps = 28/438 (6%)

Query: 9 LQPIKEISGTVK-LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+ PI + ++ + KS+S+R + + L++GT + N L ++D + L ++ LG V
Sbjct: 3 ISPIGSTAELEDIASDKSISHRFAIFSLLTQGTCKIKNYLKAQDTLHTLAIQALGAEV 62

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
E V + K P L GN+G AMR L ++A + +VL G
Sbjct: 63 EEIDG---LVYI---KAPKHIKSPNCVLDGNSGTAMRLLIGLLSAI-EDEFFVLSGDC 114

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + L LGA + + P+ + G L G K S S+Q SAL+
Sbjct: 115 YLNARPMKRVSEPLMSLGAKIYGRANANLAPICIQG-AKLDGFNYK-SNIAAQVKSALI 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG---QKYKS 244

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+AA A + + I+ +S + E+ L M G E+ + D+ +IK +K K+
Sbjct: 173 LAALFAKKESYFKEIE--LSRDHSEIILNKM--GACIEYLNE-DKTFIKINPLKEKLKA 226

Query: 245 PKNAYVEGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ V D SSA YF LA + V ++ + ++ ++LE MGAK+++ T
Sbjct: 227 FQ-VCVPNDPSSAFYFALAACILPNSKVVLKNVLLNKTR--IEAFKILEKMGAKISYNIT 283

Query: 304 SVTVTGPPREPFGFRKHLKAIDV--NMNKMVDVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ LKA++V N+ + D LA+ A G + I++ RVKE+
Sbjct: 284 NEDFESIGEICVESAPLKAVNVSENIWLIDEIPALAIAFACAQGKSIKNAKELRVKES 343

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
+R+ +I L K G ++E D + E I ++ DHR+AM+F L +
Sbjct: 344 DRIKSIVLNLQKCGIKIKEFEDGFEVEGGEA-KSAKISFGDHRIAMSF-LILGLRCGME 401

Query: 422 IRDPGCTRKTFPDYFDVL 439
+ D C + +FP++ ++L
Sbjct: 402 VDDSECIKTSFPNFVEIL 419

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>ref|YP_892408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter fetus
subsp. fetus 82-40]
sp|A0RQC5.1|AROAA_CAMFF RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABK82992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter fetus
subsp. fetus 82-40]
Length = 425

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Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 114/402 (28%), Positives = 181/402 (45%), Gaps = 36/402 (8%)

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Query: 20 KLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
K+ KS+S+R + + LS+ + + N L +ED L + LG VE
Sbjct: 16 KVSSDKSISHRAICAFSLSDKVSISKISNYLEAEDTMNSLKIIEKLGAKVEFK----- 66

Query: 80 GCGGKFPVEDAKEEVQ---LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPIG 135
G + + K+ V L GN+G AMR + AG + +VL G + ERP+
Sbjct: 67 --NGVYLITPPKKIVSPNAILECGNSGTAMRIFMGLL--AGCDGFFVLSGDKYLNERPMK 122

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLAL 194
+ L Q+GA +D G DC I G + S+ S+Q +AL++A +
Sbjct: 123 RVASPLMQIGAKID---GRDCANKAPLAIRGGELNYFAYNSSVASAQVK TALILAGLCSA 179

Query: 195 GDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQ-KYKSPKNAYVEGD 253
G + + +S + E L G+ A+ S S +K + Y P V D
Sbjct: 180 G---CKFKEPELSRDHSERML-----LGMGAQISQSGLEIEVKPLKGAYLKLPLILDVPND 231

Query: 254 ASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SS ++ +A A I G + ++ + ++ +VLE MGAK+T+T+TS T
Sbjct: 232 PSSCFFYAVAAAIIPGSKIIKNILLNKTR--IEAYKVKLEKMGAKITYTKTSSTYEDIGD 289

Query: 313 EPFGRKHLKAIDVNMNK--MPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
LK++DVN N + D A LA+ A+G + +++ RVKE +R+
Sbjct: 290 ICVQYSELKSVQVNVQNISWLIDEAPALAIAFACANGVSTLKNKELRVKECDRIAITVAA 349

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSL 412
L K G E D I K N ID++ DHR+AM+F++
Sbjct: 350 LKKCGIEAVELEDGFSIKGG-KPNSATIDSHGDHRIAMSF 390

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>ref|YP_031813.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella quintana
str. Toulouse]
sp|Q6G0X3.1|AROAA_BARQU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAF25595.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella quintana
str. Toulouse]
Length = 442

```

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.

Identities = 118/450 (26%), Positives = 204/450 (45%), Gaps = 49/450 (10%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +K+PG KS+S+R L+L L+ G T + LL S+DV A++ +G + K A
Sbjct: 15  LSGKIKIPGDKSISHRSLILGGLANGETHIHGLESDDVLNTAAAMQAMGACI--IKKAD 72

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R ++ G G + K L GNAG R + V T++ D + +RP+
Sbjct: 73  RWIIRGTGNGCLLAAEKP---LNFNGAGTGARLVMGMVGPYHMKTTFIGDA--SLSKRPM 127

Query: 135  GDLVVGLKQLGADVDCFLGTDGP-----PVRVNGIGGLPGGKVKLSGSISSQYLS 184
G ++ L+ +G +++ G P P+R ++ ++ S+Q S
Sbjct: 128  GRILNPLRLMGVEIEATHGDRPLTLTYGPKMANPIRY-----RIPIA---SAQVKS 175

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKY 242
A+L+A G +I+ +++ + E ++++ FG + E + RF GQ +
Sbjct: 176  AILLAGLNTAGTT--TVIEPILTRDHTTE--KMLKAFGAELEIKTDAEGTRFIHLNGQPH 230

Query: 243  KSPKNAYVEGDASSASY-FLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + ++ GD SSA++ +A + +T+E + + E L M AK+
Sbjct: 231  LTGQTIHIPGDPSSAAFPPIAALLVENS DITIENVLIN--KSRMGLIETLWEMDAKIELL 288

Query: 302  ETSVTVTGPPREPFGGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASW 356
T G K LK + V + P D LAV A FA+G T + +
Sbjct: 289  NQHKT--GGENVADLRVKSSMLKGVTVPKERAPSMIDEYPALAVAAFAEGKTVMLGIDEL 347

Query: 357  RVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVT AIDTYDDHRMAMAFSL- 412
RVKE++R+ A+ L EEG D+ I+ + + L + T+ DHR+AM+F +
Sbjct: 348  RVKESDRLSALAQGLKINHVDCEEGKDFLIVHGKSSAKGLGGGHVTHLDHRIAMSFLIF 407

Query: 413  AACAEVPTTIRDPGCTRKTFPDYFDVLSTF 442
+E PVTI D +FP++ +
Sbjct: 408  GLVSEKPVTTIDDKRMIATSFPEFIPFIQQL 437
```

```
>ref|ZP_01039983.1| 5-enolpyruvylshikimate-3-phosphate synthase [Erythrobacter sp.
NAP1]
gb|EAQ30454.1| 5-enolpyruvylshikimate-3-phosphate synthase [Erythrobacter sp.
NAP1]
Length = 438
```

Score = 105 bits (263), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 132/445 (29%), Positives = 205/445 (46%), Gaps = 39/445 (8%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS-VEADKAA 73
+ G +++PG KS+S+R L+ A L+ G + + LL EDV A+R LG V D
Sbjct: 12  LKGRLRVPGDKSISHRALMFAGLAVGESRIAGLLEGEVDVLATAAAMRQLGARIVREDDGT 71

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R G G + L +GN+G + R + + + G AT++ D + RP
Sbjct: 72  WRVNGAGLGLSI-----EPRAALDMNGSGTSTRLMMGLLASHGLTATFIGDA--SLSGRP 124

Query: 134  IGDVLVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+ ++ L Q+GA + G P + G P V + S+Q SA+L+A
Sbjct: 125  MNRVIEPLSQMGASFEASAGGTLPCMLR---GASPAVPVTYRLPVASQVKSALLAGLN 181

Query: 193  ALGDVEIEIIDKLIS-IPYVEMTLRLMERFGVKAHS-DSWDRFYIKGGQKYKSPKNAYV 250
G I ++I I + T R++ FG E S ++ +R G+ P + V
Sbjct: 182  TPG-----ITRVIEPIATRDHTERMRLRGFGANLEVSEENGERVIAIHGEADLKPM DVTV 235

Query: 251  EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++FL A+I G+ + VE G + + VL+ MGA + + V G
Sbjct: 236  PGDPSSAAFFLVAASIVPGSDLVVENVGLNPTRAGI--VTVLKQMGADIKELDPR-EVGG 292

Query: 310  PPREPFGGRKH--LKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P +H LK I+V+ + M D L V A A+G T + RVKE++R+
Sbjct: 293  EPVADLRVRHAPLKGIEVDPAIVPSMVDEFVLFVAAAMAEGTTTTTGLEELRVKESDRI 352

Query: 365  VAIRTELTKLGASVEEGPDYCI--TPPEKLNVT A---IDTYDDHRMAMAFSLAACAE-- 417
+ LT GA VEE D I T E L T+ + T+ DHR+AM+ ++A A
Sbjct: 353  SVMAAALTAAGARVEEHEDGLTIHGTGGEPLRGTSNARVKTHLDHRIAMSMAGVAGLASRD 412
```

Query: 418 -VPVTIRDPGCTRKTFPDYFDVLST 441
V + DP T +FP + +L +
Sbjct: 413 GVEIDDDPIAT--SFPTFMQMLLES 435

>ref|YP_379927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
chlorochromatii Cd3]
sp|Q3AQ41.1|AROA_CHLCH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB28884.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
chlorochromatii Cd3]
Length = 435

Score = 105 bits (262), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 119/443 (26%), Positives = 205/443 (46%), Gaps = 49/443 (11%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-----AK 74
LP KS+S+R ++AALSEGTT + N D LG LR G+ V+ ++
Sbjct: 11 LPPDKSISHRAAMIAALSEGTEITNFSAGFDNQSTLGVLRNAGIVVQQEEVQGAHGRTM 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + +Q N+G MR ++ + A T + D + +RP+
Sbjct: 71 RRVVITSNGLWSFTPTAPLQ--CNNSGSTMRRMSGILAAQPFQCTLIGDA--SLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTD-CPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L+Q+GA ++ L D P+ ++G L + +L + S+Q S + AA A
Sbjct: 127 KRVADPLRQMGATIE--LSPDGTAPIHISGTELRSLEYRLPVA-SAQVKSIAFAALHA 183

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G E II+ L S + E+ L L E K E R + GQ+ + K ++ D
Sbjct: 184 EG--ETRIIEPLQSRDHTEVMLGL-ETIVKKDE-----RIIVVPGQRIAAKPFIPAD 234

Query: 254 ASSASYFLAGAAITGGT--VTVEGC-----GTTSLQGDVKF---AEVLEMMGAKVTWTE 302
S+A + +A + G+ V + C L + K + ++G ++
Sbjct: 235 PSAACFIIALGLLARGEIVIRDVCLNPTRAAYLDLLAEAKAGIGVDNQVRIGGEIIGDI 294

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ G EP + + ++++P LAV++ FA G + + A R KE++
Sbjct: 295 LIDNLNG--IEPLHISDPQLVAFIIDEIP---MLAVLSAFATGSFELHNAELRTKESD 348

Query: 363 RMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAFSLAACAE 417
R+ A+ L +LG + E+ PD ++ P K+ I+++DDHR+AM+F++AA A
Sbjct: 349 RIEALVNLQRLGFACEQYPDGFVVKRTEVPQGVKT---IESFDDHRIAMSFAIAAQAT 405

Query: 418 -VPVTIRDPGCTRKTFPDYFDVL 439
+ I D +FP++F +L
Sbjct: 406 GEALDISDIEVGVSPNFFSLL 428

>ref|NP_782223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium tetani
E88]
sp|Q894D2.1|AROA_CLOTE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAO36160.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium tetani
E88]
Length = 439

Score = 105 bits (262), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 121/445 (27%), Positives = 201/445 (45%), Gaps = 41/445 (9%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+ T +LPG KS+ +R LL+ AL +G + N S D L + LG+ V K
Sbjct: 20 EVKKTYPGLPGKSVGHRSLLLIGALPKGEYKIRNFPQSRDCLTTLKIMEELGVKV---KVL 76

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K ++V G E+ K+++ GN+G R L A + A G T ++ G + R
Sbjct: 77 KDYILVNSPG---YENFKKKIDYIDCGNSGTTSR-LIAGILAGVGVETNLV-GDKSLSIR 131

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ +V L +GA+++ + D P+ G G L G + + S+Q S +L+A L
Sbjct: 132 PMKRIVDPLNSMGANIE--MEKDHMPLIFKGNELKGIDYTMEIA-SAQVKSCILLAGFL 188

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERF--GVKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
+ G ++ + P + T R+++ +K E+ + I+ K+ YV
Sbjct: 189 SEGVTKVRELS-----PTRDHTERMLKYIEGNIKIENKE-----IEIENSTIKSKDIYV 237

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD SSA+Y +A AI G + + K+ ++L+ MGA + + E + G
Sbjct: 238 PGDISSAAYIIA-CAILGEDCEIILENVLLNENRRKYLDLLKKMGANLKYLEKN-QCNG- 294

Query: 311 PREPFGF-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
E G LK I + P D ++++A FA+G T +V + KE++
Sbjct: 295 --EHVGNILVKSSFLKGISIGKEITPYIIDEIPIISLIASFAEGKTIFENVEELKYKESD 352

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPP-EKLNVT-AIDTYDDHRMAMAFSLAACAEVPV 420
R+ AI L LG E + II K+N I T++DHR+A+ F +A
Sbjct: 353 RIKAIMVNLKSLGVKTELVENNLIIYGGLSKINKEINIRTFNDHRIALTFLCSAMRNSEK 412

Query: 421 T-IRDPGCTRKTFPDYFDVLSTFVK 444
T I + C +FP+ + F +
Sbjct: 413 TYIDNWDCAISFPNSLNYFKDFFR 437

>ref|ZP_06440909.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerobaculum
hydrogeniformans ATCC BAA-1850]
gb|EFD23875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerobaculum
hydrogeniformans ATCC BAA-1850]
Length = 437

Score = 105 bits (262), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 126/455 (27%), Positives = 203/455 (44%), Gaps = 50/455 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLS 66
I ++P + I G +K+PG KS+S+R LL +LS V+N ED L LRT+G
Sbjct: 2 IEIRPQEGIVGEIKVPKDKSISHRAALLGSLSGREGIEVENFSPGEDCASTLSCLRTMGCE 61

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V D + + V G D L GN+G R + ++ N V+ G
Sbjct: 62 VNRDAVSGKVSVPKAPDGLKEPSDV-----LDAGNSGTTARLILGLISGIP-NIFAVITGD 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
++ RP+G + L +GA +D + P+ V G L GG L + S+Q +A+
Sbjct: 116 ESLKRRPMGRVAKPLVVMGAKIDGREGFKELPLAVRG-RKLTGGVHTLQVA-SAQVKTAI 173

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPK 246
L A A G + I+ ++ + E+ ++E G+ + KG + P
Sbjct: 174 LFAGLRAQGATTV--IEPTLTRDHTEI---MLEHLGIP-----IFRKLKVTVPYPA 219

Query: 247 NAY-----VEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMM 294
+ + GD S+A++++ AAIT + V V T L+ VL+ M
Sbjct: 220 STLKGASWTIPGDFSAAAFWIVAAATEKSELQIKKVNVPNTRTGLLR-----VLQRM 272

Query: 295 GAKVTWTETSVTVTGPFR-----EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPT 348
G + + ++G R K K + + M D LAV A A+G T
Sbjct: 273 G--LDYNIIEDEILSGGERMATITVRSSSLKGTVMPEEIPSMIDELPVLAVAATQAEGTT 330

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAM 408
IRD RVKE++R+ A+ L ++GA +EE D II KL+ + ++ DHR+AM
Sbjct: 331 EIRDAGELRVKESDRIHAMTEGLKRMGAQIEELQDGIWIKGKTKLSGARLKSFGDHRIAM 390

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
A ++A A+ V + C ++P +F+ L
Sbjct: 391 ALTVAGLAADDSVILEGESCVHISYPSFFEDLKAL 425

>ref|NP_711439.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
interrogans serovar Lai str. 56601]
sp|Q8F6P5.1|AROAL_EPIN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
gb|AAN48457.1|AE011307_10 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospira
interrogans serovar Lai str. 56601]
Length = 440

Score = 105 bits (262), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 121/455 (26%), Positives = 202/455 (44%), Gaps = 53/455 (11%)

Query: 16 SGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
S +++PG KSLs+R +L AALS+G + V L +ED + A LGL V+ K +
Sbjct: 10 SREIEVPGDKSLSHRSVLFAALSKGSKSVTGFLEADPLNTMSAFAKLGLKVQKVKPGEY 69

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA--GGNATYVLDGVPRMRERP 133
K V L GNAG +R L+A + G NAT L G +++RP
Sbjct: 70 EFESPGKNKL----VSPNVLDLDFGNAGTGIR-LSAGLICGLPGINAT--LTGDNLSLKKRP 122

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G ++ L +GA + + P+++ G L G + I+S + + LM A ++
Sbjct: 123 MGRIIKPLSSMGASIVGLGEKETAPLKIEG-KKLKG--FRYESPIASAQVKSCLMLAAIS 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----GGQKYKSPKNA 248
+ ++E + ++S + E R + G K E F IK G +++ P
Sbjct: 180 -SETDLEYSENILSRDHTENMFRFL--GNKIEQISPL-HFKIKPPYVLNGGEFRVP--- 231

Query: 249 YVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV-- 305
GD SSA++FL G G + ++ G + + A L+ MGAK+ +
Sbjct: 232 ---GDISAFAFLVLGLVLAKEGNLLIKNIGLNPARTGILTA--LQSMGAKIEIQNKRIEC 286

Query: 306 --TVTGPPEPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
TV P +LK ++ + +P D L+V FA+G IR R KE
Sbjct: 287 GETVGLDKTYP---SNLKKSNIPELSIPSIIDEIPILSVAGFFAEGGFEIRHAEELRAKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPD-YCIITPPEK-----LNVTAIDTYDDHRMAMA 409
++R+ + + +LG VEE D Y +K + I +Y DHR+AM+
Sbjct: 344 SDRIHTMVSNFRELGIEVEEYTDGYSFDGTSKKSSEVWTRLSTVKKIPIQSYMDHRIAMS 403

Query: 410 FSL-AACAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
F + + + + I + +FP + +L + +
Sbjct: 404 FLIFKTLGLDLQIDETSWIETSFPGFEKLLESCI 438

>ref|ZP_06924309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ATCC 51811]
gb|EFH26350.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ATCC 51811]
Length = 435

Score = 105 bits (262), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 118/448 (26%), Positives = 209/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
E+V + I +ISG +K +PG Ks+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62

Query: 62 TLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D ++ VV G + + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVEIKEDD--EKLVTSPG--YQSFNTPHQV-LYTGNSGTTRLLAGLLSGLGIES-- 115

Query: 122 VLDGVPRMRERPIGDVLVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI +++++
Sbjct: 116 VLSGDVSIGKRPMRDVLRPLKMDANIEGIEDNYTPLIIKPSVIKGI----NYQMEVA-- 169

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L +E II +L +S + E + + F + E ++
Sbjct: 170 -SAQVKSAILFA---SLFSMEPTIIKELDVSRNHTe---TMFKHFNIPIE-AEGLSINTT 221

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG
Sbjct: 222 PEAIRYIKPADFHVPGDISAFAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGGRKH---LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTA 349

```

      +      T      P      ++      L+ I +      +P      L V+AL      A G +
Sbjct: 280 GNIQLFNQ--TTGAAPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTST 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
      I+D      +VKET R+      L LG ++      D II P E      +D+ DHR+ M
Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
      ++A+ + PV I+      +FP +
Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

```

>ref|ZP_05388284.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria monocytogenes FSL J1-175]
Length = 358

Score = 105 bits (262), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 106/369 (28%), Positives = 189/369 (51%), Gaps = 31/369 (8%)

```

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
      G + +PG KS+S+R ++      A++EG TV+ + L ++D      + A + LG V+ ++ +
Sbjct: 12 GAITVPQDKSMHSRISIMFGAIAEGKTVIRHFLRADDCLGTIKAFKALG--VKIEETEEIEI 69

Query: 77 VVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
      +V G G      + K+ + L +GN+G +R +      + AG + V+ G      + +RP+
Sbjct: 70 IVHGTG----FDGLKQADGPLDIGNSGTTIRLMMGIL--AGRDFDTVILGDESIAKRPMN 123

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
      +++ L+Q+GA +      G++ P+ +NG L + + + S+Q SA++ AA A G
Sbjct: 124 RVMLPLQMQGAKMHGKDGSEFAPITINGKQSLKRMEYHMPVA-SAQVKSALIFAALQAEG 182

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
      + I      +K      + T ++ +FG + E      R +KGGQ + + + V GD S
Sbjct: 183 ETIIHEKEK-----TRDHTHEMIRQFGGEIEMDGLTIR--VKGGQTF-TGQEMTVPGDVS 234

Query: 256 SASYFLAGAAITGGT---VTVEGCGTSTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      SA++F+      IT G+      +T G T      +V+E MG +      ++S + TG
Sbjct: 235 SAAFFIVAGLITPGSEIELTHVGLNPTR---TGIFDVVEQMGGSLLVVKDSRS-TGKLA 289

Query: 313 EPFGRK--HLKAIDVNMNKMMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVAI 367
      K      LK ++      + +P +      + V+AL      A+G T I+D A +VKET R+ A+
Sbjct: 290 GTVVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTIIKDAEELKVKETNRIDAV 349

Query: 368 RTELTKLGA 376
      TEL K+GA
Sbjct: 350 ATELNMGA 358

```

>ref|ZP_07841013.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus caprae C87]
gb|EFS17555.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus caprae C87]
Length = 433

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 111/431 (25%), Positives = 196/431 (45%), Gaps = 30/431 (6%)

```

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G +++PG KS+++R ++LA+L+ G T +      L ED      +      LG+ +      +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLATGQTTIYKPLLGEDCRRTMEIFELLGVKI---TEHE 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      +++ G      + K Q L+ GN+G      R L ++      G + +L G      + +RP
Sbjct: 70 ETIIIDSPG---YQFKTPHQVLYTGNSGTTTLLAGLLSGLGIES--ILSGDVSIGKRP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      + ++ L Q+ A +      G P +      I + G + ++      + S+Q SA+L A+ +
Sbjct: 125 MDRVLPKLLQMNHISGIEGNYTPLIIKPSI--IKGIEYQMEVA-SAQVKSAILFASIFS 181

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
      + ID +S + E      + E F + E      R      Q K+ ++ +V GD

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Sbjct: 182 EEATTVTEDID--VSRNHTE---TMFEHFNIPIEIEGKTIRTSPHAIQHIKA-QDFHVP GD 235

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A IT G+ +T+ G + + +++E+MG + +VT P

Sbjct: 236 ISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVELMGGNIELN--NVTHDAEPT 291

Query: 313 EPFGRKH--LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVA 366
K+ LK I + + +P L VVAL A G I+D +VKET R+

Sbjct: 292 ASIRVKYTPTLKPITIEGDIVPKAIDELPVVALLCTQASGTCIIKDAEELKVKETNRIDT 351

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDP 425
L LG S++ D II P E +D+ DHR+ M ++A+ + P+TI

Sbjct: 352 TADMLNMLGFSLQPTNDGLIHPSEFKASATVDSQTDHRIGMMLAVASLLSSEPLTIEQF 411

Query: 426 GCTRKTFFPDYF 436
+FP +

Sbjct: 412 DAVNVSFPGFL 422

>ref|YP_002761302.1| 3-phosphoshikimate 1-carboxyvinyltransferase/cytidylate kinase
[Gemmatimonas aurantiaca T-27]
dbj|BAH38832.1| 3-phosphoshikimate 1-carboxyvinyltransferase/cytidylate kinase
[Gemmatimonas aurantiaca T-27]
Length = 672

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 127/444 (28%), Positives = 198/444 (44%), Gaps = 38/444 (8%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++GT++ PG KS+S+R L+ AAL++G T V ++L S DVH ALR +G+S+ + +

Sbjct: 8 HVAGTIRAPGDKSISHRALIFAALADGETVRDILASADVHATASALRAMGV SIP--ELS 65

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
VV G G A+ N+G R L + G + +G + RP

Sbjct: 66 TDFVVRGHGIAALTSPAR---AFDCANS GTTTRLLCGLLAGLPGRSAR-FEGDASLSRRP 121

Query: 134 IGDVLVGLKQLGADVDC--FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ + L +GA +D G D P+RV+ G G +S S+Q ALL+A

Sbjct: 122 MRRVASPLASMGAHIDFEGAPGHDGLPMRVH--GAQLRGNTNYVSAHASAQVKGALLLAG- 178

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G VE+ + + S + E R++ GV E S+ R + Q+ +

Sbjct: 179 LASG-VEVVVEPYRSRDHSE---RMLLARGVALEVSERSVR--LPAAQQVTAADVVP 232

Query: 252 GDASSASYFLAGAAITGGT VTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSV----- 305
+S+ + A G + +E C + G +VL+ MG + +E +

Sbjct: 233 DPSSATFFAALAALADSGELRLNENCLNPTRTGAF---DVLQRMGVSLDVSEQRLVG GEL 289

Query: 306 --TVTGPPEPFGFRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
T+ P + L + ++P D LA +A A G T I D A RVKE

Sbjct: 290 IGTIVVRP-----EALNGTTIEGAIEPRCIDELPMLACLASQAAGETRIADAAELRVKE 343

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS-LAACAEVP 419
++R+ A+ L LG EE PD I + T+ DHR+AMAF L A

Sbjct: 344 SDRIRAVVDNLR TLGVDAEELPDGMRIIGSRTPLRGHVITHGDHRLAMAFVGLGAIPGNQ 403

Query: 420 VTIRDPGCTRKTFFPDYFDVLSTFV 443
+TI DP C ++P ++ L+ V

Sbjct: 404 ITIDDPACVDVSYPRFWQDLAAAV 427

>ref|ZP_01746715.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sagittula stellata
E-37]
gb|EBA07679.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sagittula stellata
E-37]
Length = 438

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 122/435 (28%), Positives = 198/435 (45%), Gaps = 33/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

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++G  +PG KS+S+R L+L A++ G T V LL  +DV    A+R  G  +E
Sbjct: 9  LTGEAHVPGDKSISHRSLILGAMTVGETKVTGLLEGQDVLDTAKAMRAFGAQIEKIGETW 68

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
          VG GG    E+  +      GN+G ++R  +  +  +  AT+  D  +  +RP+
Sbjct: 69  HVHGVGVGGFLEPENVID-----CGNSGTSVRLIMGMTATSPIVATFTGDA--SLNKRPM 121

Query: 135  GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLA 193
          +  L  GA          P  V      +P  V+  +  +  S+Q  SA+L+A  A
Sbjct: 122  ARVTDPLTLFGARAYGRSSGRLPMTIVGAKEPMP---VRYATPVPSAQVKSAVLLAGLNA 178

Query: 194  LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
          G  E  +I++  +  +  E  R++  FG      D+  +  R      G+      P++  V
Sbjct: 179  PG--ETVVIERESTRDHTE---RMLAGFGASISTEDTKEGRVITLQGRPEFVPQDIVVPR 233

Query: 253  DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
          D  SSA++  +  A  I  G+  V  V  G  +  +  FA  L+  MGA  +T+  E      G  P
Sbjct: 234  DPSSAAFPVCAALIVEGSDVLPNIGLNPTRAGLFFA--LQEMGANLTF-ENMREAGGEP 290

Query: 312  ----REFPGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
          R  F      +K  I+V  +  M  D      L+VVA  FA  G  T  +  V      RVKE++R+
Sbjct: 291  VADLRAKFS-PDMKGIEVPAERAATMIDEYPVLSVVAFAAQKTHMPGVKELRVKESDRI 349

Query: 365  VAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACA-EVPV 420
          A+  L  G  V+EG  D+  +      +V      ++T+  DHR+AM+F  +  A  P+
Sbjct: 350  DAMARGLRAAGVQVDEGEDWTVHGRGFGDVAGGATVETFLDHRISFLVMGLATNAPM 409

Query: 421  TIRDPGCTRKTFPDY 435
          ++  D      +FP  +
Sbjct: 410  SVDDGQPIATSFPIF 424

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>ref|YP_002908539.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia glumae
BGR1]
gb|ACR31304.1| 5-enolpyruvylshikimate-3-phosphate synthase [Burkholderia glumae
BGR1]
Length = 451

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Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 178/377 (47%), Gaps = 26/377 (6%)

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Query: 9  LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSV- 67
          +  P  +  +  +P  SK  +  R  ++  A+L+  G  +  +  N  L  +  M  A  R  LG  +
Sbjct: 5  VNPASHLKPVMSPASKPETQRAIVTASLATGRSRIHNDLRCLETDTMKAACRQLGARIS 64

Query: 68  EADKAAKRAVVVGCGGKFP----VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
          E  D  +  V  G  GG+F      V  DAK      +G+  R+L+A  +T  +  T  +L
Sbjct: 65  EHDGFLE---VDGVGGQFTHDTLVIDAK-----GSGLVFRTLSA-ITCMRRSPT-IL 111

Query: 124  DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
          G  +R  R  +  L  L  LGA++      PV  +N  +      +L  G  +SSQ++
Sbjct: 112  TGDHTLRRRVMKPLFDALGSLGANLQHLGDAGKAPV-INWQQRISRTHAELPGDVSSQFV 170

Query: 184  SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
          +ALL+  APL+  +  +  +  ++S  Y+  T+  +  R  +  E  +  +  F  ++  G+
Sbjct: 171  TALLLLAPLSDQPITLRQREPVLKSYIAQTVDFLRRASIDIEVDERFSHFAVRPGEYVA 230

Query: 244  SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
          ++  +  D  +S  SY  L  A+  G  +  G  +  +LQG+  F  +V++  +G  KV  +
Sbjct: 231  F--DSRINADYTSLSYLLFACAVFPGEYVIRGITSDTLQGEQIFIDVVQALGVKVMHDDA 288

Query: 304  SVT-VTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          +  +      H  +V+++  P++  TL  ++LF  +G  +  +  R+  ++
Sbjct: 289  AQELLVSSVHARLSGSH---EVDVSDGPNIPTLVALSLFVEGEFRVVGGSVTRLHKSS 344

Query: 363  RMVAIRTELTKLGASVE 379
          R+  ++  TE  KLGA  ++
Sbjct: 345  RIESMVTEAAKLADIK 361

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>ref|ZP_05811043.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium

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opportunism WSM2075]
gb|EEW32753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium
opportunism WSM2075]
Length = 452

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 120/454 (26%), Positives = 195/454 (42%), Gaps = 56/454 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT ++PG KS+S+R + L+ G T + LL EDV A++ +G +E K
Sbjct: 18 LSGTARVPGDKSISHRSFMFGGLASGETRITGLLEGEDVMRTGAAMKAMGAHIE--KRG 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ G G ++ E L GNAG R V T++ D + RP+
Sbjct: 76 EWVIRGTGNGALLQ---PEGPLDFGNAGTGSRLTMGLVGTYDMETTFIGDA--SLSGRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+Q+G V D P+ ++G P ++ + S+Q SA+L+A
Sbjct: 131 GRVLEPLRQMGVQVLKATPGDRMPITLHG---PKHAAPITYRVPMASAQVKSALLAGL 186

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQYKSPKNAY 249
G +I+ +++ + E +++ FG + E + R GQ +
Sbjct: 187 NTPGIT--TVIEPVMTRDHE---KMLKGFANLSVETDERGVRHIFIEGQKGLHGQTIA 241

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA + L A I G+ +T+E + + L+ MG +
Sbjct: 242 VPGDPSSAGFPFLVAALIVPGSDITIEVLMNPTRTGLLL--TLQEMGGNIEILN----- 293

Query: 309 GPPREPFGFR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASW 356
PR G LK + V + P D LAV A FA+G T ++ +
Sbjct: 294 --PRNAGGEDVADLRVRYSELKGVTVPPERAPSMIDEYPVLAVAASFAEGETLMQGLEEL 351

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDTYDDHRM 406
RVKE++R+ A+ L G EG + P L+ T + T+ DHR+
Sbjct: 352 RVKESDRLSAVANGLKLNVDCTEGEASLAVRGKPGGKGLGHPNGLDTT-VQTHLDHRI 410

Query: 407 AMAFSLAACA-EVPVTIRDPGCTRKTFFPDYFDVL 439
AM+F + A E PVTI D +FP++ ++
Sbjct: 411 AMSFLVMGLATEKPVTTIDQAMISTSFPEFMGLM 444

>ref|ZP_01880117.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseovarius sp.
TM1035]
gb|EDM31728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseovarius sp.
TM1035]
Length = 439

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 132/443 (29%), Positives = 200/443 (45%), Gaps = 34/443 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +PG KS+S+R L+L ALS G TV+ LL EDV A+R G V D A
Sbjct: 9 LSGVADVPGDKSISHRSILGALSGETVITGLLEGEDVLDATAMRAFGAEVTRDAAGV 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V VG GG A+ + GN+G +R + A+ + AT+ D + +RP
Sbjct: 69 WHVHGVGVGGF-----AEPGHVIDCGNSGTGVRILMGAMATSPITATFTGDA--SLNKR 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L GA G P V + + S+Q SA+L+A A
Sbjct: 122 MARVTDPLALFQAQAVGRSGRLPMTIVGAEPV--PVRYVVPVPSAQVKSALLAGLNA 179

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQYKSPKNAYVE 251
G + +I++ + + E R++ FG + E +D R GQ + V
Sbjct: 180 PG--QTVVIEREATRDHE---RMLVGFAGAEITTEETDE-GRVITLTGQPELRAQTIVVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V V G + + FA + E MGA +++ E G
Sbjct: 234 RDPSSAAFPVCAALIVPGSDVLPNIGLNPTRAGL-FATLRE-MGADLSY-ENLREEGGE 290

Query: 311 P----REPFGGRKHLKAIDVNMN---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363

P R F LK I+V + M D L+VVA +A G T +R V RVKE++R
Sbjct: 291 PVADLRARF-SPDLKGIEVPPERAASMIDEYPVLSVVAAYATGETVMRGVKELRVKESDR 349
Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDT---YDDHRMAMAFSLAACAEV-P 419
+ A+ L G VE+GPD+ I+ +V T + DHR+AM+F + A P
Sbjct: 350 IEAMAAGLRAGGVEVEDGPDWWIVQGRGHGVPGGQTCASHLDHRIAMSFLVMGMASTAP 409
Query: 420 VTIRDPGCTRKTFPDYFDVLSTF 442
V + D +FP + +++
Sbjct: 410 VQVDDASPIATSFPIFESLMAQL 432

>ref|ZP_05342087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thalassiosira sp.
R2A62]
gb|EET47754.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thalassiosira sp.
R2A62]
Length = 496

Score = 105 bits (261), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 130/436 (29%), Positives = 198/436 (45%), Gaps = 34/436 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT +PG KS+S+R L+L A+S G T + LL EDV A+R G V +
Sbjct: 66 LNGTADVPKDKSISHRSLILGAMSVGETRITGLLEGEDVLDTGAMRAFGAEVTDHGGGE 125
Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRERP 133
+V VG GG A+ E + GN+G +R + ++ + AT+ D + RP
Sbjct: 126 WSVHGVGVGGF-----AEPENVIDCGNSGTGVRLIMGSMATSPITATFTGDA--SLNGRP 178
Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G + L G P V + + S+Q SA+L+A A
Sbjct: 179 MGRVTDPLALFGTQAVGRKQGRPLPMTLVGAADPV--PVRYVVPVPSAQVKSALLLAGLNA 236
Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G + +I+K + + E R++ FG + E +D R GQ P+ V
Sbjct: 237 PG--KTVVIEKEATRDETE---RMLAGFGAEITVEETDE-GRVITLTGQPELKPQTIIVP 290
Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A IT G+ V V G + + F L+ MGA +T+ E +G
Sbjct: 291 RDPSSAAPPVCAAVITPGSDVLVNPTRAGLFF--TLQDMGADLTF-ENMREESGE 347
Query: 311 P---REPFGKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F LK I+V + M D L+VVA FA+G T + V RVKE++R
Sbjct: 348 PVADLRARF-SPDLKGIEVPAERAASMIDEYPVLSVVASFAEGKTHMPGVKELRVKESDR 406
Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD---DHRMAMAFS-LAACAEVP 419
+ A+ L G +V+EG D+ + NV +T DHR+AM+F + A P
Sbjct: 407 IDAMAGLRLNGVTVDGDDWTVHGLGHGNVPGGETCASQLDHRISFVMVMGMAANAP 466
Query: 420 VTIRDPGCTRKTFPDY 435
V+I D +FP +
Sbjct: 467 VSIDGQPIATSFPIF 482

>gb|EEZ80251.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured SUP05
cluster bacterium]
Length = 434

Score = 104 bits (260), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 110/436 (25%), Positives = 204/436 (46%), Gaps = 35/436 (8%)

Query: 17 GTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +K+PG KS+S+R ++L +L+ G T V L ED L + +G+ +E +
Sbjct: 14 GNIKVPKDKSISHRSIMLGLSLANGITKVTGFLEGEDALSTLKTQAMGVKIEREGDNVTI 73
Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRERPIGD 136
VG G K + L LGN+G +MR ++ + A + V G + +RP+G
Sbjct: 74 YGVGINGL-----KKPKPLDLGNSGTSMLMSGILAAQAFDCELV--GDESLSKRPMGR 126
Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
++ L +GA +D G PP+++ G L G L + S+Q S +L+A A G

Sbjct: 127 VINPLTAMGAVIDSNDGK--PPLKITGGQSLKGDYDLPVA-SAQVKSCVLLAGLYAKGK 183

Query: 197 VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
+ P + T R+++ G + +D ++ + GG + + + V D SS

Sbjct: 184 TCVT-----EPAPTRDHTERMLKGLGYEVRVND--NQMCLTGGGEL-TATDIQVPSDISS 235

Query: 257 ASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFP 315
+++F+ A I +T+ G + V ++L++MGA +T + + G E

Sbjct: 236 SAFFMVAACIAPQADITLTGVNINPRTGTG--IDILKLMGANLTLS-NECEIGG---ELL 289

Query: 316 GRKHLKAIDVNMNMKMPDVAMTLA-----VVALFADGPTAIRDVASWRVKETERMVAI 367
+++ ++ ++P+ + LA + A A G T + RVKE++R+ +

Sbjct: 290 ADIRIQSSELKGIQIPEALVPLAIDEFFPAVFIAASCAQGETILTGAKELRVKESDRIQVM 349

Query: 368 RTELTKLGSVEEGPDYCIITPPEKLNVTI-IDTYDDHRMAMAFSLAAC-AEVPVTIRDP 425
L+ LG E D I TA I+++ DHR++M+F++A+ + P+ I

Sbjct: 350 ADGLSILGIENEVELDGIKIQQGVFKKPTAMIESHHDHRISMSFAVASLRCDYPIEINGV 409

Query: 426 GCTRKTFFPDYFDVLST 441
+FP++ D+ ++

Sbjct: 410 DNVMTSFPNFVDLANS 425

>ref|YP_001532365.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dinoroseobacter shibae DFL 12]
sp|A8LSF0.1|AROA_DINSH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV92764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dinoroseobacter shibae DFL 12]
Length = 450

Score = 104 bits (260), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 127/449 (28%), Positives = 200/449 (44%), Gaps = 36/449 (8%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P +SGT ++PG KS+S+R L+L AL+ G T V LL +DV A++ G V

Sbjct: 13 HPSGPLSGTAQVPGDKSISHRSLILGALAVGETKVTGLLEGQDVLDTARAMQAFGAEEVIQ 72

Query: 70 DKAACKRAVV-VGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+V VG GG ED + GN+G +R + A+ AT+ D

Sbjct: 73 HAPGAWSVHGVGTGGFAEPEDVID-----CGNSGTGVRLIMGAMATTPITATFTGDA--S 125

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALL 187
+R RP+G + L G G P +P V+ + + S+Q SA+L

Sbjct: 126 LRSRPMGRITDPLAGFGTTAVGRRGRLPMTLTGAADPVP---VRYTVPVPSAQVKSAVL 182

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G + +I+ + + E R++ FG + E + + + GQ P

Sbjct: 183 LAGLNAPG--QTVVIEAEATRDSHSE---RMLRGFGAEISVESAEPEGNVITLT-GQPELRP 236

Query: 246 KNAYVEGDASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V D SSA++ +A G + G V V G G + L+ MGA++++ E

Sbjct: 237 QTIVVPRDPSSAAPPVAVGLIVPGSDVLVPGIGLNPTR--AGLYTTLQEMGAELSF-ENM 293

Query: 305 VTVTGPP---REPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
G P R F ++ I+V + P D L+V+A +A G T +R V R

Sbjct: 294 REEGGEPVADLRARF-SDAMQGIIEVPPERAPSMIDEYPILSVIAAYATGRTVMRGVKELR 352

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADT---YDDHRMAMAF-SLA 413
VKE++R+ A+ L G VEE D I+ V T + DHR+AM+F

Sbjct: 353 VKESDRIDAMARGLEACGVRVEEDEDTLIVHGMGPGGVPGGATCASHLDHRIAMSFLCCG 412

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
A+ PV++ D G +FP + +++

Sbjct: 413 LAAQTPVSVDDGGPIATSFPIFEPLMTAL 441

>emb|CBE68427.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [NC10 bacterium 'Dutch sediment']

Length = 434

Score = 104 bits (260), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 117/418 (27%), Positives = 201/418 (48%), Gaps = 33/418 (7%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P+ + G + +PG KS+++R ++L +L++GT+ + L S D A T+G++++
Sbjct: 3 IDPVGPLKGELTVPGDKSITHRAILGLSLADGTSEITGALRSHDCRDTAKAFGTMGVTIQ 62

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + + GG + +++ ++ L +GN+G MR L A V AA + VL G
Sbjct: 63 EPDNGR--LQIRGGGLYGLKEPQK--VLDVGNSTGTTMR--LLAGVLAAPFFS-VLTGDRY 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALL 187
+ RP+ + V L+ +GA + G + PP+ + G + + I+S Q SA+L
Sbjct: 117 LCARPMARVTVPLRSMGATILGREGGLPPLAIAIKGTHLR---AIDYASPIASAQVKSAI 173

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
A A D + + +S + E R+ E G+ H + R + K SP
Sbjct: 174 FAGLFA--DGRTTVTPEPLSRDHTE---RMFEAVGPIPI-HRNLGL-RLQVDS-IKGISPFQ 225

Query: 248 AYVEGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVT 306
+ GD S+A++FL A I G +T+ G + + L+ MGA + + +
Sbjct: 226 MAIPGDFSAFAFFLVAALVIPGSELTIRQVGVNPTR--TGLLDALQSMGAAIEVSRRII- 282

Query: 307 VTGPPPREPFGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRV 358
V+G EP H+++ ++ + +M D AV A A GPT IR+ A RV
Sbjct: 283 VSG---EPVADLHVRSQALHGTEVTGELIPRMLDEIPIFAVAAALAGPTTIRNAELRV 339

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
KE +R+ A+ EL + G +E+ PD I L D++ DHRMAMA ++ A
Sbjct: 340 KEVDRLAALVQELRRFGVKIEQHPDGLTIQGNSSLLGCDGCDSDGWDHRMAMALAVTGLA 397

>ref|ZP_05071831.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacteriales
bacterium GD 1]
gb|EDZ62001.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacteriales
bacterium GD 1]
Length = 427

Score = 104 bits (260), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 110/425 (25%), Positives = 193/425 (45%), Gaps = 30/425 (7%)

Query: 25 KSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGK 84
KS+S+R + A L+ GT+ V N L +ED L ++ LG ++E D + G
Sbjct: 23 KSISHRSAMFAMLASGTSEVTNFLRAEDTLNSLEIVKNLGATIEDDGVTIKISSGGIKEP 82

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
F + D GN+G +R +++A G+ +VL G +R+RP+ + L+++
Sbjct: 83 FEILDG-----GNSGTGIRLFCGLLSSANGH--FVLTGDKYLKRPMKRVTTPLREI 132

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA +D ++ P+ + G L S S+Q S +++AA A D
Sbjct: 133 GAVIDGREDSNLAPLSIRG-ASLKAFDYD-SKIASAQVKSCMILALRA-----DG 181

Query: 205 LISIPYVEMTLRLMERF--GVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ S E++ ER G+ A+ + I ++ SP V D SSA +F
Sbjct: 182 ICSYTEPELSRDHTERMLOGMGADIVDGLKTTITPMKELLSPLTIRVPADPSSAFFFAV 241

Query: 263 GAAIT-GGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTW--TETSVITVTGPPPREPFGRKH 319
AAIT + +EG + ++ + LE MGA +++ T+ G R + H
Sbjct: 242 AAAITPDSDIVLEGVTLPNTR--IEAFKALERMGANISYELTDNRYEPIGDIRVKYAPLH 299

Query: 320 LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
++ N++ + D L++ A G + +++ RVKE++R+ + L G V
Sbjct: 300 AITVEDNISWLIDELPALSIACATGESVVKNAEELRVKESDRISTVVEGLRACGIEVH 359

Query: 380 EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEPVPTIRDPGCTRKTFPDYFDVL 439
E D + E L +D+ DHR+AM+F+A + + D C +FP++F++L
Sbjct: 360 EYKDGVRVVGGE-LKRATVSDGDHRIAMSFIIAGL-RCGMNVTDLDCINTSFNPFELL 417

Query: 440 STFVK 444
K
Sbjct: 418 QKITK 422

>gb|AAM16064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]
Length = 47

Score = 104 bits (259), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 47/47 (100%), Positives = 47/47 (100%)

Query: 399 DTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 445
DTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK
Sbjct: 1 DTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 47

>ref|ZP_02149098.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeobacter
gallaeciensis 2.10]
gb|EDQ09260.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Phaeobacter
gallaeciensis 2.10]
Length = 440

Score = 104 bits (259), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 127/442 (28%), Positives = 206/442 (46%), Gaps = 32/442 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G ++PG KS+S+R L+L AL+ G T + LL EDV A++ +G V
Sbjct: 9 LTGIAEVPGDKSISHRSLILGALAVGETKISGLLEGEDVLDTAKAMQAMGAIEVINHGGGN 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 133
+V VG GG A+ + + GN+G +R + + + T+ D + +RP
Sbjct: 69 WSVHGVGVGGL-----AEPDQVIDCGNSGTGVRLIMGVMATSPITVFTTGDA--SLNKR 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V P V+ + + S+Q SA+L+A
Sbjct: 122 MARVTDPLALFGTQSVGRSGGRLPMTIVGAAEPTP---VRYTVPVPSAQVKSAVLLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYSKPNAYVE 251
A G + +I+K + + E R++ FG + D+ + R GQ P+ V
Sbjct: 179 APG--QTVVIEKEATRDHSE---RMLAGFGAEITVEDTDEGRVITLTGQPELKPQVIAVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A IT G+ V V G G + + + L+ MGA +T+ E G
Sbjct: 234 RDPSSAAPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF-ENMREEGGE 290

Query: 311 PREPFGKRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P ++ +K IDV + M D L+VVA FA G T + V RVKE++R+
Sbjct: 291 PVADLRARYSPDMKIDVPPERAASMIDEYPVLSVVASFAAGKTMGTGVKELRVKESDRI 350

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--PPEKL-NVTAIDTYDDHRMAMAFS-LAACAEVPV 420
A+ L G VEEG D+ +T PE + +++ DHR+AM+F + A+ PV
Sbjct: 351 DAMARGLRANGVMVEEGDDWAVTGLGPEGVPGGGTCEFLDHRIAMSFVMVMGMGAQKPV 410

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
T+ D +FP + +++T
Sbjct: 411 TVDDGTPIATSFIFTPLMTTL 432

>ref|ZP_00998531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanicola batsensis
HTCC2597]
gb|EAQ04467.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oceanicola batsensis
HTCC2597]
Length = 451

Score = 104 bits (259), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 128/451 (28%), Positives = 198/451 (43%), Gaps = 34/451 (7%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
++ +P ++GT +PG KS+S+R L+L ALS G T + LL +DV A+R G
Sbjct: 10 MMAEPAGPLTGTADVPGDKSISHRSLILGALSGETRISGLLEGQDVLDTAKAMRAFGAE 69

Query: 67 V-EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + R VG GG A+ E + GN+G +R + A+ + AT+ D
Sbjct: 70 ITDLGGGEWRVHGVGVGGF-----AEPETVIDCGNSGTGVRILMGAMATSPVTATFSGDA 124

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-SSQYLS 184
+ RP+ + L GA G P + +P V+ + S+Q S
Sbjct: 125 --SLNRRPMPARVTDPLALFGAQAVGREGGRLPMTIIGARDPVP---VRYEVPVPSAQVKS 179

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY 242
A+L+A A G +I++ P + T R++ FG + E +D R GQ
Sbjct: 180 AVLLAGLNAPG--RTVVIERE---PTRDHTERMLAGFGAEITTEVTDE-GRITLTGQPE 233

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V D SSA++ + A I G+ V V G + E L MGA +++
Sbjct: 234 LEGQTITVPRDPSSAAFPVCAALIVPGSDVLPNIGLNPTR--AGLFETLREMGADLSY- 290

Query: 302 ETSVTVTGPP-----REPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
E G P R G K + M D L+VVA FA+G T +R V
Sbjct: 291 ENPREEGGEPVADLRARYSPGMKGIAVPPERAASMIDEYPVLSVVAFAEGRTEMRGVRE 350

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMAMAF-S 411
RVKE++R+ A+ L G VEEG D+ I+ + T+ DHR+AM+F
Sbjct: 351 LRVKESDRIDAMAVGLRANGIEVEEGEDWWIVTGCAGGAVAGGATVATHLDHRIAMSFLC 410

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
L A+ PV + D +FP + +++
Sbjct: 411 LGMAAQSPVHLDDGQPIATSFVPFPELMTAL 441

>ref|NP_907485.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Wolinella
succinogenes DSM 1740]
sp|Q7M8Y7.1|AROAWOLSU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE10385.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE [Wolinella
succinogenes]
Length = 437

Score = 103 bits (258), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 126/448 (28%), Positives = 203/448 (45%), Gaps = 41/448 (9%)

Query: 11 PIKEISGTVKLPG---SKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
P+KE +++P KS+S+R + + LS + L ED + L + LGL V
Sbjct: 8 PLKE-GFEIEIPNIASDKSISHSRAIFSLSSSPARIHRYLQGEDTLHTLQIAQQLGLEV 66

Query: 68 EADKAAKRAVVVGCGGKFP--PVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ G G F P KE + GNAG A+R + A+ G +VL+
Sbjct: 67 TKE-----GEGMVFTPPPSGIKEPFDVLDGNCAGTAIRLYVGLLAASKG--YFVLN 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYL 183
G +R RP+ +V L+ +GA + G D + I G P I+S Q
Sbjct: 116 GDAYLRRRPMNRVVKPLQSVGAQI---FGRDEGNLAPLTILGRPLAAFDYQSPIASAQVK 172

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+++AA G+ + S + E LR M + + F + G K
Sbjct: 173 SAMILAA--LQGEASFFSEPERSRDHTERMLRGMGA-RIDEDQEGRLTLFPLLG--KRL 227

Query: 244 SPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
P + D SSA +F AAI G V ++ + ++ +VLE MGA++ ++
Sbjct: 228 DPLEMTIPADPSSAFFFAVAAAIIIPGARVKLQNVLLNPTR--IEAFKVLESMGARLHYSI 285

Query: 303 TSVTVTGPPREPFGRKHLKAIDVN-----MNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
TS T L+ I V+ +++++P +A+ +A+ A G + +++
Sbjct: 286 TSETYETIGDIEVSHHTLQGITVSERISWLIDELPALAIAMAL----AQGKSRVQNAKEL 341

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
RVKE++R+ + L LG VEE D IT ID++ DHR+AM+F+LA
Sbjct: 342 RVKESDRISVVNNRLRLGVEVEEFEDGYEITGGTLQGGVTIDSHGDHRIAMSFALAGLV 401

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
VP+TI D C +FP++ ++LS+ K

Sbjct: 402 -VPLTINDSACIDVSFPNFLEILSSIAK 428

>ref|YP_001794172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoproteus
neutrophilus V24Sta]
gb|ACB39726.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoproteus
neutrophilus V24Sta]
Length = 399

Score = 103 bits (258), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 121/429 (28%), Positives = 193/429 (44%), Gaps = 45/429 (10%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ G P SK S R+LL +AL+EG TV+ + S+D M A++ L L E
Sbjct: 8 RLEGRFAAPPSPKPYSQLLLASALAEGETVIRGVESDDFTAMFRAVQPLARLYCEGG-- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G+ P D + +G +R+ A G + G +R R
Sbjct: 66 -----VVKASGREP--DFYRSFNVM--ESGFTLRTAVAVYAGVPGVTSVYYGGT--LRGR 114

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +LV L++L V+ G V +G L V++ +SSQY+S L+ A
Sbjct: 115 PIDELVEALRRL--TTVEKTAGAIV--VEGRRLGEL---DVEIRADVSSQYISGLMYLAA- 167

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+G + + + S +VE T ++ +FG + E ++ + ++G +SP V
Sbjct: 168 HVGRGVVRPVGGERKWSFVEATAEVLKFKGARVELGEAIE---VEG--PLRSPGAVDVPS 222

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S A++ + TGG V + G T + D +V MGA VT V +G
Sbjct: 223 DFSLAFLVVAGVATGGRVELLG---TLAEVDRWAIDVFRQMGADVTVDNGVVKASG--- 276

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
K +DV++ + PD+ M +A+ A + + IR V R KE++R+ + L
Sbjct: 277 -----AFTKGVDVLDGRNPDVMPVALAAATVEAESVIRGVEHLRYKESDRVATVLDVLR 331

Query: 373 KLG--ASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTRK 430
+LG A ++G Y I PP + V A T+ DHR+ + +LAA V + D K
Sbjct: 332 RLGVEARYDKGAIY-IRGPPTREV-AFQTHGDHRIGL-MALAAAKIVGGCVDDLTPVAK 388

Query: 431 TFPD---YF 436
++P YF
Sbjct: 389 SWPSAVLYF 397

>ref|ZP_07129404.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TCH70]
ref|ZP_07363611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ATCC BAA-39]
gb|EFK81409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TCH70]
gb|EFM06473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ATCC BAA-39]
gb|EFW34512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MRSA177]
Length = 435

Score = 103 bits (258), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 118/448 (26%), Positives = 208/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61
E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGPLKEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D ++ VV G + + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVEIKEDD--EKLVTSPG--YQSNTPHQV-LYTGNSGTTTRLLAGLLSGLGIES-- 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI +++++
Sbjct: 116 VLSGDVSIKGRPMRDLRPLKLM DANIEGIEDNYTPLI IKPSVIKGI----NYQMEVA-- 169

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L E II +L +S + E + + F + E ++
Sbjct: 170 -SAQVKSAILFA---SLFSKEPTIIKELDVSRNHT---TMFKHFNPIE-AEGLSINTT 221

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG
Sbjct: 222 PEAIRYIKPADFHVPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGGRKH---LK AIDVNMNKMMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +
Sbjct: 280 GNIQLFNQ--TTGAAPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTST 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M
Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFFPDYF 436
++A+ + PV I+ +FP +
Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

>ref|YP_003497302.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deferribacter
desulfuricans SSM1]
dbj|BAI81546.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Deferribacter
desulfuricans SSM1]
Length = 424

Score = 103 bits (258), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 119/447 (26%), Positives = 199/447 (44%), Gaps = 44/447 (9%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I + I+ ++G + +P KS+++R + A+++G TVV + L S D AL G+
Sbjct: 2 ISFEKIRGLNGEITVPSDKSMTHRAIFGAMAKGKTVVKSPLLSRDTIATKDALVACGVD 61

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
E +++ G + + N+G R LT A + + + G
Sbjct: 62 YELKGDG---MIINSKGYDSFLEPDNVINC--ENSGTTARLLTGLF--APQSKYFFMTGD 114

Query: 127 PRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+R+RP+ ++ L LGA + FL P + G G+ KVK S+Q
Sbjct: 115 NSLRKRPMKRVIDPLSNLGAIVHSRRGFLPLMIQPSSMKG--GIIEAKVK-----SAQVK 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
SA+++A L + D + I+K + + E L+ FGV + ++ I+ +KY+
Sbjct: 168 SAVILAG-LQI-DEPVYIEKDQTRDHTEQMLKY---FGVNL DINNGV---IEVNKKYQ 218

Query: 244 SPKNAY-VEGDASSASYFLAGAAI-TGGT VTVGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V GD SSA++F+ A + V ++ G + ++L MGA+
Sbjct: 219 LKSTEFTVPGDFSSAAFFIGAALMFENSEVVIKNVGLNKTR--TGLLKILNEMGAKI--- 273

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDV 353
V VT EP G +K +N + + D L + LFA P IRD
Sbjct: 274 --DVLVTKEGDEPIGDISIKFSSLNGGVIRGEIIPNIIDEIPLLALGLFAKSPIEIRDA 331

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AI-DTYDDHRMAMAFSL 412
RVKE++R+ +I L +GA VEE D + P +K+N + ++DDHR+AM L
Sbjct: 332 EELRVKESDRIKSIVYNLRVGAEEVEEYEDGFKVYPMKKVNDKGVLSFDDHRIAMINIL 391

Query: 413 AACAEVPVTIRDPGCTRKTFFPDYFDVL 439
+ I +FPD+ + L
Sbjct: 392 LSKRFGNFDIDSIESIDVSFPDFLERL 418

>gb|EFW32220.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MRSA131]
Length = 435

Score = 103 bits (258), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 118/448 (26%), Positives = 208/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALR 61
E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
Sbjct: 3 EMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62

Query: 62 TLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D ++ VV G + + +V L+ GN+G R L ++ G +
Sbjct: 63 LLGVEIKEDD--EKLVTSPG--YQSFNTPHQV-LYTGNSGTTTLLAGLLSGLGIES-- 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI +++++
Sbjct: 116 VLSGDVSIKRPMDRVLRLPLKMDANIEGIEDNYTPLIIPSVIKGI----NYQMEVA-- 169

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L E II +L +S + E + + F + E ++
Sbjct: 170 -SAQVKSAILFA---SLFSKEPTIIKELDVSRNHTET---MPKHFNPIE-AEGLSINTT 221

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
+Y P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG
Sbjct: 222 PEAIRYIKPADFHVPGDISAFAFFIVAALITPGSDVTIRNVGINPTRSGI--IDIVEKMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGKHKH---LKAIDVNMKNMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +
Sbjct: 280 GNIQLFNQ--TTGAAPTASIRIQYTPMLQPITIEGELVPKAIDELPIALLCTQAVGTST 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M
Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++A+ + PV I+ +FP +
Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSPFGFL 425

>ref|YP_003267971.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haliangium ochraceum
DSM 14365]
gb|ACY16078.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haliangium ochraceum
DSM 14365]
Length = 459

Score = 103 bits (258), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 136/483 (28%), Positives = 201/483 (41%), Gaps = 83/483 (17%)

Query: 7 IVLQPIKE-ISGTVKLPGSKSLSNRILLLAALSEGTTVV-----DNLLNSEDVHYMLG 58
+++P + + G +PG KS+S+R LLL AL G VV DNL + VH M
Sbjct: 4 FIVEPARSPLIGHATVPGDKSIHRALLLGALCRGKVVVRGLSGEDNLCATAHAVHAMGA 63

Query: 59 ALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
+ L A + V G G + A + + GNAG AMR L + A +
Sbjct: 64 QVSGLDALAAAPSPDREIAVSGVGLRGLRAPAGD---IDCGNAGTAMRLLCGLL--APQS 118

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV--KLSG 176
VL G + RP+ ++ L ++GA R+ G G G++ L
Sbjct: 119 FASVLVGDA SLHARPMRRVIDPLSEMGA-----RITGAEGKKPGEIYPPLRI 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS----- 230
+ +S ++AL A P+A V+ + L+ Y + R+ E G +HS+
Sbjct: 166 AAASGPM TALDYAMPVASAQVKS AV---LLCGLYADGVTRVSEP-GAARDHSERMLAHMG 221

Query: 231 ----WDRFYI----KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEG--CGTTS 280
W I KG + V D S A++ LA A I G G C +
Sbjct: 222 APIRWGGGEITLDTKGWDGALDAELIEVPADPSQA AFVLAALIVGVERVTVGRVCINDT 281

Query: 281 LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR-----EPFGRKHLKA 322
G F +VL M ++ E G P E G ++A
Sbjct: 282 RTG---FLDVLAA MNGRI---EREAMQRGGPEPVADLSVSRGAGDALQGTEIAGELVVRA 335

Query: 323 IDVNMKNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGP 382
+D ++P LAVVA A+G T +RD RVKE++R+ L LG VEE P
Sbjct: 336 VD----ELP-----ILAVVAARANGVTHVRDAGELRVKESDRIATTCAMLRALGCEVEERP 387

Query: 383 D-YCIITPPEK-LNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVL 439

D + ++ P + ID DHR+AMA ++A CAE PV + D C +FP + +VL
Sbjct: 388 DGFSVVGMPGRPFQ SARIDAAGDHR IAMAGAVAGLCAEGPVRVDDVACVDTSFPGFAEVL 447

Query: 440 STF 442

Sbjct: 448 GKL 450

>ref|YP_002956854.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micrococcus luteus
NCTC 2665]
ref|ZP_06245967.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micrococcus luteus
NCTC 2665]
gb|ACS30300.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micrococcus luteus
NCTC 2665]
Length = 476

Score = 103 bits (257), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 142/460 (30%), Positives = 205/460 (44%), Gaps = 55/460 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V+LPGSKSL+NR L+LAAL++G V+ +L S D M AL LG E
Sbjct: 31 VRGDVRLPGSKSLTNRHLVLAALADGPCVLHGVLSESRDTALMRTALTALGARFEP----- 85

Query: 75 RAVVVGCGG----KFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ GG PV E +V + G AG MR + G + DG
Sbjct: 86 ----LSDGGLRVHPMPVGEPLAGDVAVDCGLAGTVMRFVVFVAALRPGRVRF--DGDAGA 139

Query: 130 RERPIGDLVVGLKQLGADV-----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
R RP+ ++ L+QLG V D PV + G +P +V + S
Sbjct: 140 RLRPMAPVLDALRQLGVAVVEEGEPGRLPFTMTTRADAAPVAPD--GDVP--EVAVDASG 195

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIK 237
SSQ+LSA L+AA + + + + P +V MT+ ++ V + + +
Sbjct: 196 SSQFLSALLAAAGMPRGLRLRHTGEAVPSPEHVAMTVGVLRALVVDVTETGP-GAWTVA 254

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
G+ A VE D S+A FLA A TGG+VTV T + Q ++ +L GA
Sbjct: 255 PGRVPA--HEAAVEPDLNAGPFLAAAVATGGSVTVPDWPTRTTQIGDRWRRILPQFGAS 312

Query: 298 VTWT-----ETSVTVTGPPPREPFGKHLKAIDVNMKNMPDVAMTLAVVALFADGPTAI 350
V T +TVTG + + A ++ +A T A +AL A GPT +
Sbjct: 313 VALTVDRDTRSRGLTVTGAVHDDGTFRITGAGEIADTAEE--LAPTAALALLASGPTRL 370

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEG-----PDYCIITPPEKLNVT AIDTYDDH 404
+ R ET+R+ A+ E +LG +V+EG P P L+ A++TY DH
Sbjct: 371 TGIGHLRGHETDRLAALTAEEARLGITVDEGETALGFPGTDASGP---LSPALETYHHD 427

Query: 405 RMAMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTFV 443
RMA F+ VP T I D T KT PD+ + + V
Sbjct: 428 RMAF-FAAVVGLRVPGTGIVDVATTAKTMPDFPALWTALV 466

>ref|ZP_01002590.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Loktanella
vestfoldensis SKA53]
gb|EAQ06966.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Loktanella
vestfoldensis SKA53]
Length = 473

Score = 103 bits (257), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 126/435 (28%), Positives = 193/435 (44%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L A+ G T + LL +DV A+R G V D
Sbjct: 41 LQQQAHVPGDKSISHRSLILGAMCIGETRITGLLEGDDVLDTAKAMRAFGAEV-TDHGGG 99

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ V G G G F A+ + + GN+G +R + A+ T+ D + RP
Sbjct: 100 QWSVRGVGVGGF---AEPDHVIDCGNSGTGVRLIMGAMATTPITVFTTGDA--SLNGRP 153

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G + L G G P V G + + S+Q SA+L+A A

Sbjct: 154 MGRVTDPLALFGTRAVGRAGGRPLMTLVGAAGPV--PVRYVVPVPSAQVKSAVLLAGLNA 211

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
G + +I+K + + E R+++ FG D+ + R GQ P++ V

Sbjct: 212 PG--QTVVIEKEATRDHTE---RMLQGFATLTVEDTDEGRVITLTGQPELQPDIVVPR 266

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++ + A I G+ V V G + L+ MGA +T+ E + G P

Sbjct: 267 DPSSAAFVCAALIVPGSDVLVPNIGLNPT--AGLFTTLQEMGADLTF-ENLRSEGGE 323

Query: 312 ----REPFGKRHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
R F L+ I V ++ M D L+VVA FA G T + V RVKE++R+

Sbjct: 324 VADLRARF-SPDLRGITVPADRAASMIDEYPLSVVAFAQGVTDMPGVKELRVKESDRI 382

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD---DHRMAMAF-SLAACAEVPV 420
A+ L G +V+EGPD+ +T +V T DHR+AMAF + A+ PV

Sbjct: 383 DAMAQLRAAGVTVDEGPDWVRVTGVGHGHPGGVTQSRLDHRIAMAFVLMGMAAQNPF 442

Query: 421 TIRDPGCTRKTFPDY 435
+ D +FP +

Sbjct: 443 IVDDAAPITTSFPIF 457

>ref|ZP_03613284.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
capitis SK14]
gb|EEE49546.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
capitis SK14]
Length = 433

Score = 103 bits (257), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 114/432 (26%), Positives = 198/432 (45%), Gaps = 32/432 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+ G T + L ED + LG+ + +

Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLATGQTTIYKPLLGEDCRRTMEIFELLGVKI---TEHE 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+++ G + K Q L+ GN+G R L ++ G + VL G + +RP

Sbjct: 70 ETIIIDSPG---YQQFKTPHQVLYTGNSTGTTTLLAGLLSGLGIES--VLSGDVSIKRP 124

Query: 134 IGDVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L Q+ A + G P + I + G + ++ + S+Q SA+L A+ +

Sbjct: 125 MDRVLPKLLQMNHAHISGIEGNYTPLIKPSI--IKGIEYQMEVA-SAQVKSAILFASIFS 181

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ ID +S + E + E F + E R Q K+ ++ +V GD

Sbjct: 182 EEATTVEID--VSRNHTET---MFEHFNIPIEIEGKTIRTSPHAIQHIKA-QDFHVPGD 235

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A IT G+ +T+ G + + +++E+MG + +VT P

Sbjct: 236 ISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVELMGNIELN--NVTHDAEPT 291

Query: 313 EPFGRKH---LKAIDVNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETERMVA 366
K+ LK I + + +P L VVAL A I+D +VKET R+

Sbjct: 292 ASIRVKYTPTLKPITIEGDIVPKAIDELPVVALLCTQASSTCIKDAEELVKETNRIDT 351

Query: 367 IRTELTKLGASVEEGPDYCIITPPE-KLNVTAIDTYDDHRMAMAFSLAA-CAEVPVTIRD 424
L LG S++ D II P E K N T +D+ DHR+ M ++A+ + P+TI

Sbjct: 352 TADMLNMLGFSLQPTNDGLIHPSEFKANAT-VDSQTDHRIGMMLAVASLLSSEPLTIEQ 410

Query: 425 PGCTRKTFPDYF 436
+FP +

Sbjct: 411 FDAVNVSFPGFL 422

>ref|ZP_01863096.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erythrobacter sp.
SD-21]
gb|EDL50531.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erythrobacter sp.
SD-21]
Length = 450

Score = 103 bits (257), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 124/441 (28%), Positives = 207/441 (46%), Gaps = 38/441 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G +++PG KS+S+R L+ AL+ G + + LL EDV ALR +G +E D
Sbjct: 26 LTGRIRVPKDKSISHRALMFGALAVGSRITGLLEGEDVLATAAALRAMGAVIEKDGEDW 85

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG G E A L +GN+G + R L V + G A + D + RP+
Sbjct: 86 VVDGVGVGTLLQPEQA-----LDMGNSGTSTRLLMGLVASHGITAAFTGDA--SLSRPM 138

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLA 193
G ++ L +GA G P V + G+ P ++ + S+Q SA+L+A
Sbjct: 139 GRVIDPLSTMGASFTSPGGTLPV-LEGM--QPAVPIRYRLPVASQVKSAVLLAGLNT 195

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-WDRFYIKGGQKYKSPKNAYVEG 252
G + + +P + T R++ FGV+ + ++ +R G +P + V G
Sbjct: 196 PGTTTV-----IEPVPTRDHTERMLRGFGVEVQVEEADGERVISLTGTCDLTPCDITVPG 250

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++F A++ G+ + +E G + + VLE MGA++ + + V G P
Sbjct: 251 DPSSAAFFAVAASVVPGSDLVIENVGLNPTRNGIY--RVLEQMGARIGYLDQR-EVGGE 307

Query: 312 REPFGGRKH--LKAIDVNMNKMPPDVAMT-----LAVVALFADGPTAIRDVASWRVKETE 362
++ LK I+V+ PD+A + L V A A+G T + RVKE++
Sbjct: 308 VADLRVRYAQLKGIEVD----PDIASSMIDEFPVLFVAAALAEGETTVTSGLEELRVKESD 363

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFSLAACA-EV 418
R+ A+ L G +VEE D +I + I T+ DHR+AM+ ++A A E
Sbjct: 364 RLSAMAAALQLAGGTVEERDDGLVIHSGGKPLAGGGPITTHLDHRIAMSMAGVAGLAS 423

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
V++ +FP++ +L
Sbjct: 424 GVSVDSEPIATSFPNFIAL 444

>ref|ZP_01015875.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Maritimibacter
alkaliphilus HTCC2654]
gb|EAQ10494.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
bacterium HTCC2654]
Length = 441

Score = 103 bits (257), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 132/441 (29%), Positives = 196/441 (44%), Gaps = 33/441 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKAA 73
+ G +PG KS+S+R LLL A++ G T V LL EDV A+R G VE
Sbjct: 9 LKGADVVPKDKSISHRSLLLGAMAVGETRVTGLLEGEDVLATAAAMRAFGADVERLGDGE 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 133
R VG GG ED + GNAG +R + + + AT+ D +R RP
Sbjct: 69 WRVNGVGVGGAEPEDV-----IDCGNAGTGVRLIMGCMATSPITATFTGDA--SLSRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + + GA G P V +P V+ + S+Q SA+L+A
Sbjct: 122 MGRVTDPIALFGAQSYGRTGGRLPMTVVGAKNPIP---VRYRTPMASAQVKSAVLLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G E +I+ + + E R++ FG + D+ + R GQ P+ V
Sbjct: 179 APG--ETVVIEAEATRDTHE---RMLAGFGAEISVEDTDEGRVITLVGQPELKPQTIAVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ + A I G+ V V G + + F ++E MGA +T+ E G
Sbjct: 234 RDPSSAAFPVCAALIVPGSDVLVPNIPLNPTAGL-FTTLIE-MGADLT-ENEREEGGE 290

Query: 311 P----REPFG--RKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P R F K ++ + M D L+VVA FA G T + V RVKE++R+
Sbjct: 291 PVADLRARFSPDMKIRVPEERAASMIDEYPVLSVVAATGKTEMVGVHEL RVKESDRI 350

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYD---DHRMAMAFSLAACA-EVPV 420
A+ L G ++EEG D+ + V T DHR+AM+F + A + PV

Sbjct: 351 DAMARGLEANGVTIEEGRDFMTVHGLGPDGVPGGGTAAARLDHRIAMSFVMVMGMAQSPV 410

Query: 421 TIRDPGCTRKTFFPDYFDVLST 441

++ D ++FP F+ L T

Sbjct: 411 SVDDGQPIATSFP-IFEPLMT 430

>ref|ZP_05699157.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A5948]

gb|EEV83990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A5948]

Length = 432

Score = 103 bits (256), Expect = 6e-20, Method: Compositional matrix adjust.

Identities = 112/435 (25%), Positives = 201/435 (46%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +

Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVLGDGVPVRMRERPI 134

+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+

Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSGTTTTRLLAGLLSGLGIES--VLSGDVSIKRP 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190

++ LK + A+++ P P + GI +++++ S+Q SA+L A

Sbjct: 126 DRVLRPLKLM DANIEGIEDNYTPLIIKPSVIKGI---NYQMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249

+L E II +L +S + E + + F + E ++ +Y P + +

Sbjct: 178 --SLFSKEPTTIKELDVSRNHTET---MFKHFNIPIE-AEGLSINTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308

V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T

Sbjct: 232 VPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGKRH---LKAIDVNMKNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362

P ++ L+ I + +P L V+AL A G + I+D +VKET

Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVT 421

R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV

Sbjct: 348 RIDTTADMLNLLGFELQSTNDGLIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFFPDYF 436

I+ +FP +

Sbjct: 408 IKQFDVNVVSFPGFL 422

>ref|YP_809810.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oenococcus oeni
PSU-1]

sp|Q04HC7.1|AROAO_OENOB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ABJ56145.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oenococcus oeni
PSU-1]

Length = 437

Score = 103 bits (256), Expect = 7e-20, Method: Compositional matrix adjust.

Identities = 114/441 (25%), Positives = 202/441 (45%), Gaps = 30/441 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVEADKAAK 74

++G++ LPG KS+S+R +++A++S G + + N NS D L A LG VE K +

Sbjct: 12 LNSGSLLPDGKSIHSRISIMVASISRGISRIKNFSNSTDCLSTLNAFLDLG--VEIKKYGR 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATVVLGDGVPVRMRERPI 134

+V G G +D K+ + +GN+G R L + N V D + +RP+

Sbjct: 70 DLIVYGSGLD-AFKDPKKPLN--MGNSGTTTTRLLGLLAGQSFNTCLVGDA--SLSKRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

+ + ++G + G P+ V G L L + S+Q SAL+ +A A

Sbjct: 125 YRVTNPITEVGGFEFS-LTGNGTLPITVIGHPSLKAFDYHLPIA-SAQVKSALIFSALQA- 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEGD 253
D I +K + ++E+ ++ FG + + I + K S + + GD

Sbjct: 182 -DEPSIIFEKEATRNLHLEI---MLNDFGADIK---TNGLCITVMPRPKLSGRTISIPGD 233

Query: 254 ASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A++ + ++ G + + VL+ M A + +TS

Sbjct: 234 ISSAAFFMVAASLLPNSCICLKVKVGLNPTR--IGIISVLKRMNANIEVKKTSNEAEAYGD 291

Query: 313 EPFGRKHLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRVKETERMVAIRT 369
+L A+++ ++P+V L ++ L A G T I RVKET R+ +

Sbjct: 292 IIVHSSNLHAVEITSKEIPNVIDELPILTLAASLAKGRTIISGAGELRVKETRYRISVVAA 351

Query: 370 ELTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAAC---AEVPVTIRD 424
EL KLGA ++E D +I KL + + T+ DHR+ M ++AA +T+ +

Sbjct: 352 ELKKLGARIQEKSDGMVIDGCPKLQIPENNLATHGDHRIGMMLAVAALLVDTSKTITLNN 411

Query: 425 PGCTRKTFFPDYFDVLSTFVKN 445
P + ++P++F L + N

Sbjct: 412 PEAIKISYPNFFRDLDDLNN 432

>ref|YP_001202319.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium sp. ORS278]
sp|A4YJJ3.1|AROABRASO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAL74069.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Bradyrhizobium sp. ORS278]
Length = 445

Score = 103 bits (256), Expect = 7e-20, Method: Compositional matrix adjust.
Identities = 132/439 (30%), Positives = 196/439 (44%), Gaps = 33/439 (7%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+SGT+++PG KS+S+R L+L ALS G T + LL EDV ++RTLG VE + A

Sbjct: 18 LSGTIRVPGDKSISHRALILGALSVDGTRISGLLEGEDVLNTAKSMRTLGAKEVERTGEFA 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG GG A+ L GN+G R + AV AG + V DG +R RP

Sbjct: 78 WTVNGVGVGGF-----AQPAATLDFNGSGTGCRLLVMGAV--AGCPISAVFDGDASLSRSP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L +GA V P+ + G P + S+Q SA+L+A A

Sbjct: 131 MRRILDPLALMGAKVTASAEGGKLPLTLQGASN-PVPIEYRTPVASAQIKSAVLLAGLAA 189

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +I++ S + E+ L+ FG + S R GQ V

Sbjct: 190 PG--VTTVIEQEASRDHTEMLK---HFGAEIVTTPEGSHGRRIALTGQPELRGAPVIVP 244

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ L A I G+ + + T L+ L MGA + + V G

Sbjct: 245 ADPSSAAFLVLAALIVDGSIDLVSVMNPLR--TGLFTTLREMGASIEEDD---VRGD 298

Query: 311 PREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP R LK ++V + P D + LAV A +A+G T +R + RVKE++

Sbjct: 299 AGEPMARLRVRASKLKGVEVPPERAPSMIDEYLVLA VAAAYAEGTTIMRGLHELVRKESD 358

Query: 363 RMVAIRTELTKLGASVE-EGPDYCIITPPEKLVNTAIDTYDDHRMAM-AFSLAACAEVPV 420
R+ A L G VE G D + + T+ DHR+AM A + ++ PV

Sbjct: 359 RLEATAAMLRVNGVKVEITGDDLIVEGRGHVPGGGLVATHMDHRIAMSALVMGLASDKPV 418

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
T+ D +FPD+ ++

Sbjct: 419 TVDDTAFIATSFPDFIPLM 437

>ref|YP_004158380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella clarridgeiae 73]

emb|CBI75784.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella
claridgeiae 73]
Length = 442

Score = 103 bits (256), Expect = 7e-20, Method: Compositional matrix adjust.
Identities = 107/449 (23%), Positives = 199/449 (44%), Gaps = 51/449 (11%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SGT+K+PG KS+S+R ++L L+ G + + LL S+DV + ++ +G + K
Sbjct: 14 NLSGTIKIPGDKSISHRAVILGGLAHGESHIYGLLESDDVLRVTVMQAMG--AQCYYKN 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G G ++ L GN+G + R + V + T++ D + RP
Sbjct: 72 NLWIIIRGTGNGCLLQ---ARTPLNFGNSGTSARLIMGLVGSYHMKTTFLGDA--SLSRRP 126

Query: 134 IGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYL 183
+ ++ L+ +G +++ LG P P+R +V ++ S+Q
Sbjct: 127 MEHILNPLRLMGVEIEPTLGNHLPLTLYGPKMANPIRY-----RVPMA---SAQVK 174

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGK--AEHSDSWDRFYIKGGQK 241
SA+L+A G +I+ ++ + E +++++ FG + E RF GQ
Sbjct: 175 SAVLLAGLNTAGTT--TVIEPTLTRDHTE---KMLKAFGAELDIETDKEGARFISLKGQP 229

Query: 242 YKSPKNAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVK--FAEVLEMMGAKV 298
+ + + V GD SSA++ +A + +T+E L D + F + L MGA+
Sbjct: 230 HLTGQIINVPDGPSSAAFPIIAALLVEDSDITLENV---LINDSRMGFIQTLWEMGAKI 285

Query: 299 T-WTETSVTVTGPPREPFGKRHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
+ + + LK + + + P D LA+ A FA+G T + +
Sbjct: 286 ELLNQRIIGIENVADIRVRSELKGV TIPKERAPSMIDEYPALAITAAFANGTTVMMSGIK 345

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFS 411
R+KE+ R+ A+ E+G D+ I+ + + T+ DHR+AM F
Sbjct: 346 ELRIKESNRLSALAEGFKINHVCHEKGNDFLIVHGKNSIKGLGGGYVTTHLDHRIAMCFL 405

Query: 412 L-AACAEVPVTIRDPGCTRKTFPDYFDVL 439
+ +E PV I D +FP++ ++
Sbjct: 406 IFGLVSEKPVIIIDDKRMIATSFPEFIPLM 434

>gb|AAA71897.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Staphylococcus
aureus]
Length = 430

Score = 103 bits (256), Expect = 7e-20, Method: Compositional matrix adjust.
Identities = 113/435 (25%), Positives = 199/435 (45%), Gaps = 40/435 (9%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRHLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVTSPGYQV---NTPHQV-LYTGNSGTTTLLAGLLSGLGNES--VLSGDVSIKGRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI +++++ S+Q SA+L A
Sbjct: 125 DRVLRPLKLMDANIEGIEDNYTPLIIKPSVIKGI---NYQMEVA---SAQVKSAILFA- 176

Query: 191 PLALGDVEIEIIDKL-ISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQYKSPKNAY 249
+L E II +L +S + E + + F + E ++ +Y P + +
Sbjct: 177 --SLFSKEPTIIKELDVSRNHTET---MFKHFNIPIE-AEGLSINTTPEAIRYIKPADFH 230

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 231 VPGDISSAFFIVAALITPGSDVTIHNVGINQTRSGI--IDIVEKMGGNIQLFNQ--TTG 286

Query: 309 GPPREPFGKRKH---LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 287 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLLCTQAVGTSTIKDAEELVKETN 346

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVT 421
R+ L LG ++ D II P E A D DHR+ M ++A + PV
Sbjct: 347 RIDTTADMLNLLGFLQPTNDGLIIHPSE-FKTNATDILTDHRIGMMLAVACVLSSEFPVK 405

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 406 IKQFDAVNVSPFGFL 420

>ref|YP_264469.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Psychrobacter arcticus 273-4]
gb|AAZ19035.1| 3-phosphoshikimate 1-carboxyvinyltransferase / prephenate
dehydrogenase [Psychrobacter arcticus 273-4]
Length = 778

Score = 103 bits (256), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 117/460 (25%), Positives = 209/460 (45%), Gaps = 54/460 (11%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P +SGT+ +PG KS+S+R ++L +L+ G T V L ED L A R +G+ +E
Sbjct: 330 ITPSNTVSGTTITIPGDKSISHRSIMLGSLATGVTHVTGFLEGEDALATLQAFRDMGVIIE 389

Query: 69 ADKAAKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
+ VG G P + L++GN+G +MR L + A ++ VL G
Sbjct: 390 GPDNGNLTIHGVGMNGLKP-----SKTPLYMGNSGTSMRLLAGILAAQAFDS--VLTGDT 442

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIG--GLPGGKVKLSGSI-SSQYLS 184
+ +RP+ + L+Q+GA + P+ + G G P ++ + S+Q S
Sbjct: 443 SLNKRPMERIAAPLRQMGAVIQSTGQKGTAPLSITGRDSVGTPLQIEYDMPVASAQIKS 502

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LL+A A G ++ P V + T R++ FG + +R ++GG
Sbjct: 503 CLLLAGLWAEAGTTT-----VTQPEVSRDHTERMLSAFGYPV--TVDGNRISVEGGGTL 553

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K A V D SSA++F+ AAI+ + +T++ G + + ++L++M A ++ +
Sbjct: 554 KGGDIA-VPADISSAAFFMVAAAIQSDELTLKQVGINPRTGTI--IDILKLMQADISLS 610

Query: 302 -ETSVTVTGPPREPFGKRLKKAIDVNMNKMPPDVAMTLA-----VVALFADGPTAIRD 352
ET V EP ++ ++ ++P+ + LA + A A G T +
Sbjct: 611 NETHVG-----GEPVADITIRGSNLVGIEIPEYLVPLAIDEFPVLFIAASCAQGRITLTG 665

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVT-----ID 399
RVKE++R+ + L LG D II T + ++ I
Sbjct: 666 AKELRVKESDRIAVMAEGLQTLGVDCTVTEDGLIIEGKGTQSQNSDINNSQPVFGGGDIV 725

Query: 400 TYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDV 438
++ DHR+AM+F++A+ A ++I +FP + ++
Sbjct: 726 SHHDHRIAMSFVAVSLRASQQISIEGIETINTSFPGFAEL 765

>ref|ZP_01544542.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oenococcus oeni ATCC
BAA-1163]
gb|EAV39129.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oenococcus oeni ATCC
BAA-1163]
Length = 438

Score = 102 bits (255), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 116/446 (26%), Positives = 206/446 (46%), Gaps = 40/446 (8%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G++ LPG KS+S+R +++A++S G + + N NS D L A LG VE K +
Sbjct: 13 LNSLLLPKDKSISHRSIMVASISWGISRIKNFSNSTDCLSTLNAFLDLG--VEIKKYGR 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G +D K+ + + GN+G R L + N V D + +RP+
Sbjct: 71 DLIVYGSGLD-AFKDKPKPLNM--GNSGTTTTRLLGLLAGQSFNTCLVGDA--SLSKRPM 125

Query: 135 GDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ + ++G + G P+ V G L L + S+Q SAL+ +A A
Sbjct: 126 YRVNTNPITEVGGEFS-LTGNGTLPITVIGHPSLKAIFYHLPIA-SQVKSAIFLFSALQA- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEGD 253
D I +K + ++E+ ++ FG + + I + K S + + GD
Sbjct: 183 -DEPSIIFEKEATRNLHEI---MLNDFGADIK----TNGLCITVMRPKLSGRTISIPGD 234

Query: 254 ASSASYFLAGAAIT-GGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A++ + ++ G + + VL+ M A + +TS
Sbjct: 235 ISSAAFFMVAASLLPNSCICLKKVGLNPTR--IGIISVLKRMNANIEVKKTSNEA----- 287

Query: 313 EPFG-----RKHLKAIDVNMNMKMPDVAMTLAVVAL---FADGPTAIRDVASWRVKETERM 364
E +G +L A+++ ++P+V L ++ L A G T I RVKET+R+
Sbjct: 288 EAYGDIIVRSSNLHAVEITAKEIPNVIDELPILTLAASLAKGRTIISGAGELRVKETDRI 347

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAAC---AEVP 419
+ EL KLGA ++E D +I KL + + T+ DHR+ M ++AA
Sbjct: 348 SVVAELKKLKGARIQEKSDGMVIDGCPKLQIPENNLATHGDHRIGMMLAVALLDVTSKT 407

Query: 420 VTIRDPGCTRKTFPDYFDVLSTFVKN 445
+T+ +P + ++P++F L + N
Sbjct: 408 ITLNNPEAIKISYPNFRDLDYLLNN 433

>ref|NP_646171.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MW2]
ref|YP_043525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MSSA476]
ref|YP_494052.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_FPR3757]
ref|YP_499999.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus NCTC 8325]
ref|YP_001332409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus str. Newman]
ref|YP_001575291.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_TCH1516]
ref|ZP_03565461.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus str. JKD6009]
ref|ZP_06021867.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
D30]
ref|ZP_06023855.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
930918-3]
ref|ZP_06329427.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9765]
ref|ZP_06378861.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus 132]
ref|ZP_06789174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9754]
sp|Q8NWN5.1|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q6G998.1|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q05615.2|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|Q2FGX6.1|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A6QH15.1|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A8Z444.1|AROAA_STAAS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB95219.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE [Staphylococcus aureus
subsp. aureus MW2]
emb|CAG43183.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MSSA476]
gb|ABD20414.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_FPR3757]
gb|ABD30566.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus

subsp. aureus NCTC 8325]
dbj|BAF67647.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus str. Newman]
gb|ABX29412.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus USA300_TCH1516]
gb|EEW45500.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
930918-3]
gb|EEW47483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
D30]
emb|CBI49341.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TW20]
gb|EFB98961.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9765]
gb|EFG40877.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9754]
gb|ADL65472.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus str. JKD6008]
gb|EFU28124.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus CGS01]
Length = 432

Score = 102 bits (255), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 112/435 (25%), Positives = 201/435 (46%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVVTSPPG--YQSFNTPHQV-LYTGNSGTTTTRLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI +++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKLM DANIEGIEDNYTPLIIPSVIKGI----NYQMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDLK-ISPYPVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E + + F + E ++ +Y P + +
Sbjct: 178 --SLFSKEPTTIKELDVSRNHTET---MFKHFNIPIE-AEGLSINTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISSAAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGGRKH---LKAIDVNMKNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVPKAIDELPIVIALLCQAVGTSTIKDAEELVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDVNVVSFPGFL 422

>ref|ZP_06502760.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micrococcus luteus
SK58]
gb|EFD50230.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Micrococcus luteus
SK58]
Length = 476

Score = 102 bits (255), Expect = 9e-20, Method: Compositional matrix adjust.
Identities = 144/459 (31%), Positives = 205/459 (44%), Gaps = 53/459 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V+LPGSKSL+NR L+LAAL++G ++ +L S D M AL LG E
Sbjct: 31 VRGDVRLPGSKSLTNRHVLAAALADGPCILHGVLESRTALMRTALTALGARFEP----- 85

Query: 75 RAVVVGCGG----KFPV-EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129

+ GG PV E +V + G AG MR + G + DG
 Sbjct: 86 ----LSDGGLRVHMPVGEPLAGDVAVDCGLAGTVMRFPVFAALRPGRVRF--DGDAGA 139
 Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDGCPP---VRVNGIGGLPGG---KVKLSGSISSQY 182
 R RP+ ++ L+QLG V G P R + P G +V + S SSQ+
 Sbjct: 140 RLRLMAPVLDALRQLGVAVVEEGGPGRLPFTMTTRADAATVAPDGDVPEVAVDASGSSQF 199
 Query: 183 LSALLMAAPLALGDVEIEIIDKLISIP-YVEMT---LRLMERFGVKAHSDSWDRFYIKG 238
 LSA L+AA + + + + P +V MT LR +E V +W +
 Sbjct: 200 LSAALLAAAGMPRGLRLRHTGETVPSPEHVAMTAGVLRALV-VDVAETGPGAW---TVAP 255
 Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
 G+ A VE D S+A FLA A TGG+VTV T + Q ++ +L GA V
 Sbjct: 256 GRIPG--HEAAVEPDLSNAGPFLAAAVATGGSVTVDPWPTRTQIGDRWRRILPQFGASV 313
 Query: 299 TWT-----ETSVTVTGPPPREPFGGRKHLKVIDNMNMKMPDVAMTLAVVALFADGPTAIR 351
 T +TVTG + + A ++ +A T A +AL A GPT +
 Sbjct: 314 ALTVDRTDRSRGLRVTGAVHDDGAPRITGAGEIADTAEE--LAPTAALALLASGPTRLT 371
 Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEG-----PDYCIITPPEKLNVTATIDTYDDHR 405
 + R ET+R+ A+ E +LG +V+EG P P L+ A++TY DHR
 Sbjct: 372 GIGHLRGHETDRLAALTAEEARLGITVDEGETSLGFGPTDASGP---LSPALETYDHR 428
 Query: 406 MAMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTFV 443
 MA F+ VP T + D T KT PD+ + + V
 Sbjct: 429 MAT-FAAVVGLRVPGTGVDVATTAKTMPDFPALWTALV 466

>ref|YP_004139533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium ciceri
 biovar biserrulae WSM1271]
 gb|ADV09483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium ciceri
 biovar biserrulae WSM1271]
 Length = 452

Score = 102 bits (255), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 118/456 (25%), Positives = 194/456 (42%), Gaps = 54/456 (11%)

Query: 15 ISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 +SG ++PG KS+S+R + L+ G T + LL EDV A++ +G +E K
 Sbjct: 18 LSGIARVPGDKSISHRSFMFGGLASGETRITGLLEGEDVMRTGAAMKAMGAHIE--KNGD 75
 Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPI 134
 V+ G G ++ E L GNAG R V T++ D + RP+
 Sbjct: 76 EWWIRGTGNGALLQ---PEGPLDFGNAGTGSRLTMGLVGTYDMETTFIGDA--SLSGRPM 130
 Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
 G ++ L+Q+G V D P+ ++G P ++ + S+Q SA+L+A
 Sbjct: 131 GRVLEPLRQMGVQVLKATPGDRMPITLHG---PKHAAPITYRVPMASQVKSAYLLAGL 186
 Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
 G +I+ +++ + E ++++ FG + E + R GQ + +
 Sbjct: 187 NTPGIT--TVIEPVMTRDHE---KMLKGFGANLSVETDERGVRHIFIEGQKLTGTQIA 241
 Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
 V GD SSA + L A I G+ +T+E + + L+ MG +
 Sbjct: 242 VPGDPSSAGFPLVAALIVPGSDITIENVLMNPTRTGILL--TLQEMGGNIDILN----- 293
 Query: 309 GPPREPFGF-----KHLKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
 PR G LK + V + P D LAV A FA+G T ++ +
 Sbjct: 294 --PRNAGGEDVADLRVRYSELKGVIVPPERAPSMIDEYPVLAVAASFAEGETLMQGLEEL 351
 Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMA 407
 RVKE++R+ A+ LT G EG + T + T+ DHR+A
 Sbjct: 352 RVKESDRLSAVANGLTLNGVDCTEGEASLAVRGKPGGKGLGHPNGKDTTVQTHLDHRIA 411
 Query: 408 MAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
 M+F + A E PVTI D +FP++ +++
 Sbjct: 412 MSFLVMGLATEKPVTTIDDAAMIATSFPEFMGLMTAL 447

>ref|YP_186348.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus

subsp. aureus COL]
sp|Q5HFV9.1|AROA_STAAC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW36699.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus COL]
Length = 432

Score = 102 bits (255), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 112/435 (25%), Positives = 201/435 (46%), Gaps = 38/435 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EG + + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRMTDIFRLLGVEIKEDD--E 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ VV G + + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 71 KLVVTSFG--YQSFNTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI +++++ S+Q SA+L A
Sbjct: 126 DRVLRPLKLM DANIEGIEDNYTPLIIKPSVIKGI----NYQMEVA---SAQVKSAILFA- 177

Query: 191 PLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
+L E II +L +S + E + + F + E ++ +Y P + +
Sbjct: 178 --SLFSKEPTTIKELDVSRNHTET---MFKHFNIPIE-AEGLSINTTPEAIRYIKPADFH 231

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA++F+ A IT G+ VT+ G + + +++E MG + T
Sbjct: 232 VPGDISAFAFFIVAALITPGSDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--TTG 287

Query: 309 GPPREPFGKRKH---LKAIDVNMKNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETE 362
P ++ L+ I + +P L V+AL A G + I+D +VKET
Sbjct: 288 AEPTASIRIQYTPMLQPIITIEGELVPKAIDELPIVIALLCTQAVGTSTIKDAEELKVKETN 347

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ L LG ++ D II P E +D+ DHR+ M ++A+ + PV
Sbjct: 348 RIDTTADMLNLLGFELQPTNDGLIIPSEFKTNATVDSLTDHRIGMMLAVASLLSSEPVK 407

Query: 422 IRDPGCTRKTTFPDYF 436
I+ +FP +
Sbjct: 408 IKQFDAVNVSFPGFL 422

>ref|ZP_05101922.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
GAI101]
gb|EEB86224.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
GAI101]
Length = 450

Score = 102 bits (254), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 128/435 (29%), Positives = 191/435 (43%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG ++PG KS+S+R L+L A+ G T + LL +DV A+R G V D
Sbjct: 18 LSGVAQVPGDKSISHRSLILGAMCVGKTTISGLLEGDDVLDTARAMRAFGAEV-TDLGDG 76

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V G G G F A+ + + GN+G +R + A+ + AT+ D + RP
Sbjct: 77 NWSVHGVGVGGF---AEPDGVIDCGNSGTGVRLIMGAMATSPITATFTGDA--SLNGRP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L G G P V + + S+Q SA+L+A A
Sbjct: 131 MARVTDPLALFGTQSVGRKGGRLPMTIVGAADPV--PVRYVVPVPSAQVKSALLLAGLNA 188

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVEG 252
G + +I+ + + E R++ FG K D+ + R GQ ++ V
Sbjct: 189 PG--QTVVIEAEATRDHTE---RMLAGFGAKITVKDTDEGRIITLTGQPELQAQHVDPVR 243

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++ + A I G+ V V G G + L MGA +T+ E T G P

Sbjct: 244 DPSSAAFPVCAALIVPGSDVLVPGIGLNPT--AGLFTTLREMGADLTY-ENERTEGGEP 300

Query: 312 ----REFPGRKHLKAIDV---NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 R F +K I+V M D L+VVA FA G T +R V RVKE++R+

Sbjct: 301 VADLRARF-SPDMKGIEVPPARAASMIDEYPVLSVVASFAQQQTMMRGVKELRVKESDRI 359

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIIDTYD---DHRMAMAFS-LAACAEVPV 420
 A+ L G V+EGPD+ +T NV T DHR+AM+F + A PV

Sbjct: 360 DAMAKGLRANGVEVDEGPDWWAVTGLGHGNVPGGATCASQLDHRAMSFMMINGMAANAPV 419

Query: 421 TIRDPGCTRKTFFPDY 435
 ++ D +FP +

Sbjct: 420 SVDDGAPITTSFPIF 434

>ref|YP_001170040.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
 sphaeroides ATCC 17025]
 gb|ABP72735.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter
 sphaeroides ATCC 17025]
 Length = 445

Score = 102 bits (254), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 123/440 (27%), Positives = 199/440 (45%), Gaps = 31/440 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G ++PG KS+S+R L+L A++ G T + LL +DV A+R G +

Sbjct: 18 LRGRAEIPGDKSISHRALILGAMAVGETRITGLLEGQDVLDTAKAMRAFGAELIQHGPGD 77

Query: 75 RAVV-VGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
 +V VG GG P E + GN+G +R + ++ + AT+ D +R+R

Sbjct: 78 WSVHGVGVGGFTEPAE-----VIDCGNSGTGVRLIMGSMATSPITATFTGDA--SLRKR 129

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAP 191
 P+G + L GA G P V +P V + + S+Q SA+L+A

Sbjct: 130 PMGRVTDPLALFGARAYGRKGRPLMTLVGAAEPVP---VHYTVVPVSAQVKSALLAGL 186

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSWDRFYIKGGQKYKSPKNAYV 250
 A G + ++++ + + E R++ FG + + GQ P+ V

Sbjct: 187 NAPG--QTVVVEREATRDHSE---RMLRGFGAELTVEAAPEGQIITLTGQPELRPQTAV 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
 D SSA++ + A I G+ + V G + D + +LEM GA + + E G

Sbjct: 242 PRDPSSAAFPVCAALIVEGSEILVPGVSRNPTR-DGLYVTLEM-GADIAF-ENEREEGG 298

Query: 310 PPREFPGRK--HLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 P + LK ++V + P D L+VVA FADG T +R V RVKE++R+

Sbjct: 299 EPVADLRVRASELKGEVPPERAPSMIDEYPILSVVAAFADGTTIMRGVKELRVKESDRI 358

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-DTYDDHRMAMAF-SLAACAEVPVTI 422
 A+ L G +EE D ++ + A T+ DHR+AM+F L AE PV +

Sbjct: 359 DAMARGLEACGVRIEEDDTLVVHGRGSRVPGGATCATHLDHRIAMSFLVLGMAAEAPVAV 418

Query: 423 RDPGCTRKTFFPDYFDVLSTF 442
 D +FP + ++ T

Sbjct: 419 DDGSPietsfPIFMGLMRTL 438

>ref|ZP_00953711.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfitobacter sp.
 EE-36]
 gb|EAP84944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfitobacter sp.
 EE-36]
 Length = 450

Score = 102 bits (254), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 128/436 (29%), Positives = 195/436 (44%), Gaps = 34/436 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 +SG ++PG KS+S+R L+L A+ G T + LL +DV A++ G V

Sbjct: 18 LSGVAEVPGDKSISHRSLILGAMCIGETTISGLLEGDDVLDTAKAMQAFGAEVNTMGGGN 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133

Sbjct: 78 +V VG GG A+ + + GN+G +R + ++ + AT+ D + RP
WSVRGVGVGGF-----AEPDGVIDCGNSGTGVRLIMGSMATSPITATFTGDA--SLNGRP 130

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V +P V+ + + S+Q SA+L+A

Sbjct: 131 MARVTDPLALFGTQSVGRKGGRLPMTIVGAADVPV---VRYTVPVPSAQVKSAVLLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+ + + E R++ FG + D+ + R GQ ++ V

Sbjct: 188 APG--KTVVIEAEATR DHE---RMLAGFGAEISVEDTDEGRVITLTGQPELQAQHVDPV 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V V G G + L MGA +T+ E T G

Sbjct: 243 RDPSSAAFPVCAALIVPGSDVLVPGIGLNPTN--AGLFTTLREMGADLTY-ENERTEGGE 299

Query: 311 P----REPFGRKHLKAIDV---NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F LK I+V M D L+VVA FA G T +R V RVKE++R

Sbjct: 300 PVADLRKAF-SPDLKGIEVPPARAASMI DEYPVLSVVAFAQGQTMMRGVKELRVKESDR 358

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVT AIDTYD---DHRMAMAFS-LAACAEVP 419
+ A+ L G V+EGPD+ +T NV T DHR+AM+F L A P

Sbjct: 359 IDAMAKGLRANGIEVDEGPDWAVTGRGHGNVPGGATCASQLDHR IAMSFMILGMAATSP 418

Query: 420 VTIRDPGCTRKTFPDY 435
V++ D +FP +

Sbjct: 419 VSVDDGSPITTSFPIF 434

>ref|YP_765712.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium
leguminosarum bv. viciae 3841]
sp|Q1MN56.1|AROA_RHIL3 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAK05596.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) [Rhizobium leguminosarum bv. viciae 3841]
Length = 452

Score = 102 bits (254), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 122/447 (27%), Positives = 207/447 (46%), Gaps = 44/447 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G+V++PG KS+S+R ++ L+ G T + LL EDV A++ +G + K

Sbjct: 18 LTGSRVIRPGDKSISHRSFMIGGLASGETRITGLLEGEDVINTGRAMQAMGARIR--KEGA 75

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ V+ G G G DA L GNAG +R V ++T++ D + +RP

Sbjct: 76 QWVIEGTGNGALLAPDAP----LDFGNAGTGVRLTMGLVGTYDFHSTFIGDA--SLSKRP 129

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G PG + + S+Q SA+L+A

Sbjct: 130 MGRVLNPLREMGVQVSASEG-DRLPVTLRG----PGTPSPIRYRVPMASAQVKSAVLLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG + E R G+ + +

Sbjct: 185 LNTPG--VTTVIEPVMTRDHE---KMLQFGAALSVETDGDGVRTIRLEGRKLAGQVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEM--MGAKVTWTETSV 305
V GD SS ++ L A I G+ +T+ L + +L + MGA + +

Sbjct: 240 DVPGDPSSTAFLVLAALIVPGSDITI---VNVLMNPTRTGLILTLQEMGADIEVNARL 295

Query: 306 TVTGPPEPFGFRKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
G +H LK + V ++ P D LAV A FA+G T ++ + RVKE

Sbjct: 296 -AGGEDVADLRVRHSELKGVTVPEDRAPSMIDEYPILAVAAACFAEGATVMKGLEELRVKE 354

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPEKLNVT AID----TYDDHRMAMAF-SLA 413
++R+ A+ L G +EG D+ I+ P K A D T+ DHR+AM+F L

Sbjct: 355 SDRLSAVADGLKLNVDCEDEDFLIVRGRPDGKGLGNAADGRVSTHLDHRIAMSFLVLG 414

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+E VTI D +FP++ +++

Sbjct: 415 LASEHAVTIDDAAMIATSFPEFMQLMT 441

>ref|ZP_07904321.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium saburreum
DSM 3986]
gb|EFU76799.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium saburreum
DSM 3986]
Length = 416

Score = 102 bits (254), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 113/432 (26%), Positives = 203/432 (46%), Gaps = 27/432 (6%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G +++PG KS+S+R ++ +++GTT + L D + + +G+++E + +
Sbjct: 2 IKGRLRVPKDKSISHRAVMFGSIAKGTTYIKGFLTGCISTVSIFKKMGINIELNDTS- 60

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V V G + ++ KE L GN+G R ++ ++A T VL G +++RP+
Sbjct: 61 --VKVYNGLYGLKKPKE--ILDCGNSGTTTTLVSGILSAQ--EFTSVLTGDNISIQKRPM 114

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L +GA++ G P+ + G L G + K S S+Q SA+L+A A
Sbjct: 115 SRIITPLSMMGANITSNNG--FAPLTITG-SKLHGIEYK-SPVASAQVKSAILLAGLYAQ 170

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
+ K S + E+ L+ +FG A + S + + + + A +
Sbjct: 171 SPTTVTEPAK--SRDHTELMLK--KFG--ASLTSSKNSVTVNPCNELFASDIAVPSDIS 223

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
S+A + A + G + +E G + + +L+ MGA + +
Sbjct: 224 SAAFFMAAAILVPGSELVLENGVINPTRDGI--IRILKMGANIEIINHDTAFEPVAGIS 281

Query: 315 FGRKHLKAIIDVNMMKMP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
L + V + +P D LA +A A+G T I+D +VKE+ R+ + EL
Sbjct: 282 VSYSLKHSTTVEGDIIPTLIDELPILAAIACLAEGTTVIKDAGELKVKNRIHVMCNEL 341

Query: 372 TKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFS-LAACAEVPVTIRDPGCT 428
+KLG V E D IT KL NVT I T+DDHR+AM F+ L ++ + + + C
Sbjct: 342 SKLGVDVVEDGMEITGTNKLCGNVT-IATHDDHRIAMTFAVLNVLSDGEIRLDNKNVCV 400

Query: 429 RKTFFPDYFDVLS 440
++P++F+ L+
Sbjct: 401 EISYPEFFNDLN 412

>ref|YP_001236311.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium sp.
BTA11]
sp|A5E8B1.1|AROABRASB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ32405.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bradyrhizobium sp.
BTA11]
Length = 445

Score = 102 bits (253), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 135/443 (30%), Positives = 201/443 (45%), Gaps = 41/443 (9%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT+++PG KS+S+R L+L ALS G T + LL EDV A+R LG VE
Sbjct: 18 LSGTLRVPKDKSISHRALILGALSVGETRISGLLEGEDVLNTAQAMRALGAKVERHGDF 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V VG GG A+ L GN+G R + AV AG T V DG +R RP
Sbjct: 78 WTVHGVGVGGF----AQPAATLDFGNSGTGCRVMGAV--AGCPITAVFDGDASLSRSP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ +GA V P+ + G P V + S+Q SA+L+A A
Sbjct: 131 MRRILDPLELIGAKVTASAEGGKLPLTLQGASN-PVPVVYRTPVASAQIKSAVLLAGLAA 189

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +I++ S + E+ L+ FG + + R GQ V

Sbjct: 190 PG--VTTVIEQEASRDHTEMLK---HFGAEIVTTLEGTGRRIALTGQPELHGAPVIVP 244

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ L A I G+ + + T L+ + FA + E MGA + + V G

Sbjct: 245 ADPSSAAFPLVAALIVDGSIDLSDVMTNPLRTGL-FATLRE-MGASIEEDD---VRGD 298

Query: 311 PREPFGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP R L+ ++V + P D + LAV A +A+G T +R + RVKE++

Sbjct: 299 AGEPMVRLRVRASKLRGVEVPPERAPSMIDEYLVLAFAAAYAEAGTTIMRGLHELVRKESD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDTYDDHRMAM-AFSLAACA 416
R+ A L G VE D I+ P L + T+ DHR+AM A + +

Sbjct: 359 RLEATAAMLRVNGVKVEISDDDLIVEGRGHVPGGGL---VATHMDHRIAMSALVMGLAS 414

Query: 417 EVPVTIRDPGCTRKTFFPDYFDVL 439
+ PV + D +FPD+ ++

Sbjct: 415 DKPVKVDDTAFIATSFDPDFVPLM 437

>ref|YP_931265.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum
islandicum DSM 4184]
gb|ABL88922.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pyrobaculum
islandicum DSM 4184]
Length = 399

Score = 102 bits (253), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 121/433 (27%), Positives = 196/433 (45%), Gaps = 53/433 (12%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G P SK S R+LL +AL+EG TV+ + S+D M A++ L

Sbjct: 8 RLEGKFAAPPSPKPYSQLLLASALAEGETVIRGVESDDFTAMFRAVQPLAR----- 59

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLF----LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ C G V+ ++ E + + +G +R+ A G G +

Sbjct: 60 -----LYCEGGV-VKASRREPDFYRSFNMESGFTLRTAVAVYAGVPGITAVYYGGT--L 111

Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALL-M 188
+ RPI +LV L++L A V+ G + V G L V++ ISSQY+S L+ +

Sbjct: 112 KGRPIDELVEALRRLTA-VEKTAGA----IVVEG-RRLEEDFVEIRADISSQYISGLMYL 165

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA + G V + + S +VE T ++++FG E ++ I+ +SP+

Sbjct: 166 AAHVGRGIVRP--VGERKSWSFVEATAEVLKKFGAHVELGET-----IEVEGPLRSPRAV 218

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D S A++ + TGG V + G T + D +V MGA +T + V

Sbjct: 219 DVPSDFSLAFLVAVGATGGHVELLG---TLAEVDKWAIDVFRQMGADITIDNGIMRVG 275

Query: 309 GPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G + +DV++ + PD+ M +A+ A + +AIR V R KE++R+ +

Sbjct: 276 G-----VFTRGVDVLDGRNPDLVMPVALAAAMVEEESAIRGVDHLRYKESDRVATVL 327

Query: 369 TELTKLGASV--EEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEPVVTIRDPG 426
L +LG V ++G Y I PP K V A T+ DHR+ + +LAA V + D

Sbjct: 328 DVLRLRGVEVRYDKGAIY-IRGPPTKREV-AFQTHGDHRIGL-MALAAAKIVGGCVDDL 384

Query: 427 CTRKTFFD---YF 436
K++P YF

Sbjct: 385 PVAKSWPSSILYF 397

>ref|ZP_04867454.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TCH130]
gb|EES97558.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus TCH130]
Length = 435

Score = 102 bits (253), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 117/448 (26%), Positives = 208/448 (46%), Gaps = 42/448 (9%)

Query: 6 EIVLQPIKEISGTVK----LPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALR 61

Sbjct: 3 E+V + I +ISG +K +PG KS+++R ++LA+L+EG + + L ED + R
EMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDIFR 62

Query: 62 TLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
LG+ ++ D ++ VV G + + +V L+ GN+G R L ++ G +

Sbjct: 63 LLGVEIKEDD--EKLVTSPG--YQSFNTPHQV-LYTGNSGTTTLLAGLLSGLGIES-- 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGS 177
VL G + +RP+ ++ LK + A+++ P P + GI +++++

Sbjct: 116 VLSGDVSIGKRPMDRVLRLPLKMDANIEGIEDNYTPLIIKPSVIKGI----NYQMEVA-- 169

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKL-ISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S+Q SA+L A +L E II +L +S + E + + F + E ++

Sbjct: 170 -SAQVKSAILFA--SLFSKEPTIIKELDVSRNHT---TMFKHFNIPIE-AEGLSITTT 221

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
++ P + +V GD SSA++F+ A IT G+ VT+ G + + +++E MG

Sbjct: 222 PDAIQHIKPADFHVPGDISSAAFFIVAALITPGSDVTIHGINPTRSGI--IDIVEKMG 279

Query: 296 AKVTWTETSVTVTGPPREPFGKRH---LKAIDVNMKNMPDVAMTLAVVALF---ADGPTA 349
+ T P ++ L+ I + +P L V+AL A G +

Sbjct: 280 GNIQLFNQ--TTGAEPTASIRIQYTPMLQPIITIEGELVPKAIDELPIALLCTQAVGTST 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
I+D +VKET R+ L LG ++ D II P E +D+ DHR+ M

Sbjct: 338 IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++A+ + PV I+ +FP +

Sbjct: 398 LAVASLLSSEPVKIKQFDAVNVSFPGFL 425

>ref|YP_004073619.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter felis
ATCC 49179]
emb|CBY83029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter felis
ATCC 49179]
Length = 440

Score = 102 bits (253), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 117/440 (26%), Positives = 203/440 (46%), Gaps = 52/440 (11%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
LP KSLS+R ++ A L V N L +D L +TLGL V+ ++ + +

Sbjct: 17 LPADKSLSHRAVIFALLCARPCYVQNFLRGQDCLSTLHMAKTLGLRVQ--QSTPNTLKL 74

Query: 81 CGGKFPV--EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVLDGVPRMRERPIGDL 137
KF E +K L N+G MR + + ++ Y+L G + +RP+G +

Sbjct: 75 PPKKFLCFKEPSKP---LNCNRSGTTMRLFSGLLASSQFQKNHYILVGDSSLSKRPMGRV 131

Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPLALGD 196
+ L+ +GA + P+ I P +K + I S+Q SALL+A

Sbjct: 132 ITPLQVMGAQIRARANHTLAPL---SILSTPLQGMKYTSPIASAQVKSALLLAT----- 182

Query: 197 VEIEIIDKLI-SIPYV--EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---V 250
++ D LI S P + + T R+++ G K + D R + P +++ +

Sbjct: 183 --LQAKDPLIFSEPSLSRDHTERMLKALGAKIQIDRSVRL-----EPLNQPLDSFEWSI 235

Query: 251 EGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA YF LA A + V ++ + ++ +VLE MG V + S +

Sbjct: 236 PADPSSAFYFALAVALVPQSAVLLKNVLLNPTR--IEAFKVLEKMGLHVEFHPHSTQI-- 291

Query: 310 PPREPFGR---KH--LKAIDV--NMKNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP G KH LKA+++ N+ + D LAV A G + +++ RVKE++

Sbjct: 292 ---EPVGDIYVKHRPLKALEIKENIPFLIDELPALAVAMSVAKGVSQRVQNAQELRVKESD 348

Query: 363 RMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLA--ACA EVP 419
R+ + L K+G + + D + I K +++++ DHR+A++F++A AC

Sbjct: 349 RIATTLSNLAKMGITCQAYADGFSIQGSSSLKRPQEPLESGDHRIALSFAVALLACGG-- 406

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
++R+ C +FP++ ++L

Sbjct: 407 -SLRNSACMGVSFPNFIEIL 425

>ref|ZP_01125908.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrococcus mobilis
Nb-231]
gb|EAR23391.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrococcus mobilis
Nb-231]
Length = 411

Score = 101 bits (252), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 117/418 (27%), Positives = 194/418 (46%), Gaps = 30/418 (7%)

Query: 33 LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPVEDAKE 92
+LAAL+EGTT + LL EDV L A R LG+ + + +V+ G ++ + E
Sbjct: 1 MLAALAEGTTEIHGLEGEDVLATLAAFRALGIVTNGPERGR--LVIEGRGLQGLQASPE 58

Query: 93 EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFL 152
+LGN+G AMR L + AG +L G + +RP+ + L ++GA V
Sbjct: 59 P--FYLGNSTAMRLLCGLL--AGQRFDSILTGDVSLSQRPMMRVTEPLLRMGARVAAG- 113

Query: 153 GTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVE 212
T P+ + G L G ++ + S+Q S LL+A A G+ + + S+P +
Sbjct: 114 ATGTAPLHIKGGQALHGIHYEMPMA-SAQVKSCLLLAGLYAKGETCV----IESVPSRD 167

Query: 213 MTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-V 271
T R++ FG + + R + GG + + + D SSA++FL GA+I G+ +
Sbjct: 168 HTERMLTAFGYEVDRCAG--RVCLHGGGRLHAMPLLAIPADISSAAFFLVGASIAPGSDL 225

Query: 272 TVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKH--LKAIDVNMNK 329
+ G + V +L+ MGA + + + G P +H L I +
Sbjct: 226 CLMEVGLNPTRTGV--IAILKRMGADIEVLDKR-WMGGEPPVADLRVRHAALHGIHITPEM 282

Query: 330 MP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 386
+P D L V A A+G T ++ RVKE++R+ A+ L LG + E D
Sbjct: 283 VPAAIDFEFPALFVAAACAEGETLLQGAEELRVKESDRIAAMAAGLQALGITAEPQVDGIR 342

Query: 387 ITP--PEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLST 441
I P+ + A DHR+AMAF++ A A+ + I D +FP + ++ ++
Sbjct: 343 IIGGVQPGGRLHA--RGDHRIAMAFMMALRADAEIIDDRCNVATSFPGFVELAAS 397

>ref|YP_002978141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium
leguminosarum bv. trifolii WSM1325]
gb|ACS58602.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhizobium
leguminosarum bv. trifolii WSM1325]
Length = 452

Score = 101 bits (252), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 122/447 (27%), Positives = 205/447 (45%), Gaps = 44/447 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G+V++PG KS+S+R + L+ G T + LL EDV A++ +G + K +
Sbjct: 18 LTGSVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGARIR--KEGE 75

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ V+ G G G DA L GNAG +R V +T+ D + +RP
Sbjct: 76 QWVIDGTGNGALLAPDAP----LDFGNAGTGVRLTMGLVGTYDFRSTFTGDA--SLSKRP 129

Query: 134 IGDVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G PG + + S+Q SA+L+A
Sbjct: 130 MGRVLNPLREIMGVQVSASEG-DRLPVTLRG----PGTPSPIRYRVPMASAQVKSALLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
G + I+ +++ + E ++++ FG + E R G+ + +
Sbjct: 185 LNTPGITTV--IEPVMTRDHTTE--KMLQGFGAALSVETDSEGVRTIRLEGRGKLAGQVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEM--MGAKVTWTETSV 305
V GD SS ++ L A + G+ +T+ L + +L + MGA + +
Sbjct: 240 DVPGDPSSTAFPLVAALLVPGSDITI---VNVLMNPTRTGLILTLQEMGADIEVANARL 295

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360

G +H LK + V + P D LAV A FA+G T ++ + RVKE
Sbjct: 296 -AGGEDVADLRVRHSELKGVTVPEERAPSMIDEYPILAVAAACFAEGATIMKGLEELRVKE 354
Query: 361 TERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTALD---TYDDHRMAMAFSLAA 414
++R+ A+ L G +EG D+ I+ P K A D T+ DHR+AM+F +
Sbjct: 355 SDRLSAVADGLKNGVDCDEGEDFLIVRGRPDGKGLGNAADGRVSTHLDHRIAMSFLVMG 414
Query: 415 CA-EVPVTIRDPGCTRTKTFPDYFDVLS 440
A E PVTI D +FP++ +++
Sbjct: 415 LASEHPVTIDDAAMIATSFPEFMQLMT 441

>ref|YP_001526847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Azorhizobium
caulinodans ORS 571]
dbj|BAF89929.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Azorhizobium
caulinodans ORS 571]
Length = 471

Score = 101 bits (252), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 126/445 (28%), Positives = 198/445 (44%), Gaps = 35/445 (7%)

Query: 11 PIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P +SG V++PG KS+S+R L+ AL+ G T V LL EDV A LG +VE
Sbjct: 40 PSPGLSGKVRVPGDKSVSHRALIFGALARGEETRVTGLLEGEDVLTAKACALGATVERT 99
Query: 71 KAAK-RAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ R VG G K P L GN+G +R + AV AG DG
Sbjct: 100 GPGQWRVEGVGVGNFKAPA-----APLDFGNSGTGVRLMMGAV--AGNPIQATFDGDAS 151
Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R+RP+ ++ L +G + P+R+ G+ L + + S+Q SA+L+
Sbjct: 152 LRKRPMKRVLDPLAAMGVKLVVEAEGGRLPMRLEGVTDLKAFTYE-TPVPSAQVKSALL 210
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEE--HSDSWDRFYIKGGQKYKSP 245
A A G E ++++ + + E R++ FG H R +KG + K+
Sbjct: 211 AGLAASG--ETVVVEREATRDHTE---RMLAHFGADVSEPHGAHGRITLKGPELKA- 264
Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLMMGAKV----TW 300
V D SSA++ L A I G+ + + L+ L+ MGA +
Sbjct: 265 APVDVPSDPSAFLVAIVPGSDIVITDVMNPLR--TGLITLKEGASITLAER 322
Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWR 357
TE TV R + + LK + V + P D LAV A FA+G T ++ +A R
Sbjct: 323 TEGGETVAD-LRVRYSK--LKGVAVPPERAPAMIDEYPILAVAAAFAGEGTRMQGLAELR 379
Query: 358 VKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTALDITYDDHRMAMAF-SLAAC 415
VKE++R+ A+ L G + EG D + + + T+ DHR+AM+F L
Sbjct: 380 VKESDRLAAVADGLAACGVTHRIEGDDLIVTGAADVEGGGPVATHMDHRIAMSFLVLGLA 439
Query: 416 AEVPVTIRDPGCTRTKTFPDYFDVLS 440
+ V + D +FP + +++
Sbjct: 440 SRAGVKVDDVSFIATSFPTFMPMIA 464

>ref|ZP_03658338.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter cinaedi
CCUG 18818]
ref|ZP_07806023.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter cinaedi
CCUG 18818]
gb|EFR46478.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter cinaedi
CCUG 18818]
Length = 437

Score = 101 bits (252), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 113/428 (26%), Positives = 188/428 (43%), Gaps = 35/428 (8%)

Query: 25 KSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + A L+ + L ED + L + LGL VE KR ++
Sbjct: 23 KSISHRGAMFALLANAPCEIKGFLEGEDTLHTLEIAKNLGLVVE-----KRGDILHILT-- 75
Query: 85 FPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLK 142
P + +E + L GNAG MR ++ G+ +VL G + RP+G ++ L

Sbjct: 76 -PPKGGGLQEPKQVLDCGNAGTGMRLYVGLLSGVKGH--FVLSGDEYLNARPMGRVIEPLS 132

Query: 143 QLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEII 202
+GAD+ P+ + G L + S S+Q SA+++A G +

Sbjct: 133 AIGADIRGREQNKYAPLSIQG-ARLKSFNQ-SKIASAQVKSAMILAGLRTEG--KCRFY 188

Query: 203 DKLISIPYVEMTLRLMERFGVKAHS-----DSWDRFYIKGGQKYKSPKNAYVEGD 253
+ L+S + E L+ M GVK + D ++ + +K +S K V D

Sbjct: 189 EPLLSRNHTENMLKGM---GVKIQGREIQSGTNAVDGYEVEFEGSCKKLESFK-LEVPAD 244

Query: 254 ASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--TGPP 311
SSA +F A + V ++ + ++ +LE MGAKV++ S G

Sbjct: 245 PSSAFFFAVAACVLESKVLLKNVLLNKTR--IEAFKILESMGAKVSYNVRSSLYEEIGDI 302

Query: 312 REPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
GR +D N+ + D L V A G + +R+ RVKE++R++A T L

Sbjct: 303 EVQGGRLQAVQVDKNIAWLIDELPALGVCFALAKGRSEVRNAKELRVKESDRILATITNL 362

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRTK 431
+G EE D + E L + ++ DHR+AM+F++A I D C +

Sbjct: 363 RAMGIECEEFEFGSVNGGE-LKRARVSSFGDHRAMSFIAQLV-CGGEIEDSACIDVS 420

Query: 432 FPDYFDVL 439
FP++ ++L

Sbjct: 421 FPNFLELL 428

>gb|AAx21587.1| AroA [Francisella novicida]
gb|AAx21588.1| AroA [Francisella tularensis subsp. tularensis]
gb|AAx21589.1| AroA [Francisella tularensis subsp. tularensis]
gb|AAx21590.1| AroA [Francisella tularensis subsp. mediasiatica FSC147]
gb|AAx21591.1| AroA [Francisella tularensis subsp. mediasiatica]
gb|AAx21594.1| AroA [Francisella tularensis subsp. tularensis]
gb|AAx21596.1| AroA [Francisella tularensis subsp. tularensis]
gb|AAx21597.1| AroA [Francisella tularensis subsp. tularensis]
gb|ACJ54496.1| AroA [Francisella novicida]
gb|ACJ54499.1| AroA [Francisella novicida]
Length = 172

Score = 101 bits (252), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 60/143 (41%), Positives = 79/143 (55%), Gaps = 4/143 (2%)

Query: 167 LGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV

Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVK 286
D + Y +Y SP N VE D S+ASYF A AAITG T+ V S QGD+K

Sbjct: 84 --DIDENIYTANKSQYISPSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGD 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTG 309
F EVLE +G +V + + VTG

Sbjct: 142 FLEVLEKIGCQVNYNDGIEVTG 164

>gb|ACJ54494.1| AroA [Francisella sp. FSC156]
gb|ACJ54497.1| AroA [Francisella novicida]
gb|ACJ54498.1| AroA [Francisella novicida]
Length = 172

Score = 101 bits (251), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 60/143 (41%), Positives = 79/143 (55%), Gaps = 4/143 (2%)

Query: 167 LGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV

Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVK 286
D + Y +Y SP N VE D S+ASYF A AAITG T+ V S QGD+K

Sbjct: 84 --DIDENIYTANKSQYISPSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGD 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTG 309
F EVLE +G +V + + VTG
Sbjct: 142 FLEVLEKIGCQVNYNDGIEVTG 164

>ref|ZP_04808519.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pullorum
MIT 98-5489]
gb|EEQ63801.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pullorum
MIT 98-5489]
Length = 431

Score = 101 bits (251), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 116/434 (26%), Positives = 197/434 (45%), Gaps = 40/434 (9%)

Query: 20 KLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
K+ KS+S+R + + LS+ + + N L ED L + LGL V K + +V
Sbjct: 15 KIASDKSISHRCAIFSLSDKPSYIQNYLKGEDTLDTLKIARLGLGV--KEESKGMVF 71

Query: 80 GCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
P + KE ++ GNAG A+R ++A G +VL G + RP+ +V
Sbjct: 72 -----LPPKSIKEPSEILDCGNAGTAIRLYLGLLSAQKG--MFVLSGDCYLNRPMPKRVV 124

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L+ +GA + + P+ V G GL + +S S+Q SAL+++ A GD
Sbjct: 125 EPLRSIGATIFGRDNGNFAPLVVIGNQGLKSFEY-VSKIPSAQVKSALILSGLFANGDS- 182

Query: 199 IEIIDKLISIPYVEMTLRLMERFGVKAEE--HSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ + +S + E LR M G + E H I ++ P + D S
Sbjct: 183 -KYFEPELSRDHTEMLRGM---GAEIESKIHQGGDEVSVISPLKQALKPLEMNIPADPS 238

Query: 256 SASYFLAGAAI---TGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SA +F AI + G + T ++ ++LE MG K+ + E S T
Sbjct: 239 SAFFFAVAVAIMPESYGLLKNVLLNPTRIEA---FKMLEKMGVKIAYKENSNTYESIGD 294

Query: 313 -EPFGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
E K L++I+VN ++++P +A+ +A A+G + + + RVKET+R+
Sbjct: 295 IEIVSPKKLQSIIEVNEKISWLIDEIPALAIAMAC----ANGVSKVTNAKELRVKETDRIK 350

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDP 425
A+ L G +E D +IT E + + +Y DHR+AM+F++A + I
Sbjct: 351 AVVENLKLKGIEAKELDDGFVITGGE-IQKAEVSSYGDHRIAMSFAIAGLKN-GMRITQA 408

Query: 426 GCTRKTFFPDYFDVL 439
+FP++ ++L
Sbjct: 409 EYINISFPNFLEIL 422

>ref|YP_003143352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Slackia
heliotrinireducens DSM 20476]
gb|ACV22003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Slackia
heliotrinireducens DSM 20476]
Length = 439

Score = 100 bits (250), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 125/458 (27%), Positives = 209/458 (45%), Gaps = 37/458 (8%)

Query: 4 AEEIVLQPI-KEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRT 62
+E V+ P+ + + G++ +PG KS+S+R +L +A++EGT+ + +L+S+DV + ++
Sbjct: 2 SEITVINPLNRLVGSIAVPGDKSISHRSVLFSAEAGTSRISGVLDSDVRSSIRVVQQ 61

Query: 63 LGLSVEADKAAKRAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
LG V +K ++ G G + + + GN+G R + + A +
Sbjct: 62 LGAQVNLEKMPDGSLSGGITGWAAGPKQPDEPVDCGNSGTTARLIMGIL--APWDIQVE 119

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFL--GTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G +R RP+ + L ++GA FL GT P+ V G L + + S+
Sbjct: 120 ITGDASLRSRPQRVATPLARMGAR---FLPEGTYTLPMTVCGTSKLKAITYE-TPVASA 175

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEEHSDSWDRFYIKGGQ 240
Q +A+L+A A G E +++ S + E+ ++ +G + + + R G
Sbjct: 176 QVKTAVLLAGLSAEG--ETRVVEPAPSRNHTL---MLPEYGAE---TIAATRLAGVTGP 227

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
V GD SSA++ L AAI G V +EG + + F LE MG V
Sbjct: 228 VTLKAAEITVPGDPSSAAFLCAAIIIPGSAVQIEGVSLNPAR--IGFLRTLHMG--VD 283

Query: 300 WTETSVTVTGPPREPFGFR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
+ SVT G +E G HL+ +V K+ D LA+VA A G T
Sbjct: 284 ASRRSVTEGG--KEIVGLLNAEYCPHLRGCEVPTEKIASLVDEVPIALVAHAHAGITVF 341

Query: 351 RDVASWRVKETERMVAIRTELTKLGASV-EEGPD-YCIITPPEKLNVT-IDENTYDDHRMA 407
R + RVKET+R+ A+ L LG EG D Y P K+ A + ++DHR+A
Sbjct: 342 RGIDELRVKETDRVAAVIEGLGVLGVDWTEGSDLYVEGNPGLKVPKGARFNAHNDHRLA 401

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
M +++A A PV I ++P + + +
Sbjct: 402 MTWAVAGLAGNEPVQIEGYDSIAISYPTFMQDIDRLAR 439

>ref|ZP_08089003.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium symbiosum
WAL-14163]
gb|EGA95360.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium symbiosum
WAL-14163]
Length = 426

Score = 100 bits (249), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 120/448 (26%), Positives = 196/448 (43%), Gaps = 45/448 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ +SG + +PG KS+S+R ++ ++EG T V L D + +G+ +E
Sbjct: 7 RRLSGELTIPGDKSISHRSIMFGSIAEGLTEVRGFLQGADCLSTISCFTKMGIPIEN--- 63

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+ G A +E+ L GN+G R + + A + T L G +R R
Sbjct: 64 -KGETVLIHGRGLRGLTAPKEI-LDCGNSGTTTRLCIGILAAQDFDVT--LTGDESIRRR 119

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNG--IGGLPGGKVKLSGSISSQYLSALLMAA 190
P+ ++ L +GA + DC P+ + G I G+ S S+Q SA+L+A
Sbjct: 120 PMKRIMEPLSMMGAKIRSIHCNDCAPLAITGCRHGIH---YQSPVASAQVKSALLAG 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G E + + IS + E+ ++ FG ++ E++ + R P NA
Sbjct: 176 LYAEG--ETRVTESYISRNHSEL---MLSAFGADIRTTAVLR-----PGNA 219

Query: 249 Y-----VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
V GD SSA++F+A A I V + G + + V M ++
Sbjct: 220 LKGLCITVPGDISAAFFIAALIVPNSSEVLIRNVGINPTRDGI--LHVCQMNGNISIL 277

Query: 302 ETSVTVTGPPREPFGGRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
P + R L+ + + +P D LA +A +A G T IRD A +
Sbjct: 278 NRKNESGEPTADLLVRSSALQGTVIEGSIIPTLIDELPMLAAMACYAKGTTVIRDAELK 337

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-IDENTYDDHRMAMAFSLAA-CA 416
VKE+ R+ + L +GA V E D II L+ ID+ DHR+AM F++ A A
Sbjct: 338 VKESNRITVMAENLRAMGADVTETEDGMIIHGRPLHGAVIDSKKDHRIAMTFAVTALAA 397

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
E I D C ++P ++ L+ +
Sbjct: 398 EGETEILDADCVNISYPGFYSDLARLKR 425

>ref|ZP_06890569.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylosinus
trichosporium OB3b]
gb|EFH00945.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylosinus
trichosporium OB3b]
Length = 448

Score = 100 bits (249), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 124/443 (27%), Positives = 192/443 (43%), Gaps = 44/443 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ +SG + PG KS+S+R L+L L+ G T ++ LL EDV A R LG + D+

Sbjct: 18 RALSGRCRPPGDKSVSHRSLILGTAVGETAIEGLLEGEDVLR TAEACRALGARI--DRL 75

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ V G + + +E L GNAG R + V AG T DG +R+R

Sbjct: 76 GPGSWSVRGPGGLGSLLPRE--TLDFGNAGTGSRLMMGVV--AGHPITARFDGDASLRKR 131

Query: 133 PIGDLVVGLKQLGADV-DCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAA 190
P+ ++ L Q GA V + G CP + LP V+ + S+Q SA+L+

Sbjct: 132 PMRRILDPLTQQGARVLEEAEGGRCPILLRGAAEPLP---VEYKTPVASAQIKSAVLLCG 188

Query: 191 PLALGDVEIEIIDLKISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNA 248
+ G +I+ S + E +++ FG + +E R G+ P

Sbjct: 189 LNSPG--RTVVEISEASRDHTE--KMLAHFGARIASEPFGPHGRKITLEGRPELRPAV 243

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE----- 302
V D SSA++ L A I G+ + +EG L+ L+ MGA++++

Sbjct: 244 RVPADPSSAAFLVAALIVPGSEIVIEGVMINPLRNG--LLTTLQEMGARISFENRRAEG 301

Query: 303 ----TSVTVTGPPREPFGKRHLKAIDVNMNKP---DVAMTLAVVALFADGPTAIRDVAS 355
+ V L +DV + P D LAV A FA G T +R ++

Sbjct: 302 GEEVADIRVAA-----STLAGVDVPAERAPSMIDEYPILAVAAAFAGGETRMRGLSE 353

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTAIIDYDDHRMAMAF-SL 412
RVKE++R+ AI L E D I+ ++T+ DHR+AM+F +

Sbjct: 354 LRVKESDRLEAIAAGLRANAVECEISGDDLIVRGGTGRVSGGVVETHLDHRIAMSFLVM 413

Query: 413 AACAEVPTIIRDPGCTRKTFPDY 435
AE VT+ D +FPD+

Sbjct: 414 GLAAEQDVTVDDDRMIATSFPDF 436

>ref|YP_004172823.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerolinea thermophila UNI-1]
dbj|BAJ62223.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Anaerolinea thermophila UNI-1]
Length = 441

Score = 100 bits (249), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 131/465 (28%), Positives = 208/465 (44%), Gaps = 63/465 (13%)

Query: 7 IVLQPIKEISGTVKLPGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLS 66
+++ P + G V++PG KS+S+R L AAL+EG +++N L+S ML AL LG++

Sbjct: 3 LIVSPGAPLRGEVRIPGDKSISHRAALFAALAEGLIENFLDSGVTRAMLNALTALGVT 62

Query: 67 VEADKAAKRAVVVGC-GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ G K P E LF GN+ +R L A+ AAG A VLDG

Sbjct: 63 WRLEDECLEVRSPGWRRWKIPAEP-----LFCGNSATTLRLLAGALAAAGIPA--VLDG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
P +R RP+ +V L+ +G + G GG P + L + L

Sbjct: 115 TPGLRRRPMERIVDPLRAMGPITAAEG-----GGAP---LTLQARPAESPLRG 160

Query: 186 LLMAAPLALGDVE-----IEIIDKLISIPYVEMTLRLMERFGVKAHSD--- 229
+ +A V+ +E+++ +S + E R+++ GV E +

Sbjct: 161 MSHTLAVASAVKTCLLLAGLAADAPVEVVEPTLSRDHTE---RMLKGMGVALEDARLP 217

Query: 230 --SWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVK 286
+W R + Q+ P + GD S+A++ LA A+I G+ V + G G +

Sbjct: 218 GAAWVRLHPP--QQPLPPLRGSIPGDFSAAAFLLAAASIVPGSDVLIRGVGLNPTR--TG 273

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPEPFGKRHLKAIDVNMNKP-----MPDVAMTLA 338
E L MGA++ T V G EP G ++A + + M D A

Sbjct: 274 LLETLMREMGARIEITHRR-EVFG---EPVGDVVRVQASALRAGRVQGERVVAMIDEFPFAFA 329

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTAI 398
AL A+G + +RD R KE++R+ A+ E+ +LG EE PD ++ L T +

Sbjct: 330 AAALHAEGISTVRDAQELRYKESDRIAALVQEVRRLLGGIAEEHPDGFDSLGGALGGT-V 388

Query: 399 DTYDDHRMAMAFSLAACAEV-PVTIIRDPGCTRKTFPDYFDVLSTF 442
+ DHR+AMA ++A A V V I ++FPD+ L

Sbjct: 389 HPHGDHRLAMALAVAGLAGVKSVIIIEQAEIMAESFPDFVATLQAL 433

>ref|ZP_05089300.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria sp. R11]
gb|EEB70992.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ruegeria sp. R11]
Length = 449

Score = 100 bits (249), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 126/441 (28%), Positives = 204/441 (46%), Gaps = 34/441 (7%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV-EADKAA 73
+ G ++PG KS+S+R ++L AL+ G T + LL EDV A+R +G V + D +
Sbjct: 18 LKGIAEVPDGKSIHSRSLILGALAVGETKITGLLEGEDVLDTAKAMRAMGAEVTKHDDGS 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG GG A+ + + GN+G +R + + + AT+ D + +RP
Sbjct: 78 WSVHGVGVGGL-----AEPDQVIDCGNSGTGVRLIMGMATSAITATFTGDA--SLNKR 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V P V+ + + S+Q SA+L+A
Sbjct: 131 MARVTDPLALFGTKSVGRSGGRLPMTIVGAAEPTP---VRYTVPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+K + + E R++ FG + D+ + R GQ + V
Sbjct: 188 APG--KTVVIEKEATRHDSE---RMLAGFGAEITVEDTDEGRVITLTGQPELQAQVIAVP 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A IT G+ V V G G + + + L+ MGA +T+ E G
Sbjct: 243 RDPSSAAFPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF-ENMREEGGE 299

Query: 311 P---REFPGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F ++K I+V + M D L+VVA FA G T + V RVKE++R
Sbjct: 300 PVADLRKF-SPNMKGIEVPPERAASMIDEYPVLSVVASFASGKTMAGVKELRVKESDR 358

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAMAFS-LAACAEVP 419
+ A+ L G VEEG D+ +T V +++ DHR+AM+F + A+ P
Sbjct: 359 IDAMARGLRANGVMVEEGDDWAVTGMGADGVPGGGTCEFLDHRAMSFVMVMGMAQNP 418

Query: 420 VTIRDPGCTRKTFPDYFDVLS 440
VT+ D +FP + +++
Sbjct: 419 VTVDDSTPIATSFPIFTPLMT 439

>ref|ZP_00948256.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfitobacter sp.
NAS-14.1]
gb|EAP81736.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfitobacter sp.
NAS-14.1]
Length = 441

Score = 100 bits (248), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 127/436 (29%), Positives = 194/436 (44%), Gaps = 34/436 (7%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV-EADKAAK 74
+SG ++PG KS+S+R L+L A+ G T + LL +DV A++ G V
Sbjct: 9 LSGVAEVPDGKSIHSRSLILGAMCIGETTISGLLEGDDVLDTAKAMQAFGAEVTNMGGGN 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ + + GN+G +R + ++ + AT+ D + RP
Sbjct: 69 WSVRGVGVGGF-----AEPDGVIDCGNSGTGVRLIMGSMATSPITATFTGDA--SLNGRP 121

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L G G P V +P V+ + + S+Q SA+L+A
Sbjct: 122 MARVTDPLALFGTQSVGRKGGRLPMTIVGAADPVP---VRYTVPVPSAQVKSALLAGLN 178

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+ + + E R++ FG + D+ + R GQ ++ V
Sbjct: 179 APG--KTVVIEAEATRHDTE---RMLAGFGAEISVEDTDEGRVITLTGQPELQAQHVDP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V V G G + L MGA +T+ E G
Sbjct: 234 RDPSSAAFPVCAALIVPGSDVLVPGIGLNPTR--AGLFTTLREMGADLTY-ENERIEGGE 290

Query: 311 P----REFPGRKHLKAIDV---NMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P R F LK I+V M D L+VVA FA G T +R V RVKE++R
Sbjct: 291 PVADLRRAKF-SPDLKGIEVPPARAASMIIDEYPVLSVVAFAAQGTMMRGVKELRVKESDR 349

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD---DHRMAMAFS-LAACAEVP 419
+ A+ L G V+EGPD+ +T NV T DHR+AM+F L A P
Sbjct: 350 IDAMAKGLRANGIEVDEGPDWWAVTGRGHGNVPGGATCASQLDHRIAMSFMI LGMAATSP 409

Query: 420 VTIRDPGCTRKTFFPDY 435
V++ D +FP +
Sbjct: 410 VSVDDGSPITTSFPIF 425

>ref|ZP_01304551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingomonas sp.
SKA58]
gb|EAT07607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sphingomonas sp.
SKA58]
Length = 438

Score = 100 bits (248), Expect = 5e-19, Method: Compositional matrix adjust.
Identities = 122/445 (27%), Positives = 194/445 (43%), Gaps = 38/445 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+SG+V +PG KS+S+R L+L+AL+ G + V+ LL EDV A+R +G +E D
Sbjct: 11 LSGSVTPVPGDKSISHRSLMLSALAVGESRVEGLLEGEDVLATAAAMRAMGARIERDDGCV 70

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ VG GG + L +GN+G + R L + + AT++ D + +RP
Sbjct: 71 WHIHGVGVGGLL-----QPGTALDMGNSGTSTRLLMGLLASHDLTATFIGDA--SLSKRP 123

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L Q+GA G P +P V S+Q SA+L+A
Sbjct: 124 MARVTEPLAQMGASFTTSPGDRLPLTMRGACPAVPLDYVLPVA--SAQVKSAILLAG--- 178

Query: 194 LGDVEIEIIDKLIS-IPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+ I +++ IP + + R+++ FG ++ E R G+ P+ V
Sbjct: 179 ---LNTPGITRVVEPIPTRDHSERMLQGFGADLRVEQQADGARVITLIGEAEKPPQIMV 235

Query: 251 EGDASSASY-FLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++ +A + G VT+ G + + ++L MG + V G
Sbjct: 236 PGDPSSAAFPMAALVVPKSVTIANVGLNATRA--GLIDLLREMGGSIIEVNNAR-DVGG 292

Query: 310 PPREFPG-----RKHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
EP G L ++ + + P D V A A G + R + RVKE+
Sbjct: 293 ---EPVGDVLVTASVLTGVEPDPARAPSMIDEYPVAFVAAALAQGRSVFRGLEELRVKES 349

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
+R+ + L +GA VEE D II I T DHR+AM+F++A A
Sbjct: 350 DRIATMVEGLRAIGARVEEMEDGLIIEGTGGQLLPGGGPIATKLDHRIAMSFIAIAGLASR 409

Query: 419 P-VTIRDPGCTRKTFFPDYFDVLSTF 442
VTI D +FP + +L
Sbjct: 410 EGVTTIDMRPVATSFPTFIPLRLVL 434

>ref|YP_002634191.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
carnosus subsp. carnosus TM300]
sp|B9DNV0.1|AROASTACT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAL28006.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
carnosus subsp. carnosus TM300]
Length = 432

Score = 100 bits (248), Expect = 6e-19, Method: Compositional matrix adjust.
Identities = 120/471 (25%), Positives = 211/471 (44%), Gaps = 74/471 (15%)

Query: 1 MAGAEIEVLQ-PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGA 59
M E I L+ P+K G ++PG KS+++R ++L++L++G +V+ L +ED +
Sbjct: 1 MTKTETINLRGLK---GEFEVPGDKSMTHRAIMLSSLAQGSVITKPLLAEDCLRTMKI 57

Query: 60 LRTLGLS--VEADKAAKRAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAG 116
 LG++ ++ DK V V G ++ K Q L+ GN+G R + ++ G
 Sbjct: 58 FELLGVNFDIKDDK-----VFVDSPG---YQNFKTPHQSLYTGNSGTTTRIMAGLLSGIG 109

Query: 117 GNATYVLVDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
 + VL G + +RP+ ++ LK++GA + + + P+ +N + G K+
 Sbjct: 110 IQS--VLSGDESIGKRPMNRVIDPLKEMGASITG-IENNYTPLVINP-SDIQGIDYKMPV 165

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY- 235
 + S+Q SA+L A+ + T + G+ H+++ Y
 Sbjct: 166 A-SAQVKSAILFASLFS-----KTASTITEIGITRNHTETMFEHYN 205

Query: 236 ----IKGGQKYKSP-----KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQ 282
 I G P K+ V GD SSA++F+ A IT G+ +T+ G S +
 Sbjct: 206 IPLKINGNVIQITPDAITSIKVKDFTPGDISAFAFFIVAALITPGSDITIHNVGMNSTR 265

Query: 283 GDVKFAEVLEMMG--AKVTWTETS-----VTVTGPPREPFGRKHLKAIDVNMNMKP 331
 + V EM G + T TS T P E G +AID ++P
 Sbjct: 266 SGI-IDIVKEMKGNIEIINQNTSEPTASIRIQYTPDLQPAELSGELITRAID----EIP 320

Query: 332 DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE 391
 VA+ + A+G + I+D + KET R+ EL LG V D II P +
 Sbjct: 321 IVAL---LCTQANGSSVIKDAEELKFKETNRIETTSDELGLLGFEVHPTDDGFIHPSK 376

Query: 392 KLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFFDYFDVLST 441
 + ++ +Y DHR+ M ++A+ ++ + IR+ +FP++ +L +
 Sbjct: 377 FEHAASVSSYDHRIGMTLAIASLLSDETLAIRNFDVNTSFPEFLPLKS 427

>ref|YP_316829.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter
 winogradskyi Nb-255]
 sp|Q3SW64.1|AROA_NITWN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 gb|ABA03477.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter
 winogradskyi Nb-255]
 Length = 449

Score = 100 bits (248), Expect = 6e-19, Method: Compositional matrix adjust.
 Identities = 132/447 (29%), Positives = 203/447 (45%), Gaps = 29/447 (6%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--- 69
 + ++G V++PG KS+S+R L+L AL+ G T + LL EDV A++ LG VE
 Sbjct: 16 QSLTGRVRVPGDKSISHRALILGALAVGETRISGLLEGEDVLNTAKAMQALGAKVERRTD 75

Query: 70 DKAAKRAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGNATYVLVDGVP 128
 D V G G G F A E L GN+G R + AV AG DG
 Sbjct: 76 DNGGIAWSVRGVGTGGF---ATPEAPLDFGNSGTGCRLVMGAV--AGCPIRAAFDGDGS 129

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 +R RP+ ++ L+ +GA V P+ + G P V + S+Q SA+L+
 Sbjct: 130 LRSRPMRRILDPLELMGARVISQSDGGRLPLTLEGARD-PLPIVYRTPVASAQIKSAVLL 188

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
 A A G +I++ S + E+ L+ FG + + + R GQ
 Sbjct: 189 AGLSAPG--VTTVIEREASRDHTEMLK---HFGADIVSVAEGAHRKISLTGQPELHGA 243

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
 V D SSA++ + A IT G+ + ++ T L+ L MGA + +ET +
 Sbjct: 244 GVTVPADPSSAFAFFIVAALITEGSDIVLDDVMTNPLR--TGLFVTLREMGASIEESETRL 301

Query: 306 TVTGGPPREPFGRK--HLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
 G P K L+ I+V + P D + LAV A FA+G T +R + RVKE
 Sbjct: 302 D-AGEPMAQLRVKASRLRGIEVPAERAPSMIDEYLVLAFAAFAEGTTVMRGLREL RVKE 360

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACA-EV 418
 ++R+ A L G +VE D I+ ++ + T+ DHR+AM+ + CA +
 Sbjct: 361 SDRLEAAAAMLRAAGVAVEIAGDDLIVEGRVPGGGLVTTTHMDHRIAMSALVMGCASDA 420

Query: 419 PVTIRDPGCTRKTFFDYFDVLSTFVK 445
 PV + D +FPD+ ++ N

Sbjct: 421 PVKVDDIAFIATSFDPFVPMQRLGAN 447

>ref|ZP_07685443.1| hypothetical protein OSCT_1394 [Oscillochloris trichoides DG6]
gb|EF080701.1| hypothetical protein OSCT_1394 [Oscillochloris trichoides DG6]
Length = 435

Score = 100 bits (248), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 124/448 (27%), Positives = 195/448 (43%), Gaps = 41/448 (9%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V +PG KS+S+R ++ A++ G+ + N L D + +R LG+ V D+
Sbjct: 11 QLRGIVDVPGLKSSISHRAVIFNAVASGSARITNFLTGADCLSTIACIRALGVDVTQDEDE 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG G D L GN+G +R L + VL G +R RP
Sbjct: 71 VHVYGVGLQGLREPSDV-----LDCGNSGTTLRLLAGLLAGM--PIFTVLTGDASLRSP 123

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY----LSALLM 188
+V L+ LGA +D D P+ V G + GG L + S+Q L+ L
Sbjct: 124 QRRIVEPLRSLGAQIDGRQAGDRAPLAVRGT-AIRGGSYHLPVA-SAQVKSALLLAGLGG 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNA 248
+ PL L I + T R++ G++ E + + P +
Sbjct: 182 SGPLTLTG-----RIDSRDHTRMLTAMGLELEITPEQITLHPPTHVPVLPYPLSL 231

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD SSA+++ AAI +T G C + G + +VL MGA++ T
Sbjct: 232 RVPGDPSAAFWWAAAIHPNAELTTPGVCLNPTRTGAL---DVLAMGAQIEITNQRE 288

Query: 307 VTGPPPEPFGRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ P + R L+ ++ + +P D LAV A A+G T +RD R KET+
Sbjct: 289 GSEPVGDVTVRSVLRGTEIAGDLIPLRIDEIPILAVAAACAEGETVVRDAQELRAKETD 348

Query: 363 RMVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
R+ + L LG VE D I P L + ++ DHR+AMA+++AA A
Sbjct: 349 RIATVAEGLRALGGHVEPTSDGMKIVGLGGP--ALRGAQVQSHHDHRLAMAWAVAALIA 406

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
TI DP ++P +++ L T V++
Sbjct: 407 GETTIADPDSAAVSYPGFWETL-TMVQH 433

>ref|YP_003303682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurospirillum
deleyianum DSM 6946]
gb|ACZ11647.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sulfurospirillum
deleyianum DSM 6946]
Length = 428

Score = 100 bits (248), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 110/432 (25%), Positives = 191/432 (44%), Gaps = 33/432 (7%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
T K+ KS+S+R + + LS+ +++ N L +ED L + LG++++ +
Sbjct: 15 ATDKIASDKSISHRCAIFSLSDQPSLIQNYLLAEDTLCTLKIVEALGVTIQTHEEKGVF 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ P++ + + L GN+G AMR L + G +VL G + RP+
Sbjct: 75 TITP-----PIKVGEPLILDGNSGTAMRLLMGFLATCEG--FFVLHGDKYLASRPMRR 127

Query: 137 LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLALG 195
+ L+ +GA +D + P+ GI G I S+Q SAL+++AA A G
Sbjct: 128 VADPLRSIGAHIDGRNDGNFAPL---GIRGEKLNAPHYESKIASAQVKSALILAALQANG 184

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ +S + E LR G+ A+ I +K P N V D S
Sbjct: 185 IS--TFCEPELSRDHSERMLR-----GMGAKVISEGLHVSIYPQEKPLQPLNIRVPSDPS 237

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSQ-----GDVKFAEVLEMMGAKVTWTETSVTVTGP 310
S +F AAI EGC T ++ +VL MGA+V++ E
Sbjct: 238 SGFFFAVAAAIH-----EGCMVTLHNMLLNPTRIEAYKVLARMGAEVSFIEKESQYESV 291

Query: 311 PREPFGRKHLKAIDV--NMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
K L+ ++V N++ + D L++ A G + +++ RVKE++R+ ++
Sbjct: 292 GDIVIKGKSLQGVEVSENISWLIDELPALSIACAKGKSVKNAEELRVKESDRISVV 351

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCT 428
L V+E D + L I+++ DHR+AM+F++A + + I D C
Sbjct: 352 KNLRLCHIEVQEFADGYEVEGG-MLQSATINSFGDHRIAMSFAIAG-TKTAMCIEDIECI 409

Query: 429 RKTFPDYFDVLS 440
+FP++ ++LS
Sbjct: 410 NTSFPNFIELLS 421

>ref|ZP_01995870.1| hypothetical protein DORLON_01865 [Dorea longicatena DSM 13814]
gb|EDM62840.1| hypothetical protein DORLON_01865 [Dorea longicatena DSM 13814]
Length = 309

Score = 99.8 bits (247), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 89/308 (28%), Positives = 146/308 (47%), Gaps = 15/308 (4%)

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L +GA + C P+ + G L G + S S+Q SA+L+A A D
Sbjct: 8 LNTMGAHIRSLNDNGCAPLHIRP-GALHGIHYQ-SPVASAQVKSALLAGLYA--DSPTS 63

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAYF 260
+ + +S + E+ L+ + H+D +++ ++ + V GD SSA+YF
Sbjct: 64 VTEPALSRNHTELMLQGFAYVATDLHTDGTATAHVEPCKELYG-QQICVPGDISSAAYF 122

Query: 261 LAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREF--GR 317
+A A + G+ + V+ GT + F +V + MGA + ++ G R
Sbjct: 123 IAAALVPGSELLVKNVGTNFTRA--GFLKVCKAMGADIETVSQTIE-GGESRADLLVRY 179

Query: 318 KHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
HLK + + +P D +A++A FADG T IRD A +VKET R+ + L +
Sbjct: 180 SHLKGTVIEGDIPTLIDEIPMIAIMAAFADGQTVIRDAELKVKETNRIDTVTAGLKAM 239

Query: 375 GASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFP 433
GA + D II LN +I +Y DHR+AMAFS+A A + I D C ++P
Sbjct: 240 GAVITPTDDGMIEGTGHLNGASIQSYLDHRIAMAFSVAGLASDGETQIVDSQCVDVSYF 299

Query: 434 DYFDVLST 441
+++ L++
Sbjct: 300 EFYATLNS 307

>ref|YP_002607312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nautilia profundicola
AmH]
gb|ACM92625.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nautilia profundicola
AmH]
Length = 431

Score = 99.8 bits (247), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 119/437 (27%), Positives = 198/437 (45%), Gaps = 60/437 (13%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + L+ G + N L +ED L + LG VE D + + +
Sbjct: 21 KSISHRCAIFSLTNGKNTIKNYLRAEDTMNSLEIAKALGAKVEDD---GETITI---Q 73

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLGKQL 144
P + E L+ GN+G +R + AG + +VL G +R RP+ + L+ +
Sbjct: 74 APKTLQEAEDVLYCGNSGTTIRIYMGLL--AGIDGFFVLTGDQYLRRRPMKRVAEPLRSI 131

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVK---LSGSISSQYLSALLMAAPLALGDVEIE 200
GA +D D P+ V GGK+K +S S+Q SA++++A A E
Sbjct: 132 GAKIDGRKNGDLAPLAVR-----GGKLSFNYYVSKIASAQVKSAMILAALNADKPSYYE 185

Query: 201 IIDKLISIPYVEMTLRLMERFGVKA---HSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ ++S + E R+++ G K E + W + I +K P N V D SSA
Sbjct: 186 --EPMLSRDHTE--RMLKGMGAKLECIMENGKW-KVKIYPLEKKLEPLNIEVPNDPSSA 239

Query: 258 SYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
+F AAIT T ++ + ++ + LE MGA + + + EP G
Sbjct: 240 FFFAVAAAITDSTAIKNTLNPNTR--IEAYKALERMGADIEY-----VLKEDKYEPIGD 292

Query: 318 -----KHLKAIDVNMN-----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
L AI+V+ N ++P +AM +AV A+G + +++ RVKE++R+
Sbjct: 293 IIVKGAKLSAIEVSDNIPWLIIDELPALAMAMAV----AEGKSVVKNKELRVKESDRIST 348

Query: 367 IRTELTKLGASVEEGPDYCIITP--PEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTI 422
+ L G +E D IT P+K ID++ DHR+AM+F++ C + I
Sbjct: 349 VINGLKACGIEAKEFEDGYEITGGIPKK--AKIDSHGDHRIAMSAFVGLLLCG---MEI 402

Query: 423 RDPGCTRKTFPDYFDVL 439
+FP++F +
Sbjct: 403 EKAESINTSFPNFFKLF 419

>gb|ACJ54495.1| AroA [Francisella sp. FSC159]
Length = 172

Score = 99.8 bits (247), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 59/143 (41%), Positives = 78/143 (54%), Gaps = 4/143 (2%)

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV
Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
D + Y +Y SP N VE D S+ASYF A AAITG T+ V S QGD+K
Sbjct: 84 --DIDENIYTANKSQYISPSNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDII 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTG 309
F EVLE +G +V + + V G
Sbjct: 142 FLEVLEKIGCQVNYNDGIEVAG 164

>ref|YP_002287477.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oligotropha
carboxidovorans OM5]
sp|B6JCN2.1|AROALOLICO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI91612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Oligotropha
carboxidovorans OM5]
Length = 443

Score = 99.4 bits (246), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 131/436 (30%), Positives = 199/436 (45%), Gaps = 29/436 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
++G V++PG KS+S+R L+L AL+ G T + LL EDV A+ LG VE + A
Sbjct: 18 LTGRVRVPGDKSISHRALILGALAVGETKITGLLEGEDVLNTAKAMAALGAKVERVGEA 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG F DA L GN+G R AV + AT+ DG +R RP
Sbjct: 78 WRVHGVGVGG-FRAPDAP---LDFGNSGTGRLAMGAVAGSPIAATF--DGDAASLRSP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ +GA V G P +P V + S+Q SA+L+A A
Sbjct: 131 MRRILDPLELMGAKVSGGDGARLP+L+LEGARPIP--MVYRTPVASAQIKSAVLLAGLSA 188

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G E +I+ S + E R++ +FG + E + R GQ + V
Sbjct: 189 PG--ETTVIEAEASRDHTE---RMLAQFGADIVTEPEGTHGRITL+GQPELHGADVVP 243

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ + A I G+ +T+ T L+ L MGA + E+ V G
Sbjct: 244 ADPSSAAFP+VAAALIVPGSDLTLTDVMTNPLR--TGLFTTLREMGASI--EESDVRDAGE 299

Query: 311 PREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P + L+ + V + P D + LAV A FA+G T + + RVKE++R+
Sbjct: 300 PMANLRVRASKLRGVTVP+PERAPAMIDEYLVLAFAAFAEGTTRMLGLKELRVKESDRLE 359

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAMAFSLAACA-EVPVTIR 423
A L G VE D I+ ++ + T+ DHR+AM+ + CA + PV +
Sbjct: 360 ATADMLRVNGVKVEIVGDDLIVHGEGRVPGGGTVATHMDHRIAMSALVMGCASDTPVKVD 419

Query: 424 DPGCTRKTFPDYFDVL 439
D +FPD+ ++
Sbjct: 420 DTAFIATSFPDFIPMM 435

>ref|NP_371988.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Mu50]
ref|NP_374578.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus N315]
ref|YP_001442042.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Mu3]
ref|ZP_04839185.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus str. CF-Marseille]
ref|ZP_05144852.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Mu50-omega]
ref|ZP_05681565.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9763]
ref|ZP_05688020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9299]
ref|ZP_05693127.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A8115]
ref|ZP_05695512.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A6300]
ref|ZP_05697848.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A6224]
ref|ZP_05702548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A5937]
ref|YP_003282358.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ED98]
ref|ZP_06301195.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A8117]
ref|ZP_06335600.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A10102]
ref|ZP_06857845.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus MR1]
sp|P63585.1|AROA_STAAN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|P63584.1|AROA_STAAM RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A7X2G5.1|AROA_STAAl RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAB42557.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus N315]
dbj|BAB57626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Mu50]
dbj|BAF78335.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus Mu3]
gb|EEV64321.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9763]
gb|EEV73919.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A9299]
gb|EEV74244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A8115]
gb|EEV76518.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A6300]
gb|EEV79895.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A6224]
gb|EEV85731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A5937]
gb|ACY11352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
subsp. aureus ED98]
gb|EFB95368.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus
A10102]

gb|EFC05082.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A8117]
gb|ADC37631.1| 5-Enolpyruvylshikimate-3-phosphate synthase; AroF [Staphylococcus aureus 04-02981]
emb|CBX34698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus ECT-R 2]
Length = 432

Score = 99.4 bits (246), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 111/437 (25%), Positives = 199/437 (45%), Gaps = 42/437 (9%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EGT+ + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGTSNIYKPLLGEDCRRMTDIFRLLGVDIKED---E 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VV G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 DKLIVNSPG-YKAFKTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P P + GI +++++ S+Q SA+L A+
Sbjct: 126 DRVLRPLKLM DANIEGIEDNYTPLIIKPSVIKGI----NYQMEVA---SAQVKSAILFAS 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK---GGQKYKSPKN 247
+ I+ +D +S + E R F + E +R I ++ P +
Sbjct: 179 LFSNDTTVIKELD--VSRNHTETMFR---HFNIPIE----AERLSITTPDAIQHIKPAD 229

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+V GD SSA++F+ A IT + VT+ G + + +++E MG + T
Sbjct: 230 FHVPGDISAFAFFIVAALITPESDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQ--T 285

Query: 307 VTGPPPREPFGRKH---LKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVKE 360
P ++ L+ I + +P L V+AL A G + I+D +VKE
Sbjct: 286 TGAEPTASIRIQYTPMLQPIITIEGELVPKAIDELVPVIALLLCTQAVGTSTIKDAEELKVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAITDYDDHRMAMAFSLAA-CAEVP 419
T R+ L LG ++ D II P E +D+ DHR+ M ++A+ + P
Sbjct: 346 TNRIDTTADMLNLLGFELQPTNDGLIHPSEFKTNATVDSLTDHRIGMMLAVASLLSSEP 405

Query: 420 VTIRDPGCTRKTFPDYF 436
V I+ +FP +
Sbjct: 406 VKIKQFDVNVVSFPGFL 422

>ref|YP_003589561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus tusciae DSM 2912]
gb|ADG06417.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus tusciae DSM 2912]
Length = 433

Score = 99.4 bits (246), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 117/440 (26%), Positives = 189/440 (42%), Gaps = 25/440 (5%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+++++ + G V++PG KS+S+R ++ +L++G + V+ L D + +R LG+
Sbjct: 2 KLIVEMAGALKGQVRVPGDKSISHRAVMFTSLADGVS RVEGFLFGADCLSTVACMRALGV 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V+ + VG G +D L +GN+G +R L ++ G L G
Sbjct: 62 PVDIEDGTIVIVHGVGMHGLQEPDDV----LDVNGSGTTIRLLGLLS--GQTFHSCLTG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+R RP+G + L +GA +D D P+ V G L K ++ + S+Q SA
Sbjct: 115 DASIRRRPMGRVAKPLLSMGARIDGRRDGLAPLSVRG-ADLHSIKYQMPVA-SAQVKS 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+L+A A G + P + T R+++ G + G
Sbjct: 173 ILLAGLFASGVTGVREPS-----PSRDHTERMLKALGAPISKRSYTEI---GRPARLRA 224

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + GD SSA++ L I G+ + +E G + +VL MGA+ E

Sbjct: 225 MDMRIPGDLSSAFLVATLIVPGSELILEDVGVNPT--TGILDVLGAMGAQFEIEEGE 282

Query: 305 VTVTGPPEPFGGRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
P R L V + +P D LAV A A+G T IRD RVKE

Sbjct: 283 PQAGEPTARLAARSGPLVGATVGGSLIPRLIDEIPILAVAAAAAEGTTEIRDARELRVKE 342

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVP 419
T+R+ + EL K G V E D +I L ++ DHR+AMA ++A AE

Sbjct: 343 TDRIRTVAEELRKFGVQVAELEDGLMIEGGRVLKGAHCRSHGDHRIAMAMAVAGLVAEGE 402

Query: 420 VTIRDPGCTRKTFPDYFDVL 439
+ +FP + D+L

Sbjct: 403 TVVEGWEAADVSFPGFVDLL 422

>ref|ZP_01228876.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aurantimonas manganoydans SI85-9A1]
gb|EAS48526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Aurantimonas manganoydans SI85-9A1]
Length = 482

Score = 99.4 bits (246), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 126/440 (28%), Positives = 201/440 (45%), Gaps = 38/440 (8%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV +PG KS+S+R L ++ GTT V LL EDV A+R +G + D +

Sbjct: 47 LTGTVTVPGDKSISHRAFLFGGIAAGTTRVTGLLEGEDVIATGNAMRAMGAQIRKD--GE 104

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV G G +E E + GNAG +R V + AT+V D + +RP+

Sbjct: 105 TWVVEGVNGCLLE---PEGIIDFGNAGTGVRLTMGLVGSYDFGATFVGDA--SLSKRPM 159

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNG--IGGLPGGKVKLSGSISSQYLSALLMAAPL 192
G ++ L+ +G V G D P+ ++G + +V ++ S+Q SA+L+A

Sbjct: 160 GRVLDPLRLMGTQVVARSG-DRLPLSLHGPRVAAPIEYRVPMA---SAQVKSAVLLAGLN 215

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAE---HSDSWDRFYIKGGQKYKSPKNAY 249
A G +I+ +++ + E ++++ FG E ++ ++G + +

Sbjct: 216 APGIT--TVIEPVMTRDHE---KMLQGFGAALEVEETDAEGVRHIRLQGGDLRGVADFT 270

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V GD SSA + + A I G+ VTVE + E L MG + V

Sbjct: 271 VPGDPSSAGFPVVAALIVPGSDVTVENVLMNPTRS--GLVETLIEMGGSIEILNRRV-AG 327

Query: 309 GPPREPFGGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G +H L AI+V + P D LA+ A FA G T +R + RVKE++R

Sbjct: 328 GEDVADLRVRHSELTAIEVPAERAPSMIDEYPVLAMAAAFARGTTVMRGLDELRVKESDR 387

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT-PPEKLNVT-----IDTYDDHRMAMAF-SLAAC 415
+ A+ L G EEG D+ +T P+ + + T+ DHR+AM+F L

Sbjct: 388 LAAVAAGLAANGIVHEEGADWLTVTGNPDGRGLDGAYGGGTVATHLDHRIAMSFLVLGMA 447

Query: 416 AEVPVTIRDPGCTRKTFPDY 435
E VT+ D +FP +

Sbjct: 448 CERAVTVDDGRMIATSFPAPF 467

>ref|ZP_04819347.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus epidermidis M23864:W1]
gb|EES40112.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus epidermidis M23864:W1]
Length = 436

Score = 99.0 bits (245), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 108/434 (24%), Positives = 197/434 (45%), Gaps = 36/434 (8%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+ G T + L ED + + LG+S+ ++

Sbjct: 16 LKGEIEVPGDKSMTHRAIMLASLATGTTIFKPLLGEDCRRTMEIFKLLGVSITENE--- 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

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      +V+G G      + L+ GN+G R L  ++ G + VL G  + +RP+
Sbjct: 73 DTIVIGSPGYQHFTPHQ--VLYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 128

Query: 135 GDLVVGLKQLGADV----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      ++ L ++ A + D + P + GI +++++ S+Q SA+L A+
Sbjct: 129 DRVLKPLKLMNARISGVEDNYTPLIIPSTIKGIDY---QMEVA---SAQVKSAILFAS 181

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
      + + ID +S + E + E F + + + Q K+ K+ +V
Sbjct: 182 IFSKEATTVTEID--VSRNHTET---MFEHFNIPKVDGKTIQTSPNAIQHIKA-KDFHV 235

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
      GD SSA++F+ A IT G+ +T+ G + + +++E MG + + VT
Sbjct: 236 PGDISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVEQMGGNIELSH--VTEEA 291

Query: 310 PPREFPGRKH---LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKETER 363
      P K+ LK + + + +P L V+AL A G I+D +VKET R
Sbjct: 292 EPTASIRVKYTPNLKPLTIEGDIVPRAIDELPVIALLLCTQASGTCIIKDAEELKVKETNR 351

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
      + L LG ++ D II P E +D+ DHR+ M ++A+ + P+TI
Sbjct: 352 IDTTADMLGMLGFRLLQPTSDGLIHPSEFKASATVDSQTDHRIGMMLAVASLLSSEPLTI 411

Query: 423 RDPGCTRKTFPDYF 436
      +FP +
Sbjct: 412 EQFDAVNVSFPGL 425

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>ref|YP_003447473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Azospirillum sp.
      B510]
dbj|BAI70929.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Azospirillum sp.
      B510]
      Length = 452

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Score = 99.0 bits (245), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 127/449 (28%), Positives = 200/449 (44%), Gaps = 43/449 (9%)

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Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      I G++++PG KS+S+R L+L A++ G TV+ LL EDV + A+R LG E + +
Sbjct: 15 IRGSIRVPDGKSIHRSLMLGAIAVGETVIHGLLEGEDVLHTAAAMRLLGAEEREDNGQ 74

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
      R VG G +E Q+ +GN+G A R L V AG T V G
Sbjct: 75 GPGVWRVRGVGLGA-----LREPAQVLDMGNSGTAAARLLMGLV--AGHPITCVFTGDAS 126

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
      + +RP+ + L+++GA F+G P+ V G G L +L S+Q SA+
Sbjct: 127 LNKRPMPARVTKPLEEMGAR---FVGRSGGRLPLTVVGSGLVPITYRLP-VASAQVKSAL 182

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKS 244
      L+A G +I+ + + E+ LR FG V E GQ +
Sbjct: 183 LLAGLNTAG--ATTVIEAEPTRDHTELMLR---HFGASVTTERLADGALAVTVIGQPELT 237

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      + +V D SSA++ + A + G+ + + G + + L MGA + + E
Sbjct: 238 GRTIHVPADPSSAAFPVVAALLRPGSELLLNVDGMNPRR--TGLYDTLVEMGADIAF-EN 294

Query: 304 SVTVTGPPREFPGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
      G P +H LK + V ++ P D LA A A+G T + + RV
Sbjct: 295 RRDQAGEFVADLRVRHGALKGVVVPADRAPSMIDEYPVLAACAAEAGTTVMLGLKELRV 354

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAF-S 411
      KE++R+ + LT+ G SVE G D + T + T DHR+AM+F
Sbjct: 355 KESDRLAMVAEGLTRCGVSVEVGADDSLTVHGTGGTGKAPKGGATVLTAMDHRIAMSFLV 414

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
      L E PV++ D +FP + +++
Sbjct: 415 LGMATEQFVSVDGAFIDTSFPGFVGLMN 443

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>ref|ZP_01452683.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate

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dehydrogenase [Mariprofundus ferrooxydans PV-1]
gb|EAU54473.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [Mariprofundus ferrooxydans PV-1]
Length = 449

Score = 99.0 bits (245), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 120/451 (26%), Positives = 204/451 (45%), Gaps = 46/451 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE---ADK 71
+ G + +PG KS+S+R ++LAAL++G T + L ED +G+ +E +K
Sbjct: 16 LKGELTVPGDKSMSHRVLAALADGVTEIHGFLPGEDNIATARMFIDMGVRIEWNDEK 75

Query: 72 AAKRAVVVCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ R VG G K P + L GNAG +R + + AG + + + G +
Sbjct: 76 TSLRVHVGVLHGLKQP-----QGMLDAGNAGTCVRLMAGIL--AGQHFSSSTVTGDASLC 127

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVK---LSGSISSQYLSAL 186
+RP+ +V +++GA V+ + P+ ++G GK+K +S S+Q S +
Sbjct: 128 KRPMKRVVDPVRMGAKEVEGGDDGNLLPITISG-----GKLKAIDHVSEVASAQVKSCV 181

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKY 242
L+A A G + P + T R++ FG V A+ + S D +
Sbjct: 182 LLAGLYADGVTSVSE-----PKPTRDHTERMLPLFGQPVTVAADGTISLDP-----KDRL 231

Query: 243 KSPKNAY-VEGDASSASYF-LAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+P + D SSA +F +A + + G VT++ G + + V+ MGA ++
Sbjct: 232 TAPVGVVDIPADPSSACFFAVAASLVESDVTLSIGINPRRD--GWRVMNGMGAALSL 289

Query: 301 TETSVTVTGPPREPFGGRKH-LKAIDVNMNMPDVAMTLAVV---ALFADGPPTAIRDVASW 356
P + R L + V N +PD V+ A ADG + D
Sbjct: 290 ENEQVRGEEPADVRIIRSGGLHGMHVVPNDVPDAIDFPPVLFAAATLADGEFVLTDAAEL 349

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-ITYDDHRMAMAFSLAAC 415
RVKE++R+ A+ T L GA ++E PD +I L +D + DHR+AMA ++AA
Sbjct: 350 RVKESDRIAAMATALRSAGADIDEQPDGAVIRGITNLRGDDVDVAHGDHRIAMAMAVAAQ 409

Query: 416 -AEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
A+ V I + +FP++ + + N
Sbjct: 410 RADGEVRIHNAAAIATSFNPFVQLAQSVGMN 440

>ref|YP_001924782.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
populi BJ001]
sp|B1ZLG6.1|AROAMETPB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACB80247.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
populi BJ001]
Length = 453

Score = 99.0 bits (245), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 195/456 (42%), Gaps = 52/456 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ + P ++G +K PG KS+S+R ++ LS G T V+ LL +DV A++ LG
Sbjct: 8 QPVTAPAGPLTGALKPPGDKSISHRAMIFGLLSVGETRVEGLLEGDDVLRATAAVKALG 67

Query: 65 LSVEADKAAK-RAVVVCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V + + R V VG GG + PV L GNAG R + V G T
Sbjct: 68 AQVTREGEGRWRIVGVGIGMQDPVG-----VLDFGNAGTGSRLMMGVV--GGQPVTAT 119

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---S 179
DG +R+RP+ ++ + ++GA+V P+ + G P + + + S
Sbjct: 120 FDGDASLRKRPMRRILDPIKMGAEVSEAEGRVPLTLRG---PREAIPRIYELPVAS 175

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFY 235
+Q SA+L+A A G +I+K S + E LRL FG + S + R
Sbjct: 176 AQIKSAVLLAGLNAPGTT--TVIEKAASRDHTERMLRL---FGADVSVTPSGEGGHGRTV 230

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMM 294
GQ + V D SSA++ L A I G+ V + G L+ L M

Sbjct: 231 TLTGQPTLRGTDVIVPADPSSAAFPLVAALIVPGSEVILRGVMMNPLR--TGLITTLIEM 288

Query: 295 GAKVTWTETSVTVTGPPREPFR-----KHLKAIDVNMNKMP---DVAMTLAVVAL 342
GA + + RE G L+ +DV + P D LAV A

Sbjct: 289 GADIERFDE-----REEGETVADLRVRASRLRGVDVPAERAPSMIDEYPILAVAAA 340

Query: 343 FADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTAITD 400
FA+G T + + RVKE++R+ A+ L G + D I+T + T

Sbjct: 341 FAEGTTRMNLHELVRKESDRLAAVAAGLAANGVGHDIEGDDLIVTGNGGPPAGGGTVAT 400

Query: 401 YDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFFPDY 435
+ DHR+AMAF + A PVT+ D +FP +

Sbjct: 401 HLDHRIAMAFVLMGLATRKPVTVDDGAMIATSFPSF 436

>ref|ZP_01743483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
bacterium HTCC2150]
gb|EBA02168.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
bacterium HTCC2150]
Length = 448

Score = 99.0 bits (245), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 126/454 (27%), Positives = 206/454 (45%), Gaps = 50/454 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT +PG KS+S+R L+L A+S G T V LL +DV A++ G V +

Sbjct: 18 LKGTANVPKDKSISHRSLILGAMSIGETKVTGLLEGQDVLDGTGRAMQAFGAEVINHGDDGQ 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ + + GN+G +R + A+ + +T+ D + RP

Sbjct: 78 WSVHGVGVGGF----AEPDQVIDCGNSGTGVRLIMGAMATSPIASTFTGDA--SLNSRP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+G + L GA G + + IG V + S+Q SA+L+A

Sbjct: 131 MGRITDPLALFGAQS---FGRSEGRPLTIIGAAEPVPVHYKTPVPSAQVKSALLAGLN 187

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + +I++ + + E R++ FG + E +D + + G + K+ +N V

Sbjct: 188 APG--QTVVIEREATRDHSE---RMLRGFGADLSVEKTDEGNVITLMGQPELKA-QNIVV 241

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ + A I G+ V V G + + + L+ MGA +T+

Sbjct: 242 PRDPSSAAFVCAALIVEGSDVLVNPINLNPTRAGLFY--TLQEMGADLTFEN----- 292

Query: 310 PPREPFR-----KHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASW 356
PRE G ++K I V + M D L++VA FA+G T + V

Sbjct: 293 -PREEGEPVADLRKAFSPNMKGIVPAERAASMIDEYPILSIVASFAEGVTEMPGVKEL 351

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIIT----PPEKLNVTAITDYDDHRMAMAF-S 411
RVKE++R+ A+ L G +V EG D+ +T K +TA DHR+AM++

Sbjct: 352 RVKESDRIDAMAKGLRASGVNVAEGDDWSVTGLGAGGVKGGITAASEL-DHRIAMSYMC 410

Query: 412 LAACAEPVPTIRDPGCTRKTFFPDYFDVLSTFVK 445
L + P+TI D G +FP + +++ N

Sbjct: 411 LGMATQQPITIDGGPIATSFPIFLTLMAELGAN 444

>ref|YP_001038211.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum ATCC 27405]
ref|ZP_05428471.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 2360]
ref|ZP_06249375.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum JW20]
gb|ABN53018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum ATCC 27405]
gb|EEU02597.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 2360]
gb|EFB40015.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum JW20]
gb|ADU75483.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium
thermocellum DSM 1313]

Length = 423

Score = 98.6 bits (244), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 111/454 (24%), Positives = 195/454 (42%), Gaps = 65/454 (14%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+S+R +L +L++GTT ++ L+ ED + R + +S+E
Sbjct: 9 LRGEINIPGDKSISHRAILFGSLAKGTTEIEGLMMGEDCLSTIDCFRKMHVSIIEILPNKV 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G G P L G +G A+R L ++ G + VL + +P+
Sbjct: 69 KIHNGLYGLKP-----PSAPLNAGRSGTALRLLLVLS--GQPFSSVLTRNEAVLRKPV 121

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG-----SISSQYLSALLMA 189
G +V L+Q+GA++ + P+ + KL+G SI Y+ + L+
Sbjct: 122 GKVVAPLRQMGNITGRENGNICPLSIQ-----PAKLTGKTHHVSILDYIKSPLLI 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-----HSDSWDRFYIKGGQKYK 243
A L D E +I+++ S + E+ ++ FG + S + Y+ + Q
Sbjct: 174 AGL-YADGETTVIEEVKSRDHSEL---MLNYFGADIKVNGLEVTSRRVENLYAQHIQ--- 226

Query: 244 SPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTSLQGDVKFAEVLMMGAKVTWTE 302
V GD S A+YF+ AG + + ++ G + + +V + MGAK+
Sbjct: 227 -----VPGDISIAAYFITAGLIVPNSDIVIKVNGINPTRAGI--LDVYKSMGAKIEILN 278

Query: 303 TSVT-----VTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTA 349
V V+ P L + + +P D + V A A G T
Sbjct: 279 ERVVSNEKVADIRVVSSP-----LNGTTIERSMIPRLIDEIPIITVAASVAKGTTT 329

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMA 409
I + ++ KE+ ++ + EL+KLGA++ E D II E L T ++ ++D +AM+
Sbjct: 330 ITGLKGFKTKESGKLSRMIAELSKLGATLHETEDGVIIIEGKEHLKGTVVEGHNDAAIAMS 389

Query: 410 FSLAA-CAEVPVTIRDPGCTRTKTFPDYFDVLSTF 442
+A AE IR +PD+ VL+
Sbjct: 390 LCVAGLVAENETNIRKTQVLDIAYPDFITVLNKL 423

>ref|YP_003654661.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter
nitrofigilis DSM 7299]
gb|ADG92155.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter
nitrofigilis DSM 7299]
Length = 426

Score = 98.6 bits (244), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 114/426 (26%), Positives = 194/426 (45%), Gaps = 33/426 (7%)

Query: 25 KSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + LS T+ + N L +ED L + LG ++ D + V + G
Sbjct: 24 KSISHRCAMFSLLSNETSHIKNFLTAEIDLNTLSIVEQLGAEIKRDGS---TVTITPKGT 80

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
+ L GN+G AMR + + G + L G + RP+ + L+ +
Sbjct: 81 L----TEPSNVLDGNSGTAMRLFCGFLASIDG--AFTLVGDKYLHSRPMKRVANPLRSI 134

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA +D + P+ + G+ L S S+Q SA+++AA A G + + +
Sbjct: 135 GAKIDGREDGNKAPLFIKGVKELKAFTYH-SPVDSAQVKSAMILAALRANGVSKYK--EN 191

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
++ + E R+++ G K E+ DS +I K P N V D SSA +F A
Sbjct: 192 ELTRDHTE---RMLKMGAKLEN-DSEGFIIHYPLTKPLKPLNITVPTDPSSAFFFALAA 247

Query: 265 AIT-GGTVTVEGCGTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGF-----K 318
AIT VT++ + + VL+ MGA V + E EP G
Sbjct: 248 AITPNAKVTIKNVTNLNPTREAYV--VLKRMGANVEFIEKENVY-----EPMGDIVVSAN 300

Query: 319 HLKAIDV--NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L +DV N++ + D L++ A+G + + + RVKE++R+ ++ L G
Sbjct: 301 ELNGVDVSENISWLIDELPALSIAMSLANGKSKVSNKELRVKESDRISVVNNLKLKGV 360

Query: 377 SVEEGPDYCIITPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
+ +E D IT KL I+++ DHR+AM+F++A + I+D C +FP++
Sbjct: 361 TYKEFEDGYEITGG-KLKKATINSHGDHRIAMSFAIAGLNS-GMQIQDVDCILTSFPNFK 418

Query: 437 DVLSTF 442
++L T
Sbjct: 419 EILDTL 424

>ref|YP_003577287.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter capsulatus SB 1003]
gb|ADE84880.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacter capsulatus SB 1003]
Length = 447

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 121/438 (27%), Positives = 194/438 (44%), Gaps = 31/438 (7%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +PG KS+S+R L+L ALS GTT + LL +DV A++ G +V
Sbjct: 18 LSGVAAPVPGDKSISHRALILGALSVGTTRITGLLEGQDVLDLTARAMQAFGATVTRTGPGA 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V VG GG A+ + GN+G +R + + + +AT+ D +R+RP
Sbjct: 78 WTVEGVGVGGF----AEPAEVIDCGNSGTGVRLIMGCMATSPISATFTGDA--SLRKR 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+G + L GA G P V +P + S+Q SA+L+A A
Sbjct: 131 MGRVTDPLALFGARSYGRAGGRLPMTLVGAAPV--VTYTPMASAQVKSALLLAGLNA 188

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G + +I+K P + T R++ FG V E + +R + G + + + V
Sbjct: 189 PG--QTVVIEK---TPTRDHTERMLRGFGAEVTVATPEGNRITLTGQPELRA-QEVA 242

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A + G+ + V G + + L MGA + + G
Sbjct: 243 RDPSSAAFPVCAALLVPGSDILVPGVSQNPNRNLFL--TLREMGADIEFLNER-EEGGE 299

Query: 311 PREPFGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P +H L I V + D LA +A A G T +R V RVKE++R+
Sbjct: 300 PVADLRVRHSALTGIAVPPERAAAQIDEYPVLAALACASGTTVMRGVHELVRKESDRIA 359

Query: 366 AIRTELTKLGASVEEGPDYCIIT---PPEKLNVT AIDTYDDHRMAMAF-SLAACAEVPVT 421
A+ L G VEE D I+ P + T+ DHR+AM+F L ++ P++
Sbjct: 360 AMARGLEACGVRVEEDEDTLIVHGLGPDGVPGGATVATHIDHRIAMSFLVLGLVSQQPIS 419

Query: 422 IRDPGCTRKTFPDYFDVL 439
+ D +FP + D++
Sbjct: 420 VDDGSPATSFVPVFEDLM 437

>ref|ZP_01054605.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp. MED193]
gb|EAQ47096.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp. MED193]
Length = 439

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 123/449 (27%), Positives = 205/449 (45%), Gaps = 46/449 (10%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G ++PG KS+S+R L+L A++ G T + LL +DV A++ G V
Sbjct: 9 LTGVAEVPVPGDKSISHRSLILGAMAIGETKISGLLEGDDVLDTAKAMQAFGAEEVNVHGGGN 68

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ + GN+G +R + + + T+ D + RP
Sbjct: 69 WSVYGVGVGGF-----AEPGQVIDCGNSGTGVRLIMGCMATSPITVFTGDA--SLNGRP 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
+ + L GA G P V P V+ + S+Q SA+L+A
Sbjct: 122 MARVTDPLALFGAKAVGRKGGRLPMTIVGAAPTP---VRVVPVPSAQVKSALLLAGLN 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+K + + E R++ FG + DS + R G+ P+ V
Sbjct: 179 APG--KTVVIEKEATRDHSE---RMLAGFGAEITVEDSEEGRVITLTGRPELKPEIAVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I T G+ V V G G + + + L+ MGA +T+
Sbjct: 234 RDPSSAAFPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTFEN----- 283

Query: 311 PREPFGR-----KHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWR 357
PRE G ++K I+V ++ M D L+VVA FA G T + V R
Sbjct: 284 PREEGGEFVADLRKAYSPNMKGIEVPPDRAASMIDEYPVLSVVASFATGKTMMAGVKELR 343

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTAI-DTYDDHRMAMAFS-LA 413
VKE++R+ A+ L G +V+EG D+ P+ + I +++ DHR+AM+F +
Sbjct: 344 VKESDRIDAMAGGLRANGVTVDEGDDWSVEGLGPDGVPGGGICESFLDHRIAMSFVMVG 403

Query: 414 ACAEVPVTIRDPGCTRTFPDYFDVLSTF 442
A+ PVT+ D +FP + ++++
Sbjct: 404 MGAQRPVTVDDGNPITTSFPPIFEPLMTSL 432

>ref|YP_484265.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris HaA2]
sp|Q2J2F6.1|AROARHOP2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABD05354.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris HaA2]
Length = 445

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 133/444 (29%), Positives = 194/444 (43%), Gaps = 37/444 (8%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGT ++PG KS+S+R L+L AL+ G T + LL EDV A+R LG VE
Sbjct: 18 LSGTARVPGDKSISHRALILGALAVGETRISGLLEGEDVLNTARAMRALGAQVERTGDCA 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG G P L GN+G R AV AG DG +R RP
Sbjct: 78 WSVHGVGVAGFAP----PAAPLDFNGSGTGCRLAMGAV--AGSPIIATFDGDASLRSRP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+Q+GA V P+ + G P + S+Q SA+L+A A
Sbjct: 131 MRRIVDPLEQMGARVTQSADGGRPLTLQGARD-PLPITYRTPVPSAQIKSAVLLAGLSA 189

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +I+ S + E+ +++ FG V E R GQ V
Sbjct: 190 PG--VTTVIEAEASRDHTEL---MLQHFGATVVTEPEGPHGRKISLTGQPELRGAPVVVP 244

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A I G+ V + T L+ L MG + +ET G
Sbjct: 245 ADPSSAAFPVMAALIVPGSDVVLTEVMTNPLR--TGLITTLREMGLIEEETR----GD 298

Query: 311 PREPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP R L+ ++V + P D + LAV A FA+G T +R + RVKE++
Sbjct: 299 AGEPMARFRIRGSQRLRGVEVPPERAPSMIDEYLVLAFAAFAEGTTIMRGLHELVRKESD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAM-AFSLAACAEV 418
R+ A L G +VE D I+ K +V + T+ DHR+AM A + A+
Sbjct: 359 RLEATAAMLRVNGVTVEISGDDLIVE--GKGHVPGGGLVATHMDHRIAMSALVMGLAADK 416

Query: 419 PVTIRDPGCTRTFPDYFDVLSTF 442
PV + D +FPD+ ++
Sbjct: 417 PVRVDDTAFIATSFPDFVPMMQRL 440

>gb|AAN87376.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Heliobacillus
mobilis]
Length = 256

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 81/261 (31%), Positives = 122/261 (46%), Gaps = 24/261 (9%)

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSD-----SWDRFYIKGGQKYKSPKNA 248
D + + + L+S + E R++ FG K D + F GQ+ + P
Sbjct: 6 FADGKTRVTEPLLSRDHTE---RMLSSFAGAKLNRLDRGLTAEIESFPSLHGQEIEVP--- 59

Query: 249 YVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
GD SSA++ L A+I G VT+ G + + +VL MGA + E V
Sbjct: 60 ---GDISSAAFLLVAASIVPGSEVTLRNIGINPTRDGI--LDVLREMGANL-HVENERLV 113

Query: 308 TGPPREPFPGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G P + LK + +P D +AV ALFA+G T I+D A RVKET+
Sbjct: 114 AGEPVADITVQSASLKGTTIEGAIIPRLIDELPIIAVAALFAEGTTIIKDAEELRVKETD 173

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVT 421
R+ + EL KLG +VEE PD II +++ +D++ DHR+AM+ ++A A
Sbjct: 174 RIAVLAEELRLKLGVTVEETPDGMIIPGNQVKGKGTVDSHGDHRIAMSLAAGLLAADETV 233

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
IRD +FP + L +
Sbjct: 234 IRDAASIDVSFPGFAATLQSL 254

>gb|AA21584.1| AroA [Francisella tularensis subsp. holarctica]
gb|AA21585.1| AroA [Francisella tularensis subsp. holarctica]
Length = 172

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 59/146 (40%), Positives = 79/146 (54%), Gaps = 4/146 (2%)

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV
Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMHRGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
D + Y +Y S N VE D S+ASYF A AAITG T+ V S QGD+K
Sbjct: 84 --DIDENIYTANKSQYISTSNVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDII 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPR 312
F EVLE +G +V + + VTG +
Sbjct: 142 FLEVLEKIGCQVNYNDGIEVTGNNQ 167

>ref|NP_859670.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
hepaticus ATCC 51449]
sp|Q7VJV4.1|ARO_A_HELHP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAP76736.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
hepaticus ATCC 51449]
Length = 438

Score = 98.2 bits (243), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 117/437 (26%), Positives = 187/437 (42%), Gaps = 41/437 (9%)

Query: 25 KSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + A LS V+ L ED + L R LGL +E + R +
Sbjct: 23 KSISHRAAIFALLSSAPCEVEGYLMGEDTLHTLHIAARELGLEGIEQKGSVLRLLI----- 75

Query: 85 FPVEDAKEEVQLFL--GNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRERPIGDLVVLGK 142
P + E L GNAG MR ++ G+ +VL G + RP+ + L
Sbjct: 76 -PPRNGICEPHKVLDCGNAGTGMRLFAGLLSGVKGH--FVLGTGEYLNARPMKRITEPLS 132

Query: 143 QLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEII 202
+GA ++ P+ + G L K S S+Q SA+++A G +
Sbjct: 133 ATGACINGRENNAYAPLSIVG-AQLQTFDYK-STIASAQVKSAMILAGLQTAG--QSRFY 188

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-----IKGGQKYKSPKNAYVEGDASS 256
+ L+S + E LR M GV + + D Y +K K V D SS
Sbjct: 189 EPLLSRNHTENMLRGM---GVHIQERECEDGGYEVVFEGLKETNKQLEAFKFQVPADPSS 245

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFG 316
A YF A + G V ++ + ++ ++LE MGAHV + S
Sbjct: 246 AFYFAVAACVLGAKVKLNVLNKR--IEAFKILESMGAKVAYHHLSSLYEEVGDIEVQ 303

Query: 317 RKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
LKA+ V+ +++++P +++ A+ A G + + + RVKE++R+ A T
Sbjct: 304 GGSCLKAVRVDRIAWLIDEIPALSICFAL----AKGKSEVYNAKELRVKESDRIRATITN 359

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 430
L +G EE D + E L + ++ DHR+AM+F++A A I D C
Sbjct: 360 LRVMGIRCEEFDGFSVYGGE-LKRARVSSFGDHRIAMSFAIAQLA-CGGEIEDSECIDV 417

Query: 431 TFPDYFDVLS--TFVKN 445
+FP + +LS T V+N
Sbjct: 418 SFPHFLTLLSQITAVEN 434

>ref|ZP_05785141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
gb|EEX08257.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
Length = 448

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 124/441 (28%), Positives = 201/441 (45%), Gaps = 34/441 (7%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
P ++GT ++PG KS+S+R L+L A++ G T + LL EDV A+R G V +
Sbjct: 13 HPCGPLTGTAEPVPGDKSISHRSLILGAMAVGETRISGLLEGEDVLDTAKAMRAFGAEVIS 72

Query: 70 DKAAKRAVV-VGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V VG GG A+ + + GN+G +R + A+ + +AT+ D
Sbjct: 73 HGNGEWTVHGVGVGGF-----AEPDQVIDCGNSGTGVRLIMGAMATSPISATFTGDA--S 125

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALL 187
+ +RP+ + L GA G P V +P V+ + S+Q SA+L
Sbjct: 126 LNKRPMAVTDPLALFGAQAQVGRSGGRLPMTIVGAADPVP---VRYEVPVPSAQVKSAYL 182

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A A G + +I+K + + E R++ FG + E +D + G + K P
Sbjct: 183 LAGLNAPG--KTVVIEKEATRDHSE---RMLAGFGAEITVEDTDEGRVITLTGRPELK-P 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V D SSA++ + A IT G+ V V G G + L MGA +T+ E
Sbjct: 237 QVIAVPRDPSSAAPPVCAALITPGSDVLVPGIGLNPTR--AGLFTTLREMGADLTY-ENM 293

Query: 305 VTVTGPPPREPFRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRV 358
G P ++ +K IDV + M D L+VVA A G T + V RV
Sbjct: 294 REEGGEPVADLRARYSPDMKGIDVPPERAAASMIIDYVLSVVAANATGKTMGGVKELRV 353

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTIAIDTYDDHRMAMAFS-LAA 414
KE++R+ A+ L G +V+EG D+ + +++ DHR+AM+F +
Sbjct: 354 KESDRIDAMARGLRANGVTVDEGDDWWSVDGLGIGGVPGGGTCESFLDHRIAMSFMVMGM 413

Query: 415 CAEVPVTIRDPGCTRKTFPDY 435
A+ V++ D +FP +
Sbjct: 414 GAQQAVSVDDGSPATSFPIF 434

>gb|AAX21593.1| AroA [Francisella tularensis subsp. holarctica]
gb|AAX21595.1| AroA [Francisella tularensis subsp. holarctica FSC200]
gb|AAX21598.1| AroA [Francisella tularensis subsp. holarctica]
Length = 172

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 59/146 (40%), Positives = 79/146 (54%), Gaps = 4/146 (2%)

Query: 167 LPPGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV
Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMHCGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
D + Y +Y S N VE D S+ASYF A AAITG T+ V S QGD+K
Sbjct: 84 --DIDENIYTANKSQYISTSNNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIK 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPR 312
F EVLE +G +V + + VTG +
Sbjct: 142 FLEVLEKIGCQVNNYNDGIEVTGNNQ 167

>gb|AA21592.1| AroA [Francisella tularensis subsp. holarctica]
Length = 172

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 59/146 (40%), Positives = 79/146 (54%), Gaps = 4/146 (2%)

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++M FGV
Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMHCGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
D + Y +Y S N VE D S+ASYF A AAITG T+ V S QGD+K
Sbjct: 84 --DIDENIYTANKSQYISTSNNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIK 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPR 312
F EVLE +G +V + + VTG +
Sbjct: 142 FLEVLEKIGCQVNNYNDGIEVTGNNQ 167

>ref|YP_002016601.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prosthecochloris
aestuarii DSM 271]
sp|B4S4Q8.1|ARO_A_PROA2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF46954.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prosthecochloris
aestuarii DSM 271]
Length = 434

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 121/444 (27%), Positives = 196/444 (44%), Gaps = 42/444 (9%)

Query: 20 KLPGSKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVE-----ADKAA 73
LP KS+S+R L+ AL++GTT + N D LG L+ G+ + AD
Sbjct: 10 NLPPDKSISHRAALIGALADGTTEISNFSGGFDNQSTLGVLQACGIRLSQDIVQGADGRQ 69

Query: 74 KRAVVVGCGG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R VV+ G F DA L N+G MR + ++T V D + +
Sbjct: 70 TRHVVLHSSGLWSFSAPDAP----LMCNNSGSTMRFAGILAGQPFDSLTVGDN--SLMK 123

Query: 132 RPIGDLVVGLKQLGADVDCFLGTD-CPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + L+++GA + L D PV +NG L +L S+Q S + AA
Sbjct: 124 RPMKRIADPLRRMGAGIS--LSPDGTAPVGINGTRDLKPITYELPMP-SAQVKS LVAFAA 180

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A D E +I+ L S + E+ L L K E R I G K + ++
Sbjct: 181 LHA--DGESRVIELTLP SRNHTLM LLDL-----KTEALSDGRRAVIIPGGKSLEARPFHI 232

Query: 251 EGDASSASYFLA-GAAITGGTVTVEG-CGTTSLQGDVKFAEVLEMMGAKVTWTETSV--- 305
D S+A + +A G + G + + C + G + E+L GA + + V
Sbjct: 233 PADPSAACFMIALGGLVPGSEILLRDVCLNPTRAG---YIELLIGAGADIGFENRRVIGG 289

Query: 306 -TVTGPPPREPFGRKHLKAID---VNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
T+ G ID + N + ++ M LAV + A + A R KE+
Sbjct: 290 ETIGDIVVRYSGSVEPLRIDEPSIVANIIDEIPM-LAVFSACATAEFELHHAELRTKES 348

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVT AIDTYDDHRMAMAFSLAACA-EV 418
+R+ A+ + L +LG EE PD + +++ +++YDDHR+AM+F++A A E
Sbjct: 349 DRISAVVSNLQRLGLCEFPDGFVAVKGRQVRVPSGKVILESYDDHRIAMSF A IADK ALES 408

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
+ I D +FP++FD++ +

Sbjct: 409 ELEISDREIIGVSFPNFFDIIESL 432

>ref|ZP_00370175.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter upsaliensis RM3195]
gb|EAL53698.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter upsaliensis RM3195]
Length = 425

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 109/423 (25%), Positives = 178/423 (42%), Gaps = 31/423 (7%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGGK 84
KS+S+R + A LS+ T+ N L +ED L + LG VE + + V + K
Sbjct: 21 KSISRFAIFALLSDKTSRAKNYLLAEDTLNLTLLKIENLGAKVERNGSE---VCISPSAK 77

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQL 144
+ L GN+G AMR + + AG +VL G + +RP+ + LK++
Sbjct: 78 I---NEPPCILECGNSGTAMRLMIGFL--AGIEGFFVLSGDKYLNKRPMKRICEPLKKI 131

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + +G + I G + ISS + ++ A V +
Sbjct: 132 GAKI---MGREENFAPLCIEGQKLKSFNYTSEISSAQIKTAMILAGFRADKVSF-FKES 187

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E L ME A I QK P N + D SS YF+ A
Sbjct: 188 FLSRNHSENMLTFME-----APLKIRGTSLEISPLQKPLKPLNITIPNDPSSVFYFILAA 242

Query: 265 AITGGTVTVEGCGTTSLQGDVKFA--EVLEMMGAKVTWT--ETSVTVTGPPREPFGRKHL 320
I + + C L + ++LE MGA +++ E + G +
Sbjct: 243 LILPNS---QICIKNVLLNPTRIEAYKILEKMGANISYHFDEENFEKIGTIYASSSKLQA 299

Query: 321 KAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
I N++ + D A LA+ A+G + +++ RVKE++R+ A+ T L K G EE
Sbjct: 300 VEISENISWLIDEAPALAIAFALANGTSLLLKNAKELRVKESDRIKAMVTNLQKCGIKAE 359

Query: 381 GPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDV 438
D IT P+ I+++ DHR+AM+F++ + I D C +FP++ +
Sbjct: 360 LEDGFKITGGTPKS---AYIESFGDHRAMSFALGLV--CSMEIDDYSCIATSFPNFTTI 415

Query: 439 LST 441
L
Sbjct: 416 LEN 418

>ref|NP_945417.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris CGA009]
sp|Q6NDP4.1|AROARHOPA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAE25505.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris CGA009]
Length = 445

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 130/444 (29%), Positives = 197/444 (44%), Gaps = 37/444 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ GT ++PG KS+S+R L+L AL+ G T + LL EDV A+R LG VE +
Sbjct: 18 LHGTARVPGDKSISRHALILGALAVGETRISGLLEGEDVINTAKAMRALGAKVERTGDCE 77

Query: 75 -RAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R VG G A E L GN+G R AV AG DG +R RP
Sbjct: 78 WRVHGVGVAGF----ATPEAPLDFGNSGTGCRMLAGAV--AGSPIVATFDGDASLSRSP 130

Query: 134 IGDVLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+ +GA V P+ + G P + + S+Q SA+L+A A
Sbjct: 131 MRRIVDPLELMGAKVVSSEGGRLPLALQGARD-PLPILYRTPVPSAQIKSAVLLAGLSA 189

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +I+ S + E+ +++ FG + E + R GQ V

Sbjct: 190 PGIT--TVIEAEASRDHTEL---MLQHF GATIVTEAEGAHGRKISLTGQPELRGAPVVVP 244

Query: 252 GDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ +A + G + + T L+ L MGA + ++ V G

Sbjct: 245 ADPSSAAFPMAALVVPGS DIELTDVMTNPLR--TGLITTLREMGASIEDSD----VRGD 298

Query: 311 PREPFGR-----KHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP R LK ++V + P D + LAV A FA+G T +R + RVKE++

Sbjct: 299 AGEPMARFRVRGSKLKGVEVPPERAPSMIDEYLVLA VAAFAEGTTVMRGLHEL RVKESD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A---IDTYDDHRMAM-AFSLAACAEV 418
R+ A L G +VE D I+ K +V + T+ DHR+AM A ++ ++

Sbjct: 359 RLEATAAMLRVNGVAVEIAGDDLIVE--GKGHVPGGGVVATHMDHRIAMSALAMGLASDK 416

Query: 419 PVTIRDPGCTRKTRTFPDYFDVLSTF 442
PVT+ D +FPD+ ++

Sbjct: 417 PVTVDDTAFIATSFPDFVPMQRL 440

>ref|YP_002963190.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Methylobacterium
extorquens AM1]
gb|ACS39913.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Methylobacterium
extorquens AM1]
Length = 453

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 127/455 (27%), Positives = 200/455 (43%), Gaps = 50/455 (10%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
+ + P ++G++K PG KS+S+R ++L L+ G T V+ LL +DV A + LG

Sbjct: 8 QPVTASPGGPLNGSLKPPGDKSISHRAMILGLLAIGETRVEGLLEGDDVLR TASA AAKALG 67

Query: 65 LSVEADKAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ + + R V VG GG ++D + L GNAG R + V G T

Sbjct: 68 AQITREGEGRWIRIVGVGIGG---MQDP--DGVLD FGNAGTGSRLMMGVV--GGQPVTATF 120

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SS 180
DG +R+RP+ ++ + ++GA++ P+ + G P + + + S+

Sbjct: 121 DGDASLRKRP MRRILDPI LKMGAEIVSEAEGRVPLTLRG----PREAIPRYELPVASA 176

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSDW----RFYI 236
Q SA+L+A A G +I+K S + E LRL FG + + S + R

Sbjct: 177 QIKSAVLLAGLNAPGTT--TVIEKAASRDHTERMRLR L--FGAEVTVTPSGEGGHGRTVT 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
GQ + V D SSA++ L A + G+ V + G L+ L MG

Sbjct: 232 LTGQPTLRGTDVVVPADPSSAAFP LVAALVVP GSEVILRGVMNPLR--TGLITTLIEMG 289

Query: 296 AKVTWTETSVTVTGPPREPFGR-----KHLKAIDVNMNMKP---DVAMTLAVVALF 343
A + + RE G LK +DV + P D LAV A F

Sbjct: 290 ADIERLDE-----REEGETVADLRVRASRLKGVDPAPERAPSMIDEYPILAVAASF 341

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A--IDTY 401
A+G T + + RVKE++R+ A+ L G + D I+T + + T+

Sbjct: 342 AEGTTRMNGLHEL RVKESDR LAAVAAGLAANGVTHAIEGDDLIVTGNGQAPAGGGTVATH 401

Query: 402 DDHRMAMAF-SLAACAEVPVTIRDPGCTRKTFPDY 435
DHR+AMAF L A+ PVT+ D +FP +

Sbjct: 402 LDHRIAMAF LVLGLAAKSPVTVDGAMIATSFP SF 436

>ref|ZP_05570493.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ferroplasma
acidarmanus fer1]
Length = 423

Score = 97.8 bits (242), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 102/428 (23%), Positives = 182/428 (42%), Gaps = 42/428 (9%)

Query: 15 ISGTVKLP GSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISGT+ P SKS + R +L +A S + N+ SED L + ++ ++

Sbjct: 10 ISGTIYAPSSKSYTQRYVLYSAFSNKPVKIKNVSFSEDEMVS LKIAESC NATINYNRKD- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ F D+ +++G +G + R + A T + G ++ RP+
Sbjct: 69 ----IEIKPDFKCPDS-----IYVGESGTSYRLSIGLLVARKCKTT--IKGEQQLAGRPV 117

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
L+ L G + F V+G G V + G SSQ++SA+L + L
Sbjct: 118 EPLIKALSDAGTN---FKKHKGDFYMDGRNSASTG-VSIDGGTSSQFVSAMLYYYSI-L 172

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ + ++S YV +T+ + FG+ ++ + + I+ G + K +EGD
Sbjct: 173 GEGNFT-VSNMVSANYVNITINCLRNFGITVH--NNGNNYSIENGDD--YAVKEIGIEGDY 227

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
SSASYF+ T G + ++ G SLQ D + E+L + +TV
Sbjct: 228 SSASYFIVLGIPT-GNIKIKNLGIDSLQPDRIIELLNNAECIKIGGNELTVDKA---- 282

Query: 315 FGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
+K I V+ + PD+A ++V+ +F+ I + + KE++R I
Sbjct: 283 ---NFIKGIIVDASATPDIAVISVIGIFSTEGVKIYNYQRLKTKESDRWKGIEMCRAF 339

Query: 375 GASVEEGPDYC-----IITPEKLNVTADITYDDHRMAMAFSLAAC-AEVPVTIRDPGCT 428
GA+V ++ I+ PE + T DHRM M+ +A A ++
Sbjct: 340 GATVSVCFNFIEIKKILKDPESIKFT-----DHRMIMSAILIAGVIAGSHTEFKNAEKI 393

Query: 429 RKTFFPDYF 436
K++P++
Sbjct: 394 NKSYPEFL 401

>ref|ZP_07893857.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter
upsaliensis JV21]
gb|EFU71937.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter
upsaliensis JV21]
Length = 425

Score = 97.4 bits (241), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 109/421 (25%), Positives = 178/421 (42%), Gaps = 31/421 (7%)

Query: 25 KSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + A LS+ T+ N L +ED L + LG VE + + V + K
Sbjct: 21 KSISRFAIFALLSDKTSRAKNYLLAEDTLNLTLLKIIENLGAKVERNGSE---VCISPSAK 77

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
+ L GN+G AMR + + AG +VL G + +RP+ + LK++
Sbjct: 78 I----NEPPCILECGNSGTAMRLMIGFL--AGIEGFFVLSGDKYLNKRPMKRICEPLKKI 131

Query: 145 GADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + +G + I G + ISS + ++ A V +
Sbjct: 132 GAKI---MGREEANFAPLCIEGQKLKSFNYTSEISSAQVKTAMILAGFRADKVSF-FKES 187

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E L ME A I QK P N + D SS YF+ A
Sbjct: 188 FLNRNHSNMLTFME-----APLKIQTSLISPIQPLKPLNITIPNDPSSVFYFILAA 242

Query: 265 AITGGTVTEGCGTTSLQGDVKFA--EVLEMMGAKVTWT--ETSVTVTGPPREPFRKHL 320
I + + C L + ++LE MGA +++ E + G +
Sbjct: 243 LILPNS---QICIKNVLLNPTRIEAYKILEKMGANISYHFDEENFEKIGTIYASSSKLQA 299

Query: 321 KAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
I N++ + D A LA+ A+G + +++ RVKE++R+ A+ T L K G EE
Sbjct: 300 VEISENISWLIDEAPALAIAFALANGTSLKNAKELRVKESDRIKAMVTNLQKCGIKAE 359

Query: 381 GPDYCIIT--PPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDV 438
D IT P+ I+++ DHR+AM+F++ + I D C +FP++ +
Sbjct: 360 LEDGFKITGGTPKS---AYIESFGDHRVAMSFAILGLV-CSMEIDDYSCIATSFPNFTTI 415

Query: 439 L 439
L
Sbjct: 416 L 416

>ref|YP_575526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter hamburgensis X14]
sp|Q1QRT1.1|AROANITHX RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABE61066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter hamburgensis X14]
Length = 449

Score = 97.1 bits (240), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 127/436 (29%), Positives = 201/436 (46%), Gaps = 19/436 (4%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V++PG KS+S+R L+L AL+ G T + LL EDV A++ LG VE
Sbjct: 16 QSLIGRVRVPGDKSISHRALILGALAVGETRIAGLLEGEDVLNTAKAMQALGAKVERRID 75
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K +V G A E L GN+G R + AV AG DG +R R
Sbjct: 76 DKSGIVWSVRVGTSGFATPEAPLDFGNSGTGCRVMGAV--AGCPIVATFDGDGSLRSR 133
Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ ++ L+ +GA V P+ + G P V + S+Q SA+L+A
Sbjct: 134 PMRRILDPLELMGARVTGESDGGRLPLTLAGARD-PLPIVYRTPVASAQIKSAVLLAGLS 192
Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +I+ S + E+ L+ FG + + + R GQ V
Sbjct: 193 APGIT--TVIESEASRDHTEMLK---HFGAQIVSVSDGTHGRKISLTGQPELHGAATV 247
Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ + A IT G+ + + T L+ + FA + E MGA + +ET +
Sbjct: 248 PADPSSAAFPPIVAALITEGSDIVLTDVMTNPLRTGL-FATLRE-MGASIEESETRLDAGE 305
Query: 310 PPREFPGR-KHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P + R L+ ++V + P D + LAV A FA+G T +R + RVKE++R+
Sbjct: 306 PMAQLRVRASKLRGVEVPAARAPSMID EYLVLAVAAFAEGTTVMRGLHEL RVKESDRLE 365
Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL-NVTAIDTYDDHRMAM-AFSLAACAEVPTIR 423
A L G +VE D I+ ++ + T+ DHR+AM A ++ ++ PV +
Sbjct: 366 AAAAMLRVNGVAVEIAGDDLIVEGRGRVPGGGLVTTMDHRIAMSALAMGCASDAPVKVD 425
Query: 424 DPGCTRKTFFPDYFDVL 439
D +FPD+ ++
Sbjct: 426 DTAFIATSFDPDFVPM 441

>ref|YP_001989102.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris TIE-1]
sp|B3Q5Z7.1|AROARHOPT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACE98626.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris TIE-1]
Length = 445

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 130/444 (29%), Positives = 197/444 (44%), Gaps = 37/444 (8%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT ++PG KS+S+R L+L AL+ G T + LL EDV A+R LG VE +
Sbjct: 18 LHGTARVPGDKSISHRALILGALAVGETRISGLLEGEDVINTAKAMRALGAKVERTGDCE 77
Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G A E L GN+G R AV AG DG +R RP
Sbjct: 78 WRVHGVGVAGF-----ATPEAPLDFGNSGTGCRVMGAV--AGSPIVATFDGDASLRSR 130
Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+ +GA V P+ + G P + + S+Q SA+L+A A
Sbjct: 131 MRRIVDPLELMGAKVVSSEGGRLPLALQGARD-PLPILYRTPVPSAQIKSAVLLAGLSA 189
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251

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      G      +I+   S   + E+   +++ FG   +   E   +   R      GQ      V
Sbjct: 190 PG--VTTVIEAEASRDHTEL---MLQHFGATIVTEAEGAHGRKISLTGQPELRGAPVVVP 244

Query: 252 GDASSASY-FLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGTP 310
      D SSA++ +A   + G   +   +   T L+      L MGA +   ++   V G
Sbjct: 245 ADPSSAAFPMAALVVPGSDIELTDVMTNPLR--TGLITTLREMGALIEDSD----VRGD 298

Query: 311 PREPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      EP R      LK ++V   + P   D   + LAV A FA+G T +R +   RVKE++
Sbjct: 299 AGEPMARFRVRGSKLKGVEVPPERAPSMIDEYLVLAFAAAFAEGTTVMRGLHELVRKESD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAM-AFSLAACAEV 418
      R+ A   L   G +VE   D I+   K +V   + T+ DHR+AM A ++   ++
Sbjct: 359 RLEATAAMLRVNGVAVEIAGDDLIVE--GKGHVPGGGVVATHMDHRIAMSALAMGLASDK 416

Query: 419 PVTIRDPGCTRTKTFPDYFDVLSTF 442
      PVT+ D      +FPD+   ++
Sbjct: 417 PVTVDDTAFIATSFPDFVPMQRL 440

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>gb|AAx21586.1| AroA [Francisella tularensis subsp. holarctica]
Length = 172

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 59/146 (40%), Positives = 79/146 (54%), Gaps = 4/146 (2%)

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Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
      L GG +++ G SSQ+ S LLMAAP   + + I      PY++MT ++M FGV
Sbjct: 26 LDGGYIEVDGEKSSQFASGLLMAAPFMHCGLRLNSITDHKQ-PYLDMTTKVMAEFGVTV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVK 286
      D + Y      +Y S N VE D S+ASYF A AAITG T+ V      S QGD+K
Sbjct: 84 --DIDENIYTAKKSQYISTSNNYVVEPDVSTASYFWAFAAITGSTIKVMHVTKNSKQGDIK 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPR 312
      F EVLE +G +V +   + VTG +
Sbjct: 142 FLEVLEKIGCQVNNYNDGIEVTGNQ 167

```

>ref|NP_662795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium tepidum
TLS]
sp|Q8KB71.1|ARO_A_CHLTE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAM73137.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium tepidum
TLS]
Length = 434

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 114/439 (25%), Positives = 198/439 (45%), Gaps = 34/439 (7%)

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Query: 21 LPGSKSLSNRIILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA-----K 74
      LP KS+S+R L+ AL+EGTT + N      D   L LR G+S+ ++ +   +
Sbjct: 11 LPPDKSISHRAALIGALAEGTTEISNFSGGYDNQSTLSVLRDAGISIRQEELSAGDGRIE 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      R VV+   G +   +   V L N+G MR +   + A   + V D   + +RP+
Sbjct: 71 RRVVIESNGLWSFREPS--VPLMCNNSGSTMRMMAGIMAAQPFRSELVGDA--SLMKRPM 126

Query: 135 GDLVVGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      +   L+Q+GA++      PV ++G   L   + +L   + S   + +L+   A L
Sbjct: 127 KRVADPLRQMGAEI-SLSDAGTAPVVIHGKALKTIEYRL--PVPSAQVKSILVAFALH- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      D + ++II+ + S   + E+ L   G+      R I G+K   + K   V D
Sbjct: 183 ADGQSKIIEPIRSRDHTEMLML-----GLATIDRDPGVREIIIDGRKPAAKPFKVPADP 236

Query: 255 SSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP--- 311
      S+A + +A   + G   +   V + +VL+   GA +   E   + G P
Sbjct: 237 SAACFMIA-LGLLGERSEIVLRNVCLNPTRVAYIDVLQEAGAGL-GIENVRSEGGEVGD 294

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Query: 312 ---REPFGRKHLKAID--VNMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
R G K L+ D V + +V M LAV++ FA G + + A R KE++R+ A
Sbjct: 295 IIVRSCSGLKPLRISDHGVVAGVIDEVPMLAVLSAFASGEFELHNAELRTKESDRIDA 353

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKL--NVTADITYDDHRMAMAFSLAA-CAEVPVTIR 423
+ L +LG E+ D ++ + + I+ +DDHR+AM+F+AA A + +
Sbjct: 354 LVVNLQRLGFECEQYADGFVVKGRKTVASEEVEIECFDDHRIAMSFTIAEAAGASLRLS 413

Query: 424 DPGCTRKTFPDYFDVLSTF 442
D +FP++F ++ +
Sbjct: 414 DRDVAGVSFPNFFALIDSL 432

>ref|YP_001246893.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus JH9]
ref|YP_001316688.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus JH1]
ref|ZP_05644459.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A9781]
ref|ZP_05683546.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A9719]
ref|ZP_06817014.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A8819]
ref|ZP_06928521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A8796]
sp|A6U1T3.1|AROAA_STAA2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|A5ISZ4.1|AROAA_STAA9 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ABQ49317.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus JH9]
gb|ABR52401.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus JH1]
gb|EEV27792.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A9781]
gb|EEV67959.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A9719]
gb|EFG43956.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A8819]
gb|EFH37914.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus A8796]
gb|EFT85174.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus CGS03]
Length = 432

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 113/443 (25%), Positives = 204/443 (46%), Gaps = 54/443 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L+EGT+ + L ED + R LG+ ++ D +
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAEGTSNIYKPLLGEDCRRTMDIFRLLGVDIKED---E 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+VV G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 DKLVVNSPG-YKAFKTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDGCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ LK + A+++ P + GI +++++ S+Q SA+L A+
Sbjct: 126 DRVLRPLKLMADANIEGIEDNYTPLIIKPSVIKGI----NYQMEVA---SAQVKSAILFAS 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK---GGQKYKSPKN 247
+ I+ +D +S + E R F + E +R I ++ P +
Sbjct: 179 LFSNDTTVIKELD--VSRNHTETMFR---HFNIPIE---AERLSITTPDAIQHIKPAD 229

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV-----TW 300
+V GD SSA++F+ A IT + VT+ G + + +++E MG + T
Sbjct: 230 FHVPGDISAAFFIVAALITPESDVTIHNVGINPTRSGI--IDIVEKMGGNIQLFNQTTG 287

Query: 301 TETSVTVT---GPPREPF---GRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVA 354

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      E + ++      P +P      G      KAID      ++P      +A++      A G + I+D
Sbjct: 288 AEPTASIRIQYTPMLQPITIEGELVTKAID----ELP----VIALLCQAVGTSTIKDAE 339

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
      +VKET R+      L LG ++      D II P E      +D+ DHR+ M ++A+
Sbjct: 340 ELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIGMMLAVAS 399

Query: 415 -CAEVPVTIRDPGCTRKTFPDYF 436
      + PV I+      +FP +
Sbjct: 400 LLSSEPVKIKQFDAVNVSFPGFL 422

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>ref|YP_001786896.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
      A3 str. Loch Maree]
gb|ACA56282.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
      A3 str. Loch Maree]
Length = 442

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Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 110/453 (24%), Positives = 212/453 (46%), Gaps = 51/453 (11%)

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Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYEIIIGDKSIGHRSIIIGALPKGKYKYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      + V G E+ ++ ++ G N+G +R + ++ G ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQGKNSGTTVRLMAGVLSGIGAETRFI--GDESLSC 121

Query: 132 RPIGLDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+ ++ L+++GA ++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPLKFLEHSGLNFIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLME-RFGVKAHSDSWDRFYIKGG---QKYK-SPK 246
      ++ G + I++ + + E L+ ++ +K +S + ++ K +K K + K
Sbjct: 179 MSKG--KTTIVENKPTRDHTERMLKYLDASINIKNIYSKNKEKSIFKKEITIEKSKLNSK 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS--QGDVKFAEVLEMMGAKVTWTETS 304
      + YV GD SSA++ ++ A + G+ C L +G +++ VL+ MGA + E
Sbjct: 237 DIYVPGDISAFLISAALLIQGSNL---CIKNVLLNEGRIEYINVLKNMGANIE-IEKG 292

Query: 305 VVTGTPPREPFGR-----KHLKAIDVNMNMKMPDVAM---TLAVVALFADGPTAIRDVASW 356
      + G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 293 KLLNG---EPVGNIVKESYLKGITVEQHITPNIIDEIPVLSVIAAFSEGKTIFKSVEEL 349

Query: 357 RVKETERMVAIRTELTL-----KL GASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
      + KE++R+ AI L K G + EG I E I+++ DHR+A+
Sbjct: 350 KFKESDRVEAIIENLKRADVKAIIYKNGNLIIEGNKSYIDKSLE-----IESFKDHRIAL 403

Query: 409 AFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLS 440
      AF + + T I+D CT +FP+ + +
Sbjct: 404 AFLVLSLKNKKHTLIKDYQCTEISFPNLSLFLN 436

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>ref|ZP_02996348.1| hypothetical protein CLOSP0_03471 [Clostridium sporogenes ATCC
      15579]
gb|EDU37302.1| hypothetical protein CLOSP0_03471 [Clostridium sporogenes ATCC
      15579]
Length = 442

```

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 105/446 (23%), Positives = 214/446 (47%), Gaps = 37/446 (8%)

```

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++G ++ G KS+ +R L++ AL++G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYEIIIGDKSIGHRSIIIGALAKGEYKYNFPKNLDCMATLDSMKKLGVDI---KV 66

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      + V G E+ ++ ++ G N+G +R + ++ G ++ G +
Sbjct: 67 EGNTLVNNSPG---YENFNKKPEVLQGKNSGTTVRLMAGVLSGIGAETKFI--GDDSLSC 121

```

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA ++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPKFLKHDGLNSIKYNMKVA-SAQVKSCILLAGL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERF-GVKAHSDSWDRFYIKGG---QKYK-SPK 246
++ G + I++ + + E L+ ++ + ++ +S + K +K K + K
Sbjct: 179 MSKG--KTTIVEDKSTRDHTERMLKYLDAYINIRNIYSKDRKKSTFKKEVTIEKSKLNSK 236

Query: 247 NAYVEGDASSASYFLAGAA-ITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ YV GD SSA++ ++ + I G + ++ +G +++ VL MGA + E
Sbjct: 237 DIYVPGDISAFLISASLLIEGSNLCIKNVLLN--EGRIEYINVLRNMGANIE-IEKGK 293

Query: 306 TVTGGPPREPFGFR-----KHLKAIDVNMNKMVDVAM---TLAVVALFADGPTAIRDVASWR 357
+ G EP G +LK I V + P++ L+V+A F++G T + V +
Sbjct: 294 LLNG---EPVGNICVKESYLKGITVEKHIIIPNIIDEIPVLSVIAAFSEGKTIFKSVEELK 350

Query: 358 VKETERMVAIRTELTKLGA-SVEEGPDYCIITPPEKLNVT-AIDTYDDHRMAMAFSLAAC 415
KE++R+ AI L + G S + D I ++ + I+++ DHR+A+AF + +
Sbjct: 351 FKESDRVEAIIENLKRAVGKSAYKNGDLIEGKNSYIDKSLEIESFKDHRIALAFLVLSSL 410

Query: 416 AEVPVT-IRDPGCTRKTFPDYFDVLS 440
T I+D CT +FP+ + +
Sbjct: 411 RNKKHTLIKDYECTEISFPNSLSLFN 436

>ref|YP_989551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella
bacilliformis KC583]
gb|ABM45608.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella
bacilliformis KC583]
Length = 441

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 114/454 (25%), Positives = 205/454 (45%), Gaps = 58/454 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +K+PG KS+S+R L+L L+ G T + LL S+D+ + A++ +G + +
Sbjct: 15 LSGKIKIPGDKSISHRSLILGGLANGETHIHGLESDDILHTAAAMQAMGAHIRKENG- 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G ++ K L GN+ R + V++ T+ D + +RP+
Sbjct: 74 -WIIRGTNGNCLLQAQKP---LNFNGSATGARLIMGVSSYHMKTTFTGDA--SLSKRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALL 187
++ L+ +G +++ ++ P+ + G K++ I S+Q S++L
Sbjct: 128 ERILNPLRLMGTNIEAT--SNNLPLTLYG-----PKMANPICYRLPIASAQVKSSIL 177

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSP 245
+A+ G +I+ +++ + E +++E FG K E + RF GQ + +
Sbjct: 178 LASLNTAGIT--TVIEPILTRDHT---KILELFGAKLDIETNKEGTRFIHMHGQPHLTG 232

Query: 246 KNAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 304
++ + GD SSA++ +A I + +E S + + + L MGAK+ +
Sbjct: 233 QSIDIPGDPSSAAFPLIAALLIEDSDIIENVLINSSR--IGLIQTLWEMGAKIEFLNQ- 289

Query: 305 VVTGPPREPFGGRKH-----LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRD 352
R+ G LK + V + P D LAV A FA+G T +
Sbjct: 290 -----RQQGGENIADLRVRSSVLKGVTVPKERAPSMIDEYPALAVAAAFAGKTTMLG 342

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVT AIDTYDDHRMAMA 409
+ RVKE++R+ I L E+G D+ II + L I T+ DHR+AM
Sbjct: 343 IEELRVKESDRLSTIAQGLKINHVDCEKGVDFLIHGNSSKGLGGGCIKTHLDHRIAMC 402

Query: 410 FSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 442
F + A E PVTI D +FP+ +++
Sbjct: 403 FLVFGGLASEKPVITIDRRVIATSFPAFIPLMNQL 436

>ref|ZP_04056182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas uenonis
60-3]
gb|EEK15995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Porphyromonas uenonis
60-3]

Length = 428

Score = 97.1 bits (240), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 116/444 (26%), Positives = 189/444 (42%), Gaps = 62/444 (13%)

```
Query: 18 TVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
      ++ LP SKSL NR+ ++A L+ L L + D AV
Sbjct: 6 SITLPPSKSLYNRLFVMARLAH-----LPIPSLWRQIDLCEDLAV 45

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
      ++ G E ++ +G +G AMR LTA ++ V RM ERP+ L
Sbjct: 46 MLHASGS-----SEGRISVGASGTAMRLLTALFALTTEREVLLVSPVRRMTERPLAQL 98

Query: 138 VVGLKQLGADVDCFLGTD-----CPPVRVNGI-----GGLPGGKVKLSGSISSQYLSALL 187
      + L QLAD+ + P VR+ + G LP + SG SSQ ++ALL
Sbjct: 99 ITLLSQLGADLAQPSSQEPVEGLYPLVRIRPMNPQQKGLLPTLTLTP-SGLESSQTVTALL 157

Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDR--FYIKGGQKYKS 244
      + AP + + D+L S Y+++T LM+ G+ S DR Y+ G ++
Sbjct: 158 LIAPYLPGLALRWQDDQLPSASYIQLTCSLMQACGIDL----SVDRHGIYVAPGTYCEA 213

Query: 245 PKNAYVE---GDASSASYFLAGAAIT---GGTVTEGCGTTSLQGDKFAEVLEMMGAKVT 299
      + GD SSA Y L A +T + + SLQ D + E+L++ ++
Sbjct: 214 TLTRLSSHPIGWSSAQYPLQWALMTPRPCQLFLTNVPALSLQPDARALELLQISPEWLS 273

Query: 300 WTETSVTVTGPPREPFGGRKHLKAI---DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASV 356
      + ++ F +KHL+ + +++ PD A TL + L+ +R +
Sbjct: 274 AGDDTLFCFDS----EFLQKHLRKLTFGSISSLNNPDFAPTLIALLLYYQKKAQLRGLDHL 329

Query: 357 RVKETERMVAI--RTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMAMAFSL 412
      R+KE++R+ I E S E +C+ P I T DHRM MA++
Sbjct: 330 RLKESDRIALILRNGEQLDYQLSYETESGFCLAGSAPSSVHTPVPIATDADHRMVMMAWAP 389

Query: 413 AACAEVPTIIRDPGCTRKTFPDYF 436
      A + I P K++P ++
Sbjct: 390 FAWYHQ-LQIETPQAVDKSYPTFW 412
```

```
>ref|YP_032958.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella henselae
str. Houston-1]
sp|Q6G545.1|AROABARHE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAF26911.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella henselae
str. Houston-1]
Length = 442
```

Score = 96.7 bits (239), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 116/445 (26%), Positives = 201/445 (45%), Gaps = 39/445 (8%)

```
Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      +SG +K+PG KS+S+R L+L L+ G T + +L S+DV A++ LG + K
Sbjct: 15 LSGIIKIPGDKSISHRSLILGLASGETHIHGILESDDVFNTAAAMQALGACI--IKKDD 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      ++ G G + K L GNAG R + V T++ D + +RP+
Sbjct: 73 LWIIRGTGNGCLLAAQKP---LDFGNAGTGARLVGMVGPHYMKTTFIGDA--SLSKRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
      ++ L+ +G +++ G P P N I ++ ++ S+Q SA+L+A
Sbjct: 128 ARILDPLQLMGVEIEATHGNYLPLTLTYGPKMTNPI----CYRIPVA---SAQVKSAILLA 180

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD--RFYIKGGQKYKSPKN 247
      G +I+ +++ + E ++++ FG K E + + RF G + + +
Sbjct: 181 GLNTAGTT--TVIEPILTRDHTE---KMLKAFGAKLEIEKNAEGTRFIHLNGHPHLLTGQT 235

Query: 248 AYVEGDASSASY-FLAGAAITGGTVTEGCGTTSLQGDKFAEVLEMMGAKVTWTETSVT 306
      ++ GD SSA++ +A I +T+E + + + E L MGA++ T
Sbjct: 236 IHIPGDPSSAAPPIVAALLIEDSDITIENVLINNSR--MGLIETLWEMGAQIELLNQRQT 293

Query: 307 VTGPPREPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
```

G K LK + V + P D LAV A FA+G T + + RVKE+
Sbjct: 294 -GGEDVANLRVKSSVLKGVTVPKERAPSMIDEYPALAVAAFAEGKTVMLGIEELRVKES 352
Query: 362 ERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTADITYDDHRMAMAFSL-AACAE 417
+R+ + L EEG D+ I+ + L + T+ DHR+AM+F + +E
Sbjct: 353 DRLSVLAQGLKINHVDCEEQDFLIVHGKGSAGLGGGHVTTHLDRHIA MSFLIFGLVSE 412
Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
PVTI D +FP++ +
Sbjct: 413 KPVTIDDKRMIATSFPEFIPFIQQL 437

>ref|YP_758929.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hyphomonas neptunium
ATCC 15444]
sp|Q0C5R4.1|AROA_HYPNA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABI78571.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hyphomonas neptunium
ATCC 15444]
Length = 439

Score = 96.7 bits (239), Expect = 6e-18, Method: Compositional matrix adjust.
Identities = 120/445 (26%), Positives = 195/445 (43%), Gaps = 29/445 (6%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P+K ++G ++ PG KS S+R L+ L+EG + LL +DV A+ +G +V
Sbjct: 6 HPVKRLAGAIRAPGDKSCSHRALIFGGLAEGESRFGSLLEGDDVLRGTQAMEAMGATVTR 65
Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
V G G K + + L GN+G R L + AG + T L G +
Sbjct: 66 TGPGSWD-VTGVGAKGL---SSPKGVLDGFGNSGTGSRLLMGMV--AGYDLTASLTGDASL 119
Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCP-PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RP+ ++ L+Q+G + G D P + G L + S+Q SA+L+
Sbjct: 120 CSRPMNRVLNPLRQMG--LKDTAGPDGKLPFTLTGSKSLKAIRYAPP-QASAQVKSALL 176
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS---DSWDRFYIKGGQKYKSP 245
A A G E + + + + E R+++ FG +KGGQ+ +
Sbjct: 177 AGLNAEG--ETVVAEAKATRDHTE---RMLQGFGATLSFRMAPGGVHEIALKGGQRLRG- 230
Query: 246 KNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+A + GD SSA++ +A ++ G V VEG + + F +V ++MGA + E
Sbjct: 231 LDAEIPGDPSSAAFLIAAGLLSPQGDVLEGVMSNPTRS--GFYDVADLMGASLGADERG 288
Query: 305 VTVTGPDPREP-GRKHLKAIDVN---MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ G LK I V + M D LAV+A FA G T + RVKE
Sbjct: 289 EAAGERLIDIHSGYAGLKGIHVPERLVASMIDEFPILAVLAAAFATGETRVTGAEELRVKE 348
Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAM-AFSLAACAE 417
++R+ A+ L G VEE D + ++T DHR+AM A + A+
Sbjct: 349 SDRIGAVVAMLRVNGVEVEETEDGFTVQCGGRVPGGGLVETRHDRHIA MSALVMGTAAQ 408
Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
PV++ D ++P++ ++T
Sbjct: 409 KPVSVDIDSMIDTSYPEFMSHMATL 433

>ref|YP_676143.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Mesorhizobium sp.
BNC1]
sp|Q11C97.1|AROA_MESSB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABG64978.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chelativorans sp.
BNC1]
Length = 449

Score = 96.7 bits (239), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 119/451 (26%), Positives = 194/451 (43%), Gaps = 54/451 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+S+R L+ L+ G T + LL EDV A+R +G + D+

Sbjct: 18 LKGNLRVPGDKSISHRALMFGGLASGETRISGLLEGEDVLR TAEAMRAMGAQI--DRRDG 75

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ G G +E E L GNAG R LT + + T G + +RP+

Sbjct: 76 TWTIRGVNGCGLLE---PEAPLDFGNAGTGSRLTMGLVGT-YDMTRFTGDASLSKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V D P+ + G P ++ + S+Q SA+L+A

Sbjct: 131 GRVLNPLREMGTVQLQAEPGDRLPITLRG----PKHATPINYRVPMASAQVKSALLAGL 186

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAY 249
G +I+ +++ + E +++ FG ++ E R GQ +

Sbjct: 187 NTPG--VTTVIEPVMTRDHTD---KMLSGFGAAIQIETDKEGARHISIQGGTGLKGQVIA 241

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVL---EMMGAKVTWTETSVT 306
V GD SSA++ L A I G+ D+ VL G +T E

Sbjct: 242 VPGDPSSAAFLVAALIVPGS-----DILIENVLMNPTRTGLLITLQEMGAD 288

Query: 307 VTGPPREPFGRKH-----LKADIVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
+ R G + LK + V ++ P D LAV A A+G T + +

Sbjct: 289 IELLNRRSAGGEDVADLRVRSSALKGVTVPASRAPSMIDEYPILAVAASLAEGETVMLGL 348

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-PPE--KLNVTATIDTYDDHRMAMAF 410
RVKE++R+ A+ L G EG D + PE L + T+ DHR+AMAF

Sbjct: 349 EELRVKESDRLSAVAEGLKVGIDCTEGKDTLTVRGRPEGKGLGGATVTTHLDHRIAMAF 408

Query: 411 -SLAACAEVPTIRDPGCTRKTFPDYFDVLS 440
L +E PV++ D +FP++ D+++

Sbjct: 409 LVLGLASERPVSVDQSMIATSFPEFMDLMT 439

>ref|YP_002502152.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
nodulans ORS 2060]
gb|ACL61849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
nodulans ORS 2060]
Length = 466

Score = 96.7 bits (239), Expect = 7e-18, Method: Compositional matrix adjust.
Identities = 126/443 (28%), Positives = 186/443 (41%), Gaps = 44/443 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G ++ PG KS+S+R ++L LS G T ++ LL +DV A R LG ++ D +

Sbjct: 35 LRGRLRPPGDKSISHRAMILGLLSIGETRIEGLLEGDDVLR TAAAAALGAGIDRDGPGR 94

Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG + E L GNAG R + V G T DG +R+RP

Sbjct: 95 WRVRGVGIGGL-----SDPEGVLDFGNAGTGSRLMMGVV--GGQPVATATFDGDASLRKRP 147

Query: 134 IGDVLVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+ ++ L Q+GA V P+ + G P + ++ S+Q SA+L+A

Sbjct: 148 MRRILDPLVQMGA TVVAQQEGGRVPLTLRG----PDEAIPITYETPVASAQVKSALLAG 203

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLM-ERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A G +I+ + + E LRL V A + R GQ

Sbjct: 204 LNAPGTT--TVIEAAATRDHTERMLRFLGAEVAVSAHGPEGHGRAIALTGQPTLRRAEVM 261

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLMMGAKVTWTETSVTVT 308
V D SSA++ L A + G+ V +EG L+ + L MGA +T

Sbjct: 262 VPADPSSAAFLVAALIVPGSDVIEGVMNPLR--IGLITTLLEMGA DITRLNE----- 314

Query: 309 GPPREPFGRK-----HLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
RE G L + V + P D LAV A FA G T ++ +

Sbjct: 315 ---REEGETVADLRVRACRLTGTVTPPERAPAMIDEYPVLAVAAAFAGQTRMQGLHEL 371

Query: 357 RVKETERMVAIRTELTKLG-ASVEEGPDYCI-ITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
RVKE++R+ A+ L G A V EG D + + T+ DHR+AMAF +

Sbjct: 372 RVKESDRLAAVAAGLKANGVAHVVEGDDLIVHGDGGAAGGGTVATHLDHRIAMAFVLMG 431

Query: 415 CAEV-PVTIRDPGCTRKTFPDYF 436
A PVT+ D ++P +

Sbjct: 432 LASRDPVTVDGAMIATSYPSFL 454

>ref|ZP_01086603.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 5701]
gb|EAQ73594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Synechococcus sp. WH 5701]
Length = 298

Score = 96.3 bits (238), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 97/315 (30%), Positives = 141/315 (44%), Gaps = 31/315 (9%)

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALLMAAPLALGDV 197
+GADV + P+ V G L G+I S+Q SA+L+AA A D
Sbjct: 1 MGADVGRDRSGNLAPLAVQG-----TTLRGTIVGTPVASAQVKSAILLAALTA--DG 50

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-IKGGQKYKSPKNAYVEGDASS 256
+I+ S + E R++ FG E R +K G + V GD SS
Sbjct: 51 PTTVIEPSQSRDHSE---RMLRAFGANLEVGEMGRHISVKPGATLHG-QTVVVPGLDISS 106

Query: 257 ASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPF 315
A+++L AGA + G +T+E G + EVL+ MGA + V G P
Sbjct: 107 AAFWLAVAGALVPGSDLTIENVGLNPTR--TGILEVLDQMGANIEIVNPR-DVAGEPVGDL 163

Query: 316 GRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
KH LK MP D L+V A F DG + I A RVKET+R+ + +
Sbjct: 164 RVKHGPKLPKFQFGEEIMPRLVDEVPILSVAACFCDGESRISGAAELRVKETDRLAVMARQ 223

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTR 429
L +GA +EE D I L+ TA+D+ DHR+AM+ ++AA A P T+
Sbjct: 224 LKAMGAIEEHDDGMTIRGGRPLHGTALDSETDHRVAMSMAVAALMANGPSTLARSEAAA 283

Query: 430 KTFPDYFDVLSTFVK 444
++P ++D L +
Sbjct: 284 VSYPTFWDDLERLHR 298

>ref|YP_567330.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris BisB5]
sp|Q13ER0.1|AROARHOPS RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABE37429.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas palustris BisB5]
Length = 445

Score = 96.3 bits (238), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 132/439 (30%), Positives = 195/439 (44%), Gaps = 33/439 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+SGT ++PG KS+S+R L+L AL+ G T + LL +DV A+R LG VE + A
Sbjct: 18 LSGTARVPGDKSISHRALILGALAVGETRISGLLEGQDVIDTGKAMRALGARVERTGEFA 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG G A+ E L GN+G R AV AG T DG +R RP
Sbjct: 78 WTVRGVGVAGF-----AQPEAPLDFNGSGTGCRLLAMGAV--AGSPITATFDGDASLRSRP 130

Query: 134 IGDVLVGLKQLGADV-DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
+ +V L+Q+GA V G P LP + S+Q SA+L+A
Sbjct: 131 MRRIVDPLEQMGARVIQSHEGGRLPLTLQGARDPLP--ITYRTPVPSAQIKSAVLLAGLS 188

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +I+ S + E+ +++ FG E + R GQ V
Sbjct: 189 APG--VTTVIEAEASRDHTEL---MLQHFGATLVTEPEGAHGRKISLTGQPELRGARVVV 243

Query: 251 EGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
D SSA++ +A + G + + T L+ L MG + +ET TG
Sbjct: 244 PADPSSAAFPMAALLVPGSDIVLTFVMTNPLR--TGLITTLREMGAIEESETR-DDTG 300

Query: 310 PPREFPGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P F + L+ ++V + P D + LAV A FA+G T +R + RVKE++R+
Sbjct: 301 EPMAQFRIRGSRLRGVEVPPERAPSMIDEYLVLAFAAFAEGTTVMRGLHELRLVKESDRL 360

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAM-AFSLAACAEVPV 420
A L G VE D I+ K +V + T+ DHR+AM A + A+ PV
Sbjct: 361 EATADMLRVNGVKVEIVGDDLIVE--GKGHVPGGGLVATHMDHRIAMSALVMGLAADRPV 418

Query: 421 TIRDPGCTRKTFFPDYFDVL 439
+ D +FPD+ ++
Sbjct: 419 KVDDTAFIATSFPDFVPM 437

>ref|ZP_01752691.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
SK209-2-6]
gb|EBA18244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Roseobacter sp.
SK209-2-6]
Length = 441

Score = 96.3 bits (238), Expect = 8e-18, Method: Compositional matrix adjust.
Identities = 123/435 (28%), Positives = 201/435 (46%), Gaps = 32/435 (7%)

Query: 15 ISGTVKLPKSGSKSLNRILLALLSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
++G ++PG KS+S+R L+L A++ G T + LL +DV A++ G V
Sbjct: 9 LTGVAEVPKSGKSLNRILLALLSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 68

Query: 75 RAVV-VGCGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG A+ + + GN+G +R + + + T+ D + RP
Sbjct: 69 WSVHGVGVGGF-----AEPDQVIDCGNSGTGVRLLMGCMATSPISVFTTGDA--SLNGRP 121

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMAAPL 192
+ + L GA G P V +P V+ + S+Q SA+L+A
Sbjct: 122 MARVTDPLALFGAKSVGRSGGRLPMTIVGAAAPVP---VRYEVPVPSAQVKSALLMAAPL 178

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPKNAYVE 251
A G + +I+K + + E R++ FG + D+ + R GQ P+ V
Sbjct: 179 APG--KTVVIEKEATRDHSE---RMLAGFGAEISAEDTEEGRVITLTGQPELKPQVIAVP 233

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D SSA++ + A IT G+ V V G G + + + L+ MGA +T+ E G
Sbjct: 234 RDPSSAAFPVCAALITPGSDVLVPGIGLNPTRAGLFY--TLQDMGADLTF--ENMREEGGE 290

Query: 311 PREPFGRKH---LKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P K+ +K I+V + M D L+VVA FA G T + V RVKE++R+
Sbjct: 291 PVADLRKAYSPNMKGIEVPPERAASMIDEYPLSVVASFATGKTMMAGVKELRVKESDRI 350

Query: 365 VAIRTELTKLGASVEEGPDYCI--TPPEKLNVTAI-DTYDDHRMAMAFS-LAACAEVPV 420
A+ L G V+EG D+ + PE + A +++ DHR+AM+F + A+ V
Sbjct: 351 DAMARGLRANGVMVDEGDDWWSVEGMGPEGVPGGATCESFLDHRIAMSFMVMGMGAQASV 410

Query: 421 TIRDPGCTRKTFFDY 435
T+ D +FP +
Sbjct: 411 TVDDGNPITTSFPVF 425

>ref|ZP_05427835.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium
saphenum ATCC 49989]
gb|EEU03502.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Eubacterium
saphenum ATCC 49989]
Length = 425

Score = 96.3 bits (238), Expect = 9e-18, Method: Compositional matrix adjust.
Identities = 79/361 (21%), Positives = 165/361 (45%), Gaps = 27/361 (7%)

Query: 90 AKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVD 149
+ + Q+F G + +R L A ++L + +RPI L+ L GA
Sbjct: 66 SSDNKQVFTGESASTLRMLLPALAMNKPKFILSK--SLSKRPIKFLDLITDAGATCT 123

Query: 150 CFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDLKISIP 209
+ + ++ G + G L ++SSQ++S L A L E+ + +K
Sbjct: 124 TSFDEN--DRLNIDVTGKINPGTYTLTAVSSQHISGFLFALSLLYKPCELIVNEKYSDKS 182

Query: 210 YVEMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKSPKN---AYVEGDASSASYFLAGA 264
Y+ +TL ++++FG++ + DR+ I G Q Y SP + E D S+ + +L

Sbjct: 183 YINITLNVIKQFGIRYDMEKFQDRYVINIDGRQTYTSPTYNLSIAEPDFSNLTPWLIAR 242

Query: 265 AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAID 324
AI +T+ ++S Q D + +++++ A T + + EP+

Sbjct: 243 AIGSYKLTLPDLPSPPQPD---SIIMKIINAYDTMNREKIRLNSSEEEPYT----- 291

Query: 325 VNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDY 384
++++K D+ L V+A F++ T ++ ++KE++R+ +++ L K+ +

Sbjct: 292 IDISKSLDLFPPLCVLAAFSNTKTLFTNIDKLKIKESDRVKSMQDILAKINIDTSISKNT 351

Query: 385 CIIT-PPEKLN-----VTAIDTYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFPDYF 436
+I PE ++ + +++Y DHR+AMA + +C P+ + +K++P +

Sbjct: 352 LLINGNPESVSCRSPKGIHLNSYGDHRIAMAAIILSCLNTPIHLCGADALKKSYPSFL 411

Query: 437 D 437
+

Sbjct: 412 E 412

>emb|CBI81616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella
schoenbuchensis R1]
Length = 442

Score = 96.3 bits (238), Expect = 9e-18, Method: Compositional matrix adjust.
Identities = 117/451 (25%), Positives = 203/451 (45%), Gaps = 41/451 (9%)

Query: 10 QPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69
Q +SGT+K+PG KS+S+R L+L L+ G T + LL S+D+ A++ +G +

Sbjct: 10 QKSTNLSGTIKIPGDKSISHRSLILGGLANGETHIHLLESDDILQTAAAMQAMGAHIR- 68

Query: 70 DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
K V+ G G ++ + L N+G + R + V++ T+ D +

Sbjct: 69 -KENNLWVIRGTGNGCLLQ---AQTSLNFKNSGTSARLIMGVSSYHMKTTFTGDS--SL 122

Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-----SSQY 182
+RP+ ++ L +G V+ + D P+ + G K++ I S+Q

Sbjct: 123 SKRPMKRILDPLCLMGVSVEK-MCDDHLPLTYG-----PKMASPIYYRVPMAAQV 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQ 240
SA+L+A G +I+ +++ + E ++++ FG ++ E RF GQ

Sbjct: 174 KSAILLAGLNTPGIT--TVIEPILTRDHT---KMLKAFGALEIETDKKGTRFIHLNGQ 228

Query: 241 KYKSPKNAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + + V GD SSA++ +A + + +E + + + + L MGAK+

Sbjct: 229 PHLTGQIIDVPGDPSSAAFLIAALLVEDSDIIIEENVLINNSR--IGLIQTLWEMGAKID 286

Query: 300 WTETSVTVTGPPREPFGRKH-LKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVAS 355
T + R LK + V + P D LAV A FA+G T + +

Sbjct: 287 LLNQRTGGEDVADLRVRSSILKGVTVPKERAPSMIDEYPALAVAAFAEGKTTMLGIEE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMAMAFSL 412
RVKE++R+ AI L EEG D+ I+ + L + TY DHR+AM F +

Sbjct: 347 LRVKESDRLSAIAQGLKINNVDCEEVDFLIVHQNSTKSLGGGCVTTYLDHRIAMCFLV 406

Query: 413 AACA-EVPVTIRDPGCTRKTFPDYFDVLSTF 442
A E PVT+ D +FP++ ++

Sbjct: 407 FGLASEKPVTVDDTRMIATSFPEFIPLMHQL 437

>ref|ZP_06488790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. musacearum NCPPB4381]
Length = 285

Score = 96.3 bits (238), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 87/286 (30%), Positives = 141/286 (49%), Gaps = 21/286 (7%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G++ +PG KS+S+R ++ AAL++G + +D L ED LG+ +E A++

Sbjct: 16 LQGSIAIPGDKSVSHRAVMFAALADGVSQIDGFLEGEDTRSTAAIFAKLGVRIETPSASQ 75

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

```

      R V  VG  G  P  ++      L  GNAG  MR L  + A  ++  VL G  + +RP
Sbjct: 76  RIVHGVGV DGLQPPTES-----LDCGNAGTGMRLLAGLLAAQRFD S--VLVGDESLSKRP 128

Query: 134  IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      +  +  L Q+GA +D      PP+RV+G+  L G  +S  S+Q  SA+L+A  A
Sbjct: 129  MRRVTGFLAQM GARIDT-QDDGTPPLRVHGVQALHGIDF-VSPVASAQVKS AVLLAGLYA 186

Query: 194  LGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHS DSWDRFYIKGGQKYKSPKNAYVEGD 253
      G+  +      P  + T R++  FGV  + S  R  ++GGQ+ ++  A V  D
Sbjct: 187  QGETSVTEPH-----PTRDYTERMLSAFGVDIDFSPGKAR--LRGGQRLRATDIA-VPAD 238

Query: 254  ASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKV 298
      SSA++F+  A+I  G+ V +  G  +      L +MGA +
Sbjct: 239  FSSAAFFIVAASIVPGSEVVLRAVGLNPRR--TGLLAALRLMGADI 282

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>ref|ZP_05079193.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
      bacterium Y4I]
gb|EDZ47172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodobacterales
      bacterium Y4I]
Length = 448

```

Score = 96.3 bits (238), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 123/439 (28%), Positives = 199/439 (45%), Gaps = 40/439 (9%)

```

Query: 15  ISGTVKLP GSKSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G  ++PG KS+S+R L+L ALS G T +  LL  EDV  A++  G  V
Sbjct: 18  LKGVAEVP GDKSISHRSLILGALS VGETKISGLLEGEDVLD TAKAMQAFGA EVVN HGGGN 77

Query: 75  RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      +V  VG GG      A+  +  +  GN+G  R +  +  +  AT+  D  + +RP
Sbjct: 78  WSVFVG VG VGGF-----AEPDNVIDCGNSGTGARLIMGVMATSPITATFTGDA--SLNKR P 130

Query: 134  IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPL 192
      +  +  L  G      G  P  +  +P  V+  + S+Q  SA+L A
Sbjct: 131  MARVTDPLALF GTQSVGRSGGRLPMTIIGAADPVP---VRYEVPVPSAQVKS AVLFAGLN 187

Query: 193  ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHS DSWD-RFYIKGGQKYKSPKNAYVE 251
      A G  +  +I+K  +  + E  R++  FG +  D+ + R  G+  P+  V
Sbjct: 188  APG--KTVVIEKEATRDHTE---RMLAGFGAEITTEDTDEGRVITLTGRPELKPQVIAVP 242

Query: 252  GDASSASYFLAGAAITGGT-VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
      D SSA++ +  A IT G+ V V  G  +  +  +  L+ MGA +T+ E  G
Sbjct: 243  RDPSSA A FPCAALITPGSDVLVPNI GLNPTRAGLYY--TLQDMGADLTF-ENMREEGGE 299

Query: 311  P----REFPGRKHLKAIDVNMNK---MPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      P  R  F  +K I+V  +  M D  L+VVA FA+G T +  V  RVKE++R
Sbjct: 300  PVADLR AKF-SPDMKGIEVPPERAA SMIDEYPVLSVVASFAEGKTMAGVKELRVKESDR 358

Query: 364  MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI-----DTYDDHRMAMAFS-LAACA 416
      + A+  L  G +VEEG D+ +T  L +  +  +++ DHR+AM+F  +  A
Sbjct: 359  IDAMARGLRANGVTVEEGEDWWEVT---GLGIDGVPGGGTCESFLDHRIAMSFVMVMGMGA 415

Query: 417  EVPVTIRDPGCTRKTFFPDY 435
      +  V++ D      +FP +
Sbjct: 416  QNAVSVDDGSP IATSFPIF 434

```

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>ref|YP_001944126.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium limicola
      DSM 245]
sp|B3EGN4.1|ARO A_CHLL2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD91147.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium limicola
      DSM 245]
Length = 434

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Score = 96.3 bits (238), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 114/446 (25%), Positives = 196/446 (43%), Gaps = 48/446 (10%)

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Query: 21  LPGSKSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV---EADKAAK--- 74

```

Sbjct: 11 LP KS+S+R L+ +LSEG T + N D LG L G+ V E D A
LPPDKSISHRAALIGSLSEGVTETITNFSAGFDNQSTLGLVLDAGIEVSQHEIDGAYGRR I 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V++ G + E L N+G MR + A + V D + +RP+

Sbjct: 71 RKVIISSRGLWSF--TAPEKPLMCNNSGSTMRMFAGILAAQPFESLVGDS--SLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+Q+GA VD PVR+ G L + +L + S + +L+ A L

Sbjct: 127 KRVADPLRQMGAGVD-LSPAGTAPVRIRGTRDLTPLEYRL--PVPSAQVKSILVTFAALH- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
D E II+ + S + E+ L G++ +R + G+K ++ Y+ D

Sbjct: 183 ADGETRIIESIRSRNHTLML-----GLETIDRPDGERVIVIPGRKTIVARSFYIPADP 236

Query: 255 SSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
S+A + +A G + + + + V+F +L GA +T E S + G E

Sbjct: 237 SAACFIVALGLGNSSEIIIRDVCLNPTN--VEFIPLLTGAGADIT-IENSRIIGG---E 290

Query: 314 PFG-----RKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
G + LK + ++ ++++P L+V++ F+ G + + R K

Sbjct: 291 TIGDILVRSTRTLKPLVISNPTVAVGVIDELP----MLSVLSAFSSGEFELHNAEELRTK 346

Query: 360 ETERMVAIRTELTKLGASVEEGPD--YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
E++R+ AI L +LG E+ PD I + + +DDHR+AM+F++AA A

Sbjct: 347 ESDRINAIVNLERLGFDCQYDPDGRFVIGRRCRPVGVQVTVACFDDHRIAMSFAVAARAT 406

Query: 418 VP-VTIRDPGCTRKTFPDYFDVLSTF 442
+ + D +FP++F+++

Sbjct: 407 GEGIALSDSDVVGVSFPNFFFEIENL 432

>ref|ZP_07819631.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Porphyromonas asaccharolytica PR426713P-I]
gb|EFR35415.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Porphyromonas asaccharolytica PR426713P-I]
Length = 434

Score = 95.9 bits (237), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 122/451 (27%), Positives = 187/451 (41%), Gaps = 77/451 (17%)

Query: 18 TVKLPGSKSLNRIILLALALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAARKAV 77
++ LP SKSL NR+ ++A L+ + L + D AV

Sbjct: 6 SITLPPSKSLYNRLFVMARLAH-----MPIPSLWHQLDLCEDLAV 45

Query: 78 VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
++ G E ++ +G +G AMR LTA ++ V RM ERP+ L

Sbjct: 46 MLHASG-----SSEERISVGASGTAMRLLTALFALTTERKVLLVSPVRRMTERPLAQL 98

Query: 138 VVGLKQLGAD-----VDCFLGTDCPPVRVNGIG--GLPGGKVKLSGSISSQYLSAL 186
+ L QLGAD V+ C +R + GLP + SG SSQ ++AL

Sbjct: 99 IALLTQLGADLSQPASQEPVNALYPLVC--IRPMSLQQKGLPTLTLP-SGLESSQVTAL 155

Query: 187 LMAAPLAGDVEIEIID-KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+ AP + + D +L S Y+++T LM+ G++ S DR I Y +P

Sbjct: 156 LLIAPYLPFHGLALRWQDNQLPSASYIQLTCSLMQACGIEL----SVDHGI-----YVAP 206

Query: 246 KNAYVE-----GDASSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKFAEVLE 292
AY E GD SSA Y L A +T + + + SLQ D A LE

Sbjct: 207 -GAYCEATLTRLNSNPIDWSSAQYPLQWALMTPRSKILLTNVPAQSLQPD---ARALE 262

Query: 293 MMGAKVTWTETSVTVTGPPREPFGRKHLKAI---DVNMNMPDVAMTLAVVALFADGPTA 349
++ W T E F +KHL+ + ++++ PD A TL + L+

Sbjct: 263 LLQISPEWLSTGSDTLCLDSE-FLQKHLRELTFGSLSLSNPDFAPTLLIALLLYYQKKAQ 321

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASV---EEGPDYCIITPPEKLNVTATIDTYDDHR 405
+ + R+KE++R+ I +LG + E G P I T DHR

Sbjct: 322 LHGLDLLRLKESDRIALILRNGEQLGYQLTYDTESGFLAGSAPSSVHTPVPIATDADHR 381

Query: 406 MAMAFSLAACAEVPVTIRDPGCTRKTFPDYF 436
M MA++ A + I P K++P ++

Sbjct: 382 MVMAWAPFAWYHQ-LEIETPQAVDKSYPTFW 411

>ref|YP_001608574.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella tribocorum
 CIP 105476]
 sp|A9ILL7.1|ARO_A_BART1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS
 emb|CAK00579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella tribocorum
 CIP 105476]
 Length = 442

Score = 95.9 bits (237), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 114/444 (25%), Positives = 199/444 (44%), Gaps = 49/444 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 +SG +++PG KS+S+R L+L L+ G T + LL S DV A++ +G + K
 Sbjct: 15 LSGKIRIPGDKSISHRSLILGGLANGETYIHGLESADVLTASAMQAMGACI--IKKDD 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
 ++ G G + K L GNAG R + V T++ D + +RP+
 Sbjct: 73 FWIIRGTGNGCLLAAQKP---LDFGNAGTGARLVGMVGPHYMKTTFIGDA--SLSKRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLS 184
 G ++ L+ +G +++ G P P+R + V ++ SSQ S
 Sbjct: 128 GRILDPLRLMGVEIEATHGDHPLTLTYGPKMANPIRYH-----VPIA---SSQVKS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKY 242
 A+L+A G +I+ +++ + E ++++ FG ++ E R G +
 Sbjct: 176 AILLAGLNTAGIT--TVIEPVLTRDHE---KMLKAFGATLEIERDKEGARLIHLYGHPH 230

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWT 301
 + + ++ GD SSA++ + A + + +T+E + + + E L MGA + +
 Sbjct: 231 LTGQTIHIPGDPSSAAFLIIAALLVEDSDITIENVLINNSR--IGLIETLWEMGAHIEFL 288

Query: 302 ETSVTVTGPPREPFGRKH--LKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVASW 356
 T G K LK + V + P D LAV A FA+G T + +
 Sbjct: 289 NQRQT-GGEDVADLRIKSSVLKGVTVPKERAPSMIDEYPALAVAAFAEGKTVMLGIEEL 347

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVTADTYDDHRMAMAF-SL 412
 RVKE++R+ A+ L EEG D+ ++ + L + T+ DHR+AM F +
 Sbjct: 348 RVKESDRLSAVAQGLKINCVDCEEGQDFLVVYGKGSAGLGGGYVSTHLDHRIAMCFLTF 407

Query: 413 AACAEVPVTIRDPGCTRKTFPDYF 436
 +E PVTI D +FP++
 Sbjct: 408 GLVSEKPVTTIDDQRMIAATSFPEFI 431

>ref|YP_002971141.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella grahamii
 as4aup]
 gb|ACS50464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella grahamii
 as4aup]
 Length = 442

Score = 95.9 bits (237), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 116/445 (26%), Positives = 202/445 (45%), Gaps = 51/445 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
 +SG +K+PG KS+S+R L+L L+ G T + LL S DV A++ +G + + D
 Sbjct: 15 LSGKIKIPGDKSISHRSLILGGLASGETHIYGLLESADVLTAAAMQAMGACI IKKDDFW 74

Query: 73 AKRAVVVGC--GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
 R GC + P++ GNAG R + V T++ D +
 Sbjct: 75 TIRGTGNGCLLAAQKPLD-----FGNAGTGARLVGMVGPHYMKTTFIGDA--SLS 123

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSI-----SSQYL 183
 +RP+G ++ L+ +G +++ D P+ + G K++ I SSQ
 Sbjct: 124 KRPMGRILDPLRLMGVEIEA--THNDHPLTLTYG-----PKMANPIRYRVPIASSQIK 174

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQK 241
 SA+L+A G +I+ +++ + E ++++ FG ++ E + R GQ

Sbjct: 175 SAVLLAGLNTAGIT--TVIEPVLTRDHT---KMLKAFGAQLEIEKDNEGARLIHLNGQP 229

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + ++ GD SSA++ + A + + +T+E + + + E L MGA++ +

Sbjct: 230 HLTGQTIHIPGDPSSAAFLIIAALLVEDSDITIENVLINNSR--IGLIETLWEMGAQIEF 287

Query: 301 TETSVTVTGPPREPFGGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVAS 355
T G K L+ + V + P D LAV A FA+G T + +

Sbjct: 288 LNRRQT-GGEDVADLRIKSSVLRGVTVPKERAPSMIDEYPALAVAAAFAGKTVMLGIEE 346

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVTATIDTYDDHRMAMAF-S 411
RVKE++R+ A+ L EEG D+ I+ + L + T+ DHR+AM F

Sbjct: 347 LRVKESDRLSAVAQGLEINCVDCEEGQDFLIVYGKSAKGLGGHVSTHLDHRIAMCFLV 406

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYF 436
+E PVTI D +FP++

Sbjct: 407 FGLVSEKPVTTIDDKRMIATSFPEFI 431

>ref|ZP_08106814.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium symbiosum
WAL-14673]
gb|EGB19276.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium symbiosum
WAL-14673]
Length = 426

Score = 95.9 bits (237), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 118/448 (26%), Positives = 195/448 (43%), Gaps = 45/448 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ +SG + +PG KS+S+R ++ ++++G T V L D + +G+ +E

Sbjct: 7 RRLSGELTIPGDKSISHRSIMFGSIAQGLTEVRGFLQGADCLSTISCFTKMGIPIEN--- 63

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
K V+ G A +E+ L GN+G R + + A + T L G + R

Sbjct: 64 -KGETVLIHGRGLRGLTAPKEI-LDCGNSGTTTRLICGILAAQDFDVT--LTGDESICRR 119

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNG--IGGLPGGKVKLSGSISSQYLSALLMAA 190
P+ ++ L +GA + DC P+ + G I G+ S S+Q SA+L+A

Sbjct: 120 PMKRIMEPLSMMGAKIRSIHCNDCAPLAITGCRHGIH----YQSPVASAQVKSAVLLAG 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
A G E + + IS + E+ ++ FG ++ E++ + R P NA

Sbjct: 176 LYAEG--ETRVTESYISRNHSEL---MLSAFGADIRTTAVLR-----PGNA 219

Query: 249 Y-----VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
V GD SSA++F+A A I V + G + + V M ++

Sbjct: 220 LKGLCITVPGDISAAFFIAAALIVPNEVLIRNVGINPTRDGI--LHVCRQMNGNISIL 277

Query: 302 ETSVTVTGPPREPFGGRKH-LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
P + R L+ + + +P D LA +A +A G T IRD A +

Sbjct: 278 NRKNESGEPTADLLVRSSALQGTVIEGSIIPTLIDELPMLAAMACYAKGTTVIRDAELK 337

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CA 416
VKE+ R+ + L +GA V E D II L+ ID+ DHR+AM F++ A A

Sbjct: 338 VKESNRITVMAENLRAMGADVTEDEDGMIIHGGRLPHGAVIDSKKDHRIAMTFAVTALAA 397

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
E I D C ++P ++ L+ +

Sbjct: 398 EGETEILDADCVNISYPGFYSDLARLKR 425

>dbj|BAJ56431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
F30]
Length = 429

Score = 95.9 bits (237), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 112/435 (25%), Positives = 195/435 (44%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCSNNGTSMRLYSGLLSAQKG--LFVLSGDNLSNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA++ LG + I G P I+S Q S +++A A G +
Sbjct: 122 FGANI---LGREDNHFAPLVILGSPLKACDYESPIASAQVKSTFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGV--LMISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYVIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI+++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIDQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITPEKL---NVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E D +CI IT ++ N I +++DHR+AM+F++ A +P+ I + C
Sbjct: 350 EFEDGFCIEGLEIDITQLKQRLSQKNPLIQSFNDHRIAMSFAILTLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 409 ISFPQFKRLLNLFKK 423

>ref|ZP_02617066.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Bf]
ref|YP_002862363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Ba4 str. 657]
gb|EDT86381.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Bf]
gb|ACQ54506.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Ba4 str. 657]
Length = 442

Score = 95.5 bits (236), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 109/453 (24%), Positives = 211/453 (46%), Gaps = 51/453 (11%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ +L +G V N + D + +++ LG+ + K
Sbjct: 10 KSLTGEYEIIGDKSIGHRSLIIGSLPKGEYKVYNFPKNLDCMATVDSIKKLGVDI---KV 66

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G E+ ++ ++ G N+G +R + ++ G ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQKNSGTTVRLMAGVLSGIGAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA ++ + PV+ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--QDNKLPVKFLKHSGLSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLME-RFGVKAHSDSWDRFYIKGG---QKYK-SPK 246
++ G + I++ + + E L+ ++ +K +S + ++ K +K K + K
Sbjct: 179 MSGK--KTTIVENKPTRDHTERMLKYLDASINIKNIYSKNKEKSIFKKEITIEKSKLNSK 236

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL--QGDVKFAEVLEMMGAKVTWTETS 304
+ YV GD SSA++ ++ A + G+ C L +G +++ VL MGA + E
Sbjct: 237 DIYVPGDISAFLISAALLIQGSNL---CIKNVLLNEGRIEYINVLNMGANIE-IEKG 292

Query: 305 VTVTGPPREPFGFGR----KHLKAIDVNMNKMMPDVAM---TLAVVALFADGPTAIRDVASW 356
+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 293 KLLNG---EPVGNIIYKESYLKGITVEKHITPNIIDEIPVLSVIAAFSEGKTIFKSVEEL 349

Query: 357 RVKETERMVAIRTEL-----KLGSVEEGPDYCIITPEKLNVTADITYDDHRMAM 408
+ KE++R+ AI L K G + EG I E I+++ DHR+A+
Sbjct: 350 KFKESDRVEAIIENLKRADVKAIIYKNGNLIIEGNKSYIDKSLE-----IESFKDHRIAL 403

Query: 409 AFSLAACAEVPVT-IRDPGCTRKTFFDYFDVLS 440
AF + + T I+D CT +FP+ + +
Sbjct: 404 AFLVLSLKNKKHTLIKDYQCTEISFPNSLSLNF 436

>ref|YP_001644318.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
gb|ABY42690.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
Length = 367

Score = 95.5 bits (236), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 90/326 (27%), Positives = 153/326 (46%), Gaps = 34/326 (10%)

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK----LSGSISSQYLSAL 186
+RP+ + L ++ A +D P+ + G GKVK S S+Q SA+
Sbjct: 62 KRPMKRVTDPLSKMNAQIDGRENGQYTPLSIRG-----GKVKGMHYHSPVASAQVKS AV 115

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L+A G+ + + + S + E R++ FG + + ++GGQ+ K
Sbjct: 116 LLAG--LQGEIGITTVTEPMQSRDHTE---RMLRAFCTVDVNGRT--VSLQGGQQLKGA- 167

Query: 247 NAYVEGDASSASYFL-AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V GD SSA++FL AGA + + +E G + V EVL MGA ++
Sbjct: 168 DIEVPGDISAFAFLVAGAIVPNSKLVLENVGLNPTRTGV--LEVLTGMGALISIDH--- 222

Query: 306 TVTGPPPEPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWR 357
+ EP G LK I++ +P + + V+AL A +G T I++ +
Sbjct: 223 -IRNEEFEPGCDITIETSKLKGIEIGTLPRLIDEIPVIALLATQAEGITVIKNAEELK 281

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC-A 416
VKET R+ + EL KLGA +E PD II + L ++++ DHR+ M ++A+C
Sbjct: 282 VKETNRIDTVDELGLKLGAKIEATPDGMIYKQSLKGNTVNSHGDHRIGMMLAIASCI 341

Query: 417 EVPVTIRDPGCTRKTFFDYFDVLSTF 442
+ V I + ++P++F+ L+
Sbjct: 342 DGEVKIENSDAVAVSYPEFFEQALAL 367

>ref|YP_004106440.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris DX-1]
gb|ADU41707.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris DX-1]
Length = 445

Score = 95.5 bits (236), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 130/441 (29%), Positives = 196/441 (44%), Gaps = 37/441 (8%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT ++PG KS+S+R L+L AL+ G T + LL EDV A+R LG VE +
Sbjct: 18 LRGTARVPGDKSISRALILGALAVGETRISGLLEGEDVLNTAKAMRALGAKVERTGDCE 77

Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG G A E L GN+G R AV AG DG +R RP
Sbjct: 78 WRVHGVGVAGF-----ATPEGPLDFGNSGTGCR LAMGAV--AGSPVLATFDGDASLSRSP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ +V L+ +GA V P+ + G P + + S+Q SA+L+A A
Sbjct: 131 MRRIVDPLELMGAKVSSSDGGRLPLTLQGARD-PLPILYRTPVPSAQIKSAVLLAGLSA 189

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +I+ S + E+ +++ FG V E + R GQ V
Sbjct: 190 PGIT--TVIEAEASRDHTEL---MLQHFGATVVTEPEGAHGRKISLTGQPELRGAPVVVP 244

Query: 252 GDASSASY-FLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D SSA++ +A + G + + T L+ L MGA + ++ V G
Sbjct: 245 ADPSSAAFPMVAALVVPGSIDIELTDMTNPLR--TGLIATLREMGASIEDSD----VRGD 298

Query: 311 PREPFG-----KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
EP R LK ++V + P D + LAV A FA+G T +R + RVKE++
Sbjct: 299 AGEPMARFRVRGSKLKGVEVPPERAPSMIDEYLVLAFAAFAEGTTVMRGLHELVRKESD 358

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT---IDTYDDHRMAM-AFSLAACAEV 418
R+ A L G +VE D I+ K +V + T+ DHR+AM A ++ ++
Sbjct: 359 RLEATAAMLRVNGVAVEIAGDDLIVE--GKGHVPGGGVVATHMDHRIAMSALAMGLASDK 416

Query: 419 PVTIRDPGCTRKTFPDYFDVL 439
PV + D +FPD+ ++
Sbjct: 417 PVAVDDTAFIATSFDPDFVPM 437

>ref|ZP_03368422.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E98-0664]
Length = 107

Score = 95.5 bits (236), Expect = 1e-17, Method: Composition-based stats.
Identities = 54/104 (51%), Positives = 69/104 (66%), Gaps = 4/104 (3%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTD 155
+FLGNAG AMR L AA+ G VL G PRM+ERPIG LV L+Q GA++D +
Sbjct: 7 MFLGNAGTAMRPLAAALCL--GQNEIVLTGEPRMKERPIGHLVDSLQGGANIDYLEQEN 64

Query: 156 CPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
PP+R+ GG GG +++ GS+SSQ+L+ALLM APLA D I
Sbjct: 65 YPLRLRL--GGFIGGDIEVDGSVSSQFLTALMTAPLAPEDTII 106

>gb|ADI35116.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
v225d]
Length = 429

Score = 95.5 bits (236), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 113/441 (25%), Positives = 191/441 (43%), Gaps = 49/441 (11%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGK 84
KSLs+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPKACDYESPISAQVKSFILSALQAQGSSTYK-- 176

Query: 203 DKLSIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQDGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK
Sbjct: 232 ACAITPKSRLLLNKVNLPTR--IEAFEALKKMGASIEYAIQSKDLEMIGNIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI++ N + D L+V LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIEQNIASLIDEIPALSVAMLFAGKSMVKNADLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVIR 423
E D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFCIEGLEDISQLKQRFSSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
+ C +FP + +L+ F K
Sbjct: 403 NLECANISFPQFKRLNLNLFKK 423

>ref|ZP_01045034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter sp.
Nb-311A]
gb|EAQ37039.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Nitrobacter sp.
Nb-311A]
Length = 442

Score = 95.5 bits (236), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 135/447 (30%), Positives = 202/447 (45%), Gaps = 35/447 (7%)

Query: 13 KEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVE--AD 70
+ ++G V++PG KS+S+R L+L AL+ G T + LL EDV A++ LG VE AD
Sbjct: 9 QSLTGRVVRVPGDKSISHRALILGALAVGETRISGLLEGEDVLNTAKAMQALGAKVERRAD 68

Query: 71 KAAKRA-VVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
A V G G G F A E L GN+G R + AV AG DG
Sbjct: 69 DTGGIAWSVRGVGTGGF----ATPEAPLDFGNSGTGCRLVMGAV--AGCPIRAAFDGDGS 122

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+R RP+ ++ L+ +GA V P+ + G P V + S+Q SA+L+
Sbjct: 123 LRSRPMRRILDPLELMGARVISQSDGRLPLTLEGARD-PLPIVYRTPVASAQIKSAVLL 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPK 246
A A G +I++ S + E+ L+ FG V + + R GQ
Sbjct: 182 AGLSAPG--VTVIEREASRDHTEMLK---HFGADVISVADGAHGRKISLTGQPELHGA 236

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V D SSA++ + A IT G+ + + T L+ L MGA + +ET
Sbjct: 237 AVTVPADPSSAAFPIVAALITEGSDIVLSDVMTNPLR--TGLFVTLREMGASIEESETRR 294

Query: 306 TVTGPPREPFGFR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
P + R L+ I+V + P D + LAV A FA+G T +R + RVKE+
Sbjct: 295 DAGEPMAQLRVRASKLRGIEVPPERAPSMIDEYLVLAFAAFAEGTTVMRGLHELVRKES 354

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
+R+ A L G +VE D I+ P L + T+ DHR+AM+ + CA
Sbjct: 355 DRLEAAAAMLRAGGVAVEIAGDDLIVEGRGHVPGGGL---VTTHMDHRIAMSALVMGCA 410

Query: 417 -EVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ PV + D +FPD+ ++
Sbjct: 411 SDAPVKVDDIAFIATSFDPDFVPMQRL 437

>gb|ADU41323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
35A]
Length = 429

Score = 95.1 bits (235), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 112/441 (25%), Positives = 192/441 (43%), Gaps = 49/441 (11%)

Query: 25 KSLSNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRVIFSLLAQKPCVVRNFLMGEDCLSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACDYESPIASAQVKSFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQDGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK
Sbjct: 232 SCAITPKSRLLLKNVLLNPTR--IEAFALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI+++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIDQNIASLIDEIPALSIAMLFAGKSMVKNKADLRKESDRKAVVSNFKTLGIECE 349

Query: 380 EGPD-YCI-----ITPPEKLNVTATIDTYDDHRMAMAFSLAACAIEVPVTIR 423
E D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFCIEGLEDISQLKQRFSSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402

Query: 424 DPGCTRKTFFPDYFDVLSTFVK 444
+ C +FP + +L+ F K
Sbjct: 403 NLECANISFPQFKRLNLNLFKK 423

>ref|ZP_07026530.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Afipia sp. 1NLS2]
gb|EFI53672.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Afipia sp. 1NLS2]
Length = 443

Score = 95.1 bits (235), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 131/440 (29%), Positives = 194/440 (44%), Gaps = 37/440 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V++PG KS+S+R L+L AL+ G T + LL EDV A+ LG VE
Sbjct: 18 LTGKVRVPGDKSISHRALILGALAVGETKITGLLEGEDVLNTAKAMAALGAKVERTGEGA 77

Query: 75 RAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+V VG GG F D L GN+G R AV + AT+ DG +R RP
Sbjct: 78 WSVHGVGVGG-FKAPDGP----LDFGNSGTGCRLLAMGAVAGSPIAATF--DGDASLRSRP 130

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ +GA V G P +P + S+Q SA+L+A A
Sbjct: 131 MRRILDPLELMGAVVSGGDGKRLPLTLTGARDPIP--MAYRTPVASAQIKSAVLLAGLSA 188

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
G +++ S + E+ L+ +FG + E R GQ N V
Sbjct: 189 PG--VTVMETEASRDHTEMLK---QFGAEISVEKEGEHGRITLTGQPELHGANVAVP 243

Query: 252 GDASSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTTWTETSVTVTGP 310
D SSA++ L A I + +T+ T L+ L MGA + E+ V G
Sbjct: 244 ADPSSAAFPLVAALIVPDSDLTLTDVMTNPLR--TGLFTTLREMGASI--EESDVRDAGE 299

Query: 311 PREPFGRK--HLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P + L+ + V + P D + LAV A FA+G T +R + RVKE++R+
Sbjct: 300 PMANLRVRASKLRGVTVPPERAPSMIDEYLVLAFAAFAEGTTRMRGLQELRVKESDRLE 359

Query: 366 AIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADITYDDHRMAMAFSLAACA-EVP 419
A L G VE D I+ P L + T+ DHR+AM+ + CA E P
Sbjct: 360 ATADMLRVNGVKVEISGDDLIVHGEGFVPGGGL----VKTHMDHRIAMSALVMGCASEAP 415

Query: 420 VTIRDPGCTRKTFFPDYFDVL 439
V + D +FPD+ ++
Sbjct: 416 VKVDDTAFIATSFPDFIPMM 435

>ref|YP_001416018.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthobacter
autotrophicus Py2]
gb|ABS66361.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthobacter
autotrophicus Py2]
Length = 456

Score = 94.7 bits (234), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 129/456 (28%), Positives = 200/456 (43%), Gaps = 67/456 (14%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V++PG KS+S+R L+ +EG T + LL EDV A LG V +
Sbjct: 29 LTGRVRVPGDKSVSHRALIFGLFAEGITRITGLLEGEDVLNTAKACAALGARV-----TR 83

Query: 75 RAVVVGCGGKFPVEDAKEE-----VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
R G++ VE A + L GN+G +R + AV AG + T DG
Sbjct: 84 RGP-----GEWEVEGAGADGLSSPAAPLDFGNSGTGVRLMMGAV--AGQDVTATFDGDAS 136

Query: 129 MRERPIGDLVVGLKQLGAD-VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 177
+R RP+ ++ L +G + VD G P + L GS
Sbjct: 137 LRRRPMKRVLDPLTAMGVEIVDSAEGGRPL-----LTLKGSDRTKAITYET 182

Query: 178 --ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWD 232
S+Q SA+L+A A G E +I++ + + E R++ FG V+ E H
Sbjct: 183 PMPSAQVKSAVLLAGLAGAAG--ETVVIEREATRDHTE--RMLAHFGADVRVPHGAHGR 237

Query: 233 RFIYIKGGQKY-KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEV 290
R +KG +P + V D SSA++ L A I G+ VT+ L+
Sbjct: 238 RIALKGRPTLV AAPVD--VPADPSSA APLVAALIVPGSDVLTLDVMMNPLR--TGLITT 293

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKH--LKAIDVNMNMKP---DVAMTLAVVALFAD 345
L MGA + T G +H LK ++V + P D LAV A FA+
Sbjct: 294 LLEM GASIEVVAER-TEGGERVADLRVRHSRLKGVEVPPERAPAMIDEYPILAVAAFAE 352

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A-IDTYDDH 404
G TA+R ++ RVKE++R+ A+ L G + E D ++T + + T+ DH
Sbjct: 353 GVTAMRGLSELRVKESDR LA AAVADGLAACGVAHEVVGDDLLVTGATTVKGGGFPVATHMDH 412

Query: 405 RMAMAF-SLAACAEVPTIRDPGCTRKTFFPDYFDVL 439
R+AM+F L +E V++ D +FP + ++
Sbjct: 413 RIAMSFVLVGLASEQGVSVDDVAFIATSFPTFMPMM 448

>ref|ZP_01617762.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [marine gamma proteobacterium HTCC2143]
gb|EAW30355.1| 3-phosphoshikimate 1-carboxyvinyltransferase prephenate
dehydrogenase [marine gamma proteobacterium HTCC2143]
Length = 409

Score = 94.4 bits (233), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 106/420 (25%), Positives = 188/420 (44%), Gaps = 37/420 (8%)

Query: 33 LLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV-VGCGG-KFPVEDA 90
+ A++EG T V L ED L A R +G+ ++ + + + VG G K P
Sbjct: 1 MFGAVAEGVTHVKGFLGEDALATLSAFRAMGVKIDGPREGELTIHGVLNGLKQP---- 56

Query: 91 KEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC 150
+ L LGN+G AMR + + AG N L+G + +RP+G + L+ +G D++
Sbjct: 57 --SLPLDLGNSGTAMRLMAGLM--AGQNFVPTLEGDESLSKRPMGRIAEPLRLMGVDIET 112

Query: 151 FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPY 210
G PP+R+NG G + G + + S+Q S +L+A A G+ P
Sbjct: 113 EKGG R-PPLRINGTGTVNGIHYDMPMA-SAQVKSCVLLAGLYAKGETS-----TTEPAPT 165

Query: 211 VEMTLRLMERFG--VKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITG 268
+ T R+++ FG ++ E + + + G + + V D SSA++F+ A I
Sbjct: 166 RDHTERMLKGFYPIRVEGATATVQ-----GLGRLTAMDIDVPADISSA A FFMVAATIAS 220

Query: 269 GT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKH--LKAIDV 325
+ + + G + + +L+ MGA +T V G P + L I +
Sbjct: 221 NSDIMLNVHGMNPTR--IGVINILQQMGADITINNER-DVGGEVPADIRVRSLLHGIHI 277

Query: 326 NMNMKP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGP 382
+++P D L + A A G T + R KE++R+ + L LG ++
Sbjct: 278 PEDQVPLAIDEFPVLFIAACCAKGT TLTGAEE LRAKESDRIQVMVDGLRSLGVDIKGTD 337

Query: 383 DYCIIITPPEKLNVT A---IDTYDDHRMAMAFSLAAC-AEVPTIRDPGCTRKTFFPDYFDV 438
D +I V + + ++ DHR+AM+F++AA A + I +FP++ ++
Sbjct: 338 DGAVIVGNTSEGVFSGGRVSSHHDHRIAMSF AVALRATGAIFIEGSDTVATSFNPFVEL 397

>ref|YP_003471659.1| 5-Enolpyruvylshikimate-3-phosphate synthase AroF [Staphylococcus
lugdunensis HKU09-01]
ref|ZP_07911123.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
lugdunensis M23590]
gb|ADC87532.1| 5-Enolpyruvylshikimate-3-phosphate synthase AroF [Staphylococcus
lugdunensis HKU09-01]
gb|EFU84903.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
lugdunensis M23590]
Length = 431

Score = 94.4 bits (233), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 104/437 (23%), Positives = 193/437 (44%), Gaps = 36/437 (8%)

Query: 15 ISGTVKLPGSKSLSNRILL AALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + +PG KS+++R ++LA+L+ G T + L ED L + LG+ +
Sbjct: 11 LKGEITVP GDKSMTHRAIMLASLASGKTAIYQPLLGEDCLRTL NIFKLLGVDI---TIKD 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
V + G + K Q L+ GN+G R L ++ G + VL G + +RP
Sbjct: 68 DNVYIDSPG---YRNFKTPHQVLYTGNSTGTTTLLAGLLSGVGIIQS--VLSGDISIGKRP 122

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ ++ L+ + A++ + + P+ + G + G + ++ + S+Q SA+L+A+ A
Sbjct: 123 MDRILKPLQLMQANISS-VDNNYTPLIIQP-GNIHGIRYEMEVA-SAQVKSAILLASLFA 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ +I+K +S + E + + F + D K ++ ++ V GD
Sbjct: 180 --NDSTTVIEKELSRNHE---TMFKHFNIPIT-IDGKSITVPKNAIQHIKARDFTVPGD 233

Query: 254 ASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A IT G+ +T+ G + + ++ MGA + +
Sbjct: 234 ISSAAFFIVAALITPGSDITIHNVNPNTRSGI--IDIALKMGAHIELLNQTQEA----- 286

Query: 313 EPFGRKH-----LKAI DVNMNKMPPDVAMTLAVVALF---ADGPTAIRDVASWRVKETER 363
EP H LK I ++ +P L ++AL A G + I+D +VKET R
Sbjct: 287 EPTASIHVQYTPNLKPIHIDGELVPSIDELPIIALCTQATGTSTIIKDTELKVKETNR 346

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ L LG ++ D II P +D+ DHR+ M ++ + + P+ I
Sbjct: 347 IDTTADMLGLLGFDIQPTADGLIIHPSSLTRAADVDSLSDHRIGMMLAIGSLLSSEPLEI 406

Query: 423 RDPGCTRKTFPDYFDVL 439
+ +FP + L
Sbjct: 407 KQFDAVNVSFPGFSLKL 423

>gb|ADU81873.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Gambia94/24]
Length = 429

Score = 94.0 bits (232), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 113/444 (25%), Positives = 190/444 (42%), Gaps = 55/444 (12%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ V N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRTVIFSLLAQKPCFVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P + KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPKTIKEPSKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGRKDNHFAPLAIVGSPKACDYESPISAAQVKSASFILSALQAQGTSVYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSASY 259
+ +S + E+ L+ G ++ D + + P A+ + D SSA +
Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGVVKI-----SPLEKPLEAFDFTIANDPSSAFF 228

Query: 260 FLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRGK 318
F AIT + + ++ + ++ EVL+ MGA + + S +
Sbjct: 229 FALACAITPKSRLLLKNVLLNPTR--IEAFEVLKMGASIEYAIKSKDLEIIGDIYIEHA 286

Query: 319 HLKAI DVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
LKAI +N N + D L++ LFA G + +R+ R KE++R+ A+ + LG
Sbjct: 287 PLKAIAINQNTASLIDEIPALSIAMLFAGKSMVRNAKDLRAKESDRIKAVVSNFKALGI 346

Query: 377 SVEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420
EE D + I PP I +++DHR+AM+F++ A +P+
Sbjct: 347 ECEEFEFDGFYIEGLEDISQLKHFSKIKPP-----LIKSFNDHRIAMSFAVLTLA-LPL 399

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444
I + C +FP + L+ F K
Sbjct: 400 EIDNLECANISFPTFQLWLNLFFK 423

>ref|YP_458387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Erythrobacter

litoralis HTCC2594]
gb|ABC63590.1| 5-enolpyruvylshikimate-3-phosphate synthase [Erythrobacter
litoralis HTCC2594]
Length = 463

Score = 94.0 bits (232), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 130/455 (28%), Positives = 207/455 (45%), Gaps = 44/455 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSV----- 67
++G +++PG KS+S+R ++L AL+ G T V LL EDV A+R +G V
Sbjct: 28 LTGRIRVPGDKSISHRSIMLGALAIGETRVTLLEGEDVMATAAAMRAMGAQVLRQAQDG 87

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
AD A R VG GG + L +GN+G + R L V + G AT++ D
Sbjct: 88 RAD-AEWRVHVGVGGLL----QPRALTDMGNSGTSTRLLMGLVASHGITATFIGDA-- 139

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSAL 186
+ RP+ + L ++GA G P+ + G+ P ++ + S+Q SA+
Sbjct: 140 SLSGRPMSRVTEPLGRMGAFHGASGGTL-PITMEGL--CPAVPIEYRLPVASAQVKSASV 196

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSD---SWDRFYIKGGQK 241
++AA G I + +P + + R+++ FG V+ E D +R G+
Sbjct: 197 MLAALNTPG-----ITTVIEPVPTRDHSERMLKGFADVEIEEVDGATGRERAIRVRGEA 251

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
P+ V GD SSA++F+ A + G+ + +E G + EVL MG +
Sbjct: 252 DLQPQIEVPGDPSSAAFFVVAALLVEGSDLIENVGLNPTR--AGLFEVLRQMGGHIEE 309

Query: 301 TETSVTVTGPPPREPFGRKH--LKAIDVNMNKMPP--DVAMTLAVVALFADGPTAIRDVAS 355
T V G P +H L I+V+ P D L V A A+G T +
Sbjct: 310 MNTR-EVGGEVADLRVRHSALTGIEVDPAIAPSMIDEFPVLFVAASLAEGTTTTSGLEE 368

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI-----TPPEKLNVTADTYDDHRMAMAF 410
RVKE++R+ A+ LT GA++EE D +I P +A T DHR+AM+
Sbjct: 369 LRVKESDRLAAMAAALTGAGATIEEREDGLVIHGTGGAPLRGSANSATQTLLDHRIAMSM 428

Query: 411 SLAACAEVP-VTIRDPGCTRKTFPDYFDVLSTFVK 444
++A A V + D +FP++ +L V+
Sbjct: 429 AVAGLASRDGVEVDDTRPIATSFPNFMALLGGAVR 463

>ref|ZP_06622944.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Turicibacter
sanguinis PC909]
gb|EFF62765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Turicibacter
sanguinis PC909]
Length = 422

Score = 94.0 bits (232), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 109/442 (24%), Positives = 200/442 (45%), Gaps = 34/442 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSV EADKAAK 74
+SG +++ G KS+++R ++L++L+ G TV+ N L D L + G++ + A
Sbjct: 3 LSGELQVAGDKSITHRAIILSSLATGQTVIHNPPLLGADCLSTLEIFKQFGVTYQL--TAN 60

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERP 133
+ ++ G F ++ L GN+G R L ++A T V D + +RP
Sbjct: 61 QLIIDSPGVDGFTYSNSI----LDAGNSGT TARLLMGVLSALPTTLTLVGDA--SLSKRP 114

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + LKQ+GA ++ P + G L G + +L + S+Q SA+++AA A
Sbjct: 115 MKRVTSPLKQMGACIE-LTHDQTLPATIKG-QSLNGIEYELPVA-SAQVKSAIMLAAMFA 171

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ +I +P + T ++ E F + + + G Q K+P +V D
Sbjct: 172 SGETKIH-----EPVPTRDHTEKMFEDQIVYNKENRV--ITLSGPQMPKTPGQVFPAD 224

Query: 254 ASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
SSA++F+ A + G + ++ G + + +VL MG ++T G R
Sbjct: 225 ISSAAFFMVAALMVEGSDLILKNVGLNETRCGI--VDVLLQMGGRLTIQNER--YFGGER 280

Query: 313 EPFGR----KHLKAIDVNMNKMPPDVAMTLAVVALFAD--GPTAIRDVASWRVKETERMV 365

R K LK I + +P + + ++AL A G T I+D +VKET R+
Sbjct: 281 VADIRVQYTKDLKGIIEGEMIPRLIDEIPIIALLATKAMGQTIKDAEELKVKETNRID 340
Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN--TAIDTYDDHRMAMAFSLAA-CAEVPVTI 422
EL +GA++ D +I L+ + ++ DHR+AM +A+ + + I
Sbjct: 341 VTVGELKAIGANLFSTEDGMVINGDINLSYHPALVSSHGDHRIAMMLYVASLLMKNELEI 400
Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ ++PD+ + +K
Sbjct: 401 EEMQAMNISYPDFLVHMQKVLK 422

>dbj|BAJ55592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
F16]
Length = 429

Score = 94.0 bits (232), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 112/441 (25%), Positives = 192/441 (43%), Gaps = 49/441 (11%)

Query: 25 KSLSNRILLLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLAQKPCVVRNFLMGEDCLSLEIAQNLGAKVE--NTAKNSFKIT---- 64
Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMRRIIEPLKA 121
Query: 144 LGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACGYESPIASQVKSFILSALQAQGSAYK-- 176
Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231
Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLK 321
AIT + + ++ + ++ E L+ MG + + S + LK
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEALKKMGTSIEYAIQSKDLEMIGDIYIEHAPLK 289
Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI+++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIDQNIASLIDEIPALSIAMLFAKGTSMVKNKADLRSKESDRIKAVVSNFKALGIECE 349
Query: 380 EGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
E D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFCIEGLEDISQLKQRLSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402
Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
+ CT +FP + +L+ F K
Sbjct: 403 NLECTNISFPQFKRLNLNLFKK 423

>gb|EES51981.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Leptospirillum
ferrodiazotrophum]
Length = 446

Score = 93.6 bits (231), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 123/445 (27%), Positives = 202/445 (45%), Gaps = 47/445 (10%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G+V PG KS+S+R ++L + + G T + L+S D L A L + V + +
Sbjct: 25 GSVTPPGDKSISHRAVMLGSAARGRTEIRGFLDSADCRGTLEAF--LAMGVHLRRLSPHH 82
Query: 77 VVVGCGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+++ G E+ E + GN+G A+R + ++ G VL G +R RP+
Sbjct: 83 LILESPG---AENLSEPSNVLDGFGNSTAVRLMAGLLSGIPG--FRVLTGDDSLRGRPMK 137
Query: 136 DLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
+ L ++GA +D G P+ + G G + + S+Q SA+L+A A
Sbjct: 138 RVADPLSRMGARIDGRDGGSRPLPSIRG--GPLSPILYENVHRSQVKSAVLLAGLSASS 195

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
+ + +P + T RL+ FG ++ EH R + G S V G
Sbjct: 196 PSTV-----VEEVPTRDHTERLLPAFGGRVLRREEH-----RVTVWPGTL--SGTLVSVPG 243

Query: 253 DASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D SSA++FLA A +T G ++ + G + E+L +MG ++ T
Sbjct: 244 DISSAAFFLALALLTPGSSLIILRNVLNPNTR--TALLEILRLMGGRIDIERTPEEEGS-- 299

Query: 312 REPFGRKH-----LK AIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
EP G H L + V ++ +P D L+V+A FA G T IR A RVKE++R
Sbjct: 300 -EPAGTLHPSFSSLTGVQVPLSLIPGAIDEIPILSVLAFAHGRTEIRGAELRVKESDR 358

Query: 364 MVAIRTELTKLGASVEEGPDYCIIT---PPEKLNVT AIDTYDDHRMAMAFSLAACAEVP- 419
+ + L +G +VEE PD I P L +ID+ DHR+AM+ ++ A +P
Sbjct: 359 IAGMVAALRAVGVAVEEFPDGLAIEGEGPDRALAGASIDSLDHRIAMSAVLAT-RLPR 417

Query: 420 ---VTIRDPGCTRKTFPDYFDVLST 441
+ I +FP + D+ ++
Sbjct: 418 GEFLEIAGTDFVETSFPGFPDLFNS 442

>ref|YP_779383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisA53]
sp|Q07UI1.1|AROA_RHOP5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABJ04403.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisA53]
Length = 445

Score = 93.6 bits (231), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 130/438 (29%), Positives = 201/438 (45%), Gaps = 31/438 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+ G V++PG KS+S+R L+L ALS G T + LL EDV A++ LG VE + A
Sbjct: 18 LQGRVRVPGDKSISHRALILGALSVGETTITGLLEGEDVLNTAKAMQALGAKVERTGEFA 77

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERP 133
R VG GG A+ + L GN+G R + AV AT+ DG +R RP
Sbjct: 78 WRVNGVGVGGF-----AQPDAALDFGNSGTGCR LVMGAVAGCPAATF--DGDASLSRP 130

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSI-SSQYLSALLMAAP 191
+ +V L+ +GA V P+ + G LP ++ + S+Q SA+L+A
Sbjct: 131 MKRIVDPLQLMGASVIASAEKGKLP LTLQGAKNPLP---IEYRTPVASAQIKSAVLLAGL 187

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAY 249
A G +I++ S + E+ +++ FG + + R GQ
Sbjct: 188 SAPG--VTTVIEQEASRDHTEL---MLQHFGAQIVSVPEGVHGRKISLTGQPELRGAPVV 242

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D SSA++ + A I G+ + + T L+ + FA + E MGA + +E
Sbjct: 243 VPADPSSAAFPMAALIVPGSDLVLTDMTNPLRTGL-FATLRE-MGASIESELR-DDA 299

Query: 309 GPPREPFGRK--HLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
G P F + LK + V + P D + LAV A FA+G T +R + RVKE++R
Sbjct: 300 GEPMATFRVRASKLKGVTVPPERAPSMIDEYLVLAFAAFAEGTTRMRGLQELRVKESDR 359

Query: 364 MVAIRTELTKLGASVE-EGPDYCIITPPEKLNVT AIDTYDDHRMAM-AFSLAACAEVPVT 421
+ A L G V EG D + + T+ DHR+AM A + ++ PV
Sbjct: 360 LEATAAMLRVNGVDVAIEGDDLIVEGRGHVPGGLVATHMDHRIAMSALVMGLASDQPVQ 419

Query: 422 IRDPGCTRKTFPDYFDVL 439
+ D +FPD+ ++
Sbjct: 420 VDDTAFIATSFPDFIPMM 437

>ref|ZP_08053835.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter suis
HS1]
gb|EFX42704.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter suis
HS1]
Length = 416

Score = 93.6 bits (231), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 114/435 (26%), Positives = 204/435 (46%), Gaps = 51/435 (11%)

Query: 27 LSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGKFP 86
+S+R+LL A + V +LL +D L +R LGL V+ K A + + +F
Sbjct: 1 MSHRVLLCALFTNPKCFVQDLLMGQDCLSTLSIVRALGLRVQ--KEAPNILKLTTPKQFL 58

Query: 87 VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVLDGVPRMRERPIGDLVVGLKQLG 145
+ ++V L N+G MR L+ +++ Y+L G + ERP+G +VV LKQ+G
Sbjct: 59 RFNEPKKV-LHCHNSGTTMRLLSGLSSSTTQQNHYLIGDVSLSERPMGRVVVPLKQMG 117

Query: 146 ADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKL 205
A + P+ + + G +S S+Q SALL+A A + +
Sbjct: 118 AQIRGRAHNTLAPLSI--VSTPLQGINYVSPLASQKLSALLLATLQAKSASTLS--EPS 173

Query: 206 ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF-LAGA 264
+S + E+ L+ + A + +++ K + ++ D SSA YF LA
Sbjct: 174 LSRNHTEMLQTL----GANLKMNKQTIFLEPLDKPLESFSWHIPNDPSSAFYFALAVM 228

Query: 265 AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGFGR---KH-- 319
+ V ++ + ++ +VLE MGA++++T T E G KH
Sbjct: 229 LVPQSAVLLKRVLLNPTR--IEAFKVLKMGAKQISYTPTEYMGA---EEVGDIYVKHAS 282

Query: 320 LKAIDVNMN-----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
LKAII++ N ++P +A+ +AV A G + +++ RVKE++R+ I L K
Sbjct: 283 LKAINLESNIAFLIDELPALAVAMAV---AKGVSVVKNQELRVKESDRITITILANLKK 338

Query: 374 LGASVEEGPDYCI-----TPPEKLNVTATIDYDDHRMAMAFSLA--ACAEPVTIRDP 425
+G + D I +P E L ++++DHR+A++F++A AC I++
Sbjct: 339 MGIECQAFKDGFSIQGGTLKSPQEPL-----ESFNDHRIALSFAIALACGG--EIKNT 390

Query: 426 GCTRKTFFPDYFDVLS 440
C +FP + ++L+
Sbjct: 391 ECMAISFPKFEEILN 405

>ref|YP_001398032.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. doylei 269.97]
gb|ABS43964.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. doylei 269.97]
Length = 423

Score = 93.6 bits (231), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 186/431 (43%), Gaps = 34/431 (7%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++G N L ++D L ++ LG +E + + +
Sbjct: 12 IAADKSISHRFAIFSLLTQGENKARNYLLAQDTLNTLEIIKNLGAKIEQKDSCVKIIP-- 69

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 70 -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKFLNNRPMRRISKP 122

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 123 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSAFRA----- 173

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
D + + + ++ E +KA S D I +K +N + D SS
Sbjct: 174 --DNICTFSEISLSRNHSENMLKAMKAPMRVSNLGLNLEISPLKPLKAQNIIPNDPSS 231

Query: 257 ASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWETSVTVTGPPRE 313
A YF LA + + ++ + ++ ++L+ MGA+ T T+ G R
Sbjct: 232 AFYFALAAIILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRV 289

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ + + N+ + D A LA+ A G + + + RVKE++R+ + L
Sbjct: 290 ESSKLNIEVKNIAWLIDEAPALAIAPALAKGKSNLVNAKELRVKESDRIAVMVENLKL 349

Query: 374 LGASVEEGPDYCIITPEKLNVTATIDYDDHRMAMAFSLA--CAEVPVTIRDPGCTRKT 431

Sbjct: 350 G +E D I +L + I +Y DHR+AM+F++ C + I D C + +
CGVEAKEFDGFEIEGGCELSKSSIKISYGDHRIAMSFALLGLLCG---IEIDSDSCKITS 406

Query: 432 FPDYFDVLSTF 442
FP++ ++LS

Sbjct: 407 FPNFIEILSNL 417

>ref|ZP_06054530.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (epsp
synthase) (epsps) [alpha proteobacterium HIMB114]
gb|EEY74299.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (epsp
synthase) (epsps) [alpha proteobacterium HIMB114]
Length = 665

Score = 93.6 bits (231), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 105/452 (23%), Positives = 200/452 (44%), Gaps = 46/452 (10%)

Query: 15 ISGTVKLPGSKLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G V+L KSLR ++ A+++ G + + ED + A++ LG+ V +K
Sbjct: 17 IKGLVELSSDKLSIRGVIFASIAYGISKIKIKSPGEDAETAIAKALGIKVRNKDLY 76

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+G G +K +++ N+G +R LT + + NA + G + +RP
Sbjct: 77 TVYGLGIG-----YYSKRTLKISFNNSGTTLRLLTPLIAGSKVNAK--ITGDKSLSKRPY 129

Query: 135 GDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ LKQ ++ + P+++ G VK+ S S+Q +SA +A ++
Sbjct: 130 R--LEFLKQFLMNLKP-TNSQYLPKIKGHENCIQSNVKIEKS-SAQMVSAATIAGMISY 185

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMER--FGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G+ IE + + + T R+++ + +K ++ S ++G + K +N +
Sbjct: 186 GETIIEAPNNV-----RDHTTRVLKYLDYPIKVQNKKSQIIVQGRRLKPLQYNINPS 240

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTTSQGDVVKFAEVLEMMGAKVTWTETS----- 304
D SS+++ +A A +T G+ + ++ + + F ++L+ MGAK+ ++
Sbjct: 241 DPSSSAFLIAIAILTKGSEIKIKNVCLNPYR--IGFIKILKKMGAKIIFSNNKSYFGPEV 298

Query: 305 --VTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+T + P+ LK I + N++ D L +V LF + ++ + K
Sbjct: 299 GDITASYSPPK-----LKGITIKPNEVASIIDEIPILLIVTLFCKPKSIFNNLTCLKFK 351

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL----NVTADTYD-DHRMAMA-FSLA 413
E++R+ + L GA+V D II V I Y DHR+ MA F LA
Sbjct: 352 ESDRLRVMYENLILCGANVIRVKDNLIINGINNRFYSSEVPIIKNYSKDHRCMAFFCLA 411

Query: 414 ACAEVPVTIRDPGCTRTKTFPDYFDVLSTFVK 445
A + + I D +FP++ ++ N
Sbjct: 412 AVSRKKIQINDFDSVSVFPNFKLTINDLKYN 443

>dbj|BAJ57933.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
F32]
Length = 429

Score = 93.2 bits (230), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 113/435 (25%), Positives = 195/435 (44%), Gaps = 37/435 (8%)

Query: 25 KLSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KLSL+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KLSLHRAVIFSLAQKPCVVRNFMGDCSSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLGKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA V LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKV---LGREDNHFAPLVILGSPLKADYESPIASAIKSAFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SS +F
Sbjct: 177 ENELSRNHTIEMLK---SLGANIQNQDGV--LTISPLEKPLEAFDFTIANDPSSVFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPEPFGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI+++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIDQNIASLIDEIPALSIAMLFAGKSKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITP-PEKLNVT---IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E D +CI IT ++L+ I +++DHR+AM+F++ A +P+ I + C
Sbjct: 350 EFEDGFCIEGLEEDITQLKQRLSQKKPLIQSFNDHRIAMSFALITLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 409 ISFPQFKRLNLNLFKK 423

>ref|ZP_06159238.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Slackia exigua ATCC
700122]
gb|EEZ61946.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Slackia exigua ATCC
700122]
Length = 439

Score = 93.2 bits (230), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 125/462 (27%), Positives = 209/462 (45%), Gaps = 45/462 (9%)

Query: 4 AEEIVLQPI-KEISGTVKLPKSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRT 62
+E +V++P+ K + G++++PG KS+S+R +LL+A++EGT+ + +L+S+DV + ++
Sbjct: 2 SESVIRPLEKPLRGSIRVPGDKSISHRAVLLSAMAEGTSQIRGVLDSDVRSSIRVVQQ 61

Query: 63 LGLSVEAD---KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
LG V + G G K P ++ + L GN+G R L + G A
Sbjct: 62 LGAQVNLQIMPDGSLGAITGWAKGP---SQPDGPLDCGNSGTTARLLMGILAPWGIEA 118

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGGLPGGKVKLSGS 177
L G + RP+ ++ L ++GA F D P+ G G L +
Sbjct: 119 E--LTGDES LARRPMQRVMTPLSRMGAR---FSPQDAQTLPI TERGTGRL--DPITYESP 171

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
++S L ++ A L+ D E +I+ S + E+ ++ FG AE + + +K
Sbjct: 172 VASAQLKTAVLLAGLS-ADGETRVIEPAPSRNHTEL---MLPAFG--AETTAATRVASVK 225

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G ++ + V GD SSA++ L AA+ G + VEG + + F LE MG
Sbjct: 226 GPVTLRA-TDVVVPDGPSSAAFLLCAAALCPGSAIQVEGVS LNPAR--IGFLRTLEHMG- 281

Query: 297 KVTWTETSVTVTGPPPEPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGP 347
V + S G +E G L +V K+ D LA+VA A G
Sbjct: 282 -VNASRRSDGAKG--KELSGILSVEYCDRLHGCEVPAEKIATVIDEVPILALVAAHAKGV 338

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASV-EEGPDYCIITPPEKLNVT---IDTYDD 403
T R RVKET+R A+ L +G +G D I P + +A D D
Sbjct: 339 TVFRGADEL RVKETDRAAAVIEGLALMGIDAWMDGSDLFIEGDP-MFSTSAGLRFDKGD 397

Query: 404 HRMAMAFSLAA-CAEVPVTIRDPGCTRKTTFPDYFDVLSTFVK 444
HR+AM +++A C P+ I+ ++P + D + +
Sbjct: 398 HRLAMTWAVAGLCGANPIEQGFDAVSVSYPGFLDDIRMLAR 439

>sp|A7H3F2.2|AROA_CAMJD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 428

Score = 93.2 bits (230), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 186/431 (43%), Gaps = 34/431 (7%)

Query: 21 LPSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R ++ L++G N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSIHRFAIFSLLTQGENKARNYLLAQDTLNTLEIIKNLGAKIEQKDCSVKIIP-- 74

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKFLNNRPMRRISK 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSAFRA----- 178

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
D + + + ++ E +KA S D I +K +N + D SS
Sbjct: 179 --DNICTFSEISLSRNHSENMLKAMKAPMRVSNLGLNLEISPLKKPLKAQNIIPNDPSS 236

Query: 257 ASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
A YF LA + + ++ + ++ ++L+ MGAK+ T T+ G R
Sbjct: 237 AFYFALAAIILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRV 294

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ + + N+ + D A LA+ A G + + + RVKE++R+ + L
Sbjct: 295 ESSKLNIGIEVKDNIAWLIDEAPALAIAPALAKGKSNLVNAKELRVKESDRIAVMVENLKL 354

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
G +E D I +L + I +Y DHR+AM+F++ C + I D C + +
Sbjct: 355 CGVEAKEFDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCG---IEIDSDCIKTS 411

Query: 432 FPDYFDVLSTF 442
FP++ ++LS
Sbjct: 412 FPNFIEILSNL 422

>ref|YP_002266615.1| 3-phosphoshikimate 1-carboxyvinyl transferase [Helicobacter pylori
G27]
sp|B5Z850.1|AROA_HELPG RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACI27749.1| 3-phosphoshikimate 1-carboxyvinyl transferase [Helicobacter pylori
G27]
Length = 429

Score = 93.2 bits (230), Expect = 8e-17, Method: Compositional matrix adjust.
Identities = 110/435 (25%), Positives = 193/435 (44%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ V N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCFVRNFMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLGKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTAIKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACDYESPISASQVKSAFILSALQAQGISAYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ + A+ + I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK-----SLGADIQNGVLMISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VTVTGPPREPFGGRKH 319
AIT + + ++ + ++ EVL+ MGA + + S + + G
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEVLKKMGASIEYAIQSKDLEIIGDIYIEHAPLK 289

Query: 320 LKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
+ID N+ + D L++ LFA G + +++ R KE++R+ A+ + L LG E
Sbjct: 290 AISIDQNIASLIDEIPALSIAMLFAKGSVMKNAKDLRSKESDRIKAVVSNLKGALGIECE 349

Query: 380 EGPDYCII-----TPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E D I P K +++ I +++DHR+AM+F++ A +P+ I + C

Sbjct: 350 EFEDGFYIEGLEDISPLKQHLSQKKPPLIQSFNDHRIAMSFAILTLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444

+FP + +L+ F K

Sbjct: 409 ISFPQFKRLLNQFKK 423

>ref|YP_003928924.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
SJM180]

gb|ADO02607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
SJM180]

Length = 429

Score = 93.2 bits (230), Expect = 8e-17, Method: Compositional matrix adjust.
Identities = 111/444 (25%), Positives = 191/444 (43%), Gaps = 55/444 (12%)

Query: 25 KSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84

KSLS+R ++ + L++ V N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLLAQKPCFVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQ 143

P KE ++ N+G +MR + ++A G +VL G + RP+ ++ L+

Sbjct: 65 -PPTAIKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLRA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202

GA + LG + I G P I+S Q SA +++A A G +

Sbjct: 122 FGARI---LGRENNHFAPLVILGSPLKACHYESLIASQVKSAFILSALQAQGTSAK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY--VEGDASSASY 259

+ +S + E+ L+ G ++ D + + P A+ + D SSA +

Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGVLEKI-----SPLEKPLEAFDFTIANDPSSAFF 228

Query: 260 FLAGAAITGGT-VTVEGCGTTSLOGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRK 318

F AIT + + ++ + ++ EVL+ MGA + + S +

Sbjct: 229 FALACAITPKSHLLKNVLLNPTR--IEAFEVLKMGASIEYAIQSKDLEIIGDIYIEHA 286

Query: 319 HLKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376

LKAI +N N + D L++ LFA G + +++ R KE++R+ A+ + LG

Sbjct: 287 PLKAIAINQNTASLIDEIPALSIAMFLAKGKSMVKNKADLRAKESDRIKAVVSNFKALGI 346

Query: 377 SVEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPV 420

EE D + I PP I +++DHR+AM+F++ A +P+

Sbjct: 347 ECEEFEEDGFYIEGLEDISPLKQRFSRKPP-----LIQSFNDHRIAMSFAILTLA-LPL 399

Query: 421 TIRDPGCTRKTFPDYFDVLSTFVK 444

I + C +FP + +L+ F K

Sbjct: 400 EIDNLECANISFPQFKRLLNLFKK 423

>ref|ZP_04797190.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis W23144]

gb|EES36193.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis W23144]

Length = 436

Score = 92.8 bits (229), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 101/437 (23%), Positives = 198/437 (45%), Gaps = 42/437 (9%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G +++PG KS+++R ++LA+L++G + + L ED + + LG+++E

Sbjct: 16 LKGEIEVPGDKSMTHRAIMLASLAKGISTIEPLLGEDCRRTMDIFKQLGVITIEEQD--- 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

+++ G + +V L+ GN+G R L ++ G + +VL G + +RP+

Sbjct: 73 NSIINSFG-YQNFTTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 128

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190

++ L ++ A++ P P + GI +++++ S+Q SA+L+A+

Sbjct: 129 DRVMKPLLKMNAISGIDNNYTPLIIPSTIKGINY----QMEVA---SAQVKSAILLAS 181

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250

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      +      + ID +S + E   L   F +      +      ++ P++ +V
Sbjct: 182 LFSKEATTLTEID--VSRNHTET---LFAHFNIPISIQGKTIQ-TLPYAIEHIQPRDFHV 235

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
      GD SSA++F+  A IT G+ +T+  G   + +  +++++ MG + +  S
Sbjct: 236 PGDISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMGGNIELSNVSKGA-- 291

Query: 310 PPREPFGRKH-----LKAIDVNMNMKMPDVAMTLAVVALF---ADGPTAIRDVASWRVKE 360
      EP   H      L A+ + + +P      L V+AL  A      I+D  +VKE
Sbjct: 292 ---EPTASIHVTYTPNLNAVTIKGDLPVRAIDELPVIALLLCTQASNSCIIKDAEELKVKE 348

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVP 419
      T R+      L LG +++  D II P E +  +D+  DHR+ M ++A+ +  P
Sbjct: 349 TNRIDTTADMLNLLGFNLQPTHDLIIHPSEFRSNATVDSQTDHRIGMMLAVASLLSSEP 408

Query: 420 VTIRDPGCTRKTFPDYF 436
      + I      +FP +
Sbjct: 409 LKIEQFDVNVVSFPGF 425

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>ref|YP_003927283.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
      PeCan4]
gb|AD007233.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
      PeCan4]
      Length = 429

```

Score = 92.8 bits (229), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 111/441 (25%), Positives = 191/441 (43%), Gaps = 49/441 (11%)

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Query: 25  KSLSNRIILLAAALSEGTTVVDNLLNSEVDVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
      KSLs+R ++ + L++  VV N L  ED   L + LG VE  AK + +
Sbjct: 11  KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85  FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
      P   KE ++  N+G +MR + ++  G +VL G + RP+ ++  LK
Sbjct: 65  -PPTALKEPNKILNCNNSGTSMLRYSGLLSTQKG--LFVLSGDNSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
      GA +  LG +      I G P      I+S Q  SA +++A  A G  +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPKACDYESPISAAQVKSASFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
      + +S + E+ L+  G ++ D   I +K  + +  D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLK 321
      AIT + + ++      + ++  E L+ MGA + +  S +      LK
Sbjct: 232 ACAITPKSRLLLNKVNLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
      AI+++ N   + D   L++  LFA G + +++  R KE++R+ A+ +  LG  E
Sbjct: 290 AINIDQNIASLIDEIPALSIAMLFAGKGSVMKNAKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
      E D +CI      PP      I +++DHR+AM+F++  A +P+ I
Sbjct: 350 ELEDGFCIEGLEDISQLKQRLSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
      + C  +FP +  +L+ F K
Sbjct: 403 NLECANISFPQFKRLNLFKK 423

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>ref|YP_003728473.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
      B8]
emb|CBI66009.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
      B8]
      Length = 429

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Score = 92.8 bits (229), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 114/443 (25%), Positives = 194/443 (43%), Gaps = 53/443 (11%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTAIKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID 203
GA + P+ + G L + S S+Q SA +++A A G V + +
Sbjct: 122 FGAKILGREDNHFAPLVILG-SSLKACHYE-SPIASQVKSASFILSALQAQG-VSVYKEN 178

Query: 204 KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSASYF 260
+L S + E+ L+ G ++ D + + P A+ + D SSA +F
Sbjct: 179 EL-SRNHTEIMLK---SLGADIQNQDGVLEKI-----SPLEKPLEAFDFTIANDPSSAFFF 229

Query: 261 LAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKH 319
AIT + + ++ + ++ EVL+ MGA + + S +
Sbjct: 230 ALACAITPKSRLLLNKVNLLNPTR--IEAFEVLKKMGASIEYAIQSKDLEMIGDIYVEHAP 287

Query: 320 LKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
LKAI + N + D L+V LFA G + +++ R KE++R+ A+ + LG
Sbjct: 288 LKAISIEQNIASLIDEIPALSVAMLFAGKGSVMKNKDLRSKESDRIKAVVSNFKALGIE 347

Query: 378 VEEGPD-----YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPT 421
EE D + I PP I +++DHR+AM+F++ A +P+
Sbjct: 348 CEEFEDGFYIEGLEDISPLKQCFSRKPP-----LIKSFNDHRIAMSFVAVTLA-LPLE 400

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + CT +FP + +L+ F K
Sbjct: 401 IDNLECTNISFPQFKRLLNLFKK 423

>ref|ZP_06371976.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 414]
gb|EFC32822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 414]
Length = 428

Score = 92.8 bits (229), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 108/432 (25%), Positives = 190/432 (43%), Gaps = 36/432 (8%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG ++ ++ V
Sbjct: 17 IAADKSISHRFAIFSLTQEENKAQNYLLAQDTLNTLEI IKNLGAKIK-----QKGSCVN 71

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 72 ITP--PKEILSPNCVLDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + G + P+ + G L K S S+Q +A++++A D
Sbjct: 128 LAQIGARIYGRDGANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSA--FRDNDVCT 183

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
+ +S + E L+ M+ + SD+ I +K +N + D SSA YF
Sbjct: 184 FSEVSLSRNHSNMLKAMK---APIKVSNDGLSLEISPLKKPLKAQNIVIPNDPSSAFYF 240

Query: 261 -LAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG-- 317
LA + + ++ + ++ ++L+ MGAK+ +T+T E G
Sbjct: 241 ALAAIILPNSQIILKNILLNPTR--IEAYKILQKMGAKL-----EITITQNDFETIGEIK 293

Query: 318 ---KHLKAIDV--NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELT 372
L AI+V N+ + D A LA+ A G + +++ RVKE++R+ + L
Sbjct: 294 VETSKLNAIEVKDNIAWLIDEAPALAIAFALAKGKSILKNAKELRVKESDRIAVVIENLK 353

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRK 430
G +E D I L + I +Y DHR+AM+F++ C V I D C +
Sbjct: 354 LCGIKAKELEDGFEIEGGDLKSSIKISYGDHRIAMSFALIGLLCG---VEIDSDCIKT 410

Query: 431 TFPDYFDVLSTF 442

+FP++ ++LS
Sbjct: 411 SFPNFIEILSNL 422

>gb|ACB05442.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [*Lolium rigidum*]
Length = 63

Score = 92.8 bits (229), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 55/62 (88%), Positives = 59/62 (95%), Gaps = 1/62 (1%)

Query: 73 AKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
AKRAVVVGCGG+FP+E DAKEEV+LFLGNAG AMR+LTAAGV AAGGNATYVLDGVPRMRE
Sbjct: 2 AKRAVVVGCGGRFPIEKDAKEEVKLFLGNAGTAMRALTAAVVAAGGNATYVLDGVPRMRE 61

Query: 132 RP 132
RP
Sbjct: 62 RP 63

>dbj|BAJ60090.1| 3-phosphoshikimate 1-carboxyvinyltransferase [*Helicobacter pylori* F57]
Length = 429

Score = 92.4 bits (228), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 113/442 (25%), Positives = 190/442 (42%), Gaps = 51/442 (11%)

Query: 25 KSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMLRYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLVILGSPLKACDYESPISAQVKSALFILSALQAQSSIIK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ + I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANLQNQNGV--LIISPLEKPLESFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGTIVTVEGCGTTSLSQGDVKAFA--EVLEMMGAKVTWTETSVTVTGPPREPFGRKHL 320
AIT + + L + E L+ MGA + + S + L
Sbjct: 232 ACAITPKSRL---LKNVLLNPTRIGAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPL 288

Query: 321 KAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASV 378
KAI+++ N + D L++ LFA G + +++ R KE++R+ A+ + LG
Sbjct: 289 KAINIDQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAVVSNFKALGVEC 348

Query: 379 EEGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
EE D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 349 EEFEDGFCIEGLEDISQLKQRLSQKPP-----LIQSFNDHRIAMSFAILTLA-LPLEI 401

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
+ CT +FP + +L+ F K
Sbjct: 402 DNLECTNISFPQFKRLNLNLFKK 423

>gb|ACB05438.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [*Lolium rigidum*]
gb|ACB05439.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [*Lolium rigidum*]
Length = 63

Score = 92.0 bits (227), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 56/63 (88%), Positives = 58/63 (92%), Gaps = 1/63 (1%)

Query: 72 AAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AKRAVVVGCGG+FPVE DAKEEV+LFLGNAG AMR LTAAGV AAGGNATYVLDGVPRMR

Sbjct: 1 GAKRAVVVGCGRFPVEKDAKEEVKFLGNAGTAMRPLTAAVVAAGGNATYVLDGVPRMR 60

Query: 131 ERP 133

ERP

Sbjct: 61 ERP 63

>ref|NP_207199.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
26695]
sp|P56197.1|AROA_HELPY RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAD07470.1| 3-phosphoshikimate 1-carboxyvinyltransferase (aroA) [Helicobacter
pylori 26695]
Length = 429

Score = 92.0 bits (227), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 113/452 (25%), Positives = 192/452 (42%), Gaps = 71/452 (15%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGRK 84
KSLS+R ++ + L++ V N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLAQKPCFVRNFLMGEDCLSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTTIKEPNKILNCNNSGTTMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLVILGSPLKACHYESPIASQVKSAFILSALQAQGASTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSASY 259
+ +S + E+ L+ G + D + + P A+ + D SSA +
Sbjct: 177 ESELSRNHTEIMLK---SLGADIHNQDGVLEKI-----SPLEKPLEAFDFTIANDPSSAFF 228

Query: 260 FLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETST-----VTVTGP 310
F AIT + + ++ + ++ EVL+ MGA + + S + V
Sbjct: 229 FALACAITPKSRLLLKNVLLNPTR--IEAFEVLKMGASIEYAIQSKDLEMIGDIYVEHA 286

Query: 311 PREPFGRKHLKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P LKAI+++ N + D L++ LFA G + +++ R KE++R+ A+
Sbjct: 287 P-----LKAINIDQNIASLIDEIPALSIAMLFAGKGSVMKNAKDLRAKESDRIKAVV 338

Query: 369 TELTKLGASVEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSL 412
+ LG EE D + I PP I +++DHR+AM+F++
Sbjct: 339 SNFKALGIECEEFEFGFYVEGLEDISPLKQRFSSRIKPP-----LIKSFNDHRIAMSFV 392

Query: 413 AACAEVPVTIRDPGCTRKTFFDYFDVLSTFVK 444
A +P+ I + C +FP + +L+ F K
Sbjct: 393 LTLA-LPLEIDNLECANISFPQFKHLLNQFKK 423

>ref|ZP_05363634.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter showae
RM3277]
gb|EET79669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter showae
RM3277]
Length = 424

Score = 92.0 bits (227), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 120/424 (28%), Positives = 189/424 (44%), Gaps = 38/424 (8%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGRK 84
KS+S+R + + LS+ + V N L +ED L ++ LG +E +K + + K
Sbjct: 21 KSISHRCAIFSLSDKPSRVKNYLKAEIDLNTLEIVKNLGAHIE-EKEGELIITPSANLK 79

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
P V L GN+G AMR + A+ G +VL G + RP+ + L +
Sbjct: 80 EP-----SVVLECGNSGTAMRLFMGFLAASEG--FFVLSGDEFLNRRPMARVAKPLISV 131

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEIID 203
GA +D G D P+ I G K I+S Q SAL++A + G E+ +

Sbjct: 132 GAKIDGANGGDHAPL---AIRGKKLEYFKFDSKIASAQVKSALILAGLKSNG---CELSE 185

Query: 204 KLISIPYVEMTLRLMER-----FGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+S + E L+ M GVK E ++ + P V D SSA

Sbjct: 186 PELSRDHTERMLKMGASLQILPCGVKVEPMNAPLK-----PLEICVPNDPSSA 234

Query: 258 SYFLAGAAITGGTGTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPPREPFGR 317
+F AAI + V + + V+ ++L MGA+VT+ ETS T

Sbjct: 235 FFFAVAAAIIPNSHIVLKNMLLN-KTRVEAFKILAKMGAQVTFKETSGETYESIGEIEIKY 293

Query: 318 KHLKAIDV--NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
LKA+DV N++ + D LA+ A G +++R+ RVKE++R+ + L K G

Sbjct: 294 APLKAVDVSENIWLIDEVPALAIAFANAQGTSSVRNAKELRVKESDRIAIMVQGLRKCG 353

Query: 376 ASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFPDY 435
VEE D + E N ID+ DHR+AM+F++ + + I +FP++

Sbjct: 354 LEVEEFEDGFSVKGGEA-NCIIDSNGDHRIAMSAVLGL-KCGMVIEKSEFIATSPFNF 411

Query: 436 FDLV 439
+L

Sbjct: 412 SGIL 415

>ref|YP_001129873.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Prosthecochloris
vibrioformis DSM 265]
sp|A4SD12.1|ARO_APROVI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABP36371.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium
phaeovibrioides DSM 265]
Length = 433

Score = 92.0 bits (227), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 109/444 (24%), Positives = 198/444 (44%), Gaps = 45/444 (10%)

Query: 21 LPSKSLSNRILLALLAALSEGTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK----- 74
LP KS+S+R L+ AL+EG T + N D LG L G+ + ++

Sbjct: 11 LPPDKSISHRAALIGALAEGVTEITNFSGGFDNQSTLGVLGACGIPLTQEEVPGPWGGTI 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + + ++ N+G MR + + + V DG + +RP+

Sbjct: 71 RRVVIESKGLWSFRPSGAPLEC--NNSGSTMRMMAGILAGQPFGSELVGDG--SLMKRPM 126

Query: 135 GDLVVLGKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ L+ +GA V+ + P+R+ G L +L S+Q S + AA A

Sbjct: 127 QRVAGPLRDMGAGVE-LSESGTAPMRIAGTKELRPVYRLPVP-SAQVKSILVAFALHAE 184

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G E II+ ++S + E+ L G++A D +R + G++ + V D

Sbjct: 185 G--ESRIIEPVLSDHTELML-----GLEAEVDG-ERVIVVPGRRRIEARPFLVPADP 235

Query: 255 SSASYFLAGAAITGGT--VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPP- 311
S+A + +A A + G+ + + C + F +++ G ++T E TV G

Sbjct: 236 SAACFIVALALLAPGSEIMIRDVCLNPT--RAAFLDIMIAAGGQIT-IENRRTVGGEDI 291

Query: 312 -----REPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
EP + +++++P LAV+++FA G + + R KE

Sbjct: 292 GDILARGGGVLEPLSISDPGVVARVIDEIP---MLAVLSVFASGSFEVSNAGELRTKEC 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--AIDTYDDHRMAMAFSLAACAE-V 418
+R+ A+ L +LG EE PD ++ + + ++ +DDHR+AM+F++AA A +

Sbjct: 348 DRLNALAVNLQRLGCLCEESPDGMRVSGGVRAQHSPVVVECFDDHRIAMSAFAIARATGM 407

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTF 442
+ + D +FP++F +L +

Sbjct: 408 DIELSDSAVVGVSFPNFFALLESL 431

>ref|ZP_06373720.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 1336]
gb|EFC30749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni

subsp. jejuni 1336]
Length = 428

Score = 92.0 bits (227), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 186/431 (43%), Gaps = 34/431 (7%)

Query: 21 LPSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEEKDSCVKIIP-- 74

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNNRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNYKSEIS-SAQVKTAMILSAFRA----- 178

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
D + + + ++ E +KA S D I +K +N + D SS
Sbjct: 179 --DNICTFSEISLSRNHSENMLKAMKAPIRVSNLGLSLEISPLKKPLKAQNIIPNDPSS 236

Query: 257 ASYF-LAGAAITGGTIVTEGCGTTSLGQDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
A YF LA + + ++ + ++ ++L+ MGAK+ T T+ G R
Sbjct: 237 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQDNFETIGEIRV 294

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ + + N+ + D A LA+ A G +++ + RVKE++R+ A+ L
Sbjct: 295 ESSKLNIGIEVKDNIAWLIDEAPALAIAPALAKGKSSLINAKELRVKESDRITAMVENLKL 354

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
G E D I +L + I +Y DHR+AM+F++ C V I D C + +
Sbjct: 355 CGVEARELDDGFEIGRCELKSSKIKSYGDHRIAMSFALGLLCG--VEIDSDCIKTS 411

Query: 432 FPDYFDVLSTF 442
FP++ ++LS
Sbjct: 412 FPNFIEILSNL 422

>ref|ZP_05068167.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Octadecabacter
antarcticus 238]
gb|EDY93406.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Octadecabacter
antarcticus 238]
Length = 450

Score = 92.0 bits (227), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 119/437 (27%), Positives = 188/437 (43%), Gaps = 36/437 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +PG KS+S+R L+L AL+ G T + LL +DV A+ G V +
Sbjct: 18 LRGEAHVPGDKSISHRSLILGALAVGETKITGLLEGQDVLDTGRAEAFGAQVINHGGGE 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V + E + GN+G +R + A+ + T G + RP+
Sbjct: 78 WSVHG----VGVGFGGEPENVIDCGNSGTGVRLIMGAMATC--DMTFTFTGDASLNGRPM 131

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGK-----VKLSGSISSQYLSALLMA 189
G + L G G P V G K + S+Q SA+L+A
Sbjct: 132 GRVTDPLALFGTIAVGRAGRPLPMTVV-----GAKDPVPVRYVVPVPSAQVKSALLA 184

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWD-RFYIKGGQKYKSPKNA 248
A G E +I+K + + E R++ FG D+ + R GQ P+
Sbjct: 185 GLNAPG--ETVVIEKEATRDHTE---RMLVGFADLTVEDTDEGRVITLVGQPELKPQTI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSVTV 307
V D SSA++ + A + G+ V V G + + + L+ MGA +T+
Sbjct: 240 IVPRDPSSAAFPVCAALLAEGSDVLVPNIGLNPTRAGLFY--TLQDMGADLTFFENMREEG 297

Query: 308 TGPPREPFGF--KHLKAIDV---NMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
P + R ++ I+V M D L+VV+ FA G T +R V RVKE++
Sbjct: 298 GEPVADLRARYSPNMHGIEVPPARAASMIDEYPVLSVVSFAKGTVMRGVKELRVKESD 357

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD---DHRMAMAFSLAACA-EV 418
R+ A+ L G +V+EGPD+ I+T NV T + DHR+AM+F + A
Sbjct: 358 RIDAMAKGLRAAGVTVDGPDWWIVTGLGFGNVAGGITAESRLDHRAMSFVLMGLATNA 417

Query: 419 PVTIRDPGCTRKTFPDY 435
P+++ D G +FP +
Sbjct: 418 PMSVDDGGPIATSFPIF 434

>gb|EFV89034.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus epidermidis FRI909]
Length = 433

Score = 92.0 bits (227), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 101/437 (23%), Positives = 198/437 (45%), Gaps = 42/437 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L++G + + L ED + + LG+++E
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAKGISTIEYELLGEDCRRTMDIFKQLGVITIEEQ---D 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++++ G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 NSIIINSPG-YQNFTTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ L ++ A++ P P + GI +++++ S+Q SA+L+A+
Sbjct: 126 DRVMKPLLKMANISGIDNNYTPLIIPSTIKGI----NYQMEVA---SAQVKSAILLAS 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
+ + ID +S + E L F + + + ++ P++ +V
Sbjct: 179 LFSKEATTLTEID--VSRNHTET---LFAHFNIPIISIQGKTIQ-TLPYAIEHIQPRDFHV 232

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
GD SSA++F+ A IT G+ +T+ G + + +++++ MG + + S
Sbjct: 233 PGDISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMGNGIELSNVSKGA-- 288

Query: 310 PPREFPGRKH-----LKAIIDVNMNMPDVMATLAVVALF---ADGPTAIRDVASWRVKE 360
EP H L A+ + + +P L V+AL A I+D +VKE
Sbjct: 289 ---EPTASIHVITYTPNLNAVITIKGDLVPRAIDELPVIALLLCTQASNSCIIKDAEELKVKE 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVP 419
T R+ L LG +++ D II P E + +D+ DHR+ M ++A+ + P
Sbjct: 346 TNRIDTTADMLNLLGFNLQPTHDLIIHPSEFGSNATVDSQTDHRIGMMLAVASLLSSEP 405

Query: 420 VTIRDPGCTRKTFPDYF 436
+ I +FP +
Sbjct: 406 LKIEQFDVNVVSFPGFL 422

>ref|YP_001997916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobaculum parvum NCIB 8327]
sp|B3QQU6.1|ARO_A_CHLP8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACF10716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobaculum parvum NCIB 8327]
Length = 434

Score = 92.0 bits (227), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 115/445 (25%), Positives = 195/445 (43%), Gaps = 46/445 (10%)

Query: 21 LPGSKSLSNRILLALASEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK----- 74
LP KS+S+R ++ +L+EGTT + N D L LR LG+SV D+
Sbjct: 11 LPPDKSISHRAAIIIGSLAEGTTEITNFGSGGFDNQSTLSVLRDLGISVRQDEVPAAGDGRIV 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R VV+ G + + E L N+G MR + + A + V D + +RP+
Sbjct: 71 RHVVIENGLWSFREPSE--PLMCNNSGSTMRRMAGILAAQPFSELVGDA--SLMKRPM 126

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

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      +   L+ +GAD+          PV +NG   L   +   L   +   S   + +L+   A   L
Sbjct: 127 KRVADPLRM MGADI-SLS DAGTAPV VINGTKDLK TIEYLL--PVPSAQV KSLVALAALH- 182

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHS DSWD--RFYIKGGQKYKSPKNAYVEG 252
      D + +II+ + S + E+ L L          E D D R I G+K + K V
Sbjct: 183 ADGQSKIIEPIRSR DHTEMLGL-----ETIDRPDGVREI IIDGRKPIAAKPFK VPA 234

Query: 253 DASSASYFLAGAAI--TGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTG P 310
      D S+A + +A +          V + C +          V + +VL+ GA +          V
Sbjct: 235 DPSAACFMIALG LGERSEIVLRDVC LNPT---RVAYIDVLQEAGAGLGIE----NVRSE 287

Query: 311 PREPFGRKHLKAI-DVNMNKM P DVAMT-----LAVVALFADGPTAIRDVASWRVKE 360
      EP G   +++ +   ++ D A+          LAV++ FA G   + +   R KE
Sbjct: 288 GGEPVGDIVVRSCSS LAPLRISDHAVVAGVIDELPMLAVLSAFATGEFELHNATELRTKE 347

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVT AIDTYDDHRMAMAF-SLAACAE 417
      ++R+ A+ + L +LG + E+ PD ++ P          I+ +DDHR+AM+F A A
Sbjct: 348 SDRIEAVVSNLERLGFACEQYPDGFVVKGRPTV NREEAVIECFDDHRIAMSFAIAAEAAG 407

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
      + + D          +FP++F ++ +
Sbjct: 408 ASLRLSDREVAGVSFPNFFALIESL 432

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>gb|EGC91177.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Turicibacter sp.
HGF1]
Length = 422

Score = 91.7 bits (226), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 108/442 (24%), Positives = 200/442 (45%), Gaps = 34/442 (7%)

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Query: 15  ISGTVKLP GSKSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      +SG +++ G KS+++R ++L++L+ G TV+ + L D L + G++ + A
Sbjct: 3   LSGELQVAGDKSITHRAIILSSLATGQTVIHDP LLGADCLSTLEIFKQFGVTYQL--TAN 60

Query: 75  RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      + ++ G F ++ L GN+G R L ++A T V D + +RP
Sbjct: 61  QLIIDSPGVDGFTYSNSI----LDAGNSGTTARLLMGVLSALPTTLTLVGDA--SLSKRP 114

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
      + + LKQ+GA ++ P + G L G + +L + S+Q SA+++AA A
Sbjct: 115 MKRVTSP LKQMGACIE-LTHDQTLPATIKG-QSLNGIEYELPVA-SAQVKSAIMLAAMFA 171

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKA EHS DSWDRFYIKGGQKYKSPKNAYVEGD 253
      G+ +I          +P + T ++ E F + +          + G Q K+P +V D
Sbjct: 172 SGETKIH-----EPVPTRDHTEKMFEDFQIVYNKENRV--ITLSGPQMPKTPGQVFVPAD 224

Query: 254 ASSASYFLAGA-AITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
      SSA++F+ A + G + ++ G + + +VL MG ++T          G R
Sbjct: 225 ISSAAFFMVAALMVEGSDLILKNVGLNETRCGI--VDVLLQMGGRLTIQNER--YFGGER 280

Query: 313 EPFGR----KHLKAIDVNMNKM P DVAMTLAVVALFAD---GPTAIRDVASWRVKETERMV 365
      R K LK I + +P + + ++AL A G T I+D +VKET R+
Sbjct: 281 VADIRVQYTKDLKGIIIEGEMIPRLIDEIPIIALLATKAMGQTI IKDAEELKVKETNRID 340

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN V--TAIDTYDDHRMAMAFSLAA-CAEVPVTI 422
      EL +GA++ D +I L+ + ++ DHR+AM +A+ + + I
Sbjct: 341 VTVGELKAIGANLFSTEDGMVINGDINLSYHPALVSSHGDHRIAMMLYVASLLMKNELEI 400

Query: 423 RDPGCTRKTFPDYFDVLSTFVK 444
      + ++PD+ + +K
Sbjct: 401 EEMQAMNISYPDFLVHMQKVLK 422

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>gb|ACB05437.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 63

Score = 91.7 bits (226), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 55/63 (87%), Positives = 58/63 (92%), Gaps = 1/63 (1%)

Query: 72 AAKRAVVVGC GGFVPE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AKRAVVVGC GG+FP+E DAKEEV+LFLGNAG AMR LTAAV AAGGNATYVLDGVPRMR
Sbjct: 1 GAKRAVVVGC GRFPFIEKDAKEEVKLFLGNAGTAMRPLTAAVVAAGGNATYVLDGVPRMR 60

Query: 131 ERP 133
ERP
Sbjct: 61 ERP 63

>gb|ACX99551.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
52]
Length = 429

Score = 91.7 bits (226), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 111/435 (25%), Positives = 190/435 (43%), Gaps = 37/435 (8%)

Query: 25 KSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGC GGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA V LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKV---LGREDNHFAPLVILGSPLKACNYESPIASQVKSAFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ + I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLK 321
AIT + + + + + ++ EVL+ MG + + S + LK
Sbjct: 232 ACAITPKSRLLLKNNVLLNPTR--IEAEVLKMGVSIIEYVIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI ++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AISIDQNIASLIDEIPALSIAMLFAKGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPDYCIITPPEKL-----NVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E D I E + N I +++DHR+AM+F++ A +P+ I + C
Sbjct: 350 EFEDGFGYIEGLEEDITQLKQRLSQKNPLIKSFNDHRIAMSFALITLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 409 ISFPQFKRLNLNLFKK 423

>gb|ADO05722.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Sat464]
Length = 429

Score = 91.3 bits (225), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 112/441 (25%), Positives = 190/441 (43%), Gaps = 49/441 (11%)

Query: 25 KSLSNRI LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGC GGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACDYESPIASQVKSAFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ + I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQGV--LTILPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + + + + + + E L+ MGA + + S + LK
Sbjct: 232 SCAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI + N + D L++ LFA G + +++ R KE++R+ AI + LG E
Sbjct: 290 AISIEQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAIIVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
E D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFCIEGLEDISQLKQRFSSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
+ C +FP + +L+ F K
Sbjct: 403 NLECANISFPQFKRLLNLFKK 423

>gb|ADU83434.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Lithuania75]
Length = 429

Score = 91.3 bits (225), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 109/435 (25%), Positives = 190/435 (43%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ +V N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCIVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTTLKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLVILGNPLKACDYESPISAQVKSAFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ENELSRNHTEIMLK---SLGADIQNQDGV--LMISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + + + + + + E L+ MGA + + S + LK
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI++ N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AINIEQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
E D I E ++ I +++DHR+AM+F++ A +P+ I + C
Sbjct: 350 EFEDGFYIEGLEDISQLKQRFSSQKKPLIKSFNDHRIAMSFAILTLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 409 ISFPQFKRLLNQFKK 423

>ref|YP_627732.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
HPAG1]
sp|Q1CSL4.1|AROA_HELPH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABF85058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
HPAG1]
Length = 429

Score = 91.3 bits (225), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 116/443 (26%), Positives = 193/443 (43%), Gaps = 53/443 (11%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84

Sbjct: 11 KSLS+R ++ + L++ V N L ED L + LG VE AK + +
KSLSHRAVIFSLLAQKPCFVRNFMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK

Sbjct: 65 -PPTAIKEPSKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G V +

Sbjct: 122 FGARI---LGREDNHFAPLVIVGSPLKACNYESPIASQVKSFAVL SALQAQG-VSVYKE 177

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
++L S + E+ L+ G K + D I +K + + D SSA +F

Sbjct: 178 NEL-SRNHTEIMLK---SLGAKIHNQDGV--LMISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS-----VTVTGPPRE 313
AIT + + + + + ++ E L+ MGA + + S + V P

Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEALKMGASIEYVIQSKDLEMIGDIYVEHAP-- 287

Query: 314 PFGRKHLKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
LKAI + N + D L++ LFA G + +++ RVKE++R+ A+ +

Sbjct: 288 -----LKAISIEQNIASLIDEIPALSIAMLFAGKGMVKNKDLRVKESDRKAVISNF 341

Query: 372 TKLGASVEEGPDYCI-----TPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPT 421
LG EE D I P K + I +++DHR+AM+F++ A +P+

Sbjct: 342 KALGIECEEFEFDGFYIEGLEDISPLKQRFQSKKPLIKSFNDHRIAMSFAILTLA-LPLE 400

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + C +FP + +L+ F K

Sbjct: 401 IDNLECANISFPQFKRLLNLFKK 423

>ref|ZP_08054927.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter suis
HS5]
gb|EFX41538.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter suis
HS5]
Length = 416

Score = 91.3 bits (225), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 113/440 (25%), Positives = 203/440 (46%), Gaps = 61/440 (13%)

Query: 27 LSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCGGKFP 86
+S+R+LL A + V +LL +D L +R LGL V+ K A + + +F

Sbjct: 1 MSHRVLLCALFTNPKCFVQDLLMGQDCLSTLSIVRALGLRVQ--KEAPNILKLTTPPKQFL 58

Query: 87 VEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT-YVLDGVPRMRERPIGDLVVGLKQLG 145
+ ++V L N+G MR L+ +++++ Y+L G + ERP+G +VV LKQ+G

Sbjct: 59 RFNEPKKV-LHCHNSGTTMRLLSGLSSSTTQQNHYLIGDVSLSERPMGRVVVPLKQMG 117

Query: 146 ADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKL 205
A + P+ + + G +S S+Q SALL+A A + +

Sbjct: 118 AQIRGRAHNTLAPLSI--VSTPLQGINYVSPLASQLKSALLLATLQAKSASTLS--EPS 173

Query: 206 ISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF-LAGA 264
+S + E+ L+ + A + +++ K + ++ D SSA YF LA

Sbjct: 174 LSRNHTEMLMLQTL-----GANLKMNQITIFLEPLDKPLESFSWHIPNDPSSAFYFALAVM 228

Query: 265 AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTGTGPPREPFGFGR----- 317
+ V ++ + ++ +VLE MGA++++T P E G

Sbjct: 229 LVPQSAVLLKRVLLNPTR--IEAFKVLKMGQAISYT-----PTEYMGAEVGDY 277

Query: 318 -KH--LKAI DVNMN-----KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
KH LKAI++ N ++P +A+ +AV A G + +++ RVKE++R+

Sbjct: 278 VKHASLKAINLESNIAFLIDELPALAVAMAV---AKGVSVVKNAQELRVKESDRITTTTL 333

Query: 369 TELTKLGASVEEGPDYCI-----TPPEKLNVTIDTYDDHRMAMAFSLA--ACAEPV 420
L K+G + D I +P E L +++++DHR+A++F++A AC

Sbjct: 334 ANLKKMGIECQAFKDGFSIQGGTLKSPQEPL-----ESFNDHRIALSFAIALACGG--- 385

Query: 421 TIRDPGCTRKTFPDYFDVLS 440
I++ C +FP + ++L+

Sbjct: 386 EIKNTECMAISFPKFEEILN 405

```
>ref|NP_764708.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis ATCC 12228]
sp|Q8CSI1.1|AROA_STAES RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AA004750.1|AE016747_247 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis ATCC 12228]
Length = 433
```

Score = 90.9 bits (224), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 102/450 (22%), Positives = 200/450 (44%), Gaps = 68/450 (15%)

```
Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++PG KS+++R ++LA+L++G + + L ED + + LG+++E
Sbjct: 13 LKGEIEVPGDKSMTHRAIMLASLAKGISTIEPLMGEDCRRRTMDIFKLLGVITIEEQ---D 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++++ G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 70 NSIIINSPG-YQNFIPTPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKGRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDGP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
++ L ++ A++ P P + GI +++++ S+Q SA+L+A+
Sbjct: 126 DRVMKPLLKMNANISGIDNNYTPLIIPSTIKGI----NYQMEVA---SAQVKSAILLAS 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFY-----IKGGQ----- 240
L S +T F V H+++ + I+G
Sbjct: 179 -----LFSKEATTLT-----EFDVSRNHTETLFAHFNIPISIQGKTIQTIP 219

Query: 241 ---KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGA 296
++ P++ +V GD SSA++F+ A IT G+ +T+ G + + +++ MG
Sbjct: 220 YAEIHQPRDFHVPDGISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMG 277

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLK-----AIDVNMNKMMPDVAMTLAVVALF---ADGP 347
+ + S EP H+K A+ + + +P L V+AL A
Sbjct: 278 NIELSNVSKGA-----EPTASIHVKYTPNLNAVTIKGDLPRAIDELPVIALLCTQASNS 332

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMA 407
I++ +VKET R+ L LG +++ D II P E + +D+ DHR+
Sbjct: 333 CIIKNAEELKVKETNRIDTTADMLNLLGFNLQPTHGLIHPSEFRSNATVDSQTDHRIG 392

Query: 408 MAFSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
M ++A+ + P+ I +FP +
Sbjct: 393 MMLAVASLLSSEPLKIEQFDAVNVSPGFL 422
```

```
>ref|YP_001910521.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Shi470]
sp|B2UUF9.1|AROA_HELP RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACD48491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Shi470]
Length = 429
```

Score = 90.9 bits (224), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 111/441 (25%), Positives = 190/441 (43%), Gaps = 49/441 (11%)

```
Query: 25 KSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLAQKPCVVRNFMGDCLLSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTALKEPNKILNCSNNGTSMRLYSGLLSAQKG--LFVLSGDNSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACDYSPIASAQVKSFAFILSALQAQGSSTYK-- 176
```

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ + I +K + + D SSA +F
Sbjct: 177 ENELSRNHTIEMLK---SLGANIQNQGV--LTILPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPPREPFGRKHLK 321
AIT + + + + + E L+ MGA + + S + LK
Sbjct: 232 SCAITPKSRLLLKNNVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI + N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AISIEQNIASLIDEIPALSIAMFLAKGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-YCI-----ITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
E D +CI PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFCIEGLEDISQLKQRFSSQKKPP-----LIQSFNDHRIAMSFAILTLA-LPLEID 402

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
+ C +FP + +L+ F K
Sbjct: 403 NLECANISFPQFKRLNLNLFKK 423

>ref|YP_188611.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis RP62A]
ref|ZP_06284969.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis SK135]
sp|Q5HP79.1|AROA_STAEQ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW54418.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis RP62A]
gb|EFA87654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis SK135]
Length = 433

Score = 90.5 bits (223), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 102/448 (22%), Positives = 199/448 (44%), Gaps = 68/448 (15%)

Query: 17 GTVKLPGSKSLSNRIALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRA 76
G +++PG KS+++R ++LA+L++G + + L ED + + LG+++E +
Sbjct: 15 GEIEVPGDKSMTHRAIMLASLAKGISTIIYEPLMGEDCRRTMDIFKLLGVITIEEQ---DNS 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 72 I IINSPG-YQNFITPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIKRPMDR 127

Query: 137 LVVGLKQLGADVDCFLGTDGCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
++ L ++ A++ P P + GI +++++ S+Q SA+L+A+
Sbjct: 128 VMKPLLKMNANISGIDNNYTPLIIKPSTIKGI----NYQMEVA---SAQVKSAILLAS-- 178

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-----IKGGQ----- 240
L S +T F V H+++ + I+G
Sbjct: 179 -----LFSKEATTLT-----EFDVSRNHTETLFAHFNIPISIQGTIQTIPYA 221

Query: 241 -KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ P++ +V GD SSA++F+ A IT G+ +T+ G + + +++++ MG +
Sbjct: 222 IEHIQPRDFHVPGDISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMGGNI 279

Query: 299 TWTETSVTVTGPPREPFGRKHLK-----AIDVNMNKMMPDVAMTLAVVALF---ADGPTA 349
+ S EP H+K A+ + + +P L V+AL A
Sbjct: 280 ELSNVSKGA-----EPTASIHVKYTPNLNAVTIKGDLPVRAIDELPVIALLLCTQASNSCI 334

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
I++ +VKET R+ L LG +++ D II P E + +D+ DHR+ M
Sbjct: 335 IKNAEELKVKETNRIDTTADMLNLLGFNLQPTHGLIIHPSEFRSNATVDSQTDHRIGMM 394

Query: 410 FSLAA-CAEVPTIRDPGCTRKTFPDYF 436
++A+ + P+ I +FP +
Sbjct: 395 LAVASLLSSEPLKIEQFDAVNVVSFPGFL 422

>ref|ZP_07598734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium meliloti AK83]
gb|EFN25898.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium meliloti AK83]
Length = 455

Score = 90.5 bits (223), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 110/445 (24%), Positives = 198/445 (44%), Gaps = 38/445 (8%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ GT+++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 17 DLKGTTLRIPGDKSISHRSFMFGGLAAGETRITGLLEGEDVINTGKAMQAMGARIRKEGGT 76

Query: 74 KRAVVVGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
VG G E L GNAG R V ++T++ D + +RP
Sbjct: 77 WIIDGVNGALL-----APEAPLDFGNAGTGCRLTMGLVGVYDFDSTFIGDA--SLTKRP 129

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 130 MGRVLDPLREMGVQVKSAG--DRLPVTLRG----PKTPNPITYRVPMSAQVKSALLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
G +++ ++ + E ++++ FG + E R G+ + +
Sbjct: 185 LNTPGIT--TVVEPVMTDRDTE---KMLQGFGANLTVETDAEGVRTIRLEGRKLTGQVI 239

Query: 249 YVEGDASSASY--FLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ +AG + G +T+ + + L+ MGA + +
Sbjct: 240 DVPGDPSSTAFLVAGLIVPGSDITILNVLMNPTRTGLIL--TLQEMGANIEVMNKRL-A 296

Query: 308 TGPPREPFPGRKH--LKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G +H LK + V ++ P D LAV A FA+G T + + RVKE++
Sbjct: 297 GGEDVADLRVRHSELKGVTVPEDRAPSMIDEYPVLAVAAFAEGTTVMNGLEELRVKESD 356

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPE-----KLNVTADITYDDHRMAMAFSLAACA 416
R+ A+ L G +EG ++ K++ + T+ DHR+AM+F + A
Sbjct: 357 RLSAVADGLKLVGDCDEGEASLVVRGPGGKGLGKISGGQVKTHLDHRIAMSFLVMGLA 416

Query: 417 -EVPVTIRDPGCTRTKTFPDYFDVLS 440
E PVT+ D +FP++ ++
Sbjct: 417 SEHPVTVDATMIATSFPEFMGLMT 441

>ref|YP_001390821.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum F str. Langeland]
gb|ABS42069.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum F str. Langeland]
gb|ADF99267.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum F str. 230613]
Length = 442

Score = 90.5 bits (223), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 107/455 (23%), Positives = 208/455 (45%), Gaps = 55/455 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYIEIGDKSIGHRSIIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVGCCKGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G E+ ++ ++ G N+G +R + ++ ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQKNSGTTVRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA ++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPLKFLKHSGLSIKYNMEIA-SAQVKSICILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++ G I + ++++ Y++ ++ + + + S S I+ + +
Sbjct: 179 MSKGGTTIVENKSTRDHTERMLK--YLDASINIRNIYSKDKKSSSKKEITIEKSKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLS--QGDVKFAEVLEMMGAKVTWTE 302
K+ YV GD SSA++ ++ A + G+ C L +G +++ VL MGA + E

Sbjct: 235 SKDIYVPGDISSAAFLISAALLIQGSNL---CIKNVLLNEGRIEYINVLRNMGANIE-IE 290

Query: 303 TSVTVTGPPPREPFGR----KHLKAIDVNMNKMPPDVAM---TLAVVALFADGPTAIRDVA 354

+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 291 KGKLLNG--EPVGNIVKESYLKGITVERHITPNIIDEIPVLSVIAAFSEKTTFKSVE 347

Query: 355 SWRVKETERMVAIRTELT-----KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406

+ KE++R+ AI L K G + EG I P E I+++ DHR+
Sbjct: 348 ELKFESDRVEAIIENLKRADVKAIIYKNGDLIEGNSYIDKPLE-----IESFKDHRI 401

Query: 407 AMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLS 440

A+AF + + T I+D CT +FP+ + +
Sbjct: 402 ALAFLVLSLKNKKHTLIKDYQCTEISFPNSLSLNF 436

>ref|YP_001368591.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ochrobactrum anthropi
ATCC 49188]
sp|A6WUV8.1|AROAO_OCHA4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABS12762.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ochrobactrum anthropi
ATCC 49188]
Length = 450

Score = 90.5 bits (223), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 112/445 (25%), Positives = 193/445 (43%), Gaps = 45/445 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + D A
Sbjct: 18 LTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGAKIRKGDGAW 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134

VG G + E L GNAG R V +++ D + +RP+
Sbjct: 78 IINGVGNGCLL----QPEAALDFGNAGTGARLTMGLVGTDMRTSFIGDA--SLSKRPM 130

Query: 135 GDLVVGKQLGADVDCFLGTDGP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189

G ++ L+++G V+ G P P N I +V ++ S+Q SA+L+A
Sbjct: 131 GRVLNPLREMGVQVEAAEGDRMPLTLIGPKTANPI----TYRVPMA---SAQVKSAYLLA 183

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247

G +I+ +++ + E ++++ FG + E R GQ +
Sbjct: 184 GLNTPG--VTTVIEPVMTDRDTE--KMLQGFGADLSVETDKDGVRRHIRTGQKLGIGQT 238

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDV----KFAEVLEMMGAKVTWT 301

V GD SS ++ L A + G+ VT+ + + +E++ A++
Sbjct: 239 IDVPGDPSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLILTLQEMGADIEVLNARLAGG 298

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRV 358

E + LK + V + P D LA+ A FA+G T + + RV
Sbjct: 299 EDVADLR-----VKASKLKGVVPPERAPSMIDEYPVLAIAAAFAEGETVMDGLDELRV 352

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEK-LNVTATIDTYDDHRMAMAFSLAAC 415

KE++R+ A+ L G EG + P K L + T+ DHR+AM+F +
Sbjct: 353 KESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVATHLDHRIAMSFLVMGL 412

Query: 416 A-EVPVTIRDPGCTRKTFPDYFDVL 439

A E PVT+ D +FP++ D++
Sbjct: 413 ASEKPVTVDDSTMIATSFPEFMDMM 437

>dbj|BAJ41481.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lactobacillus
paraplantarum]
Length = 277

Score = 90.5 bits (223), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 85/277 (30%), Positives = 133/277 (48%), Gaps = 26/277 (9%)

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238

S+Q SAL+ AA L I I++KL + + E+ ++ +FG D+ +
Sbjct: 5 SAQVKSALIFAA-LQAKQSSI-IVEKLPTNRNHTI---MLHQFGAHI RTVDN-KVIIVDP 58

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G+K + V GD SSA++FL A I VT++G + + ++L+ MGAK
Sbjct: 59 GEKLVG-QEVTVPDGMSSAAFFLVAAITVPHSKVTLKGVNLPTRTGI--IDILQQMGAK 115

Query: 298 VTWTETSVTVTGPPREPFG-----RKHLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTA 349
+ E T EP G L+ I + +P V L +VAL A DG +
Sbjct: 116 LLIEEQFST-----GEPSGDITVENSALRPIHLTAEDIPAVIDELPLVALLAACSDGQST 170

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMA 407
IR RVKET+R+ + EL KLG V+E PD +I P + +D+Y DHR+
Sbjct: 171 IRGAQELRVKETDRIKTVVAELRKLGVQVKELPDGMVIDGRPSWDIQDPQLDSYGDHRLG 230

Query: 408 MAFSLAAC-AEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
M ++AA A+ P+ + ++P +F L+T +
Sbjct: 231 MMDAIAALKADQPLQLAHEDAVAVSYPGFFADLATLL 267

>ref|ZP_04825363.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis BCM-HMP0060]
ref|ZP_06613244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis M23864:W2(grey)]
gb|EES58227.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis BCM-HMP0060]
gb|EFE59705.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
epidermidis M23864:W2(grey)]
Length = 436

Score = 90.5 bits (223), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 102/448 (22%), Positives = 199/448 (44%), Gaps = 68/448 (15%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +++PG KS+++R ++LA+L++G + + L ED + + LG+++E +
Sbjct: 18 GEIEVPGDKSMTHRAIMLASLAKGISTIEYPLMGEDCRRTMDIFKLLGVTTIEEQ---DNS 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+++ G + +V L+ GN+G R L ++ G + VL G + +RP+
Sbjct: 75 IIINSPG-YQNFITPHQV-LYTGNSGTTTLLAGLLSGLGIES--VLSGDVSIGKRPMDR 130

Query: 137 LVVGLKQLGADVDCFLGTDCP----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
++ L ++ A++ P P + GI +++++ S+Q SA+L+A+
Sbjct: 131 VMKPLLKMNANISGIDNNTPLIIPSTIKGI---NYQMEVA---SAQVKSAILLAS-- 181

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY-----IKGGQ----- 240
L S +T F V H+++ + I+G
Sbjct: 182 -----LFSKEATTTL-----EFDVSRNHTETLFAHFNIPISIQGKTIQTIPYA 224

Query: 241 -KYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ P++ +V GD SSA++F+ A IT G+ +T+ G + + +++ MG +
Sbjct: 225 IEHIQPRDFHVPDGISSAAFFIVAALITPGSDITIHNVGINPTRSGI--IDIVKQMGGINI 282

Query: 299 TWETETSVTVTGPPREPFGRKHLK-----AIDVNMNKMPPDVAMTLAVVALF---ADGPTA 349
+ S EP H+K A+ + + +P L V+AL A
Sbjct: 283 ELSNVSKGA-----EPTASIHVKYTPNLNAVITIKGDLVPRAIDELPVIALLTQASNSCI 337

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMA 409
I++ +VKET R+ L LG +++ D II P E + +D+ DHR+ M
Sbjct: 338 IKNAEELKVKETNRIDTTADMLNLLGFNLQPTHGLIHPSEFRSNATVDSQTDHRIGMM 397

Query: 410 FSLAA-CAEVPVTIRDPGCTRKTFPDYF 436
++A+ + P+ I +FP +
Sbjct: 398 LAVASLLSSEPLKIEQFDAVNVSFPGFL 425

>gb|ADC28481.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni IA3902]
Length = 428

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 102/431 (23%), Positives = 185/431 (42%), Gaps = 34/431 (7%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80

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      + KS+S+R  + + L++      N L ++D      L  ++ LG +E  +  + +
Sbjct: 17  IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDCSCVKIIP-- 74

Query: 81  CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
      P E      L GN+G AMR +  + AG + +VL G  + RP+  +
Sbjct: 75  -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
      L Q+GA +      + P+ + G L      K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNFKSEIS-SAQVKTAMILSAFRA----- 178

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
      D + +  + ++      E      +KA S D      I +K      +N + D SS
Sbjct: 179 --DNVCTFSEISLSRNHSENMLKAMKAPIRVSNDGLSLEINPLKKPLKAQNIIPNDPSS 236

Query: 257 ASYF-LAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
      A YF LA  +      + ++      + ++ ++L+ MGAK+ T T+      G R
Sbjct: 237 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQDNFETIGEIRV 294

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      + +  + N+  + D A LA+      A G +++ +      RVKE++R+  + L
Sbjct: 295 ESSKLNIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRVKESDRIAVMVENLKL 354

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
      G E D I      +L + I +Y DHR+AM+F++      C      + I D C + +
Sbjct: 355 CGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFALLGLLCG---IEIDSDCIKTS 411

Query: 432 FPDYFDVLSTF 442
      FP++ ++LS
Sbjct: 412 FPNFIEILSNL 422

```

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>ref|ZP_03223145.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Campylobacter jejuni
      subsp. jejuni CG8421]
gb|EDZ32403.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Campylobacter jejuni
      subsp. jejuni CG8421]
Length = 428

```

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 102/431 (23%), Positives = 185/431 (42%), Gaps = 34/431 (7%)

```

Query: 21  LPSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
      + KS+S+R  + + L++      N L ++D      L  ++ LG +E  +  + +
Sbjct: 17  IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDCSCVKIIP-- 74

Query: 81  CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
      P E      L GN+G AMR +  + AG + +VL G  + RP+  +
Sbjct: 75  -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
      L Q+GA +      + P+ + G L      K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLYIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRA----- 178

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
      D + +  + ++      E      +KA S D      I +K      +N + D SS
Sbjct: 179 --DNVCTFSEISLSRNHSENMLKAMKAPIRVSNDGLSLEINPLKKPLKAQNIIPNDPSS 236

Query: 257 ASYF-LAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
      A YF LA  +      + ++      + ++ ++L+ MGAK+ T T+      G R
Sbjct: 237 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQDNFETIGEIRV 294

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
      + +  + N+  + D A LA+      A G +++ +      RVKE++R+  + L
Sbjct: 295 ESSKLNIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRVKESDRIAVMVENLKL 354

Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
      G E D I      +L + I +Y DHR+AM+F++      C      + I D C + +
Sbjct: 355 CGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFALLGLLCG---IEIDSDCIKTS 411

Query: 432 FPDYFDVLSTF 442
      FP++ ++LS

```

Sbjct: 412 FPNFIEILSNL 422

>ref|YP_001000570.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 81-176]
gb|EAQ72379.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 81-176]
Length = 423

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 186/427 (43%), Gaps = 26/427 (6%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R ++ L++ N L ++D L ++ LG +E + + +
Sbjct: 12 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCSVKIIP-- 69

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 70 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRP MRRISKP 122

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 123 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRADNVCTFS 180

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
I +S + E L+ M + ++ + D I +K +N + D SSA YF
Sbjct: 181 EIS--LSRNHSENMLKAM-KAPIRVSNDDL--SLEINPLKKPLKAQNIIPNDPSSAFYF 235

Query: 261 -LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPREPFGFR 317
LA + + ++ + ++ ++L+ MGAK+ T T+ G R +
Sbjct: 236 VLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRVESSK 293

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + N+ + D A LA+ A G +++ + RVKE++R+ + L G
Sbjct: 294 LNGIEVKDNIAWLIDEAPALAIAPALAKGKSSLINAKELRVKESDRIAMVMENLKL CGVE 353

Query: 378 VEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDY 435
E D I +L + I +Y DHR+AM+F++ C + I D C + +FP++
Sbjct: 354 ARELDDGFEIEGGCELKSSKISYGDHRIAMSFAILGLLCG---IEIDSDCIKTSFPNF 410

Query: 436 FDVLSTF 442
++LS
Sbjct: 411 IEILSNL 417

>ref|NP_384359.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium
meliloti 1021]
ref|ZP_07586162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium
meliloti BL225C]
sp|Q92SV5.1|AROA_RHIME RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAC41690.1| Putative 3-phosphoshikimate 1-carboxyvinyltransferase
[Sinorhizobium meliloti 1021]
gb|EFN32857.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium
meliloti BL225C]
Length = 455

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 110/445 (24%), Positives = 200/445 (44%), Gaps = 38/445 (8%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ GT+++PG KS+S+R + L+ G T + LL EDV A++ +G + K
Sbjct: 17 DLKGTLRIPGDKSISHRSFMFGGLAAGETRITGLLEGEDVINTGKAMQAMGARIR--KEG 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMRERPI 133
++ G G + E L GNAG R V ++T++ D + +RP
Sbjct: 75 DTWIIDVGNGALL---APEAPLDFGNAGTGCRLTMGLVGVDYDFDSTFIGDA--SLTKRP 129

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A

Sbjct: 130 MGRVLDPLREMGVQVKS AEG-DRLPVTLRG----PKTPNPITYRVPMAS AQVKS AVLLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKA EHS DSWDRFYIKGGQKYKSPKNA 248
G +++ ++ + E +++++ FG + E R G+ + +

Sbjct: 185 LNTPGIT--TVVEPVMT RDHTE--KMLQGFGANLTVETDAEGVRTIRLEGRGKLTGQVI 239

Query: 249 YVEGDASSASY-FLAGAAITGGTVTVVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ +AG + G +T+ + + L+ MGA + +

Sbjct: 240 DVPGDPSSTAFPLVAGLIVPGSDITILNVLMNPTRTGLIL--TLQEMGANIEVMNKRL-A 296

Query: 308 TGPPREPFGGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
G +H LK + V ++ P D LAV A FA+G T + + RVKE++

Sbjct: 297 GGEDVADLRVRHSELKGVTVPEDRAPSMIDEYPVLAVAAFAEGTTVMNGLEELRVKESD 356

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPE-----KLNVT AIDTYDDHRMAMAFSLAACA 416
R+ A+ L G +EG ++ K++ + T+ DHR+AM+F + A

Sbjct: 357 RLSAVADGLKLVGDCDEGEASLVVRGRPGGKGLGKISGGQVKTHLDHRIAMSFLVMGLA 416

Query: 417 -EVPVTIRDPGCTRKTTFPDYFDVLS 440
E PVT+ D +FP++ +++

Sbjct: 417 SEHPVTVDATMIATSFPEFMGLMT 441

>sp|A1VZM9.2|AROA_CAMJJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 428

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 186/427 (43%), Gaps = 26/427 (6%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +

Sbjct: 17 IAADKSISHRFAIFSLTQEENKAQNYLLAQDTLNTLEI IKNLGAKIEQKDCVCKIIP-- 74

Query: 81 CGGKFVPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +

Sbjct: 75 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A

Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRADNVCTFS 185

Query: 201 IIDKLISIPYVEMTLRLMERFGVKA EHS DSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
I +S + E L+ M + ++ + D I +K +N + D SSA YF

Sbjct: 186 EIS--LSRNHSENM LKAM-KAPIRVSNDDL--SLEINPLKKPLKAQNIIPNDPSSAFYF 240

Query: 261 -LAGAAITGGTVTVVEGCGTTS LQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPREPFG 317
LA + + ++ + ++ ++L+ MGAK+ T T+ G R +

Sbjct: 241 VLAAILPKSQIILKNILLNPTR--IEAYKILQMGAKLEMTITQNDFETIGEIRVESSK 298

Query: 318 KHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + N+ + D A LA+ A G +++ + RVKE++R+ + L G

Sbjct: 299 LNGIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRVKESDRIAVMVENLKL CGVE 358

Query: 378 VEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTTFDY 435
E D I +L + I +Y DHR+AM+F++ C + I D C + +FP++

Sbjct: 359 ARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCG---IEIDSDCIKTSFPNF 415

Query: 436 FDLVSTF 442
++LS

Sbjct: 416 IEILSNL 422

>ref|ZP_03609839.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter rectus
RM3267]
gb|EEF14217.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter rectus
RM3267]
Length = 424

Score = 90.1 bits (222), Expect = 6e-16, Method: Compositional matrix adjust.

Identities = 119/420 (28%), Positives = 186/420 (44%), Gaps = 30/420 (7%)

```
Query: 25  KLSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
           KS+S+R  + + LS+  + V N L +ED    L  ++ LG  +E +K  + +      K
Sbjct: 21  KSISHRCAIFSLSDRPSRVKNYLKAEDTLNLTLEIVKNLGAHIE-EKEGELIITPSANLK 79

Query: 85  FPFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
           P      V L  GN+G AMR      + A+ G  +VL G  + RP+  + L  +
Sbjct: 80  EP-----SVVLECGNSGTAMRLFMGFLAASEG--FFVLSGDEFLNRRPMARVAKPLISV 131

Query: 145  GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEIID 203
           GA +D   G D  PP+   I G      K      I+S Q  SAL++A  + G   E+ +
Sbjct: 132  GAKIDGANGGDHAPL---AIRGKKLEYFKFDSKIASAQVKSALILAGLKSNG---CELSE 185

Query: 204  KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK--SPKNAYVEGDASSASYFL 261
           +S  + E  L+ M      H      +K G      P      V  D SSA +F
Sbjct: 186  PELSRDHTERMLKGMGAGLQILPHG-----VKVGPMSTPLKPLEICVPNDPSSAFFFA 238

Query: 262  AGAAITGGTIVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREFPGRKHLK 321
           AAI  + V      + + V+  ++L  MGA+VT+  ETS T      LK
Sbjct: 239  VAAAIIPNSHIVLKNMMLN-KTRVEAFKILSKMGAQVTFKETSGTYESIGEIEIKHTPLK 297

Query: 322  AIDV--NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
           A+DV  N++ + D   LA+   A G  ++R+   RVKE++R+  +   L K G  VE
Sbjct: 298  AVDVSENISWLIDEVPALAIAFANAQGTSSVRNAKELRVKESDRIAIMVQGLRKCGLEVE 357

Query: 380  EGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
           E D  +   E N   ID+  DHR+AM+F++  + + I      +FP++ +L
Sbjct: 358  EFEDGFSVKGGEA-NCAIIDSSGDHRIAMSFVAVLGL-KCGMVIEKSEFIATSFNPFSGIL 415
```

```
>ref|YP_002301651.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
P12]
sp|B6JMP3.1|AROHA_HELP2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACJ08171.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
P12]
Length = 429
```

Score = 90.1 bits (222), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 114/440 (25%), Positives = 186/440 (42%), Gaps = 47/440 (10%)

```
Query: 25  KLSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
           KSL+S+R  ++ + L++  VV N L  ED    L  + LG  VE   AK  + +
Sbjct: 11  KSLSHRAVIFSLAQKPCVVRNFLMGEDCLSLEIAQNLAGAVE--NTAKNSFKIT---- 64

Query: 85  FPFVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
           P      KE  ++   N+G +MR  + ++A G  +VL G  + RP+  ++ LK
Sbjct: 65  -PPTAIKEPSKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNSLSRPMKRIIEPLKA 121

Query: 144  LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
           A  +   LG  +      I G P      I+S Q  SA +++A  A G
Sbjct: 122  FEARI---LGREDNHFAPLVIVGSPLKACNYESPIASAQVKSALFALSALQAQG----- 171

Query: 203  DKLISIPYVEMTL-RLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSAS 258
           S   Y E  L R      +K+  +D  D+  +      + P  A+  + D SSA
Sbjct: 172  ----SSTYKENELSRNHTEIMLKSLGADIQDQNGVLMVSPLEKPLEAFDFTIANDPSSAF 227

Query: 259  YFLAGAAITGGTIVTVEGCGTTSLSQGDVKFA--EVLEMMGAKVTWTETSVTVTGPPREFPG 316
           +F      AIT  + +      L  +      E L+  MGA  + +   S  +
Sbjct: 228  FFALACAITPKSRLL---LKNVLLNPTRIGAFEALKKMGASIEYAIQSKNLEMIGDIYIE 284

Query: 317  RKHLKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
           LKAI++  N   + D   L++  LFA G  + +R+   R KE++R+  A+  +   L
Sbjct: 285  HAPLKAINIEQNIASLIDEIPALSIAMLFAKKGSMVRNAKDLRAKESDRIKAVVSNFKAL 344

Query: 375  GASVEEGPDYCI-----TPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPVTIRD 424
           G   EE  D  +      P K  +      I  +++DHR+AM+F++  A +P+ I  +
Sbjct: 345  GIECEEFEFGFYVEGLEDISPLKQRFSGKKPPLIKSFNDHRIAMSFVAVLTLA-LPLEIDN 403
```

Query: 425 PGCTRKTFPDYFDVLSTFVK 444
C +FP + +L+ F K
Sbjct: 404 LECANISFPQFKRLNLNLFKK 423

>gb|ADU84995.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
SouthAfrica7]
Length = 429

Score = 90.1 bits (222), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 113/437 (25%), Positives = 192/437 (43%), Gaps = 41/437 (9%)

Query: 25 KSLSNRILLLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLAKKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPPTLKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLVILGSPLKACNYESPISAAQVKSASFILSALQAQGISAYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF-L 261
+ +S + E+ L+ + A D I +K + + D SSA +F L
Sbjct: 177 ESELSRNHTEIMLK-----SLGANIKDQNGVLKISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 262 AGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VTVTGPPREPFGGRKH 319
A A + + ++ + ++ EVL+ MGA + + S + +TG
Sbjct: 232 ACAIVPKSRLLLKNVLLNPTR--IEAEVLKKMGAHIEYVIQSKDLEITGDIY--IEHAP 287

Query: 320 LKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
LKAI +N N + D L + LFA G + +++ R KE++R+ A+ + L L
Sbjct: 288 LKAIVINQNIASLIDEIPALGIAMLFAGQSMVKNAKDLRSKESDRIKALISNLKALEIE 347

Query: 378 VEEGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
EE D I E ++ I +++DHR+AM+F++ + +P+ I + C
Sbjct: 348 CEEFEDGFYIEGLEDISQLKQRFSSQKKPPIIKSFNDHRIAMSFALISLI-LPLEIDNLEC 406

Query: 428 TRKTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 407 ANISFPQFKHLLNLNLFKK 423

>ref|YP_301370.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Staphylococcus
saprophyticus subsp. saprophyticus ATCC 15305]
sp|Q49XS0.1|AROA_STAS1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
dbj|BAE18425.1| 5-enolpyruvylshikimate-3-phosphate synthase [Staphylococcus
saprophyticus subsp. saprophyticus ATCC 15305]
Length = 432

Score = 90.1 bits (222), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 100/415 (24%), Positives = 194/415 (46%), Gaps = 47/415 (11%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G +++PG KS+++R ++L +L+ G + + L ED + + LG+ +E ++ +
Sbjct: 15 GEIEVPGDKSMTHRAIMLGSLATGKSTIYKPLLGEDCLRTVEIFKLLGVQIEVNE--DKI 72

Query: 77 VVVGCGGKFPVEDAKEEVQ-LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ G K+ K Q L+ GN+G R L A + G T VL G + +RP+
Sbjct: 73 EIDSPGYKY---FKTPHQVLYTGNSGTTTR-LVAGLLCGLGIET-VLSGDESIGKRPMD 126

Query: 136 DLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
++ L+ + A++ D + P ++GI +++++ S+Q SA+L A+
Sbjct: 127 RIMKPLRYMNANITGINDNYTPLIIPASISGITY----EMEVA---SAQVKSAILFASL 179

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKNAYV 250
A +I+ D + T + E F + A ++D + + G ++ P + +V

Sbjct: 180 FANEPTKIKEFDTRN-----HTETMFEHFNIPVAVNNDIEMPSL--GIEHIKPADFHV 232

Query: 251 EGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET----- 303
GD SSA+YF+ IT G+ +T+ G + + V +M G + +T

Sbjct: 233 PGDISSAAYFIVAGLITPGSDITIHNVGINPTRSGI-IDIVTQMEGNITLNFQTDNPEPT 291

Query: 304 -SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALF---ADGPTAIRDVASWRVK 359
S+ V P ++K I ++ + +P + +VAL A+G + +++ +VK

Sbjct: 292 ASIRVQYSP-----NMKPIHIDGDLVPRAIDEIPIVALLCTQANGTSIVKEAEELKVK 344

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
ET R+ L LG +++ D II P ++++ DHR+ M ++A+

Sbjct: 345 ETNRIDTTANMLNLLGFTLQPTNDGLIIHPSAFEQTATVNSFTDHRIGMMLAIAS 399

>gb|ADN80165.1| 5-Enol pyruvyl shikimate-3-phosphate synthase [Helicobacter pylori
908]
Length = 429

Score = 90.1 bits (222), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 113/438 (25%), Positives = 193/438 (44%), Gaps = 43/438 (9%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
KSLS+R ++ + L++ V N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLLAQKPCFVRNFLMGEDCLSSLEIAQNLAGKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK

Sbjct: 65 -PPTAIKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKV 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +

Sbjct: 122 FGARI---LGREDNHFAPLAIVGSPLKACDYESPIASQVKSASFILSALQAQGISAYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSASY 259
+ +S + E+ L+ G ++ D + + P A+ + D SSA +

Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGVLKI-----SPLEKPLEAFDFTIANDPSSAFF 228

Query: 260 FLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRK 318
F AIT + + ++ + ++ EVL+ MGA + + S +

Sbjct: 229 FALACAITPKSRLLLNVLNPNTR--IEAFEVLKMGASIEYAIQSKDLEIIGDIYIEHA 286

Query: 319 HLKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
LKAI +N N + D L++ LFA G + +R+ R KE++R+ A+ + LG

Sbjct: 287 PLKAIINQNTASLIDEIPALSIAMFLAKGKSMVRNAKDLRAKESDRIKAVVSNFKALGI 346

Query: 377 SVEEGPD-YCI-----ITPPE----KLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
EE D + I I+P + K+ I +++DHR+AM+F++ +P+ I +

Sbjct: 347 ECEEFEFGFYIEGLGDISPLKQHSKIKPPIIKSFNDHRIAMSFAVLTLI-LPLEIDNLE 405

Query: 427 CTRKTFPDYFDVLSTFVK 444
C +FP + L+ F K

Sbjct: 406 CANISFPTFQLWLNLFKK 423

>gb|ACX98152.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
51]
Length = 429

Score = 89.7 bits (221), Expect = 7e-16, Method: Compositional matrix adjust.
Identities = 110/435 (25%), Positives = 189/435 (43%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGCGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLAGKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK

Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMRRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202

GA + LG + I G P + I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGRDENHFAPLVILGSPLKACEYESPIASQVKSALQAGSSTYK-- 176
Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F
Sbjct: 177 ESELSRNHTEIMLK---SLGADIQNQDGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231
Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK
Sbjct: 232 SCAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYVIQSKDLEMIGDIYIEHAPLK 289
Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI + N + D L++ LFA G + +++ R KE++R+ A+ + LG E
Sbjct: 290 AISIEQNIASLIDEIPALSIAMLFAKGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349
Query: 380 EGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPTIRDGPCTR 429
E D I E + I +++DHR+AM+F++ A +P+ I + C
Sbjct: 350 EFEDGFIIEGLEEDITQLKQRFSSQKKPLIKSFNDHRIAMSFALITLA-LPLEIDNLECAN 408
Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K
Sbjct: 409 ISFPQFKRLNLNLFKK 423

>gb|ADG03677.1| 5-enolpyruvylshikimate 3-phosphate synthase [Ochrobactrum anthropi]
Length = 450

Score = 89.7 bits (221), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 113/453 (24%), Positives = 191/453 (42%), Gaps = 61/453 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + D A
Sbjct: 18 LTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGAKIRKGDGAW 77
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG G + E L GNAG R V +++ D + +RP+
Sbjct: 78 IINGVNGCLL-----QPEAALDFGNAGTGARLTMGLVGTYDMRTSFIGDA--SLSKRPM 130
Query: 135 GDLVVGLKQLGADVDCFLGTDGP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
G ++ L+++G V+ G P P N I +V ++ S+Q SA+L+A
Sbjct: 131 GRVLNPLREMGVQVEAAEGDRMPLTLIGPKTANPI----TYRVPMA---SAQVKSAYLLA 183
Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247
G +I+ +++ + E L GNAG + E R GQ +
Sbjct: 184 GLNTPG--VTTVIEPVMTRDHTE---KMLQGFGADLSVETDKDGVHRITGQGGKLGQT 238
Query: 248 AYVEGDASSASYFLAGAAI-----TGGETVTVEGCGTTSLQGDVKFAEV 290
V GD SS ++ L A + TG +T++ G + + A
Sbjct: 239 IDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLILTLQEMGADIEVLNARLAGG 298
Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAI 350
++ +V ++ V P R P M D LA+ A FA+G T +
Sbjct: 299 EDVADLRVKASKLKGVVPPERAP-----SMIDEYPVLAIAASFAEGETVM 344
Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK-LNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L G EG + P K L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVATHLDHRIA 404
Query: 408 MAFSLAACAEVPTTIRDPGCTRKTTFPDYFDVL 439
M+F + A E PVT+ D +FP++ D++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMDMM 437

>sp|A8FLU4.2|AROJA_CAMJ8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAA61554.1| 5-enolpyruvylshikimate-3-phosphate synthetase [Campylobacter
jejuni]
gb|ADN91065.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni M1]
gb|EFV11554.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni

subsp. jejuni 327]
Length = 428

Score = 89.7 bits (221), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 184/427 (43%), Gaps = 26/427 (6%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R ++ L++ N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCVCKIIP-- 74

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNNRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSAFRANNVCAFS 185

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
I +S + E L+ M+ S+ I +K +N + D SSA YF
Sbjct: 186 EIS--LSRNHSENMLKAMK---APIRVNSDGLSLEISPLKKPLKAQNIIPNDPSSAFYF 240

Query: 261 -LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPREPFGFR 317
LA + + ++ + ++ ++L+ MGAK+ T T+ G R +
Sbjct: 241 ALAAIILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRVESSK 298

Query: 318 KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + N+ + D A LA+ A G +++ + RVKE++R+ + L G
Sbjct: 299 LNGIEVKDNIAWLIDEAPALAIAFALAKGKSSLINAKELRVKESDRIAVMVENLKLGCVE 358

Query: 378 VEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDY 435
E D I +L + I +Y DHR+AM+F++ C + I D C + +FP++
Sbjct: 359 ARELDDGFEIEGGCELKSSKISYGDHRIAMSFAILGLLCG---IEIDSDCIKTSFPNF 415

Query: 436 FDVLSTF 442
++LS
Sbjct: 416 IEILSNL 422

>ref|XP_002163382.1| PREDICTED: hypothetical protein [Hydra magnipapillata]
Length = 874

Score = 89.7 bits (221), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 45/76 (59%), Positives = 52/76 (68%), Gaps = 5/76 (6%)

Query: 369 TELTKLGASVEEGPDYCIITPPEKL---NVTADTYDDHRMAMAFSLAAC--AEVPVTIR 423
TEL KLGA+V EG DY +TPP + +I TYDDHR+AM FSLAA A+VPV I
Sbjct: 3 TELRKLGA+VVEGQDYIQVTPPAGIADWKAASIHTYDDHRVAMCFSLAAFNPAQVPVRIE 62

Query: 424 DPGCTRKTFPDYFDVL 439
DP C KTFPDYF+ L
Sbjct: 63 DPKCVAKTFPDYFEAL 78

>ref|YP_001482408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 81116]
gb|ABV52431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 81116]
Length = 423

Score = 89.7 bits (221), Expect = 8e-16, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 184/427 (43%), Gaps = 26/427 (6%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R ++ L++ N L ++D L ++ LG +E + + +
Sbjct: 12 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCVCKIIP-- 69

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 70 -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNNRPMRRISKP 122

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 123 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSAFRANNVCAFS 180

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
I +S + E L+ M+ S+ I +K +N + D SSA YF
Sbjct: 181 EIS--LSRNHSENMLKAMK---APIRVSNDGLSLEISPLKPLKAQNIIPNDPSSAFYF 235

Query: 261 -LAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPREPFGFR 317
LA + + ++ + ++ ++L+ MGAK+ T T+ G R +
Sbjct: 236 ALAAIILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRVESSK 293

Query: 318 KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + N+ + D A LA+ A G +++ + RVKE++R+ + L G
Sbjct: 294 LNGIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRVKESDRIAVMVENLKL CGVE 353

Query: 378 VEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFFDY 435
E D I +L + I +Y DHR+AM+F++ C + I D C + +FP++
Sbjct: 354 ARELDDGFEIEGGCELKSSKIKSYGDHRIAMSF AILGLLCG---IEIDSDCIKTSFPNF 410

Query: 436 FDVLSTF 442
++LS
Sbjct: 411 IEILSNL 417

>ref|YP_001639594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
extorquens PA1]
gb|ABY30523.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
extorquens PA1]
Length = 472

Score = 89.7 bits (221), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 127/455 (27%), Positives = 199/455 (43%), Gaps = 50/455 (10%)

Query: 5 EEIVLQPIKEISGTVKVLPGSKSLSNRIILL AALSEGTTVDNLLNSEDVHYMLGALRTL 64
+ + P ++G++K PG KS+S+R ++L L+ G T V+ LL +DV A + LG
Sbjct: 27 QPVTAYPGGPLNGSLKPPGDKSISHRAMILGLLAIGETRVEGLLEGDDVLR TAAAKALG 86

Query: 65 LSVEADKAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ + + R V G GG ++D + L GNAG R + V G T
Sbjct: 87 AQITREGEGRWRIVGAGIGG---MQDP--DGVLD FGNAGTGSRLMMGVV--GGQPVTATF 139

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SS 180
DG +R+RP+ ++ + ++GA++ P+ + G P + + + S+
Sbjct: 140 DGDASLRKRPMRRLDPILKMGAIEVSEAEGGRVPLTLRG----PREAIPRYELPVASA 195

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD----RFYI 236
Q SA+L+A A G +I+K S + E LRL FG + + S + R
Sbjct: 196 QIKSAVLLAGLNAPGTT--TVIEKAASRDHTERMLRL--FGAEVTVTPSGEGGHGRTVT 250

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
GQ + V D SSA++ L A + G+ V + G L+ L MG
Sbjct: 251 LTGQPTLRGTDVVVPADPSSAAFPLVAALVVPGEVILRGVMMNPLR--TGLITTLIEMG 308

Query: 296 AKVTWTETSVTVTGPPREPFGFR-----KHLKAIDVNMNMKMP---DVAMTLAVVALF 343
A + + RE G LK +DV + P D LAV A F
Sbjct: 309 ADIERLDE-----REEGGETVADLRVRASRLKGVDPVPAERAPSMIDEYPILAVAASF 360

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT A--IDTY 401
A+G T + + RVKE++R+ A+ L G + D I+T + + TY
Sbjct: 361 AEGTTRMNGLHEL RVKESDR LAAVAAGLAANGVTHAIEGDDLIVTGNGQAPAGGGTVATY 420

Query: 402 DDHRMAMAF-SLAACAEVPVTIRDPGCTRKTFFDY 435
DHR+AMAF L A+ PVT+ D +FP +
Sbjct: 421 LDHRIAMAFVLGLA AKSPVTVDDGAMIATSFPSF 455

>ref|ZP_01068463.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni CF93-6]
ref|ZP_01071533.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni HB93-13]

ref|ZP_01100716.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 84-25]
ref|YP_002344294.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]
sp|P0C630.1|ARO_A_CAMJE RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|EAQ56614.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni CF93-6]
gb|EAQ60266.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni HB93-13]
gb|EAQ94049.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 84-25]
emb|CAL35016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]
gb|EFV06887.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni DFVF1099]
Length = 428

Score = 89.7 bits (221), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 102/431 (23%), Positives = 185/431 (42%), Gaps = 34/431 (7%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCSCVKIIP-- 74

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRA----- 178

Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
D + + + ++ E +KA S D I +K +N + D SS
Sbjct: 179 --DNVCTFSEISLSRNHSENMLKAMKAPIRVSNDGLSLEINPLKKPLKAQNIIPNDPSS 236

Query: 257 ASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTGTGPPRE 313
A YF LA + + ++ + ++ ++L+ MGA+ T T+ G R
Sbjct: 237 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFFETIGEIRV 294

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ + + N+ + D A LA+ A G +++ + RVKE++R+ + L
Sbjct: 295 ESSKLNIEVKDNIWLIDEAPALAIAFALAKGKSSLINAKELRVKESDRIAVMVENLKL 354

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
G E D I +L + I +Y DHR+AM+F++ C + I D C + +
Sbjct: 355 CGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCG---IEIDSDCIKTS 411

Query: 432 FPDYFDVLSTF 442
FP++ ++LS
Sbjct: 412 FPNFIEILSNL 422

>gb|EFV09124.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 305]
Length = 423

Score = 89.7 bits (221), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 101/431 (23%), Positives = 185/431 (42%), Gaps = 34/431 (7%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 12 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCSCVKIIP-- 69

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 70 -----PKEILSPNCILDGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 122

Query: 141 LKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200

L Q+GA + + P+ + G L K S S+Q +A++++A A
 Sbjct: 123 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRA----- 173
 Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
 D + + + ++ E +KA S D I +K +N + D SS
 Sbjct: 174 --DNVCTFSEISLSRNHSENMLKAMKAPIRVSNDGLSLEINPLKKPLKAQNIIPNDPSS 231
 Query: 257 ASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
 A YF LA + + ++ + ++ ++L+ MGAK+ T T+ G R
 Sbjct: 232 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFETIGEIRV 289
 Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
 + + + N+ + D A LA+ A G +++ + R+KE++R+ + L
 Sbjct: 290 ESSKLNIGIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRIKESDRIAVMVENLKL 349
 Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
 G E D I +L + I +Y DHR+AM+F++ C + I D C + +
 Sbjct: 350 CGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFALLGLLCG---IEIDSDCIKTS 406
 Query: 432 FPDYFDVLSTF 442
 FP++ ++LS
 Sbjct: 407 FPNFIEILSNL 417

>ref|YP_001191935.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Metallosphaera sedula
 DSM 5348]
 gb|ABP96011.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Metallosphaera sedula
 DSM 5348]
 Length = 391

Score = 89.4 bits (220), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 115/432 (26%), Positives = 180/432 (41%), Gaps = 60/432 (13%)

Query: 14 EISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
 I G VK P SKSL R + L+ L+E ++NL S+DV + A+++L
 Sbjct: 9 RIKGRVKAPPSKSLGIRYVFLSLLTE--VSLENLPESDDVRVAINAVKSL----- 56
 Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPMRERP 133
 ++ K+E L+LG + +R + + A G LDG +R RP
 Sbjct: 57 -----KEGKDE--LYLGGSATTLRMIIPVILAMGRRVK--LDGDDTLRRRP 98
 Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
 + L+ L ++ P+ V G G + ++ G SSQY+S L+ A L
 Sbjct: 99 LN---ALRWLPKGK---FSSNSLPMTVEG---SLGPETQIEGWESSQYISGLIYAYCLR 147
 Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
 G+ I +I + S Y+ MT ++ G K + +K+ V GD
 Sbjct: 148 -GEGRIRVIPPISRGYIFMTADVISSIGGKVTIQGEEITVECRNLKRF----GGSVPGD 202
 Query: 254 ASSASYFLAGAAITGGTVTVEGC-GTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--TGP 310
 + AS++ GA +TGG V + S GD +++ GA+ +E V TG
 Sbjct: 203 YALASFYAVGAVLTGGEVEITNLYAPPSYVGHDVVRMVKEAGAESYVSENWIVRDTGV 262
 Query: 311 PREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
 R P I V++N +PD+A +LA + G + I D R+KE++R+ I
 Sbjct: 263 -RVP-----ISVSINDVPLAPSLAALMAVIPGESRIMDSERLRIKESDRISTILNT 313
 Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRK 430
 L G S + E ++ DHR+AM A V I C K
 Sbjct: 314 LASFGISGSYSAGTITVKGGEPRR-GEVECPKDHRIAMMAGDLAL-RVGGKITSACVKNK 371
 Query: 431 TFPDYFDVLSTF 442
 + P Y+ LS
 Sbjct: 372 SNPGYWSDSLAL 383

>ref|YP_002421176.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
 chloromethanicum CM4]
 sp|B7KZL6.1|AROAMETC4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
 AltName: Full=5-enolpyruvylshikimate-3-phosphate
 synthase; Short=EPSP synthase; Short=EPSPS

gb|ACK83248.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
chloromethanicum CM4]
Length = 453

Score = 89.4 bits (220), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 126/455 (27%), Positives = 200/455 (43%), Gaps = 50/455 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEVDHYMLGALRTL 64
+ + P ++G++K PG KS+S+R ++L L+ G T V+ LL +DV A + LG
Sbjct: 8 QPVTATPGGPLNGSLKPPGDKSISHRAMILGLLAIGETQVEGLLEGDDVLRATAAAKALG 67

Query: 65 LSVEADKAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ + + R V VG GG ++D + L GNAG R + V G T
Sbjct: 68 AQITREGEGRWRIVGVGIGG---MQDP--DGVLDGFGNAGTGSRLMMGVV--GGQPVTATF 120

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SS 180
DG +R+RP+ ++ + ++GA++ P+ + G P + + + S+
Sbjct: 121 DGDASLRKRPMRRILDPIKMGAEIVSEAEGRVPLTLRG----PREAIPRIYELPVASA 176

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSDW----RFYI 236
Q SA+L+A A G +I+K S + E R++ FG + + S + R
Sbjct: 177 QIKSAVLLAGLNAPGTT--TVIEKAASRDHTE---RMLHLFGAETVTPSGEGGHGRTVT 231

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMG 295
GQ + V D SSA++ L A I G+ V + G L+ L MG
Sbjct: 232 LTGQPTLRGTDVVVPADPSSAAFPLVAALIVPGSEVILRGVMMNPLR--TGLITTLIEMG 289

Query: 296 AKVTWTETSVTVTGPPREPFGF-----KHLKAIDVNMNMKMP---DVAMTLAVVALF 343
A + + RE G LK +DV + P D LAV A F
Sbjct: 290 ADIERLDE-----REEGETVADLRVRASRLKGVDPAPERAPSMIDEYPILAVAASF 341

Query: 344 ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTY 401
A+G T + + RVKE++R+ A+ L G + D I+T + + T+
Sbjct: 342 AEGTTRMNGLHELVRKESDRLAAVAAGLAANGVTHAIEGDDLIVTGNGQAPAGGGTVATH 401

Query: 402 DDHRMAMAF-SLAACAEVPVTIRDPGCTRKTFFDY 435
DHR+AMAF L A+ PVT+ D +FP +
Sbjct: 402 LDHRIAMAFVLGLAALKSPVTVDDGAMIATSFPSF 436

>ref|ZP_07399237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
duerdenii ATCC BAA-1640]
gb|EFM25794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
duerdenii ATCC BAA-1640]
Length = 171

Score = 89.4 bits (220), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 49/165 (29%), Positives = 93/165 (56%), Gaps = 11/165 (6%)

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVA 334
G S QGD K ++L+ GA +T ++ ++ G HL + +V+ ++ PD+
Sbjct: 3 GLNLESSQGDKKVVQILKKAGAILTCSDDCISSNGS-----HLNSFEVDFSETPDFL 54

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
L+VVA + G + ++ ++KE+ R+ + L LGA V++ D II E L+
Sbjct: 55 PILSVVAALSKGQSVLKGGERLKLKESNRIESTFQMLKSLGADVKKRDDGLIIQGREILD 114

Query: 395 VTAIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFFDYFD 437
+++++DHR+ M+ ++A+ C E PV+I + G +K++P++FD
Sbjct: 115 GGIVNSFNDHRIVMSATMASIKCKE-PVSIVNAGAVKKSYPNFFD 158

>gb|ADU80242.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
India7]
Length = 429

Score = 89.4 bits (220), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 109/435 (25%), Positives = 187/435 (42%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLALLAALSEGTTVDNLLNSEVDHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK

Sbjct: 65 -PPTTLKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G +

Sbjct: 122 FGAKI---LGREDNHFAPLAILGSPLKACNYESPIASQVKSASFILSALQAQGSSTYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ D I +K + + D SSA +F

Sbjct: 177 ENELSRNHTEIMLK---SLGADIQNQDGV--LMISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
IT + + ++ + ++ E L+ MGA + + S + LK

Sbjct: 232 ACVITPKSRLLLKLVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI + N + D L++ LFA G + +++ R KE++R+ A+ + L LG

Sbjct: 290 AISIEQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAVISNLKALGIECG 349

Query: 380 EGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E D I E + I +++DHR+AM+F++ A +P+ I + C

Sbjct: 350 EFEDGFYIEGLEEDITQLKQRFSSQKKPLIQSFNDHRIAMSFAILTLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K

Sbjct: 409 ISFPQFKRLLNLFKK 423

>gb|AD004216.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
Cuz20]
Length = 429

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 109/435 (25%), Positives = 190/435 (43%), Gaps = 37/435 (8%)

Query: 25 KSLSNRILLLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +

Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFLMGEDCLSSLEIAQNLGAKVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK

Sbjct: 65 -PPTALKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P + I+S Q SA +++A A G +

Sbjct: 122 FGAKI---LGREDNHFAPLVILGSPLKACEYESPIASQVKSASFILSALQAQGSAYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
+ +S + E+ L+ G ++ + I +K + + D SSA +F

Sbjct: 177 ENELSRNHTEIMLK---SLGANIQNQGV--LTISPLEKPLEAFDFTIANDPSSAFFFAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLK 321
AIT + + ++ + ++ E L+ MGA + + S + LK

Sbjct: 232 SCAITPKSRLLLKLVLLNPTR--IEAFEALKKMGASIEYAIQSKDLEMIGDIYIEHAPLK 289

Query: 322 AIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
AI + N + D L++ LFA G + +++ R KE++R+ A+ + LG E

Sbjct: 290 AISIEQNIASLIDEIPALSIAMLFAGKSMVKNKDLRSKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPDYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E D I E ++ I +++DHR+AM+F++ A +P+ I + C

Sbjct: 350 EFEDGFYIEGLEDISQLKQRFSSQKKPLIQSFNDHRIAMSFAILTLA-LPLEIDNLECAN 408

Query: 430 KTFPDYFDVLSTFVK 444
+FP + +L+ F K

Sbjct: 409 ISFPQFKRLLNLFKK 423

>ref|ZP_07476226.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. B01]
gb|EFM58016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. B01]
Length = 450

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 114/454 (25%), Positives = 196/454 (43%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNGC-----LLQPEAPLDFGNAGTGARLTMGVLGTYDMKTSFIGNDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----TYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTDRDTE---KMLQGFADLTVETDKDGVHRIRIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TQQTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L GA EG + + L ++T+ DHR+A
Sbjct: 345 DGLDELRVKESDRLLAAVARGLEANGADCTEGEMSLTVRGRPGGKGLGGGTVEHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 438

>ref|YP_003057713.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
B38]
emb|CAX29537.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) [Helicobacter pylori B38]
Length = 429

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 112/439 (25%), Positives = 192/439 (43%), Gaps = 45/439 (10%)

Query: 25 KSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KSLS+R ++ + L++ VV N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAQKPCVVRNFMGDCSSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTAKEPNKILNCNNSGTSMLRYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
GA + LG + I G P I+S Q SA +++A A G
Sbjct: 122 FGAKI---LGREDNHFAPLVILGNPLKACHYESPIASQVKSASFILSALQAQG----- 171

Query: 203 DKLISIPYVEMTL-RLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY---VEGDASSAS 258
+S+ Y E L R +K+ +D ++ + + P A+ + D SSA
Sbjct: 172 ---VSV-YKESELSRNHTEIMLKS LGADIQNQDGVLKISPLEKPLEAFDFTIANDPSSAF 227

Query: 259 YFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETS--VTVTGPPPREPF 315
+F AIT + + ++ + ++ E L+ MGA + + S + + G
Sbjct: 228 FFALACAITPKSHLLKNVLLNPTR--IEAFEALKKMGAHIEYVIQSKDLEIIGDIYIEH 285

Query: 316 GRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375

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+ID N+ + D L++ LFA G + +++ R KE++R+ A+ + LG
Sbjct: 286 APLKAISIDQNIASLIDEIPALSIAMLFAGKSMVKNADLRSKESDRIKAVVSNFKALG 345

Query: 376 ASVEEGPDYCI-----TPPEKLNVT-----IDYDDHRMAMAFSLAACAEVPTIRDP 425
      EE D I P K + I +++DHR+AM+F++ A +P+ I +
Sbjct: 346 IECEEFEDGFYIEGLEDISPLKQRFQSKKPPLIKSFNDHRIAMSAFVLTALA-LPLEIDNL 404

Query: 426 GCTRKTFPDYFDVLSTFVK 444
      C +FP + +L+ F K
Sbjct: 405 ECANISFPQFKRLNLNLFKK 423

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>ref|NP_223697.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
J99]
sp|Q9ZKF7.1|AROA_HELPJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAD06557.1| 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYL TRANSFERASE [Helicobacter pylori
J99]
Length = 429

```

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 111/441 (25%), Positives = 189/441 (42%), Gaps = 49/441 (11%)

```

Query: 25 KSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
      KSLS+R ++ + L++ V N L ED L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLAQKPCFVRNFMGDCLSLEIAQNLGAKVE--NTAKNSFKIT---- 64

Query: 85 FVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
      P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPTTIKEPNKILNCNNSGTSMRLYSGLLSAQKG--LFVLSGDNLSLNARPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
      GA + LG + I G P I+S Q SA +++A A G +
Sbjct: 122 FGAKI---LGREDNHFAPLAIVGGPLKACDYESPIASQVKSASFILSALQAQGISAYK-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLA 262
      + +S + E+ L+ G ++ D + I +K + + D SSA +
Sbjct: 177 ESELSRNHTEIMLK---SLGANIQNQDGVLK--ISPLEKPLESFDFTIANDPSSAFFLAL 231

Query: 263 GAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VTVTGPPREPFGGRKH 319
      AIT + + ++ + ++ EVL+ MGA + + S + V G
Sbjct: 232 ACAITPKSRLLLKNVLLNPTR--IEAFEVLKKMGAHIEYVIQSKDLEVIGDIYIEHAPLK 289

Query: 320 LKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVE 379
      +ID N+ + D L++ LFA G + +R+ R KE++R+ A+ + LG E
Sbjct: 290 AISIDQNIASLIDEIPALSIAMLFAGKSMVRNAKDLRAKESDRIKAVVSNFKALGIECE 349

Query: 380 EGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
      E D + I PP I +++DHR+AM+F++ A +P+ I
Sbjct: 350 EFEDGFYIEGLGDASQLKQHFSKIKPP-----IIKSFNDHRIAMSAFVLTALA-LPLEID 402

Query: 424 DPGCTRKTFPDYFDVLSTFVK 444
      + C +FP + L+ F K
Sbjct: 403 NLECANISFPTFQLWLNLFKK 423

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>ref|ZP_03305162.1| hypothetical protein ANHYDRO_01599 [Anaerococcus hydrogenalis DSM
7454]
gb|EEB35416.1| hypothetical protein ANHYDRO_01599 [Anaerococcus hydrogenalis DSM
7454]
Length = 241

```

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 65/254 (25%), Positives = 128/254 (50%), Gaps = 32/254 (12%)

```

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGV---KAHSDSWDRFYIKGGQKYK 243
      ++AA G I++ +K SI Y+++T +++ F V K +HS YI + K
Sbjct: 1 MLAASKLKGTKYIKLSEKPESIGYIDITRKVLKDFNVVKKDKHS-----YIENPELK 54

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303

```

Sbjct: 55 SPKN VEGD S+A++F GA + G + + SLQ D + E+ + +
SPKNYIVEGDWSNAAFY-GANLLGSKIKISNLDKNSLQKDREIVEICQKIKK----- 106

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
++ K + +++++PD+ +A++ D + I + R+KE++R

Sbjct: 107 -----CKEENKELKIDISQIPDLCPVAILLTSLDKTSYIINGERLRLKESDR 154

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTI 422
+ + L LGA+ + D I+ K++ +D+++DHR+ MA S+ + A+ + I

Sbjct: 155 LESTSKMLNDLGANCQILGDGLKISG--KISGGVVDSEFNDHRIVMAASIGSLLAKEDIII 212

Query: 423 RDPGCTRKTFPDYF 436
++ K++P +F

Sbjct: 213 KNYKAVNKSYPSFF 226

>ref|ZP_06499379.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. syringae FF5]
Length = 145

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 57/138 (41%), Positives = 79/138 (57%), Gaps = 8/138 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L+ GT+ + L S+D M ALR +G V+ D+

Sbjct: 14 RPLVGRVSPPGSKSITNRALLAGLARGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R

Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDC 150
PIG LV L+++G +V

Sbjct: 126 PIGPLVDALQRMGVEVSA 143

>ref|ZP_05635999.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas syringae
pv. tabaci ATCC 11528]
Length = 146

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 57/138 (41%), Positives = 80/138 (57%), Gaps = 8/138 (5%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V PGSKS++NR LLLA L++GT+ + L S+D M ALR +G V+ D+

Sbjct: 14 RPLVGRVSPPGSKSITNRALLAGLAKGTSRLTGALKSDDTRVMSEALRLMG--VQVDEP 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV G + + LFLGNAG A R LTAA+ G+ +V+DG MR+R

Sbjct: 72 DDSTFVVTSSGHW---QAPQQALFLGNAGTATRFLTAALANFEGD--FVVDGDEYMRKR 125

Query: 133 PIGDLVVGLKQLGADVDC 150
PIG LV L+++G +V

Sbjct: 126 PIGPLVDALQRMGVEVSA 143

>ref|YP_003068413.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Methylobacterium
extorquens DM4]
emb|CAX24555.1| 3-enolpyruvylshikimate-5-phosphate synthetase [Methylobacterium
extorquens DM4]
Length = 436

Score = 89.0 bits (219), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 126/445 (28%), Positives = 196/445 (44%), Gaps = 50/445 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G++K PG KS+S+R ++L L+ G T V+ LL +DV A + LG + + +

Sbjct: 1 MNGSLKPPGDKSISHRAMILGLLAIGETRVEGLLEGDDVLRATAAAKALGAQITREGGR 60

Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
R V VG GG ++D + L GNAG R + V G T DG +R+RP

Sbjct: 61 WRIVGVGIGG---MQDP--DGVLDGFGNAGTGSRLMMGVV--GGQPVATATFDGDASLRKRP 113

Query: 134 IGD LVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+ ++ + ++GA++ P+ + G P + + + S+Q SA+L+A

Sbjct: 114 MRRILDPILKMGAIEVSEAEGRVPLTLRG----PREAIPRIYELPVASAQIKSAVLLAG 169

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKSPK 246
A G +I+K S + E LRL FG + + S + R GQ

Sbjct: 170 LNA PGTT--TVIEKAASRDHTERMLRL--FGAEVSVTPSGEGGHGRTVTTLTGQPTLRGT 224

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V D SSA++ L A + G+ V + G L+ L MGA + +

Sbjct: 225 DVVVPADPSSA APLVAALVPGSEVILRGVMNPLR--TGLITTLIEMGADIERLDE-- 280

Query: 306 TVTGPPPREPFGR-----KHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDV 353
RE G LK +DV + P D LAV A FA+G T + +

Sbjct: 281 -----REEGETVADLRVRASRLKGVDVPAERAPSMIDEYPILAVAASFAEGTTRMNGL 334

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT--IDTYDDHRMAMAF- 410
RVKE++R+ A+ L G + D I+T + + T+ DHR+AMAF

Sbjct: 335 HELRVKESDRLAAVAAGLAANGVTHAIEGDDLIVTGDGQAPAGGGTVATHLDHRIAMAFL 394

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDY 435
L A PVT+ D +FP +

Sbjct: 395 VLGLAARSPVTVDGAMIATSFPSF 419

>ref|ZP_04679202.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ochrobactrum
intermedium LMG 3301]
gb|EEQ94708.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Ochrobactrum
intermedium LMG 3301]
Length = 450

Score = 89.0 bits (219), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 113/455 (24%), Positives = 191/455 (41%), Gaps = 65/455 (14%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D

Sbjct: 18 LTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGAKIRKEGDVW 77

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V GC + E L GNAG R V +++ D + +R

Sbjct: 78 IINGVGNCG-----LLQPEAALDFGNAGTGARLTMGLVGTYDMKTSFIGDA--SLSKR 128

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
P+G ++ L+++G V+ G P P N I +V ++ S+Q SA+L

Sbjct: 129 PMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPI----TYRVPM---SAQVKSAVL 181

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A G +I+ +++ + E +++ FG + E R GQ

Sbjct: 182 LAGLNTPG--VTTVIEPVMTRDHTE---KMLQGFGADLTVETDKDGVHRITGQGKLVG 236

Query: 246 KNAYVEGDASSASYFLAGAAI-----TGGT VTVEGCGTTSLQGDVKFA 288
+ V GD SS ++ L A + TG +T++ G + + A

Sbjct: 237 QTIDVPGDPSSAFPLVAALLVEGSDVTIRNVLMNPTRTGLILTLQEMGADIEVLNARLA 296

Query: 289 EVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPT 348
++ +V ++ V P R P M D LA+ A FA+G T

Sbjct: 297 GGEDVADLRVRASKLKGVVVPPERAP-----SMIDEYPVLAIAASFAEGET 342

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK-LNVT AIDTYDDHR 405
+ + RVKE++R+ A+ L G EG + P K L + T+ DHR

Sbjct: 343 VMDGLDEL RVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVATHLDHR 402

Query: 406 MAMAF-SLAACAEVPVTIRDPGCTRKTFPDYFDVL 439
+AM+F + AE PVT+ D +FP++ D++

Sbjct: 403 IAMSFLVMGLAAEKPVTVDDSNMIATSFPEFMDMM 437

>sp|P0A2Y4.1|AROA_PSES2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate

synthase; Short=EPSP synthase; Short=EPSPS
sp|P0A2Y5.1|ARO_ACHSL RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
Length = 449

Score = 88.6 bits (218), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 113/455 (24%), Positives = 191/455 (41%), Gaps = 65/455 (14%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 18 LTGEIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGAKIRKEGDVW 77

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V GC + E L GNAG R V +++ D + +R
Sbjct: 78 IINGVGNGC-----LLQPEAALDFGNAGTGARLTMLGLVGTDMKTSFIGDA--SLSKR 128

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
P+G ++ L+++G V+ G P P N I +V ++ S+Q SA+L
Sbjct: 129 PMGRVLNPLREMGVQVEAADGDRMPLTLIGPKTANPI----TYRVPMA---SAQVKSAVL 181

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 182 LAGLNTPG--VTVIEPVMTRDHTTE---KMLQGFGADLTVDKDGVRHIRTGQGLVG 236

Query: 246 KNAYVEGDASSASYFLAGAAI-----TGGTVTVEGCGTTSLQGDVKFA 288
+ V GD SS ++ L A + TG +T++ G + + A
Sbjct: 237 QTIDVPGDPSSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLILTLQEMGADIEVLNARLA 296

Query: 289 EVLEMMGAKVWTETSTVTGTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVALFADGPT 348
++ +V ++ V P R P M D LA+ A FA+G T
Sbjct: 297 GGEDVADLRVRASKLKGVVVPPERAP-----SMIDEYPVLAIAASFAGET 342

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK-LNVTADITYDDHR 405
+ + RVKE++R+ A+ L G EG + P K L + T+ DHR
Sbjct: 343 VMDGLDELVRKESDRLA AVARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVATHLDHR 402

Query: 406 MAMAF-SLAACAEVPTVIRDPGCTRKTFPDYFDVL 439
+AM+F + AE PVT+ D +FP++ D++
Sbjct: 403 IAMSFLVMGLAAEKPTVDDSNMIATSFPEFMDMM 437

>ref|YP_425387.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodospirillum rubrum
ATCC 11170]
sp|Q2RXP5.1|ARO_A_RHORT RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABC21100.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Rhodospirillum rubrum
ATCC 11170]
Length = 451

Score = 88.6 bits (218), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 126/447 (28%), Positives = 194/447 (43%), Gaps = 43/447 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EADKAAK 74
+SG +++PG KS+S+R L+L L+ G T + LL EDV A+ +G ++ + A
Sbjct: 18 LSGRIRVPDKSISHRALMLGGLAVGRTEIRGLLEGEDVIATAHAMEAMGARIDRQETAD 77

Query: 75 RAVV-----VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
A V VG GG D L +GNAG R L + A + T +L G +
Sbjct: 78 GAGVWTVVDGKGLAEPADV-----LDMGNAGTGARLLMGLL--ATHDLTAILTGDAASL 130

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCP--PVRVNGIGG-LP-GGKVKLSGSISSQYLSA 185
R RP+ + L GA F+G P+ V G LP +V + S+Q SA
Sbjct: 131 RGRPMKRVTDPALFGA---SFVGRSGGRLPMAVRGTATPLVSYRVPVP---SAQVKS 184

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G E +I+ + + + E R++ FG ++ D GQ
Sbjct: 185 VLLAGLNTPG--ETTVIEPVATRDHTTE---RMLGHFGAALRLGRDDQGATTITLTGQPEL 239

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLMMGAKVWTWE 302

V D SSA++ L A + + VT+ G G + + + L MGA + +
Sbjct: 240 RAAPVEVPADPSSAAFLVAALVPESHVTLAGVGMNPQR--IGLIDTLREMGADILIRD 297
Query: 303 TSVTVTGPPPREPFGRKH-LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ P + R L I+V + P D LAV A A G T + + RV
Sbjct: 298 PRIEAGEFPVADLEVRASALTGIEVPAARAPSMIDEYPILAVAAACARGTTTRMHGELGELRV 357
Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTADITYDDHRMAMAF-SLA 413
KE++R+ A+ T L G V D I+ T P+ A++ DHR+ MAF L
Sbjct: 358 KESDRLSAVATGLAACGVDTVGDGTLIVHGKGTVPKGGATVAVNL--DHRIGMAFLVLG 415
Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLS 440
+ VTI D +FP + +++
Sbjct: 416 LVSAEAVTIDDGRAIDTSFPGFVTLMT 442

>ref|YP_178972.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
RM1221]
sp|Q5HUR3.1|AROA_CAMJR RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAW35307.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
RM1221]
gb|ADT72664.1| 5-Enolpyruvylshikimate-3-phosphate synthase / AroF [Campylobacter
jejuni subsp. jejuni S3]
Length = 428

Score = 88.6 bits (218), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 102/431 (23%), Positives = 184/431 (42%), Gaps = 34/431 (7%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSIHFRFAIFSLTQEENKAQNYLLAQDTLNTLEIINKLGAKIEQKDCVCIIP-- 74
Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMREPIGDLVVG 140
P E L GN+G AMR + + AG +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGIFGFFVLSGDKYLNRRPMRRISKP 127
Query: 141 LKQLGADVDCFLGTDPCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QKLKAFNFKSEIS-SAQVKTAMILSAFRA----- 178
Query: 201 IIDKLISIPYVEMTLRLMERF--GVKAEHSDSWD--RFYIKGGQKYKSPKNAYVEGDASS 256
D + + + ++ E +KA S D I +K +N + D SS
Sbjct: 179 --DNVCTFSEISLSRNHSENMLKAMKAPIRVSNDGLSLEINPLKKPLKAQNIIPNDPSS 236
Query: 257 ASYF-LAGAAITGGT VTVEGCGTTSLSQGDVKFAEVLEMMGAKV--TWTETSVTVTGPPRE 313
A YF LA + + ++ + ++ ++L+ MGA+ T T+ G R
Sbjct: 237 AFYFVLAAILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMTITQNDFFETIGEIRV 294
Query: 314 PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
+ + + N+ + D A LA+ A G +++ + RVKE++R+ + L
Sbjct: 295 ESSKLNIGIEVKDNIAWLIDEAPALAI AFALAKGKSSLINAKELRVKESDRIAMVENLKL 354
Query: 374 LGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKT 431
G E D I +L + I +Y DHR+AM+F++ C + I D C + +
Sbjct: 355 CGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFALLGLLCG---IEIDSDCIKTS 411
Query: 432 FPDYFDVLSTF 442
FP++ ++LS
Sbjct: 412 FPNFIEILSNL 422

>sp|A8Z6D5.1|AROA_CAMC1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABW74752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter
concisus 13826]
Length = 428

Score = 88.2 bits (217), Expect = 2e-15, Method: Compositional matrix adjust.

Identities = 109/431 (25%), Positives = 189/431 (43%), Gaps = 43/431 (9%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R ++ LS+ + V N L + D L + LG +E D A+ +
Sbjct: 17 IAADKSIHRCAMFSLSDKPSRVRYNLKIVELGAKIE-DNGAEIIIT-- 73

Query: 81 CGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
P + KE ++ GN+G AMR + A G +VL G + RP+ +
Sbjct: 74 -----PPQKIKEPNEILECGNSGTAMRLFMGLLAAQDG--FFVLSGDKYLNSRPMARIAK 126

Query: 140 GLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVE 198
L ++GA +D + P+ I G + I+S Q SALL+AA + G
Sbjct: 127 PLNEMGAKIDGANNANNAPL---CIRGTKFERFSFDSKIASAQVKSALLLAALYSNG--- 180

Query: 199 IEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + +S + E R++ G + + ++ + SP + V D SSA
Sbjct: 181 CKFSEPELSRDHTE---RMLAGMGANIKRDEL--EITLEPMRSPLSPLDIDVPNDPSSAF 235

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS-----VTVTGP 310
+F A I + + + + ++ VLE MGA++ + +TS + V
Sbjct: 236 FFAVAALIIPNSHIILKNILLN-KTRIEAYRVLEKMGAEIKFHKTSKYEDIGDIEVRY 294

Query: 311 PREPFGRKHLKAIDV--NMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P +LK I+V N++ + D A LA+ A G + + + RVKE++R+
Sbjct: 295 P-----NLKGIEVSENISWLIDEAPALAIACAKGQSKLTNAKELRVKESDRIAVTI 347

Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDPGCT 428
L + G E D II E T ID++ DHR+AM+F++ + + I
Sbjct: 348 NALKQCGVDASELEDGFIINGSEAKFAT-IDSHGDHRIAMSFAILGL-KCGMQIEKSEFI 405

Query: 429 RKTFPDYFDVL 439
+FP++ ++L
Sbjct: 406 ATSFPNFAEIL 416

>ref|YP_023380.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Picrophilus torridus
DSM 9790]
sp|Q6L1G5.1|ARO_A_PICTO RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
gb|AAT43187.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Picrophilus torridus
DSM 9790]
Length = 411

Score = 88.2 bits (217), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 90/432 (20%), Positives = 187/432 (43%), Gaps = 44/432 (10%)

Query: 17 GTVVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + P SKS S R +L +A S + N+ S+D L R G +E + +
Sbjct: 12 GVINAPSSKSFQRYIILYSAFNSIPVTLKNVSFSDDERIALEIARACGADIEFNDSLTIK 71

Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 136
C +E+ G +G ++R L + AA T++ + ++ RP+ D
Sbjct: 72 PDFRC-----PDEINA--GESGTSRL-LATGLLAARRCKTFIHEEASLLK-RPLDD 118

Query: 137 LVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGD 196
L+ L + F D + ++ +P + + G SSQ++S+++M L G
Sbjct: 119 LIKTLSEKNV---VFNNLD-NGIMIDASNSIPSDSI-IDGGRSSQFVSSMMMYHSLTSGS 173

Query: 197 VEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
++ ++S Y+++T++ + FG+ S+ + F G+ +EGD SS
Sbjct: 174 LKAL---NIVSNDYIKITIKTLNDFGISVYSSNGFFEF----GKTLMKGNKICIEGDYSS 226

Query: 257 ASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPF 316
A++++ + G + ++ + S Q D ++ +E + +
Sbjct: 227 AAFWIV-LGLFKGDIEIKNLKSDSCQPDAA-----IINIINGISERKIDIYNNKIVVHK 279

Query: 317 RKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
+ L + +++K PD+A L+++ +F+D I + +KE+ R I + GA
Sbjct: 280 TRFLGDLYIDVDKNPDLAPPLSIIGIFSDVAVHILNRYRLEIKESNREENIISMARSFGA 339

Query: 377 SVEEGPDYCI-----ITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRK 430
+E+ + + I+ PE++ ++ DHRM M+ +A + + + K
Sbjct: 340 LIEKNDNEMVIRRGKISLPERI-----SFS DHRMIMSSIIAGLISSGDILYENIENINK 393

Query: 431 TFPDYFDVLSTF 442
++P + + LS
Sbjct: 394 SYPGFLNDLSNL 405

>ref|NP_111838.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoplasma
volcanium GSS1]
sp|Q978S3.1|AROA_THEVO RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
dbj|BAB60484.1| 5-enolpyruvylshikimate 3-phosphate synthase [Thermoplasma volcanium
GSS1]
Length = 410

Score = 88.2 bits (217), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 109/431 (25%), Positives = 193/431 (44%), Gaps = 42/431 (9%)

Query: 16 SGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG ++P SKS + R +L +A + V++ + + D + ++G ++ + R
Sbjct: 11 SGIAEMPSSKSFTQRYVLASAFLNKSVVLNGITITNDDDVAMRIAESVGSITITINN---R 67

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
++ + K P E +++G +G + R L+ + AA G T + G + +RPI
Sbjct: 68 SIKISSNFKCPPE-----IYVGESGTSYR-LSIGLLAASGCVTRI-KGEDSLAKRPIE 118

Query: 136 DLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA-APLAL 194
L++ L + G F + V+G V++ GS SSQ++S+L++ A
Sbjct: 119 PLLMALGENGVK---FERNEAGFYNV DGRNS-QKKHVEIEGS-SSQFVSSLMLYYAKKGG 173

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ I SI YV +T R++ G A + I +K+ + VE D
Sbjct: 174 GEFTARNIK---SIGVYITKRVLVLDLGYFANIERT---ITINPTGVWKTATID--VEPDY 225

Query: 255 SSASYFLAGAAITGGT-VTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
SS ++F+ ++ V + +Q D + +L++ + + V E
Sbjct: 226 SSMAFFMVLGLLSDSVDVRFRIKRISRIQPD---SVILDLFKNNILINGEEIRVISGINE 282

Query: 314 PFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
P ++D +MN PD+ L+V+ +F+ IR+ + KE+ R I +
Sbjct: 283 PV-----SVDADM--PDLCPPLSVIGIFSKYGVQIRNYERLKTESNRYEGIIDLAER 334

Query: 374 LGASVEE-GPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKT 431
GA+VE+ G D I P + + +Y DHRM MA S+A+ P I + T K+
Sbjct: 335 FGANVEDNGQDLFI--KPGSVRFPDVISYKDHMMIMAASIASLIGGFPTVIENAEKTAKS 392

Query: 432 FPDYFDVLSTF 442
FP +F LS F
Sbjct: 393 FPGFFAELSKF 403

>ref|YP_001758244.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
radiotolerans JCM 2831]
sp|B1M0N9.1|AROA_METRJ RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACB27561.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium
radiotolerans JCM 2831]
Length = 449

Score = 87.8 bits (216), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 127/456 (27%), Positives = 188/456 (41%), Gaps = 50/456 (10%)

Query: 11 PIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P + G ++ PG KS+S+R ++L LS+G T V+ LL +DV A + LG VE
Sbjct: 14 PGAPLRGRLRPPGDKSISHRSMLGLLSQGETRVEGLLEGDDVLRATAAAKALGAGVERL 73

Query: 71 KAAK-RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ R VG GG D L GNAG R + V G T DG +
Sbjct: 74 GPGRWRVQGVGIGGLGDPADV-----LDFGNAGTGSRLMMGVV--GGQPVTTATFDGDASL 126

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL---SGSISSQYLSAL 186
R RP+ ++ L ++G V P+ + G P + + + + S+Q SA+
Sbjct: 127 RSRPMRRILDPLTRMGTVLSEAEGGRVPLTLRG----PREAIPITYETPAASAQIKSAV 182

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKY 242
L+A A G +I+ + + E LRL FG V+ R GQ
Sbjct: 183 LLAGLNAPG--VTTVIEAAATRDHTERMLRL---FGAAVSVEPHGPGGHGRKVALTGQPT 237

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ V D SSA++ L A I G+ V +EG L+ + L MGA++
Sbjct: 238 LRGTDVVVPADPSSAFLVAALIVPGSDVVGVMNPLR--IGLITTLLEMGAIQIERV 295

Query: 302 ETSVTVTGPPPREPFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTA 349
RE G L +DV + P D LAV A FA+G T
Sbjct: 296 AE-----REEGETVADLRVRASRLNGVDVPAERAPAMIDEYPVLAVASFAEGRTR 347

Query: 350 IRDVASWRVKETERMVAIRTELTKLGA-SVEEGPDYCI-ITPPEKLNVTATIDTYDDHRMA 407
+ + RVKE++R+ A+ L G EG D + ++T+ DHR+A
Sbjct: 348 MSGLHELVRVKESDRLAAVAAGLAANGVRHTVEGDDLVVEGDGAAAPGGGTVEHLDHRIA 407

Query: 408 MAF-SLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
MAF + A PVT+ D +FP + +
Sbjct: 408 MAFLVMGLAARNPVTVDGAMIATSFPSFLPTMQAL 443

>ref|ZP_00367067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter coli
RM2228]
ref|ZP_07401214.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter coli
JV20]
gb|EAL57713.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter coli
RM2228]
gb|EFM37777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter coli
JV20]
Length = 426

Score = 87.8 bits (216), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 105/430 (24%), Positives = 190/430 (44%), Gaps = 37/430 (8%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L +ED L + LG V+ + ++ +
Sbjct: 16 IAADKSISHRFIFSLTQSENRAKNYLLAEDTLNLTAKIENLGAKVKREGSSVSIMP-- 73

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 74 -----PSEILSPNCVLECGNSTAMRLMIGFL--AGVSGFFVLSGDKYLNRRPMKRICKP 126

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L ++GA + + P+ + G L K S S+Q +A++++A A D +
Sbjct: 127 LSEIGAKIYGREQANLAPLCIEG-QKLKAFDYKSEIS-SAQVKTAMILSAFRA--DKTSK 182

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
+ +S + E L+ M + SD + I + ++ + D SSA YF
Sbjct: 183 FSEISLSRNHSENMLKAM--NAPLKISDDYLSLEISPLNQAQDILIPNDPSSAFYF 239

Query: 261 -LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKH 319
LA + V ++ + ++ ++L+ MGAK+ + +T E G H
Sbjct: 240 ALAAIILPNSKVVLKNILLNPTR--IEAYKILQKMGAKL-----EIKITQNDFETIGEIH 292

Query: 320 -----LKAIDV--NMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 372
LKA++V N+ + D A LA+ A G + + + RVKE++R+ A L
Sbjct: 293 ASSSELKAVEVKENIAWLIDEAPALAIAPALAKGSKLINAKELRVKESDRIAATVENLK 352

Query: 373 KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRK 430
G + +E D I + + I +Y DHR+AM+F++ C + I + C +
Sbjct: 353 LCGVNAKELEDGFEIEGSQ-IKKAKIKSYGDHRIAMSFALIGLLCG--MEIDESECIKT 408

Query: 431 TFPDYFDVLS 440
+FP++ D+L+
Sbjct: 409 SFPNFMIDILT 418

>ref|YP_001253986.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. ATCC 3502]
ref|YP_001383824.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. ATCC 19397]
ref|YP_001387374.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. Hall]
emb|CAL83016.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. ATCC 3502]
gb|ABS34318.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. ATCC 19397]
gb|ABS36189.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A str. Hall]
Length = 442

Score = 87.4 bits (215), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 106/455 (23%), Positives = 208/455 (45%), Gaps = 55/455 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYEIIGDKSIGHRSLIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G E+ ++ ++ G N+G +R + ++ ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQKNSGTTVRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA+++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAEIES--KDNKLPLKFLKHSGLSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYVEMTLRLMERFGVKAHEHSDSWDRFYIKGGQKYKS 244
++ G I + +++ Y++ ++ + + + S S I+ + +
Sbjct: 179 MSKGGKTTIVENKSTRDHTERMLK--YLDASINIRNIYSKDKKKSSSKKEITIEKSKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL--QGDVKFAEVLEMMGAKVTWTE 302
K+ YV GD SSA++ ++ A + G+ C L +G +++ VL MGA + E
Sbjct: 235 SKDIYVPGDISAFLISAALLIQQSNL---CIKNVLLNEGRIEYINVLNRNMGANIE-IE 290

Query: 303 TSVTVTGPPREPFGFR-----KHLKAIDVNMNMKMPDVAM---TLAVVALFADGPTAIRDVA 354
+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 291 KGKLLNG---EPVGNIVKESYLKGITVEKHITPNIIDEIPVLSVIAAFSEGKTIFKSVE 347

Query: 355 SWRVKETERMVAIRTELT-----KLGASVEEGPDYCIITPPEKLNVTADITYDDHRM 406
+ KE++R+ AI L K G + EG I E I+++ DHR+
Sbjct: 348 ELKFKESDRVEAIIENLKRADVKAIFYKNGDLIIEGNRSYIDKSLE-----IESFKDHRI 401

Query: 407 AMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLS 440
A+AF + + T I+D CT +FP+ + +
Sbjct: 402 ALAFLVLSLKNKHTLIKDYQCTEISFPNSLSLFN 436

>ref|YP_001490938.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter butzleri
RM4018]
sp|A8EWE5.1|AROARCB4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABV68268.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter butzleri
RM4018]
Length = 425

Score = 87.0 bits (214), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 107/433 (24%), Positives = 189/433 (43%), Gaps = 39/433 (9%)

Query: 21 LPGSKSLSNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + S T+ + N L +ED L + LG ++ D +
Sbjct: 20 IASDKSISHRCAMFSLFSNQTSYIKNYLTAEDTLNLTLSIVEQLGAKIKRDGYSVEIT--- 76

Query: 81 CGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
P E + GN+G AMR + + G +++L G +R RP+ +
Sbjct: 77 -----PTSTLTPEPSDVLDCGNSGTAMRLFCGLLASVEG--SFILTGDKYLRNRPMPKRVAD 129

Query: 140 GLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ +GA +D + P+ + G+ L S S+Q SA+++AA A G
Sbjct: 130 PLRSIGALIDGRENGKAPLFIRGVKELKPFTYH-SPVDSAQVKSAMILAALRANGISRY 188

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAHE-SDSWDRFYIKGGQKYKSPKNAYVEGDASSAS 258
+ + ++ + E R++ G E+ +D + + G + P N V D SSA
Sbjct: 189 K--ENELTRDHTE---RMLNGMGATLEYDNDGFINIHPLNG--HLKPLNITVPTDPSSAF 241

Query: 259 YFLAGAAITGGT-VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPPREPFG- 316
+F AAIT + V ++ + V+ +VL+ MG V + E EP G
Sbjct: 242 FFAVAAAITSKSRVLKVNLTLPNTR--VEAYQVLKRMGVIVNFIEKENVY-----EPIGD 294

Query: 317 ----RKHLKAIDV--NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L +DV N++ + D L++ A G + + + RVKE++R+ ++
Sbjct: 295 IEVINNELNGVDVSENISWLIDELPALSIAMSLAKGSKSVNAKELRVKESDRISVVNN 354

Query: 371 LTKLGASVEEGPD-YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTR 429
L E D Y I+ L ID++ DHR+AM+F+AA + I D C
Sbjct: 355 LKLCKVDFTEFEDGYEIVGG--SLQKAVIDSHGDHRIAMSFIAIAGL-NCDMDIEDIQICIE 411

Query: 430 KTFPDYFDVLSTF 442
+FP++ ++L +
Sbjct: 412 TSFPNFKEILDSL 424

>ref|YP_001773239.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium sp.
4-46]
sp|B0UC54.1|AROAMETS4 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACA20805.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacterium sp.
4-46]
Length = 449

Score = 87.0 bits (214), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 127/447 (28%), Positives = 188/447 (42%), Gaps = 52/447 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G ++ PG KS+S+R ++L LS G T V+ LL +DV A R LG ++ D +
Sbjct: 18 LRGLRPPGDKSISHRAMILGLLSLGETRVEGLLEGDDVLRATAAARALGAGIDRDGPGR 77

Query: 75 -RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R VG GG + E L GNAG R + V G T DG +R+RP
Sbjct: 78 WRVRGVGIGGL-----SDPEGVLDFGNAGTGSRLMMGVV--GGQPVATATFDGDASLRKRP 130

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+ ++ L Q+GA + P+ + G P + ++ + S+Q SA+L+A
Sbjct: 131 MRRILDPLVQMQAQILSEQAGGRVPLTLRG---PEEAIPITYATPVASQVKSAVLLAG 186

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKYKSPK 246
A G +I+ + + E LRL FG V A R GQ
Sbjct: 187 LNAPGTT--TVIEAAATRDHTERMLRL---FGAEVTVAAGHPAGHGRAIALTGQPTLRRAA 241

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSV 305
V D SSA++ + A I G+ V +EG L+ L MGA +
Sbjct: 242 EVIVPADPSSAAFPIVAALIVPGSDVIEGVMNPLR--TGLITTLIEMGADIARLNE-- 297

Query: 306 TVTGPPREPFGP-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDV 353
R+ G L + V + P D LAV A FA+G T ++ +
Sbjct: 298 -----RDEGETVADLRVRASRLAGTVPPERAPAMIDEYPVLAVAAAFAGETTRMQGL 351

Query: 354 ASWRVKETERMVAIRTELTKLG-ASVEEGPDYCIITP--PEKLNVTADITYDDHRMAMAF 410
RVKE++R+ A+ L G A EG D + P T + T+ DHR+AMAF
Sbjct: 352 HELRVKESDRLAADVGLRANGVAHAVEGDDLIVHGDGRPAPGGGT-VATHLDHRIAMAF 410

Query: 411 -SLAACAEVPVTIRDPGCTRKTTFPDYF 436
+ A PVT+ D ++P +

Sbjct: 411 LVMGLAAGEPVTVDGAMIATSYPAFL 437

>ref|ZP_01870782.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio shilonii AK1]
gb|EDL50621.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Vibrio shilonii AK1]
Length = 94

Score = 87.0 bits (214), Expect = 6e-15, Method: Composition-based stats.
Identities = 51/96 (53%), Positives = 69/96 (71%), Gaps = 3/96 (3%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
E + LQPI+++SGTV LKSGKS+SNR LLLAAL+EGTT + NLL+S+D+ +ML AL +LG
Sbjct: 2 ESLTLQPIQKVSQTVNLPKSGKSVSNRALLLAALAEAGTTTLNLLDSDDIRHMLNALSSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGN 100
+ + + + +V G G F V + KE LFLGN
Sbjct: 62 VEYQLSEDKTQCIVKGLGQPFVSEPKE---LFLGN 94

>ref|YP_220807.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
1 str. 9-941]
sp|P0C100.1|AROAB_BRUAB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|AAX73446.1| AroA, 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella
abortus bv. 1 str. 9-941]
Length = 450

Score = 86.7 bits (213), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHSFMMFGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGVLGTYDMKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHT---KMLQDFGADLTVDKDGVRHIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TQQTIDVPGDPSSTAFPLVAALLVEGSEVTIRNVLNPNTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVVPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTTPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 438

>ref|YP_003105996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella microti CCM
4915]
gb|ACU47047.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella microti CCM
4915]
Length = 450

Score = 86.7 bits (213), Expect = 6e-15, Method: Compositional matrix adjust.

Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNGC-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 ILLAGLNTPG--VTTVIEPVMTRDHT--KMLQGFADLTVDKDGVRHRIIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TGQTIDVPGDPSSTAFLVAALLVEGSDVTIRNVLNPNTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFFDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMMA 438

>ref|YP_002803900.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A2 str. Kyoto]
gb|AC084572.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
A2 str. Kyoto]
Length = 442

Score = 86.7 bits (213), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 106/455 (23%), Positives = 207/455 (45%), Gaps = 55/455 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYIEIIGDKSIGHRSIIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ V G E+ ++ ++ G N+G +R + ++ ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQKNSGTTIRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA ++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPLKFLKHSGLNSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++ G I + ++++ Y++ ++ + + + S S I+ + +
Sbjct: 179 MSKGKTTIVENKSTRDHTERMLK--YLDASINIRNIYSKDKKSSSKKEITIEKSKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL--QGDVKFAEVLEMMGAKVTWTE 302
K+ YV GD SSA++ ++ A + G+ C L +G +++ VL MGA + E
Sbjct: 235 SKDIYVPGDISAFLISAALLIQGSNL---CIKNVLLNEGRIEYINVLRNMGANIE-IE 290

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMPPDVAM---TLAVVALFADGPTAIRDVA 354
+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 291 KGKLLNG---EPVGNIVKESYLKGITVEKHITPNIIDEIPVLSVIAAFSEGKTIFKSVE 347

Query: 355 SWRVKETERMVAIRTEL-----KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406
+ KE++R+ AI L K G + EG I E I+++ DHR+
Sbjct: 348 ELKFKESTRVEAIIENLKRADVKAIIYKNGDLIEGNSYIDKSLE-----IESFKDHRI 401

Query: 407 AMAFSLAACAEVPT-IRDPGCTRKTFPDYFDVLS 440
A+AF + + T I+D CT +FP+ + +
Sbjct: 402 ALAFLVLSLKNKKHTLIKDYQCTEISFPNSLSLFN 436

>ref|YP_413526.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
biovar Abortus 2308]
ref|YP_001934058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus S19]
ref|ZP_05153594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
6 str. 870]
ref|ZP_05158286.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
2 str. 86/8/59]
ref|ZP_05189948.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
4 str. 292]
ref|ZP_05464130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
9 str. C68]
ref|ZP_05868229.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 6
str. 870]
ref|ZP_05871453.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 4
str. 292]
ref|ZP_05873173.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 2
str. 86/8/59]
ref|ZP_05896519.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
9 str. C68]
sp|Q2YPN6.1|AROA_BRUA2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|B2S7T0.1|AROA_BRUA1 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAJ09979.1| ATP/GTP-binding site motif A (P-loop):EPSP synthase
(3-phosphoshikimate
1-carboxyvinyltransferase):3-phosphoshikimate 1-carbo
[Brucella melitensis biovar Abortus 2308]
gb|ACD71584.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus S19]
gb|EEX56363.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 4
str. 292]
gb|EEX58083.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 2
str. 86/8/59]
gb|EEX62810.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 6
str. 870]
gb|EEX81502.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
9 str. C68]
Length = 450

Score = 86.7 bits (213), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMLGLVGTMDKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKS 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHT---KMLQGFADLTVETDKDGVRRHIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TGQTIDVPGDPSSTAFLVAALLVEGSEVTIRNVLNMPNTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPREPFGFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +

Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYFVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407

+ RVKE++R+ A+ L G EG + + L + T+ DHR+A

Sbjct: 345 DGLDELRVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440

M+F + A E PVT+ D +FP++ +++

Sbjct: 405 MSFLVMGLASEKPVTVDSTMIATSFPEFMGMMA 438

>ref|YP_001626705.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis ATCC 23445]
ref|YP_002731802.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis ATCC 23457]
ref|ZP_05162669.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 5 str. 513]
ref|ZP_05169101.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis M163/99/10]
ref|ZP_05170996.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis B2/94]
ref|ZP_05175201.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M644/93/1]
ref|ZP_05178063.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M13/05/1]
ref|ZP_05444323.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis M292/94/1]
ref|ZP_05450350.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella neotomae 5K33]
ref|ZP_05453454.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis bv. 3 str. Ether]
ref|ZP_05456591.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M490/95/1]
ref|ZP_05459650.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti B1/94]
ref|ZP_05467452.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis bv. 2 str. 63/9]
ref|ZP_05756423.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. F5/99]
ref|ZP_05932309.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M13/05/1]
ref|ZP_05935536.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti B1/94]
ref|ZP_05953953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis M163/99/10]
ref|ZP_05955882.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis B2/94]
ref|ZP_05960319.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M644/93/1]
ref|ZP_05963343.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella neotomae 5K33]
ref|ZP_05995059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 5 str. 513]
ref|ZP_06002849.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. F5/99]
ref|ZP_06100312.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella pinnipedialis M292/94/1]
ref|ZP_06106529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis bv. 3 str. Ether]
ref|ZP_06109773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M490/95/1]
sp|B0CI45.1|AROABRUSI RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
sp|C0RG90.1|AROABRUMB RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS
gb|ABY37135.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis ATCC 23445]
gb|ACN99847.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis ATCC 23457]
gb|EEX86492.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti B1/94]
gb|EEX89685.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti M13/05/1]
gb|EEX97308.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti

M644/93/1]
gb|EEX99404.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella
pinnipedialis B2/94]
gb|EEY03623.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella neotomae
5K33]
gb|EEY07279.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella
pinnipedialis M163/99/10]
gb|EEY27120.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. F5/99]
gb|EEY29029.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 5
str. 513]
gb|EEZ07674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti
M490/95/1]
gb|EEZ10874.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 3 str. Ether]
gb|EEZ19006.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 2 str. 63/9]
gb|EEZ30213.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella
pinnipedialis M292/94/1]
Length = 450

Score = 86.7 bits (213), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGVLGTYDMKTSFIDGA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTGP--VTTVIEPVMTRDHTD---KMLQGFADLTVETDKDGVHRIRIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TQQTIDVPGDPSSTAFLVAALLVEGSDVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVPPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADITYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFFDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 438

>ref|NP_697067.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis 1330]
ref|YP_001591902.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella canis ATCC
23365]
ref|ZP_05167035.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 3
str. 686]
ref|ZP_05837797.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 4
str. 40]
ref|ZP_05999624.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 3
str. 686]
sp|Q8G3C4.1|AROABRUSU RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
sp|A9M6N0.1|AROABRUC2 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|AAN28982.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis 1330]
gb|ABX61131.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella canis ATCC
23365]
gb|EEW91925.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 4
str. 40]
gb|EEY33594.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella suis bv. 3
str. 686]
Length = 450

Score = 86.7 bits (213), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNGC-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI---AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHTD---KMLQGFADLTVDKDGVRHIRIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TGQTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMPNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPFPREPFR-----KHLKAIDVNMNKMPP--DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVRASKLKGVVPPERAPSMIDEYPLVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMLGLASEKPVTVDDSTMIATSPFEFMGMMA 438

>ref|ZP_06792105.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. NVSL
07-0026]
gb|EFG37020.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. NVSL
07-0026]
Length = 450

Score = 86.3 bits (212), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNGC-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI---AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHTD---KMLQGFADLTVDKDGVRHIRIVGQGKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302

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      + +   V GD SS ++ L  A +   G+ VT+           + +   L+ MGA +   +
Sbjct: 235 TGQTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMPNTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAI 350
      PR   G           LK + V   + P   D   LA+ A FA+G T +
Sbjct: 293 -----PRLTGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTATIDTYDDHRMA 407
      +   RVKE++R+ A+   L   G   EG   +   + L   + T+ DHR+A
Sbjct: 345 DGLDELRVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
      M+F +   A E PVT+ D   +FP++   +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMA 438

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>ref|ZP_02614795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
      NCTC 2916]
gb|EDT80941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
      NCTC 2916]
      Length = 442

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Score = 86.3 bits (212), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 102/451 (22%), Positives = 207/451 (45%), Gaps = 47/451 (10%)

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Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++G ++ G KS+ +R L++ AL +G   V N   + D   L +++ LG+ +   K
Sbjct: 10 KSLTGEYIEIGDKSIGHRSLIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      + V   G   E+ ++ ++   G N+G +R +   ++   ++ G   +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQGKNSGTTVRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+ ++ L+++GA ++   + P++   GL   K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPKFLKHSGLNSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ++ G   I   +   ++++   Y++ ++ +   +   + S S   I+ +   +
Sbjct: 179 MSKGKTTIVENKSTRDHTERMLK--YLDASINIRNIYSKDKKKSSSKKEITIEKSKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL--QGDVKFAEVLEMMGAKVTWTE 302
      K+ YV GD SSA++ ++ A +   G+   C   L +G +++ VL MGA +   +
Sbjct: 235 SKDIYVPGDISAFLISAALLIQGS---NLCIKNVLLNEGRIEYINVLNRNMGANIEIKK 291

Query: 303 TSVTVTGPPPREPFGRK-HLKAIDVNMNKMPPDVAM---TLAVVALFADGPTAIRDVASWRV 358
      +   P   + ++ +LK I V   + P++   L+V+A F++G T + V   +
Sbjct: 292 GKLLNGEPVGNIVKESYLKGITVEKHITPNIIDEIPVLSVIAAFSEGKTIFKSVEELKF 351

Query: 359 KETERMVAIRTEL-----KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
      KE++R+ AI   L   K G + EG   I   E   I+++ DHR+A+AF
Sbjct: 352 KESDRVEAIIENLKRADVKAIIYKNGDLIEGNRSYIDKSLE-----IESFKDHRIALAF 405

Query: 411 SLAACA-EVPVT-IRDPGCTRKTFPDYFDVLS 440
      + +   T I+D CT +FP+   + +
Sbjct: 406 LVLSLKNKKHTLIKDYQCTEISFPNSLSLFN 436

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>ref|ZP_08032456.1| EPSP synthase [Actinomyces sp. oral taxon 171 str. F0337]
gb|EFW28280.1| EPSP synthase [Actinomyces sp. oral taxon 171 str. F0337]
      Length = 220

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Score = 86.3 bits (212), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 62/199 (31%), Positives = 102/199 (51%), Gaps = 11/199 (5%)

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Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
      +E D S+A FLA A + GG V++   T + Q   + EVL +G +VT T+ ++T G
Sbjct: 6 IEPDLNAGPFLAAALVAGGRVSIHPWPTATTQAGDAWREVLPRLGGEVTLTDGTLTARG 65

Query: 310 PPREFGRKHLKAIDVNMNKMPPDVAMTLAVVALF--ADGPTA-IRDVASWRVKETERMVA 366
      R   L   I   +++ + ++A T+A +A   A G T+ +   +A R ET+R+ A

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Sbjct: 66 TGR-----LTGIHADLSDVGELAPTVAALATLAGAQGHTSTLTGIAHLRGHETDRLAA 118

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRDPG 426
+ ++ LG EE D II P L+ A+ +Y DHRMA ++ + V++ D

Sbjct: 119 LAAQIRLLGGEAEESNDGLIIR-PAPLHGAALRSYADHRMATFAAIIGLSVDGVSLDDVE 177

Query: 427 CTRKTFPDYFDVLSTFVKN 445
CT KT P + D+ + +

Sbjct: 178 CTSKTLPGFTDLWAAMLAT 196

>ref|YP_001781111.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Bl str. Okra]
gb|ACA44749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Clostridium botulinum
Bl str. Okra]
Length = 442

Score = 86.3 bits (212), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 106/455 (23%), Positives = 207/455 (45%), Gaps = 55/455 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYIEIIGDKSIGHRSLIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI--KV 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
+ V G E+ ++ ++ G N+G +R + ++ ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQKNSGTTVRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA ++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAKIES--KDNKLPKFLKHSGLNSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++ G I + ++++ Y++ ++ + + + S S I+ + +
Sbjct: 179 MSKGGKTIVENKSTRDHTEMLK--YLDASINIRNIYSKDKKKSSSKEITIEESKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSL--QGDVKFAEVLEMMGAKVTWTE 302
K+ YV GD SSA++ ++ A + G+ C L +G +++ VL MGA + E
Sbjct: 235 SKDIYVPGDISAFLISAALLIQGSNL---CIKNVLLNEGRIEYINVLNRMGANIE-IE 290

Query: 303 TSVTVTGPPREPFGFR-----KHLKAIDVNMNMKMPDVAM---TLAVVALFADGPTAIRDVA 354
+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 291 KGKLLNG---EPVGNIVKESYLKGITVERHITPNIIDEIPVLSVIAAFSEGKTIFKSVE 347

Query: 355 SWRVKETERMVAIRTELT-----KLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406
+ KE++R+ AI L K G + EG I E I+++ DHR+
Sbjct: 348 ELKFKESDRVEAIIENLKRAVDKAIYKNGDLIEGNSYIDKSLE-----IESFKDHRI 401

Query: 407 AMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLS 440
A+AF + + T I+D CT +FP+ + +
Sbjct: 402 ALAFLVLSLKNKKHTLIKDYQCTEISFPNSLSLFN 436

>ref|ZP_05822047.1| 5-enolpyruvyl shikimate 3-phosphate synthase [Brucella abortus NCTC
8038]
gb|EEW80290.1| 5-enolpyruvyl shikimate 3-phosphate synthase [Brucella abortus NCTC
8038]
Length = 461

Score = 86.3 bits (212), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 27 QALTGEIRIPGDKSISHRSMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 86

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 87 VWIINGVGNGC-----LLQPEAPLDFGNAGTGARLTMGVLVGTYDMKTSFIGDA--SLS 137

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185

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      +RP+G ++ L+++G V+  G  P      P  N I      +V ++  S+Q  SA
Sbjct: 138 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 190

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
      +L+A      G      +I+ +++  + E  + + + + FG  +  E      R      GQ
Sbjct: 191 VLLAGLNTPG--VTTVIEPVMTRDHTe---KMLQGFADLTVETDKDGVVRHIRIVGQGKL 245

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      + +  V GD SS ++ L  A +  G+ VT+      + +      L+ MGA +  +
Sbjct: 246 TQQTIDVPGDPSSTAFLVAALLVEGSEVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 303

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI 350
      PR      G      LK + V  + P  D      LA+ A FA+G T +
Sbjct: 304 -----PRLAGGEDVADLRVKASKLKGVVPPPERAPSMIDEYPLAIAASFAEGETVM 355

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407
      +  RVKE++R+ A+  L  G  EG  +      + L  + T+ DHR+A
Sbjct: 356 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 415

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
      M+F +  A E PVT+ D      +FP++  +++
Sbjct: 416 MSFLVMGLASEKPVTVDSTMIATSFPEFMGMMMA 449

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>sp|Q46550.1|AROA_DICNO RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
      AltName: Full=5-enolpyruvylshikimate-3-phosphate
      synthase; Short=EPSP synthase; Short=EPSPS
emb|CAA82544.1| enolpyruvylshikimate 3-phosphate synthase [Dichelobacter nodosus]
      Length = 443

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Score = 86.3 bits (212), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 114/448 (25%), Positives = 194/448 (43%), Gaps = 38/448 (8%)

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Query: 11 PIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P+  +SG + + G KS+S+R LLLAAL+EG T +  L  D      ALR LG+ ++ +
Sbjct: 10 PVSALSGEITICGDKSMRALLAALAEGQTEIRGFLACADCLATRQALRALGVDIQRE 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      K      VG  G  P      +  L + N+G +MR L  + A      VL G  +
Sbjct: 70 KEIVTIRGVGFLGLQP-----PKAPLNMQNSGTSMRLLAGILAAQ--RFESVLCGDESLE 122

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMA 189
      +RP+  ++ L Q+GA +      P      I G P  +  +  + S+Q  S L++A
Sbjct: 123 KRPMQRIITPLVQMGAIVSHSNFTAPL----HISGRPLTGIDYALPLPSAQLKSCILILA 178

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
      LA G  +      IS + E  R++ FG  E      ++ + GGQK
Sbjct: 179 GLLADGTTTLHTCG--ISRDHTE---RMLPLFGGGALEIKK--EQIIVTGGQKLHGCVLDI 231

Query: 250 VEGDASSASYFLAGAAIT-GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      V GD S+A++F+  A I      V +  G  +  +  +L+ MG ++
Sbjct: 232 V-GDLSAAAFMVAALIAPRAEVVIRNVGINPTRAII--ITLLQKMGGRIELHHQRFWGA 288

Query: 309 GPPRE-PFGRKHLKAIDV-----NMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
      P  +      L+ I V      + + + + P      + A  A+G T +  + + RVKE
Sbjct: 289 EPVADIVVYHSLRGITVAPEWIANAIIDELP----IFFIAACAEGTTFVGNLSELRVKE 344

Query: 361 TERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMAMAFSLAAC-AE 417
      ++R+ A+  L  LG + + G D+  I      +      + + + + DHR+AM+ ++A  A
Sbjct: 345 SDRLAAMAQNLQTLGVACDVGADFIHIYGRSDRQFLPARVNSFGDHRAMSLAVAGVRAA 404

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
      + I D      + P + D  +  N
Sbjct: 405 GELLIDDGAVAAVSMQPFRDFAAAIGMN 432

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>ref|ZP_03784612.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti str.
      Cudo]
gb|EEH15273.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ceti str.
      Cudo]
      Length = 480

```

Score = 85.9 bits (211), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 111/452 (24%), Positives = 195/452 (43%), Gaps = 53/452 (11%)

Query: 13 KEISGTVKLPKSGSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + K
Sbjct: 46 QALTGEIRIPGDKSISHRSMFGLASGKTRITGLLEGEDVINTGRAMQAMGARIR--KE 103

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 132
++ G G ++ E L GNAG R V +++ D + +R
Sbjct: 104 GDVWIINGVGNCLLQ---PEAPLDFGNAGTGARLTMLVGTYDMKTSFIGDA--SLSKR 158

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
P+G ++ L+++G V+ G P P N I +V ++ S+Q SA+L
Sbjct: 159 PMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI---AYRVPMA---SAQVKSALL 211

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
+A G +I+ +++ + E ++++ FG + E R GQ +
Sbjct: 212 LAGLNTPG--VTTVIEPVMTRDHT---KMLQGFADLTVDKDGVRHIVGQGLTG 266

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 267 QTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLIL--TLQEMGADIEIID-- 322

Query: 305 VTVTGPPEPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 323 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDG 376

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTATIDTYDDHRMAMA 409
+ RVKE++R+ A+ L G EG + + L + T+ DHR+AM+
Sbjct: 377 LDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIAMS 436

Query: 410 FSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
F + A E PVT+ D +FP++ +++
Sbjct: 437 FLVMDGLASEKPVTVDDSTMIATSFPEFMGMA 468

>ref|ZP_05180057.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. 83/13]
ref|ZP_06095941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. 83/13]
ref|ZP_07472782.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. NF 2653]
gb|EEZ32059.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. 83/13]
gb|EFM61237.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. NF 2653]
Length = 450

Score = 85.9 bits (211), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSMFGLASGETRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCLLQ---PEAPLDFGNAGTGARLTMLVGTYDMKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI---TYRVPMA---SAQVKS 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHT---KMLQGFADLTVDKDGVRHIHIVGQGL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TGQTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPEPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVRASKLKGVVPPERAPSMIDEYPVLAIAAPFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELRVKESDRDLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 404

Query: 408 MAFSLAACAEVPTTIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 438

>ref|ZP_07891778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter butzleri
JV22]
gb|EFU69888.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Arcobacter butzleri
JV22]
Length = 425

Score = 85.9 bits (211), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 109/434 (25%), Positives = 187/434 (43%), Gaps = 41/434 (9%)

Query: 21 LPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + S T+ + N L +ED L + LG ++ D +
Sbjct: 20 IASDKSISHRCAMFSLFSNQTSYIKNYLTAEDTLNLTLSIVEQLGAKIKRDGSYVEIT--- 76

Query: 81 CGGKFPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
P E + GN+G AMR + + G +++L G +R RP+ +
Sbjct: 77 -----PTSTLTPEPSDVLDCGNSGTAMRLFCGLLASVEG--SFILTGDKYLRNRPMKRVAD 129

Query: 140 GLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ +GA +D + P+ + G+ L S S+Q SA+++AA A G
Sbjct: 130 PLRSIGALIDGRENGKAPLFIIRGVKELKPFTYH-SPVDSAQVKSAMILAAALRANG---- 184

Query: 200 EIIDKLISIPYV-EMTLRLMERFGVKAHEH-SDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
I K + T R++ G E+ +D + + G + P N V D SSA
Sbjct: 185 --ISKYKENELTRDHTERMLNGMGAILEYDNDGFINIHLNG--HLKPLNITVPTDPSSA 240

Query: 258 SYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
+F AAIT + V ++ + V+ +VL+ MG V + E EP G
Sbjct: 241 FFFAVAAAITPKSRVLKKNVTLPNTR--VEAYQVLKRMGVIVNFIEKENVY-----EPIG 293

Query: 317 -----RKHLKAIDV--NMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
L +DV N++ + D L++ A G + + + RVKE++R+ ++
Sbjct: 294 DIEVINNELNGVDVSENISWLIDELPALSIAMSLAKGKSKVSNAKELRVKESDRISVVN 353

Query: 370 ELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTTIRDPGCT 428
L E D Y I+ L ID++ DHR+AM+F++A + I D C
Sbjct: 354 NLELCKVDTFEFEDGYEIVGG--SLQKAVIDSHGDHRIAMSFAIAGL-NCMDIEDIQCI 410

Query: 429 RKTFFPDYFDVLSTF 442
+FP++ ++L +
Sbjct: 411 ETSFPNFKEILDSL 424

>ref|ZP_04593499.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus str.
2308 A]
ref|ZP_06931151.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
5 str. B3196]
gb|EEP63548.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus str.
2308 A]
gb|EFH33949.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
5 str. B3196]
Length = 480

Score = 85.9 bits (211), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 46 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 105

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 106 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGLVGTYDMKTSFIGNA--SLS 156

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 157 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKS 209

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 210 VLLAGLNTPG--VTTVIEPVMTRDHTe---KMLQGFADLTVEtdKdGVRHirivGQgKL 264

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 265 TGQTIDVPGDPSSTAFLVAALLVEGSEVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 322

Query: 303 TSVTVTGPPREPFGFR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 323 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 374

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTaidTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 375 DGLDELRVKESDRLAAVARGLEANGVdCTEGEMSLTVRGRPGGKGLGGGTvATHLDHRIA 434

Query: 408 MAFSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 435 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 468

>ref|ZP_07475325.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. B02]
gb|EFM58630.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella sp. B02]
Length = 449

Score = 85.9 bits (211), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGLASGETRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTmGLVGTyDMKTSfIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----TYRVPMA---SAQVKS 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHTe---KMLQGFADLTVEtdKdGVRHirivGQgKL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TGQTIDVPGDPSSTAFLVAALLVEGSDVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPREPFGFR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVRASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTaidTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELRVKESDRLAAVARGLEANGVdCTEGEMSLTVRGRPGGKGLGGGTvATHLDHRIA 404

Query: 408 MAFSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMA 438

>ref|YP_001258071.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ovis ATCC
25840]
gb|ABQ60885.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella ovis ATCC
25840]
Length = 461

Score = 85.5 bits (210), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

```

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 27 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 86

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 87 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 137

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 138 KRPMGRVLNPLREMGVQVEAAEGDWMLPLTLIGPRTANPI---AYRVPMA---SAQVKSA 190

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 191 VLLAGLNTPG--VTTVIEPVMTRDHTD---KMLQGFADLTVDKDGVRHRIIVGQGKL 245

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 246 TGQTIDVPGDPSSTAFLVAALLVEGSDVTIRNVLNPNTRTGLIL--TLQEMGADIEIID 303

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 304 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVM 355

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 356 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 415

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 416 MSFLVMLGLASEKPVTVDDSTMIATSFPEFMGMA 449

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>ref|ZP_05448692.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 1 str. Rev.1]
ref|ZP_05833592.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 1 str. 16M]
ref|ZP_06104787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 1 str. Rev.1]
sp|Q8YEG1.2|AROABRUME RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EEW88214.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 1 str. 16M]
gb|EEZ15589.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
bv. 1 str. Rev.1]
Length = 450

```

Score = 85.1 bits (209), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 194/454 (42%), Gaps = 57/454 (12%)

```

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI---AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTRDHTD---KMLQGFADLTVDKDGVRHRIIVGQGKL 234

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Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TQQTIDVPGDPSSSTAFPLVAALLVEGSDVTIRNVLNPNTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +
Sbjct: 293 -----PRLAGGEDVADLRVKASKLKGVVVPPERAPSMIDEYPLAIAASFAEGETVM 344

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDTYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A
Sbjct: 345 DGLDELVRKESDRLLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTGTHLDHRIA 404

Query: 408 MAFSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
M+F + A E PVT+ D +FP++ +++
Sbjct: 405 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMMA 438

>ref|ZP_01070338.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 260.94]
gb|EAQ58161.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni 260.94]
Length = 428

Score = 85.1 bits (209), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 100/427 (23%), Positives = 182/427 (42%), Gaps = 26/427 (6%)

Query: 21 LPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
+ KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 17 IAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDCSCVKIIP-- 74

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
P E L GN+G AMR + + AG + +VL G + RP+ +
Sbjct: 75 -----PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKP 127

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
L Q+GA + + P+ + G L K S S+Q +A++++A A
Sbjct: 128 LTQIGARIYGRNEANLAPLCIEG-QNLKAFNYKSEIS-SAQVKTAMILSAFRADNVCIFS 185

Query: 201 IIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF 260
I +S + E L+ M+ S+ I +K +N + D SSA YF
Sbjct: 186 EIS--LSRNHSENMLKAMK---APIRVNSDGLSLEISPLKKPLKAQNIIPNDPSSAFYF 240

Query: 261 -LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW--TETSVTVTGPPPREPFGR 317
LA + + ++ + ++ ++L+ MGAK+ T+ G R +
Sbjct: 241 ALAAIILPKSQIILKNILLNPTR--IEAYKILQKMGAKLEMIITQNDFETIGEIRVESSK 298

Query: 318 KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
+ + N+ + D A LA+ A G +++ + RVKE++R+ + L G
Sbjct: 299 LNGIEVKDNIAWLIDEAPALAIAPALAKGKSLINAKELRVKESDRIAMVMENLKLGCVE 358

Query: 378 VEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDY 435
E D I +L + I +Y DHR+ M+F++ C + I D C + +FP++
Sbjct: 359 ARELDDGFEIEGGCELKSSKISYGDHRITMSFAILGLLCG---IEIDSDCIKTSFPNF 415

Query: 436 FDLVSTF 442
++LS
Sbjct: 416 IEILSNL 422

>ref|ZP_05626392.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter
gracilis RM3268]
gb|EEV16469.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter
gracilis RM3268]
Length = 424

Score = 85.1 bits (209), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 114/418 (27%), Positives = 184/418 (44%), Gaps = 26/418 (6%)

Query: 25 KSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + L+E T+ + N L +ED L + LG SV+ + ++
Sbjct: 21 KSISHRAAIFSLAAEETSKISNYLAAEDTLNLTIVELLGASVQ--RVEGEILIT----- 73

Query: 85 FPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P E KE V L GN+G AMR + AG +VL G + ERP+ + L +
Sbjct: 74 -PPEIIKEPNVPLDCGNSGTAMRLFMGFL--AGCEGFFVLCGDRYLSEPRMRRVADPLCK 130

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID 203
+GA + G + P+ V +G G S S+Q +AL++AA G + +
Sbjct: 131 VGAKIYGRAGGEKAPIAV--LGQKLGIFYEYASKIASAQVKTALILALRGSG---CKFSE 185

Query: 204 KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAG 263
+S + E L+ M A+ S + + P ++ D SSA +F
Sbjct: 186 PELSRDHSERLMKAM----GAQISQNGLEIEVAPLSSPLKPFEIFIPNDPSSAFFFAVA 240

Query: 264 AAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VTVTGPPREPFGGRKHLK 321
AAIT G+ V + + ++ E+L+ MGA+V + +TS G + H
Sbjct: 241 AAITPGSCIVLKNMLLN-KTRIEAYEILKRMGAEVKFHKTSEIYEIQIGDIEVAYAPLHAV 299

Query: 322 AIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEG 381
+ N++ + D A LA+ A G + +R+ A RVKE +R+ L G E
Sbjct: 300 EVSENIISWLIDEAPALAIAFACAQGSVLRNAAELRVKECDRIKVTCEGLRACGIKAREL 359

Query: 382 PDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEPVPTIRDPGCTRKTFPDYFDVL 439
D I E N I DHR+AM+F++ + I D C +FP++ +L
Sbjct: 360 QDGWQIEGGEA-NAAIITPCGDHRIAMSFAILG-LRSGMIIEDSDCIATSPFNFAAIL 415

>emb|CBZ03356.1| 5-Enolpyruvylshikimate-3-phosphate synthase [Clostridium botulinum
H04402 065]
Length = 442

Score = 85.1 bits (209), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 105/455 (23%), Positives = 207/455 (45%), Gaps = 55/455 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G ++ G KS+ +R L++ AL +G V N + D L +++ LG+ + K
Sbjct: 10 KSLTGEYIEIIGDKSIGHRSLIIGALPKGEYKVYNFPKNLDCMATLDSIKKLGVDI---KV 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLG-NAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ V G E+ ++ ++ G N+G +R + ++ ++ G +
Sbjct: 67 EGNVLEVNSPG---YENFNKKPEVLQGNKSGTTVRLMAGILSGIRAETRFI--GDESLSC 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ L+++GA+++ + P++ GL K + + S+Q S +L+A
Sbjct: 122 RPMKRIIEPLEKMGAEIES--KDNKLPKFLKHSGLNSIKYNMEIA-SAQVKSCILLAGL 178

Query: 192 LALGDVEI-----EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++ G I + ++++ Y++ ++ + + + S S I+ + +
Sbjct: 179 MSKGGKTIVENKSTRDHTERMLK--YLDASINIRNIYSKDKKKSSSKKEITIEKSKL--N 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL--QGDVKFAEVLEMMGAKVTWTE 302
K+ YV GD SSA++ ++ A + + C L +G +++ VL MGA + E
Sbjct: 235 SKDIYVPGDISAFLISAALLIQDS---NLCIKNVLLNEGRIEYINVLNRNMGANIE-IE 290

Query: 303 TSVTVTGPPREPFGFR-----KHLKAIDVNMNMKMPDVAM---TLAVVALFADGPTAIRDVA 354
+ G EP G +LK I V + P++ L+V+A F++G T + V
Sbjct: 291 KGKLLNG---EPVGNIIYVKESYLKGITVERHITPNIIDEIPVLSVIAAFSEGKTIFKSVE 347

Query: 355 SWRVKETERMVAIRTELT-----KLASVEEGPDYCIITPPEKLNVTDAIDTYDDHRM 406
+ KE++R+ AI L K G + EG I E I+++ DHR+
Sbjct: 348 ELKFKESDRVEAIIENLKRADVKAIIYKNGDLIIEGNRSYIDKSLE-----IESFKDHRI 401

Query: 407 AMAFSLAACAEPVPT-IRDPGCTRKTFPDYFDVLS 440
A+AF + + T I+D CT +FP+ + +
Sbjct: 402 ALAFLVLSLKNKKHTLIKDYQCTEISFPNSLSLFN 436

>ref|ZP_05922163.1| LOW QUALITY PROTEIN: 3-phosphoshikimate 1-carboxyvinyltransferase
[Enterococcus faecium TC 6]
gb|EEW66073.1| LOW QUALITY PROTEIN: 3-phosphoshikimate 1-carboxyvinyltransferase
[Enterococcus faecium TC 6]
Length = 266

Score = 84.7 bits (208), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 79/254 (31%), Positives = 128/254 (50%), Gaps = 16/254 (6%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
          LQ I + GTV++P KS+S+R ++ A++EGTT + N L +ED L A + LG+ +E
Sbjct: 1  LQQIHGLRGTVRIPADKSISHRSIMFGAIAEGTTTQIQLRAEDCLSTLHAFQQLGVEIE 60

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
          ++ + + G G V+ + + +GN+G +R L + AG T L G
Sbjct: 61 EEEVIK--IHGRGSHSFVQPTES---IDMGNSGTTIRLLMGIL--AGQPFTTTLFGDAS 113

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
          + +RP+G ++ L+++GAD+ P+ V G L + + + S+Q SALL
Sbjct: 114 LSKRPMGRVMEPLREMGADLQGEENDQYLPITVTGTRSLSPIRYNMPVA-SAQVKSALLF 172

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
          AA A G I++K S + E +R +FG + D + G QK +
Sbjct: 173 AALQAEGTS--VIVEKERSRNHTEEMIR--QFGGRITVEDKT--IIVTGPQKLTG-QQI 224

Query: 249 YVEGDASSASYFLA 262
          V GD SSA++FLA
Sbjct: 225 TVPGDISSAFFLA 238
```

```
>ref|NP_540834.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
          bv. 1 str. 16M]
gb|AAL53098.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella melitensis
          bv. 1 str. 16M]
Length = 480
```

Score = 84.7 bits (208), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 111/452 (24%), Positives = 195/452 (43%), Gaps = 53/452 (11%)

```
Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
          + ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + K
Sbjct: 46 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIR--KE 103

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
          ++ G G ++ E L GNAG R V +++ D + +R
Sbjct: 104 GDVWIINGVNGNCLLQ---PEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLSKR 158

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
          P+G ++ L+++G V+ G P P N I +V ++ S+Q SA+L
Sbjct: 159 PMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSAYL 211

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSP 245
          +A G +I+ +++ + E ++++ FG + E R GQ +
Sbjct: 212 LAGLNTPG--VTTVIEPVMTRDHT---KMLQGFADLTVETDKDGVHRIRIVGQKLTG 266

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
          + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 267 QTIDVPGDPSSTAFPLVAALLVEGSDVTIRNVLMNPRTGLIL--TLQEMGADIEIID-- 322

Query: 305 VVTGTPPREPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
          PR G LK + V + P D LA+ A FA+G T +
Sbjct: 323 -----PRLAGGEDVADLRVKASKLKGVVPPERAPSMIDEYPVLAIAASFAEGETVMDG 376

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCII---TPPEKLNVT AIDTYDDHRMAMA 409
          + RVKE++R+ A+ L G EG + + L + T+ DHR+AM+
Sbjct: 377 LDELRLVKESDRLA AVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTGTHLDHRIAMS 436

Query: 410 FSLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
          F + A E PVT+ D +FP++ +++
Sbjct: 437 FLVMGLASEKPVTVDDSTMIATSFPEFMGMA 468
```

```
>ref|ZP_05156657.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Brucella abortus bv.
          3 str. Tulya]
ref|ZP_05929437.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 3
          str. Tulya]
```

gb|EEX83624.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brucella abortus bv. 3
str. Tulya]
Length = 450

Score = 84.7 bits (208), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 112/447 (25%), Positives = 194/447 (43%), Gaps = 43/447 (9%)

Query: 13 KEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S+R + L+ G T + LL EDV A++ +G + E D
Sbjct: 16 QALTGEIRIPGDKSISHRSFMFGGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 75

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +
Sbjct: 76 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGVLGTMDKTSFIGNA--SLS 126

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA
Sbjct: 127 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 179

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ
Sbjct: 180 VLLAGLNTPG--VTTVIEPVMTDRDTE---KMLQGFADLTVETDKDGVHRIRIVGQKGL 234

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 235 TQQTIDVPDPSSTAFPLVAALLVEGSEVTIRNVLMNPTRTGLIL--TLQEMGADIEIID 292

Query: 303 TSVTVTGPPREPFGGRK--HLKAIDVMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ G K LK + V + P D LA+ A FA+G T + + R
Sbjct: 293 PHL-AGGEDVADLRVKASKLKGVVVPPERAPSMIDEYPVLAIASFAEGETVMDGLDELRL 351

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
VKE++R+ A+ L G EG + + L + T+ DHR+AM+F +
Sbjct: 352 VKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIAMSFLVMG 411

Query: 415 CA-EVPVTIRDPGCTRKTFFPDYFDVLS 440
A E PVT+ D +FP++ +++
Sbjct: 412 LASEKPVTVDDSTMIATSFPEFMGMMA 438

>gb|AAK62987.2|AF387597_1 EPSP synthase [Nicotiana sylvestris]
gb|AAK62988.2|AF387598_1 EPSP synthase 1 [Nicotiana tabacum]
Length = 52

Score = 84.3 bits (207), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 39/50 (78%), Positives = 45/50 (90%)

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+ +++EE+QLFLGNAG AMR LTAAVT AGG++ YVLDGVPRMRERPIGDL
Sbjct: 3 KKSEEEIQLFLGNAGTAMRPLTAAVTVAGGHSRYVLDGVPRMRERPIGDL 52

>gb|AAK62989.2|AF387599_1 EPSP synthase [Nicotiana tomentosiformis]
Length = 52

Score = 84.3 bits (207), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 38/50 (76%), Positives = 46/50 (92%)

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+++++E+QLFLGNAG AMR LTAAVT AGG++ YVLDGVPRMRERPIGDL
Sbjct: 3 KNSEQEIQLFLGNAGTAMRPLTAAVTVAGGHSRYVLDGVPRMRERPIGDL 52

>gb|AAK27445.1|AF326475_1 5-enolpyruvyl shikimate 3-phosphate synthase [Brucella abortus]
Length = 480

Score = 84.3 bits (207), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 113/454 (24%), Positives = 193/454 (42%), Gaps = 57/454 (12%)

Query: 13 KEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EAD 70
+ ++G +++PG KS+S R + L+ G T + LL EDV A++ +G + E D

Sbjct: 46 QALTGEIRIPGDKSISTRSMFGLASGKTRITGLLEGEDVINTGRAMQAMGARIRKEGD 105

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V GC + E L GNAG R V +++ D +

Sbjct: 106 VWIINGVGNCG-----LLQPEAPLDFGNAGTGARLTMGLVGTMDKTSFIGDA--SLS 156

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+RP+G ++ L+++G V+ G P P N I +V ++ S+Q SA

Sbjct: 157 KRPMGRVLNPLREMGVQVEAAEGDRMPLTLIGPRTANPI----AYRVPMA---SAQVKSA 209

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
+L+A G +I+ +++ + E ++++ FG + E R GQ

Sbjct: 210 VLLAGLNTPG--VTTVIEPVMTRDHT---KMLQGFADLTVDKDGVRHIRIVGQGKL 264

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V GD SS ++ L A + G+ VT+ + + L+ MGA + +

Sbjct: 265 TGQTIDVPGDPSSTAFLVLPALLVEGSEVTIRNVLNPNTRTGLIL--TLQEMGADIEIID 322

Query: 303 TSVTVTGPPPREPFGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAI 350
PR G LK + V + P D LA+ A FA+G T +

Sbjct: 323 -----PRLAGGEDVADLRVKASKLKGVVVPPERAPSMIDEYPVLAIXASFAEGETVM 374

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTATIDYDDHRMA 407
+ RVKE++R+ A+ L G EG + + L + T+ DHR+A

Sbjct: 375 DGLDELVRKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGLGGGTVATHLDHRIA 434

Query: 408 MAFSLAACA-EVPVTIRDPGCTRKTFFDYFDVLS 440
M+F + A E PVT+ D +FP++ +++

Sbjct: 435 MSFLVMGLASEKPVTVDDSTMIATSFPEFMGMMMA 468

>gb|AAK62986.2|AF387596_1 EPSP synthase 2 [Nicotiana tabacum]
Length = 52

Score = 84.3 bits (207), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 38/50 (76%), Positives = 46/50 (92%)

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+++++E+QLFLGNAG AMR LTAAVT AGG++ YVLDGVPRMRERPIGDL

Sbjct: 3 KNSEQEIQFLGNAGTAMRPLTAAVTVAGGHSRYVLDGVPRMRERPIGDL 52

>ref|YP_001209041.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dichelobacter nodosus
VCS1703A]
sp|A5EWS0.1|ARO_A_DICNV RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS

gb|ABQ13246.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Dichelobacter nodosus
VCS1703A]
Length = 442

Score = 83.6 bits (205), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 113/444 (25%), Positives = 191/444 (43%), Gaps = 30/444 (6%)

Query: 11 PIKEISGTVKLPKSGKSLNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P+ +SG + + G KS+S+R LLLAAL+EG T + L D ALR L + + + +

Sbjct: 9 PVSALSGEITICGDKSMHRALLLAALAEQGTEIRGFLPCADCLATAQALRALWVDIQRE 68

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
K VG G P + L + N+G +MR L + A VL G +

Sbjct: 69 KEIVTIRGVGFLGLQP-----PKAPLNMQNSGTSMRLLAGILAAQ--RFESVLCGDESLE 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSI--SSQYLSALLMA 189
+RP+ ++ L Q+GA + P I G P + + S+Q S L++A

Sbjct: 122 KRPMQRIITPLVQMGAKIVSHSNFTAPL----HISGRPLTGIDYALPLPSAQLKSCLILA 177

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
LA G + IS R++ FG E ++ + GGQK

Sbjct: 178 GLLADGTTRLHTCG--ISRDHTE---RMLPLFGGALETQK--EQIIVTGGQKLHGCVLEI 230

Query: 250 VEGDASSASYFLAGAAIT--GGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308

V GD S+A++F+ A I V + G + + +L+ MG ++
Sbjct: 231 V-GDLSAAAFFMVAALIAPRAEVVIRNVGINPTRSAI--ITLLQKMGGRIELHHQRFWGA 287
Query: 309 GPPRE-PFGRKHLKAIDVNMNKMMPDVAMTLA---VVALFADGPTAIRDVASWRVKETERM 364
P + L+ I V + + L + A A+G T + +++ RVKE++R+
Sbjct: 288 EPVADIVVYHSKLRGITVAPEWIANAIDELPIFFIAAACAEGTTTFVGNLSELRVKESDRL 347
Query: 365 VAIRTELTKLGASVEEGPDYCI--TPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVT 421
A+ L LG + + G D+ I + +++++ DHR+AM+ ++A A +
Sbjct: 348 AAMAQNLQTLGVACDVGADFIHIYGRSDRQFLPARVNSFGDHRIAMSLAVAGVRAAGELL 407
Query: 422 IRDPGCTRKTTPDYFDVLSTFVK 445
I D + P + D + N
Sbjct: 408 IDDGAVAAVSMPPQFRDFAAAIGMN 431

>ref|ZP_03636944.1| hypothetical protein HOLDEFILI_04270 [Holdemania filiformis DSM
12042]
gb|EEF65600.1| hypothetical protein HOLDEFILI_04270 [Holdemania filiformis DSM
12042]
Length = 293

Score = 83.6 bits (205), Expect = 6e-14, Method: Compositional matrix adjust.
Identities = 65/245 (26%), Positives = 114/245 (46%), Gaps = 16/245 (6%)

Query: 18 TVKLPGSKSLSNRILLALASEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAV 77
TV +P SKS+++R ++ AAL++G +++ ++ S+D+ + +R LG +E + + R
Sbjct: 52 TVAIPPSKSMAHRAICAALAQGESLIHHVDYSDDILTTIDGMRKLGAHIELEGS D V R V Q 111
Query: 78 VVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDL 137
+ P + + ++F +G +R + G + G R+ +RP
Sbjct: 112 GI-----PDFNQLQSEEIFCKESGSTLRFFIPIFSLTGKRVRF--GQNRLLQRP---- 159
Query: 138 VVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
+QL + + G L G + L G ISSQ++S LL A D
Sbjct: 160 QTVYQQLFEAQGFHYSQTAEWIEIEG--ALQPGDITLRGDISSQFISGLLFALVCRKEDS 217
Query: 198 EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSA 257
+ I S YVE+TL++++ FGV A D I GGQ+Y++ + VE D S
Sbjct: 218 TLHIEPPFESRSYVELTLQMLQDFGVHAYFEDELTLRIPGGQRYQACETT-VESDYSQL 275
Query: 258 SYFLA 262
++ A
Sbjct: 276 GFYAA 280

>ref|ZP_06522794.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis GM 1503]
gb|EFD74938.1| 3-phosphoshikimate 1-carboxyvinyltransferase aroA [Mycobacterium
tuberculosis GM 1503]
Length = 263

Score = 82.8 bits (203), Expect = 9e-14, Method: Compositional matrix adjust.
Identities = 79/233 (33%), Positives = 116/233 (49%), Gaps = 26/233 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALAS----EGTTVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+ TV +PGSKS +NR L+LAAL+ G + + L S D ML AL+TLGL V+
Sbjct: 13 VRATVTVPGSKSQTNRALVLAALAAQGRGASTISGALRSRDTLM DAL QTLGLRVD-- 70
Query: 71 KAAKRAVVVCGCGKFPVEDAKEE---VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 127
G G + V E ++ G AG +R + AA G+ DG
Sbjct: 71 -----GVGSELTVSGRIEPPGARVDCGLAGTVLRFVPP--LAALGSVPVTFDGDQ 119
Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ R RPI L+ L++LG VD GT P RV G G L GG V + S SSQ++S LL
Sbjct: 120 QARGRPIAPLLDALRELGVAVD---GTGLP-FRVRGNGSLAGGTVAIDASASSQFVSGLL 175
Query: 188 MAAPLALGDVEIEII-DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
++A + ++ L S P++ MT ++ + GV + S +R+ ++ G
Sbjct: 176 LSAASFDTGLTVQHTGSSLP SAPHIAMTAAML RQAGVDIDDSTP-NRWQVRPG 227

>gb|AAX21644.1| AroA [Wolbachia persica]
Length = 172

Score = 82.8 bits (203), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 55/146 (37%), Positives = 76/146 (52%), Gaps = 4/146 (2%)

Query: 167 LPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
L GG +++ G SSQ+ S LLMAAP + + I PY++MT ++ME FGV
Sbjct: 26 LSGGNIEVDGEKSSQFASGLLMAAPFMRHGLRLNSITDYKQ-PYLDMTTKVMEEFGVIV- 83

Query: 227 HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK 286
D Y +Y SP N VE D S+ASYF A AAITG + + + K
Sbjct: 84 --DIDKNIYTVKKSQYISPSNYVVEPDVSTASYFWAFAAITQSLRLCMLLKSLSKVISK 141

Query: 287 FAEVLEMMGAKVTWTETSVTVTGPPR 312
F EVLE +G +V + + + VTG +
Sbjct: 142 FLEVLENIGCQVNYCDDGIEVTGSDK 167

>ref|ZP_03655937.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
canadensis MIT 98-5491]
ref|ZP_04870155.1| 5-enolpyruvylshikimate-3-phosphate synthase [Helicobacter
canadensis MIT 98-5491]
ref|ZP_07803665.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
canadensis MIT 98-5491]
gb|EES89335.1| 5-enolpyruvylshikimate-3-phosphate synthase [Helicobacter
canadensis MIT 98-5491]
gb|EFR48120.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
canadensis MIT 98-5491]
Length = 436

Score = 82.8 bits (203), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 115/437 (26%), Positives = 197/437 (45%), Gaps = 36/437 (8%)

Query: 20 KLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
++ KS+S+R + + LS+ +++ N L ED L + LGL V + V+
Sbjct: 17 ETAAKDSISHRCAIFSLSDKPSLIRNYLKGEDTLDLSLNIARKLGLEVREE--GNEMVLT 74

Query: 80 GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVV 139
P + + L GNAG A+R ++A G +VL G + +RP+ +V+
Sbjct: 75 P-----PPSIQEPKSILECGNAGTAIRLYLGLLSAQKG--LFVLSGDCYLNKRPMKRVL 127

Query: 140 GLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEI 199
L+ +GA + + P+ V G G L S S+Q SALL++ A GD
Sbjct: 128 PLRSIGAVILGREDGNLAPLVVVGNGNLQSFDT-SQIPSAQVKSALLSGLFAKGDSRY 186

Query: 200 EIIDKLISIPYVEMTLRLMERFGVKAEHS-DSWDRFYIKG---QKYKSPKNAYVEGDAS 255
+ +S + E R++ GV+ E + I+ QK K P + D S
Sbjct: 187 R--EPESLSDHTE---RMLSGMGVELESKMNGMGEVEIRLSPLKQKLK-PLIMEIPADPS 240

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQ-GDVKFAEVLEMMGAKVTWTETSVTVTGPPR-E 313
SA +F AAI + V L ++ +LE MG K+ + ETS T E
Sbjct: 241 SAFFFALAAAIMPNSHLV--LKNILLNPTRIEAFRILEKMGVKIIYKETSNTYESIGDIE 298

Query: 314 PFGRKHLKAIDVN-----MNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
F + L++++V+ ++++P +A+ +A A G + +++ RVKET+R+ A+
Sbjct: 299 IFSPQSLQSVSEKISWLIDEIPALAIAMAC---AKGISRVKNAKELRVKETDRIKAV 354

Query: 368 RTELTKLGSASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGC 427
L G E D I E + + +Y DHR+AM+F++A + I
Sbjct: 355 VENLKLGCIEANELEDGFEIKGGE-IQRAEVSSYGDHRIAMSFIAIAGLKN-GMEITQAEY 412

Query: 428 TRKTFPDYFDVLSTFVK 444
+FP++ ++LS +
Sbjct: 413 INISFPNFLEILSKITQ 429

>emb|CBL42035.1| 5-enolpyruvylshikimate-3-phosphate synthase [butyrate-producing
bacterium SS3/4]
Length = 276

Score = 82.4 bits (202), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 79/294 (26%), Positives = 131/294 (44%), Gaps = 30/294 (10%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L + G + +PG KS+S+R ++ +++GTT + N L S D +G R +G+ +E
Sbjct: 3 LHKADHVRGEITVPGDKSISHRSVMFGSIAKGTTEIHNFLSADCLSTIGCFRRMGIDIE 62

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
VV GK A L GN+G R ++ + A N L G
Sbjct: 63 NKNG-----VVTVHGKGMHGLAAPAETLDCGNSGTTTRLISGIL--APQNFVTLTGDES 115

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI--SSQYLSALL 187
+++RP+ ++ L +GAD+ G DC P+R I G P + + + S+Q S++L
Sbjct: 116 IQKRPMKRIIEPLSMMGADIRSVRGNDCAPLR---ICGKPLAGIHYTSKVASAQVKSSIL 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS----WDRFYIKGGQKYK 243
+A A D I + +S + E+ L+ FG + E + W + G +
Sbjct: 173 LAGLYA--DGLTSITEPQVSRNHTELMLKF---FGAELESKGTTVTIWPATELFGNR--- 224

Query: 244 SPKNAYVEGDASSASYFL-AGAAITGGTTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
V GD SS+ YF+ AG + V ++ G + +V E MGA
Sbjct: 225 ----IDVPGDISSSVYFVAAGLILPNSEVLIKNVGINPTRAG--LIKVCEAMGA 272

>pdb|2PQD|A Chain A, A100g Cp4 Epsps Liganded With (R)-Difluoromethyl
Tetrahedral Reaction Intermediate Analog
Length = 445

Score = 82.4 bits (202), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 118/452 (26%), Positives = 200/452 (44%), Gaps = 54/452 (11%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 13 LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNAG R V ++T++ D + +RP+
Sbjct: 73 IIDGVNGGGLL-----APEAPLDFGNAGTGCRLTMGLVGVDYDFDSTFIGDA--SLTKRPM 125

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 126 GRVLNPLREMGVQVKSEGD-DRLPVTLRG---PKTPTPITYRVPMASAQVKSALLAGL 180

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG +D ++G K +
Sbjct: 181 NTPGIT--TVIEPIMTRDTE---KMLQGFGANLTVETDADGVRTIRLEGRKLTG-QVI 234

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +
Sbjct: 235 DVPGDPSSTAFLVAALLVPGSDVTILNVLMNPTRTGLIL--TLQEMGADIEVIN----- 287

Query: 308 TGPPREPFGR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V ++ P D LAV A FA+G T + +
Sbjct: 288 ---PRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEE 344

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K + A+ T+ DHR+AM+
Sbjct: 345 LRVKESDRLSAVANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVATHLDHRIAMS 404

Query: 410 F-SLAACAEVPVTIRDPGCTRTFPDYFDVLS 440
F + +E PVT+ D +FP++ D+++
Sbjct: 405 FLVMGLVSENPTVDDATMIATSFPEFMDLMA 436

>pdb|2GGD|A Chain A, Cp4 Epsp Synthase Ala100gly Liganded With S3p And
Glyphosate
Length = 455

Score = 82.0 bits (201), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 118/452 (26%), Positives = 200/452 (44%), Gaps = 54/452 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 18 LSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNAG R V ++T++ D + +RP+
Sbjct: 78 IIDGVGNGGLL-----APEAPLDFGNAGTGCRLTMGLVGVYDFDSTFIGDA--SLTKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 131 GRVLNPLREMGVQVKSEGD-DRLPVTLRG----PKTPTPITYRVPMASQVKSALLAGL 185

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ ++ + E ++++ FG +D ++G K +
Sbjct: 186 NTPGIT--TVIEPIMTRDHT---KMLQGFANLTVETDADGVRTIRLEGRKLTG-QVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +
Sbjct: 240 DVPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLIL--TLQEMGADIEVIN----- 292

Query: 308 TGPPREPFGFR-----KHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V ++ P D LAV A FA+G T + +
Sbjct: 293 ---PRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEE 349

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K + A+ T+ DHR+AM+
Sbjct: 350 LRVKESDRLSAVANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATAHLDRHRIAMS 409

Query: 410 F-SLAACAEVPTVIRDPGCTRTFPDYFDVLS 440
F + +E PVT+ D +FP++ D+++
Sbjct: 410 FLVMGLVSENPTVDDATMIATSFPEFMDLMA 441

>ref|YP_001407856.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter curvus
525.92]
sp|A7GXB4.1|AROACAMC5 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|EAU00796.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter curvus
525.92]
Length = 424

Score = 81.3 bits (199), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 107/436 (24%), Positives = 192/436 (44%), Gaps = 28/436 (6%)

Query: 7 IVLQPIK-EISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 65
I+ +PI E+S ++ KS+S+R + + LS+ + V N L + D L +RTL
Sbjct: 5 ILNEPINVELS---RIAADKSISHRCAIFSLSDKPSHVRNYLKAGDTLNTLDIVRTLGA 61

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
++ + + ++ P + + +V L GN+G +MR + A G +VL G
Sbjct: 62 QIQ--ERGEVITP-----PEKILEPDVLECGNSGTSMLFMGLLAAQDG--FFVLSG 112

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + L +GA +D + P+ + G L K S S+Q SA
Sbjct: 113 DKYLNRRPMAVAKPLVAVGAKIDGANEANTAPLCIRG-KKLERFKYD-SPVASAQVKS 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LL+AA + G E + +S + E L+ G+ A+ ++ +P
Sbjct: 171 LLLAALYSNG---CEFSEPELSRDHTERMLK-----GMGAKIKTQGASIALEPMSTPLAP 222

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSV 305
+ V D SSA +F A I + V + ++ ++L+ MGA + + E S
Sbjct: 223 LDIDVPNDPSSAFFFAVAACIIPNSHIVLK-NVLLNETRIEAYKILQKMGADIKFKEISG 281

Query: 306 TVTGPPREPFGKRHLKAIDV--NMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
L A++V N++ + D A LA+ A G + +++ RVKE +R
Sbjct: 282 KYESIGDIEIRYAALNAVEVSENISWLIDEAPALAI AFANAKGTSVLKNAKELRVKECDR 341

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLAACAEVPTIR 423

+ L K G E D ++ + + ID++ DHR+AM+F++ + + I
Sbjct: 342 IAVTVAGLKCKGKIKARELEDGFEVSGSDA-SCAIIDSHGDHRIAMSFVAVLGL-KCGMIIE 399

Query: 424 DPGCTRKTFPDYFDVL 439
+FP++ +L

Sbjct: 400 KSEFIATSFPNFVSIL 415

>ref|YP_374215.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium luteolum DSM 273]
sp|Q3B659.1|AROA_PELLD RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ABB23172.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Chlorobium luteolum DSM 273]
Length = 433

Score = 80.9 bits (198), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 108/442 (24%), Positives = 191/442 (43%), Gaps = 47/442 (10%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK-----AAK 74
LP KS+S+R L+A+LS+G T + N D LG L+ G+ V ++ A
Sbjct: 11 LPPDKSISHRAALIASLSDGETEIMNFSAGFDNQSTLGVQLACGIPVRQEEVPGPWGTAI 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VV+ G + + +Q N+G MR + + AG L G + +RP+
Sbjct: 71 LRVVIKSKGLWSLTPPSAPLQ--CNNSGSTMRFSGIL--AGQPFQSELVGDASLLKRP 126

Query: 135 GDLVVGLKQLGADVDCF-LGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ L Q+GA V +GT PV + G L +L ++S + +L+ A L
Sbjct: 127 RRIADPLIQMGAGVSLSPIGT--APVVITGSKDLHAIDYRL--PVASAQVKSLVAFAGLH 182

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
+ E I + L S + E+ L L R ++ +R + G++ + + + D
Sbjct: 183 -AEGETRIYEPLSSRNHTEMLGLEPRV-----ENEERVIVVPGRRQREARPFQIPAD 234

Query: 254 ASSASYFLA-GAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP- 311
S+A + ++ G G + + + F ++L GA VT E TV G
Sbjct: 235 PSAACFIVSLGLLARGSEIMIRDVCLNPTRA--AFLDILIRAGAAVT-IENRRTVGGESI 291

Query: 312 -----REPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
EP + + + +++++P L V++ FA + + R KE+
Sbjct: 292 GDILVEGTRDMEPLVISDPQEVIAIAIDELP----MLGVLSAFATERFELMNAGELRTKES 347

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDHRMAMAFSLA--ACAE 417
+R+ A+ L +LG + P +T ++ +DDHR+AM+F++A AC E
Sbjct: 348 DRIEALALNLERLGFVCHQEPGGLSVTGRKGRPSGPVVVECFDDHRIAMSFVAVASKACGE 407

Query: 418 VPVTIRDPGCTRKTFPDYFDVL 439
+ + D +FP++F +L
Sbjct: 408 -DIELSDREVAGVSFPNFFSL 428

>ref|YP_003109953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidimicrobium ferrooxidans DSM 10331]
gb|ACU54280.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Acidimicrobium ferrooxidans DSM 10331]
Length = 434

Score = 80.9 bits (198), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 120/441 (27%), Positives = 200/441 (45%), Gaps = 31/441 (7%)

Query: 6 EIVLQP-IKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++V++P SG ++ P KS+S+R LL A L+ GTT+V+ L + DV L A+R G
Sbjct: 2 DLVIRPGAHAPSGVLEPPDPKSIHRALLGALLARGTTIVEGLSRALDVTATLEAIRAFG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V +++A + G G + VE E + +GN+G R T G V+D
Sbjct: 62 -AVVSEIRANGTLEIDGPGIEGLVE---PEGVIDVGNSGTLARLGLGVATLVPG--LVVID 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFGLTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G +R RP+ ++ L+ LGA +D G P V G L GG ++L ++S +
Sbjct: 116 GDASVRRRPMARVIEPLRSLGAVIDARGGARWLPAAVRG-ARLAGGTIEL--RVASAQVK 172

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+ L+ A + +++ + + P+ E L L+ + E +D R + G

Sbjct: 173 SALLLA-GLGAASAVSVVEPVATRPHTTEELLGLLGLEVDEEELADGRHRVSVPVGPTRPV 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGC--GTTSLQGDVKFAEVLEMMGAKV-TWT 301
+ +++A + +A AA G + V G G T + +VL MGA++

Sbjct: 232 ERIVVARDPSAAAFFVVAAAATPGARLEVRGAYLGPTR----TGyLDVLRMGAEIEVLG 287

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+V V G L A + +++P D LAV A G + I A RV

Sbjct: 288 RDTVIVRG-----AALGATTIVADEVPSLIDEVPLAVAFAAARGTSRIEGAELRV 339

Query: 359 KETERMVAIRTELTKLGASVEEGPD-YCIITPPEKLNVTATIDTYDDHRMAMAFSL-AACA 416
KE++R+ L GA+VE D + + P +D+ DHR+AM+ ++ AA

Sbjct: 340 KESDRIETTARMLEAFGATVETSHDGFVVEGTPSPSGPVLVDSVRDHRIAMSAAVWAATQ 399

Query: 417 EVPVTIRDPGCTRKTFFDYFD 437
+ IRD ++P + D

Sbjct: 400 GIGARIRDAEWVATSYPGFVD 420

>gb|ADI18937.1| 5-enolpyruvylshikimate-3-phosphate synthase [uncultured SAR11
cluster bacterium HF0010_09016]
Length = 441

Score = 80.9 bits (198), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 106/453 (23%), Positives = 198/453 (43%), Gaps = 32/453 (7%)

Query: 7 IVLQPIKEISGTVKLPKSKSLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I+ + I + + PG KSL R +L+++L+ G + NLL SEDV + A+R LG+

Sbjct: 6 IIKKKIGNYNKKITIPGDKSLIRWVLISLANGISQAKNLLMSIEDVIATINAIKRLGVR 65

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-- 124
+ + + VG G K+ + + N+G R L + N+ Y +

Sbjct: 66 AKINNICKICKIHGVGING----FKYKKNLVIDAQNSGTGLRLLAGLLI----NSPYPIKII 117

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +R + LK+ GA++ P+ + G L + L S+Q S

Sbjct: 118 GDKSLSKRDFKRIAQPLKKFGANLR-LKNNYTLPLTIKGSQNLKPIRY-LENKGSQVKS 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++ A G I+ S + E + + + +K + ++D I +K K

Sbjct: 176 CIIFAGARTNGKTIICKQ---SRDHSERIFKYL-KLPIKIKRKKNYDLIEISKVKKIK- 230

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P N + D SS ++F+A A++G + +T++ + V +L+ MG K+++

Sbjct: 231 PINYKIPSDLSSCAFFIALTALSGKSKLTIKEVNINPRTGTG--LTILKKMGVKISFFNK 288

Query: 304 SVTVTGPPREPFGFR--KHLKAIDV--NMNMKMP-DVAMTLAVVALFADGPTAIRDVASWRV 358
+ P + F + K LK+I+ N+N D + L ++A A G + +++

Sbjct: 289 KIYKGEPDIADIFIQSPKMLKSINCPNSLNSAAIDEFLVFLIAAKAKGVSFKNLDELNK 348

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTAI--DTYDDHRMAMAFSLAA 414
KE+ R+ L +G V + I P K N I + DHR+ M +AA

Sbjct: 349 KESPRLKWGSKILKMMGVKVIITKNSIKIFGNPELKTNNKIIKKNYLDHRVFMSTVIAA 408

Query: 415 CAEVP---VTIRDPGCTRKTFFDYFDVLSTFVK 444
+ +I +P + +FP++ +++ K

Sbjct: 409 LSFTDGGVWSIANPESVKTSFPNFKIINQLKK 441

>pdb|2PQB|A Chain A, Cp4 Epsps Liganded With (R)-Difluoromethyl Tetrahedral
Intermediate Analog
pdb|2PQC|A Chain A, Cp4 Epsps Liganded With (R)-Phosphonate Tetrahedral
Reaction Intermediate Analog
Length = 445

Score = 80.1 bits (196), Expect = 6e-13, Method: Compositional matrix adjust.

Identities = 117/452 (25%), Positives = 199/452 (44%), Gaps = 54/452 (11%)

```
Query: 15  ISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 13  LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 72

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNA R V ++T++ D + +RP+
Sbjct: 73  IIDGVGNGGLL-----APEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDA--SLTKRPM 125

Query: 135  GDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 126  GRVLNPLREMGVQVKSEGD-DRLPVTLRG---PKTPTPITYRVPMASQVKSALLAGL 180

Query: 192  LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG +D ++G K +
Sbjct: 181  NTPGIT--TVIEPIMTRDHTD---KMLQGFGANLTVETDADGVRTIRLEGRKLTG-QVI 234

Query: 249  YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +
Sbjct: 235  DVPGDPSSTAFLVAALLVPGSDVTILNVLMPNPTRTGLIL--TLQEMGADIEVIN----- 287

Query: 308  TGPPREPFGFR-----KHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V ++ P D LAV A FA+G T + +
Sbjct: 288  ---PRLAGGEDVADLRVSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEE 344

Query: 356  WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK---LNVTAIDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K + A+ T+ DHR+AM+
Sbjct: 345  LRVKESDRLSAVANGLKLVDCDEGETSLVVRGRPDGKGLGNASGA AVATHLDHRIAMS 404

Query: 410  F-SLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
F + +E PVT+ D +FP++ D+++
Sbjct: 405  FLVMGLVSENPTVDDATMIATSFPEFMDLMA 436
```

```
>ref|YP_001697683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
sphaericus C3-41]
gb|ACA39553.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
sphaericus C3-41]
Length = 186
```

Score = 79.7 bits (195), Expect = 8e-13, Method: Compositional matrix adjust.
Identities = 59/182 (32%), Positives = 88/182 (48%), Gaps = 7/182 (3%)

```
Query: 261  LAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE-PFGRKH 319
+AGA +T+E G + + EVL MGA +T + P
Sbjct: 1  MAGAICHNSQLTLENVGVNPTRDGI--IEVL SKMGATMTVMPNDNSQAEPTATIQITST 58

Query: 320  LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L + + +P D LA++A A G T I+D +VKET+R+ A+ EL KLGA
Sbjct: 59  LSGTTIEGDMIPRLIDEIPILALLATQAHGQTIKDAEELVKETDRITAVVAELKKLGA 118

Query: 377  SVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDY 435
++E D II P L ++ TY DHR+ M ++AA E PVT+ D C ++P +
Sbjct: 119  NIEATNDGMIIIEGPTPLKGASLKTYGDHRIGMMGAVAALMTEGPVTLDDAQCIASVYPSF 178

Query: 436  FD 437
F+
Sbjct: 179  FE 180
```

```
>sp|Q9R4E4.2|AROA_AGRSC RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
pdb|2GG4|A Chain A, Cp4 Epsp Synthase (Unliganded)
pdb|2GG6|A Chain A, Cp4 Epsp Synthase Liganded With S3p
pdb|2GGA|A Chain A, Cp4 Epsp Synthase Liganded With S3p And Glyphosate
Length = 455
```

Score = 79.7 bits (195), Expect = 9e-13, Method: Compositional matrix adjust.
Identities = 117/452 (25%), Positives = 199/452 (44%), Gaps = 54/452 (11%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 18 LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 77

Query: 75 RAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNA R V ++T++ D + +RP+
Sbjct: 78 IIDGVGNGGGLL-----APEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDA--SLTKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 131 GRVLNPLREMGVQVKSEGD-DRLPVTLRG----PKTPTPITYRVPMASQVKSALLAGL 185

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG +D ++G K +
Sbjct: 186 NTPGIT--TVIEPIMTRDHT---KMLQGFGANLTVETDADGVRTIRLEGRKLTG-QVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +
Sbjct: 240 DVPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLIL--TLQEMGADIEVIN----- 292

Query: 308 TGPPREPFGFR-----KHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V ++ P D LAV A FA+G T + +
Sbjct: 293 ---PRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEE 349

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K + A+ T+ DHR+AM+
Sbjct: 350 LRVKESDRLSAVANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATHLDHRIAMS 409

Query: 410 F-SLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
F + +E PVT+ D +FP++ D+++
Sbjct: 410 FLVMGLVSENPTVDDATMIATSFPEFMDLMA 441

>gb|AAL67577.1|AF464188_1 CP4EPSPS [Glycine max]
gb|AA017037.1| CP4EPSPS protein [synthetic construct]
Length = 455

Score = 79.7 bits (195), Expect = 9e-13, Method: Compositional matrix adjust.
Identities = 117/452 (25%), Positives = 199/452 (44%), Gaps = 54/452 (11%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 18 LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 77

Query: 75 RAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNA R V ++T++ D + +RP+
Sbjct: 78 IIDGVGNGGGLL-----APEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDA--SLTKRPM 130

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 131 GRVLNPLREMGVQVKSEGD-DRLPVTLRG----PKTPTPITYRVPMASQVKSALLAGL 185

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG +D ++G K +
Sbjct: 186 NTPGIT--TVIEPIMTRDHT---KMLQGFGANLTVETDADGVRTIRLEGRKLTG-QVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +
Sbjct: 240 DVPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLIL--TLQEMGADIEVIN----- 292

Query: 308 TGPPREPFGFR-----KHLKAIDVNMNMP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V ++ P D LAV A FA+G T + +
Sbjct: 293 ---PRLAGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMNGLEE 349

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K + A+ T+ DHR+AM+
Sbjct: 350 LRVKESDRLSAVANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAATHLDHRIAMS 409

Query: 410 F-SLAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
F + +E PVT+ D +FP++ D+++

Sbjct: 410 FLVMGLVSENPVTVDATMIATSFPEFMDLMA 441

>ref|YP_664289.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
acinonychis str. Sheeba]
sp|Q17YI6.1|AROA_HELAH RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
emb|CAJ99290.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter
acinonychis str. Sheeba]
Length = 429

Score = 79.3 bits (194), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 111/446 (24%), Positives = 185/446 (41%), Gaps = 59/446 (13%)

Query: 25 KSLSNRILLLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVCGGK 84
KSLS+R ++ + L++ V N L D L + LG VE AK + +
Sbjct: 11 KSLSHRAVIFSLLAKKPCFVRNFLMGGDCLSSLEIAQNLGARVE--NIAKNSFKIT---- 64

Query: 85 FPVEDAKEEVQLF-LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQ 143
P KE ++ N+G +MR + ++A G +VL G + RP+ ++ LK
Sbjct: 65 -PPWALKEPRKILNCNNSGTSMLYSGLLSAQKG--LFVLSGDNLSLRPMKRIIEPLKA 121

Query: 144 LGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEII 202
G + LG + I G P I+S Q SA +++A A G
Sbjct: 122 FGTKI---LGREDNHFAPLVILGSPLKADYESPIASAQVKSAFILSALQAQGTSTYR-- 176

Query: 203 DKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYF-L 261
+ +S + E+ L+ + A D I +K + + D SSA +F L
Sbjct: 177 ESELSRNHTEIMLK-----SLGANIKDQDGVLKISPLEKPLEAFDFKIANDPSSAFFFAL 231

Query: 262 AGAAITGGTVTVEGCGTTSLQGDKVFAEVLMMGAKVTWTETSVTVTGPPPREPFGRKH-- 319
A A + + ++ + ++ EVL+ MG T + E G +
Sbjct: 232 ACAILPKSRLLLKNVLLNPTR--IEAFEVLLKMG-----THIECVIKSKDLEIIGDIYIE 284

Query: 320 ---LKAI--DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKL 374
LKAI D N+ + D L + LFA G + +++ R KE++R+ A+ + L L
Sbjct: 285 HALLKAITIDQNIASLIDEIPALGIAMLFAGKSVVKNKADLRSKESDRIKALISNLKAL 344

Query: 375 GASVEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
G EE D + I PP I +++DHR+AM+F++ +
Sbjct: 345 GIECEEFEFGFYIEGLEDISQLKQRFSGIKPP-----IIKSFNDHRIAMSFAILTLM-L 397

Query: 419 PVTIRDPGCTRKTFPDYFDVLSTFVK 444
P+ I + C +FP + +L+ F K
Sbjct: 398 PLEIDNLECANISFPQFKRLNLNLFKK 423

>dbj|BAD94823.1| 5-enol-pyruvylshikimate-3-phosphate synthase class 2 precursor
[Agrobacterium sp. CP4]
Length = 527

Score = 79.0 bits (193), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 115/444 (25%), Positives = 199/444 (44%), Gaps = 38/444 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G + +
Sbjct: 90 LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIRKEGDTW 149

Query: 75 RAVVVCGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
VG GG E L GNA R V ++T++ D + +RP+
Sbjct: 150 IIDGVNGGGLL-----APEAPLDFGNAATGCRLTMGLVGVYDFDSTFIGDA--SLTKRPM 202

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A
Sbjct: 203 GRVLNPLREMGVQVKSEGD-DRLPVTLRG---PKTPTPITYRVPMASQVKSALLAGL 257

Query: 192 LALGDVEIEIIDLKISIPYVEMTLRLMERFGVK---AEHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG +D ++G K +
Sbjct: 258 NTPGIT--TVIEPIMTCDHTE---KMLQGFGANLTVETDADGVRTIRLEGRKLTG-QVI 311

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA + +
Sbjct: 312 DVPGDPSSTAFLVAALLVPGSDVTILNVLMPNTRTGLIL--TLQEMGADIEVINLRLAG 369

Query: 308 TGPPREPFGGRKH-LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ R LK + V ++ P D LAV A FA+G T + + RVKE++R
Sbjct: 370 GEDVADLRVRSSSTLKGVTVPEDRAPPMIDEYPILAVAAFAEGATVMNGLEELRVKESDR 429

Query: 364 MVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMAF-SLAACA 416
+ A+ L G +EG ++ P K + A+ T+ DHR+AM+F + +
Sbjct: 430 LSAVANGLKLNQVDCDEGETSLVVGRPDGKGLGNASGAAVATHLDHRIAMSFLVMGLVS 489

Query: 417 EVPVTIIRDPGCTRKTFPDYFDVLS 440
E PVT+ D +FP++ D+++
Sbjct: 490 ENPVTVDATMIATSFPEFMDLMA 513

>gb|EDZ73130.1| YDR127Wp-like protein [Saccharomyces cerevisiae AWRI1631]
Length = 535

Score = 79.0 bits (193), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 56/138 (40%), Positives = 75/138 (54%), Gaps = 11/138 (7%)

Query: 5 EEIVLQPIKEI---SGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
+E ++ P K+I V PGSKS+SNR L+LAAL EG + NLL+S+D +ML A+
Sbjct: 401 DETLVYPFKDIPADQQKVVIIPGSKSISNRALILAALEGQCKIKNLLHSDDTKHMLTAV 460

Query: 61 RTL-GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMR---SLTAAVTAAG 116
L G ++ + + VV G GG A L+LGNAG A R SL A V +
Sbjct: 461 HELKGATISWEDNGETVVVEGHGGSTLSACADP---LYLGNAGTASRFLTSLAALVNSTS 517

Query: 117 GNATYVLDGVPRMRERPI 134
VL G RM++RPI
Sbjct: 518 SQKYIVLTGNARMQQRPI 535

>ref|ZP_08072352.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylocystis sp.
ATCC 49242]
gb|EFY00154.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Methylocystis sp.
ATCC 49242]
Length = 410

Score = 78.6 bits (192), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 115/423 (27%), Positives = 176/423 (41%), Gaps = 30/423 (7%)

Query: 32 LLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVV-VGCGGKF-PVED 89
++ L+ G T ++ LL EDV A R LG + +V G G P E
Sbjct: 1 MIFGLLAVGETRIEGLLEGEDVLRTAQACRQLGAKIVRHAPGSWSVWGAGLGSLLQPT- 59

Query: 90 AKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGLDVLVGLKQLGADV- 148
L GNAG R + V AG DG +R+RP+ ++ L GA V
Sbjct: 60 -----TLDGFGNAGTGSRLMMGVV--AGHPIVARFDGDASLRKRPMRRIPLDPLALQGAQVL 112

Query: 149 DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEIIDKLIS 207
+ G P V LP V+ ++S Q SA+L+ + G +I+ S
Sbjct: 113 EQAEGGRLPLVLQGAPEPLP---VEYKTPVASAQIKSAVLLCGLNSPG--RTVVIEAEAS 167

Query: 208 IPYVEMTLRLMERFGVK--AEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAA 265
+ E +++ FG K +E + R G+ + V D SSA++ + A
Sbjct: 168 RDHTE---KMLAHFGAKVTSEPYGAHGRKITLEGRPELVAREVVRPADPSSAAFPIVAAL 224

Query: 266 ITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGR-KHLKAI 323
I G+ + VEG T L+ L+ MGA +T + R L+ +
Sbjct: 225 IAPGSDIVVEGVMTNPLRSG--LLTTLQEMGADITLDNRRDEGGEEVADVLRARFSSLRGV 282

Query: 324 DVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEE 380
DV + P D LAV A FA G T +R ++ RVKE++R+ AI L G E
Sbjct: 283 DVPAERAPSMIDEYPILAVAAFAQGETRMRGLSELRVKESDRLAIAAGLAVNGVDCEI 342

Query: 381 GPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA-EVPVTIIRDPGCTRKTFPDYFDVL 439
D I+ ++T+ DHR+AM+F + A + VT+ D +FP + ++

Sbjct: 343 VGDDLIVRGGA VKGGGVVETHLDHRIAMSFLVMGLASQSKVTVDDETMIA TSFPSFRALM 402

Query: 440 STF 442

T

Sbjct: 403 ETL 405

>ref|ZP_08142635.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas sp. TJI-51]
gb|EGB96080.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas sp. TJI-51]
Length = 290

Score = 78.6 bits (192), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 84/287 (29%), Positives = 129/287 (44%), Gaps = 20/287 (6%)

Query: 157 PPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLR 216
PP+ + G L G L + S+Q S LL+A A G + P + T R

Sbjct: 1 PPLTIRGGHRLKGLTYTLPMA-SAQVKSCLLLAGLYAEGKTTVTE-----PAPTRDHTER 54

Query: 217 LMERFGVKAHSDSDWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEG 275
++ FG E + ++ G K + + V D SSA++FL A+I G+ + +E

Sbjct: 55 MLRGFGYAVESNGPVA--SLQSGGKLTA TR-IEVPADISSAAFFLVAASIAEGSELVLEH 111

Query: 276 CGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRK--HLKAIDVNMNKMPP-- 331
G + V ++L +MG ++ E V G P + LK ID+ +P

Sbjct: 112 VGINPRTGTG--IDILRLMGGDISL-ENQREVGGEPVADLRVRGAKLKGIDIPPELVPLA 168

Query: 332 -DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPP 390
D L V A A+G T +R RVKE++R+ + L LG E PD II

Sbjct: 169 IDEFPVLVFAAACAEGRTVLRGAEEELRVKESDRIQVMADGLLTLGIKCEPTPDGIIID-G 227

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYF 436
+L + + DHR+AMAFS+A+ A P+ I D +FP++

Sbjct: 228 GQLGGGEVHGHDHRIAMAFSVASLRASAPIRIHDCANVATSFPNFL 274

>gb|ADU03259.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus suis]
Length = 235

Score = 78.2 bits (191), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 64/232 (27%), Positives = 122/232 (52%), Gaps = 17/232 (7%)

Query: 12 IKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++++ G +++PG KS+S+R ++ +L++G T V ++L EDV + R LG+ +E +
Sbjct: 7 VEKLQGVIRVPGDKSISHRSIIFGSLAKGVTRVHDILRGEDVLSTMQVFRDLGVKIEDNG 66

Query: 72 AAKRAVVVGCGG-KFPVEDAKEEVQFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
VG G + P D L +GN+G ++R ++ + AG + + G +
Sbjct: 67 DIVEVHGVGFDGLQVPKND-----LDMGNSGTSIRLISGVL--AGQDFEATMFGDDSL 118

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
+RP+ + + L Q+G ++ D PP+ + G L + +L + S+Q SAL+ AA
Sbjct: 119 KRPMDRVTIPLSQMGVEISGQTERDLPLTIKGNKNLKPIRYQLPVA-SAQVKSALIFAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSDWDRFYIKGGQKY 242
A G E I++K ++ + E ++ +FG + E + R I+GGQ++
Sbjct: 178 LQAEG--ESVIVEKELTRNHTE---DMIVQFGGQLEVNGKEIR--IQGGQEF 222

>ref|ZP_04126962.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar sotto str. T04001]
gb|EEM41408.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar sotto str. T04001]
Length = 170

Score = 78.2 bits (191), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 78/161 (48%), Gaps = 5/161 (3%)

Query: 289 EVLEMMGAKVTWTETSVTVTGPPRE-PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFA--- 344
+VLE MGA T + + P LK I++ + +P + + V+AL A

Sbjct: 10 DVLEKMGATFTVDLINEGASEPAANITITETSSLKGIEIGGDIIPRLIDEIPVIALAATQA 69

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDH 404
+G T I+D +VKET R+ + ELTKLGA +E D II L +++Y DH

Sbjct: 70 EGITVIKDAHELKVKETNRIDTVVAELTKLGARIEATDDGMIYGKSALKGNTVNSYGDH 129

Query: 405 RMAMAFSLAAC-AEVPVTIRDPGCTRKTFFPDYFDVLSFVK 444
R+ M ++A C AE I D ++P +FD L K

Sbjct: 130 RIGMMLAIAGCLAEGKTIIEDAEAVGVSYPFFDELQKLAK 170

>ref|YP_002828058.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium fredii
NGR234]
sp|C3MC80.1|AROA_RHISN RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase;
AltName: Full=5-enolpyruvylshikimate-3-phosphate
synthase; Short=EPSP synthase; Short=EPSPS
gb|ACP27305.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium fredii
NGR234]
Length = 448

Score = 77.8 bits (190), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 118/452 (26%), Positives = 201/452 (44%), Gaps = 52/452 (11%)

Query: 14 EISGTVKLPGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ GTV++PG KS+S+R + L+ G T + LL EDV A++ +G + K

Sbjct: 17 DLKGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGAKIR--KEG 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G G + E L GNAG R V ++T++ D + +RP

Sbjct: 75 DTWIINGVGNGALL---APEAPLDFGNAGTGCRLTMTGLVGVYDFDSTFIGDA--SLTKRP 129

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A

Sbjct: 130 MGRVLDPLREMGVQVKSAGG-DRLPVTLRG----PKTPNPITYRVPMASAQVKSAYLLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNA 248
G +I+ +++ + E ++++ FG + E + R G+ + +

Sbjct: 185 LNTPGIT--TVIEPVMTRDHE--KMLQGFGANLSVETDTAGVVRTIRLEGRGKLTGQVI 239

Query: 249 YVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD SS ++ L A + G+ VT+ + + L+ MGA +

Sbjct: 240 DVPGDPSSTAFLVAALLVPGSDVTILNVLMNPTRTGLIL--TLQEMGANIEVMN----- 292

Query: 308 TGPPREPFGFGR-----KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
PR G LK + V + P D LAV A FA+G T + +

Sbjct: 293 ---PRLAGGEDVADLRVRYSELKGVTVPEERAPSMIDEYPVLAVAAFAEGATVMNGLDE 349

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK-LNVT---IDTYDDHRMAMA 409
RVKE++R+ A+ L G +EG ++ P K L A + T+ DHR+AM+

Sbjct: 350 LRVKESDRLSAVADGLKLVGDCDEGEASLVVRGRPGGKGLGNAAGGQVKTHLDHRIAMS 409

Query: 410 F-SLAACAEVPVTIRDPGCTRKTFFPDYFDVLS 440
F L +E PVT+ D +FP++ D+++

Sbjct: 410 FLVLGLASEHPVTVDDATMIATSFPEFMDLMT 441

>ref|ZP_03806227.1| hypothetical protein PROPEN_04629 [Proteus penneri ATCC 35198]
gb|EEG83858.1| hypothetical protein PROPEN_04629 [Proteus penneri ATCC 35198]
Length = 65

Score = 77.8 bits (190), Expect = 3e-12, Method: Composition-based stats.
Identities = 40/55 (72%), Positives = 41/55 (74%)

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K VEGDASSASYFLA AAI GGT V G G SLQGD+ FA VLE MGAKV W

Sbjct: 9 KKYLVEGDASSASYFLAAAAIKGGTVRVTGIGKNSLQGDHIFASVLEKMGAKVRW 63

>ref|ZP_03510971.1| 3-phosphoshikimate 1-carboxyvinyltransferase protein [Rhizobium
etli 8C-3]
Length = 166

Score = 76.6 bits (187), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 48/120 (40%), Positives = 69/120 (57%), Gaps = 6/120 (5%)

Query: 319 HLK AIDVNMNKM P D V A M T L A V V A L F A D G P T A I R D V A S W R V K E T E R M V A I R T E L T K L --GA 376
HL A +++ ++M D T+AV+A F P +A+ RVKE +R+ A+ T L + G
Sbjct: 4 H L P A - E I D G S Q M Q D A V P T I A V L A A F N A T P V R F V G I A N L R V K E C D R I R A L S T G L N N I R E G L 62
Query: 377 S V E E G P D Y C I I T P P E K L N V T ---A I D T Y D D H R M A M A F S L A A C A E V P V T I R D P G C T R K T F P 433
+V E E G D + + P T I D T + D H R + A M + F + L A + T I D P C K T F P
Sbjct: 63 A V E E G D D L I V H S D P A L A G Q T L P A E I D T F A D H R I A M S F A L A G L K I D G I T I L D P D C V G K T F P 122

>ref|ZP_02862022.1| hypothetical protein ANASTE_01235 [Anaerofustis stercorihominis DSM 17244]
gb|EDS71533.1| hypothetical protein ANASTE_01235 [Anaerofustis stercorihominis DSM 17244]
Length = 426

Score = 75.5 bits (184), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 72/332 (21%), Positives = 150/332 (45%), Gaps = 18/332 (5%)

Query: 30 R I L L L A A L S E G T T V D N L L N S E D V H Y M L G A L R T L G L S V E A D K A A K R A V V V G C G G K F P V E D 89
R L + + + T + + + N + L + + + L L L G + D + + + G + P +
Sbjct: 25 R Y L I C S L F T N E T S I I K N V L L D K E T K E I L D I L S L L G A R I T V D E F K G K R K T L R I K G S Y P F D I 84
Query: 90 A K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P I G D L V V G L K Q L G A D V D 149
E E + L G N + R + + + + L + + + P + + G
Sbjct: 85 K L E E I D L --G N N L N L L R T F A P I L L I S --K T K F N L K Y K N T I I Q N P L N S F Y S L F F E K G F - T K 139
Query: 150 C F L G T D C P P V R V N G I G G L P G G K V K L S G S I S S Q Y L S A L L M A A P L A L G D V E I E I D K L I S I P 209
+ P + + + G + + I + L S L L P A + + I + +
Sbjct: 140 I Q M E K G E Y P L K I K T --G I D K S V F Y I R A D I E K E C L S T L L S M L P R A Y R A S K V I I V G E I K D K A 197
Query: 210 Y V E M T L R L M E R F G V K A E H S D S W D R F Y I K G G Q K Y K S P K N A Y V E G D A S S A S Y F L A G A A I T G G 269
Y V T + + + + F + + + + F I K Y + P N V E D + A S + + + A + G
Sbjct: 198 Y V N R T I Q I L K D F E I D V R N N N - F K E F D I - I N T K Y E - P C N V T V E N D F T M A S I W I T A S A L - G H 253
Query: 270 T V T V E G C G T T S L Q G D V K F A E V L E M M G A K V T W T E T S V T V T G P P R E P F G R K H L K A I D V N M N K 329
V V + S Q + K + + L + + G + + + P R + A + + + + K
Sbjct: 254 K V M V K D L N L K S R Q D N K K L L D I L K V I G I D I F A S P N G D I I A R P N R ----- I N A F N I D I S K 306
Query: 330 M P D V A M T L A V V A L F A D G P T A I R D V A S W R V K E T 361
+ P D + L A V + A A D G + + + V V K + T
Sbjct: 307 V P D L M P Y L A V I A S V A D G T S K L K N V E D I Y V K D T 338

>ref|ZP_02164769.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hoeftlea phototrophica DFL-43]
gb|EDQ35464.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Hoeftlea phototrophica DFL-43]
Length = 420

Score = 75.5 bits (184), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 112/438 (25%), Positives = 186/438 (42%), Gaps = 61/438 (13%)

Query: 33 L L A A L S E G T T V D N L L N S E D V H Y M L G A L R T L G L S V --E A D K A A K R A V V V G C G G K F P V E D A 90
+ L + G T + L L E D V A + + + G S + E D V G C
Sbjct: 1 M F G G L A N G E T R I T G L L E G E D V I N T G K A M Q A M G A S I R K E G D A W V I N G V G N G C ----- L L 53
Query: 91 K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L D G V P R M R E R P I G D L V V G L K Q L G A D V D C 150
E L G N A G R V + T + V D + R P + G + + L + + G V
Sbjct: 54 A P E K P L D F G N A G T G C R L T M G L V G P Y D F D T T F V G D A --S L S R R P M G R V L D P L R L M G V Q V R S 111
Query: 151 F L G T D C P P V R V N G I G G L P G G K V K L S G S I ---S S Q Y L S A L L M A A P L A L G D V E I E I D K L I S 207
G D P V + + G P + S + S + Q S A + L + A G + I + + +
Sbjct: 112 E D G - D R L P V T L H G ---P L A P A I S Y R V P M A S A Q V K S A V L L A G L N V P G --V T T V I E P V M T 164
Query: 208 I P Y V E M T L R L M E R F G V K A E H S D S W D --R F Y I K G G Q K Y K S P K N A Y V E G D A S S A S Y F L A G A A 265
+ E + + + F G + E D R G + + + V G D S S + + L A
Sbjct: 165 R D H T E ---K M L A G F A Q L E V E T G A D G V R T I R L E G R G T L T A Q I I D V P G D P S S T A F P L V A A L 221

Query: 266 ITGGT-VTVEGCGTTSIQGDVKFAEVLEM--MGAKVTWTETSVTVTGPPREPFGFGR----- 317
+ + VT+ L + + +L + MGA + + PR+ G
Sbjct: 222 LVPDSVTIRNV----LMNETRTGLILTLQEMGANIEIID-----PRQAGGEDVADL 269

Query: 318 ----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE 370
L ++V ++ P D LAV A FA+G T + + RVKE++R+ A+
Sbjct: 270 RVRSSSETGVNVPADRAPSMIDEYPVLAVAASFAEGETVMTGLDELRVKESDRLSAVARG 329

Query: 371 LTKLGASVEEGPDYCIIT-PPEKLNVT-----IDTYDDHRMAMAFSLAACA-EVPVTI 422
L G EG D+ + P+ + A + T+ DHR+AM+F + A E PV +
Sbjct: 330 LEINGVDCTEGDDWLSVRGRPDGKGLGARSEKAVVKTWLDHRIAMSFLVMGLASEHPVHV 389

Query: 423 RDPGCTRKTFPDYFDVLS 440
D +FP++ D+++
Sbjct: 390 DDSAIIATSFPEFMDMMT 407

>gb|ABC00780.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 53

Score = 74.7 bits (182), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 46/53 (86%), Positives = 49/53 (92%), Gaps = 1/53 (1%)

Query: 82 GGFKEPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
GG+FP+E DAKEEV+LFLGNAG AMR LTAAGV AAGGNATYVLDGVPRMRERP
Sbjct: 1 GGRFPIEKDAKEEVKLFLGNAGTAMRPLTAAVVAAGGNATYVLDGVPRMRERP 53

>gb|EFV96997.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus
agalactiae ATCC 13813]
Length = 229

Score = 72.8 bits (177), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 60/235 (25%), Positives = 106/235 (45%), Gaps = 14/235 (5%)

Query: 217 LMERFGVKAHSDSWDR-FYIKGGQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVE 274
++ +FG H D D+ + GGQ ++ V GD SSA++++ AG I + +E
Sbjct: 1 MIRQFG---GHLDIKKEIRLNGGQSLVG-QDIRVPGDISSAAFVIVAGLIIPNSHIILE 56

Query: 275 GCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVA 334
G + + +V+ MG K+ + V HL+A ++ +P +
Sbjct: 57 NVGINETRTGI--LDVVSVMGKGKIKLSSVDNQVKSATL-TVDYSHLQATHISGAMIPRLI 113

Query: 335 MTLAVVALFA---DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE 391
L ++AL A G T I D +VKET+R+ + L ++GA + D II
Sbjct: 114 DELPIIALLATQAQGTTVIADAQELVKVETDRIQVVESLQMGADITATADGMIIRGNT 173

Query: 392 KLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLSFVK 444
L+ ++D + DHR+ M ++AA E V + ++P++ + L V
Sbjct: 174 PLHAASLDCHGDHRIGMMIAIAALLVKEGEVDLSGEEAINTSYPNFLEHLEGLVN 228

>gb|ABZ09592.1| putative EPSP synthase (3-phosphoshikimate
1-carboxyvinyltransferase) [uncultured marine
microorganism HF4000_APKG8D23]
Length = 394

Score = 72.8 bits (177), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 71/199 (35%), Positives = 99/199 (49%), Gaps = 16/199 (8%)

Query: 21 LPGSKSLSNRIILLALSEGTTVVD-NLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
LP SKS R L LAA +EG TV+ + EDV M LR LG +E ++A + V
Sbjct: 17 LPPSKSHMMRWLALAAQAEGETVLSFDSEPGEDVLSMAECLRLGAGIE--QSASQSVT 74

Query: 80 GCGGK-FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLV 138
G G F ++ E L GN+G A R LTA AAG + LDG +R R + L
Sbjct: 75 GVGADGF---SEPEGVLDCGNSGTAAFLTA--IAAGLASAVALDGDASLRRRDLALN 128

Query: 139 VGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVE 198
L++ G C + +D P+ VNG G G+ L SSQ LSALL+A+P +

Sbjct: 129 SALREFG---CEISSDAVPLSVNGPAG--PGRAYLEVSSSSQPLSALLLASPGYSARLH 182

Query: 199 IEIIDKLISIPYVEMTLRL 217
 + + + +S Y ++ L

Sbjct: 183 LGLSEGSVSRGYSRLSFEL 201

>emb|CBL42034.1| 5-enolpyruvylshikimate-3-phosphate synthase [butyrate-producing
 bacterium SS3/4]
 Length = 107

Score = 72.4 bits (176), Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 39/107 (36%), Positives = 61/107 (57%), Gaps = 1/107 (0%)

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI 398
 ++A FA+G T IRD A +VKE+ R+ + L +GA VEE D II + L+ +
 Sbjct: 1 MMACFAEGTTVIRDAELKVKESNRRIAMVENLRAMGADVEETEDGMIHGGKPLHGAVV 60

Query: 399 DTYYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
 D++ DHR+AM F++AA A+ I D C ++P +++ L K
 Sbjct: 61 DSHKDHRIAMTFAVAALAADGETEIIDADCVDISYPAFYEELEKLTK 107

>ref|YP_261736.1| prephenate dehydrogenase /3-phosphoshikimate
 1-carboxyvinyltransferase [Pseudomonas fluorescens Pf-5]
 gb|AAY93899.1| prephenate dehydrogenase, putative/3-phosphoshikimate
 1-carboxyvinyltransferase [Pseudomonas fluorescens Pf-5]
 Length = 447

Score = 72.4 bits (176), Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 113/448 (25%), Positives = 182/448 (40%), Gaps = 64/448 (14%)

Query: 21 LPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVG 80
 LP KS+S+R++L AAL+ + +L + V +L AL+ LGL V + + +
 Sbjct: 27 LPSDKSISHRMILFAALARHPVRLRDLNRGKAVTLLLDALQQLGLEVTGQTPQ---TLE 83

Query: 81 CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVG 140
 G+F + A E ++ LG + A R L + G N ++DG +R RP +V
 Sbjct: 84 ISGEFAL--ATHERRVDLGPSSAAARLLIGMLV--GLNVPCIVDGDETLRNRPFDWIVEP 139

Query: 141 LKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
 L Q+GA ++ P+R++ GG ++ S+Q +S LL A A
 Sbjct: 140 LNQMGAHLEYLGRPGALPIRIHQ-AAFRGGAAQIHIG-SAQAISTLLFAGVAA----- 190

Query: 201 IIDKLISIPY----VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASS 256
 K +SI Y + T R++ FG DR + Q + P++ + + S
 Sbjct: 191 --RKPMISIRYPVVARHTQRIINSFG-----DRLLEQLQIHQPRDCAIPEEISI 239

Query: 257 ASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEV-----LEMMGAKVTWTETS 304
 +AI C Q + F V L G +T S
 Sbjct: 240 PR---DPSAIAYPAALFLLCNRHQEQQRLSFDNVCLNPTRLGFFNWLLACGFNLTLLEVDS 296

Query: 305 VTVTGPPREPFGGRKHL-----KAIDV----NMNKMPD-VAMTLAVVALFADGPTAIRDV 353
 + EP GR L +A D+ + M D V + LA+ + G D+
 Sbjct: 297 IRHG----EPVGRLLLRGGQPRAHDLRDKHQFHAMIDEVPLALAIISCVLP-GSATFSDL 351

Query: 354 ASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDYDDHRMAM-AFS 411
 KE++R+ A R+ L LG + +G D + AI T+ DHR++M A
 Sbjct: 352 YELTFKESDRIAATRSMNLALGLDYQVDGYDVRVEGGQVPSVQGAIPTFGDHRLSMTAHV 411

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVL 439
 L + TI + C + +FP + L
 Sbjct: 412 LLLAHGLQATILEGHYQTSFPGFAQCL 439

>ref|ZP_06221622.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
 influenzae HK1212]
 gb|EFA29383.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
 influenzae HK1212]
 Length = 104

Score = 72.0 bits (175), Expect = 2e-10, Method: Composition-based stats.
Identities = 43/107 (40%), Positives = 59/107 (55%), Gaps = 4/107 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL+ LG+ + + G GG F +++ + LFLGNAG AMR LTAA+
Sbjct: 1 MLNALKALGVRYQLSDDKTICEIEGLGGAFNIQN---NLSLFLGNAGTAMRPLTAALCLK 57

Query: 116 GGNAT-YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRV 161
G + +L G PRM+ERPI LV L+Q GAD+ PP+ +
Sbjct: 58 GKTESEIILTGEPRMKERPILHLVDALRQAGADIRYLENEGYPPLAI 104

>ref|ZP_06223002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae HK1212]
gb|EFA28002.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Haemophilus
influenzae HK1212]
Length = 103

Score = 71.6 bits (174), Expect = 2e-10, Method: Composition-based stats.
Identities = 43/105 (40%), Positives = 58/105 (55%), Gaps = 4/105 (3%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAA 115
ML AL+ LG+ + + G GG F +++ + LFLGNAG AMR LTAA+
Sbjct: 1 MLNALKALGVRYQLSDDKTICEIEGLGGAFNIQN---NLSLFLGNAGTAMRPLTAALCLK 57

Query: 116 GGNAT-YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPV 159
G + +L G PRM+ERPI LV L+Q GAD+ PP+
Sbjct: 58 GKTESEIILTGEPRMKERPILHLVDALRQAGADIRYLENEGYPPL 102

>gb|ACB05434.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 53

Score = 71.6 bits (174), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 45/53 (84%), Positives = 48/53 (90%), Gaps = 1/53 (1%)

Query: 82 GGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
GG+FP+E DAKEEV+LFLGNA AMR LTAAG AAGGNATYVLDGVPRMRERP
Sbjct: 1 GGRFPIEKDAKEEVKLFLGNNAVTAAMRPLTAAVVAAGGNATYVLDGVPRMRERP 53

>ref|NP_147921.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeropyrum pernix K1]
dbj|BAA80401.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Aeropyrum pernix K1]
Length = 419

Score = 71.6 bits (174), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 113/440 (25%), Positives = 179/440 (40%), Gaps = 48/440 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+V++P +I G + P SK + L + L+ G + + L S DV + A+R G
Sbjct: 2 NLVVKP-SQIGGEIIPSSKGHTIAALFASLLAGGRSKISEPLYSRDVTATYAVRRFVG 60

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V+ +R ++V P V ++ + S+ A A G + Y G
Sbjct: 61 LVQK---GERDLIVDS---PPRPWWPRVNCRRSSTVLRHSIVTAALAPGISLVY---G 110

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNG---IGGLPGGKVKLSGSISSQY 182
P+ +L LK++GA+V G PPV V G G G V S S
Sbjct: 111 DSHTNSTPVSSELGALKKIGAEVVTNGR--PPVAVKGPLARGCCEGETVGASDGESLAA 168

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L A+ S +V + L ++ FG K S+D GG Y
Sbjct: 169 LLLASPLLGFAIKRAGTH-----SWHHVAVALHVLGRFGAKI----SFD-----GGIYY 213

Query: 243 K----SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
P V GD +A+ L AI G +TV QG+ F +L GAK+
Sbjct: 214 PDKPYGPGAYAVPGDYVNAAPLLLAGAIAAG-RITVRRLDPEDPQGEKVFNLIAQAGAKL 272

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
E+SV V G L+ + +++++ P +A LAV+A +A G + I+ ++ R+

Sbjct: 273 KAGESSVEVVG-----TGSLEGFEADVSETPSLAPVLAVLAAYAKGRSVIKGISHLRL 325

Query: 359 KETERMVAIRTELTKLGASVEE--GPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACA 416
KE + + + L +L + G D + + Y D RM MAF++A A

Sbjct: 326 KEGGNLKLPLMSNLRRLKVKAKPRCGGDCLEVYGEYVEGGTAKGYGDPRMTMAFAVAGLA 385

Query: 417 EVPVTIRDPGCTRKTFPDYF 436
+R G +R + DY+

Sbjct: 386 SRK-GVRVTGASR--YRDYY 402

>ref|YP_001329109.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium medicae
WSM419]
gb|ABR62274.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sinorhizobium medicae
WSM419]
Length = 456

Score = 71.6 bits (174), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 112/451 (24%), Positives = 202/451 (44%), Gaps = 50/451 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ GTV++PG KS+S+R + L+ G T + LL EDV A++ +G + K

Sbjct: 17 DLKGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGRAMQAMGAKIR--KEG 74

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
++ G G + E L GNAG R V ++T++ D + +RP

Sbjct: 75 DTWIIDVGNGGALL---APEAPLDFGNAGTGCRLTMGLVGVYDFDSTFIGDA--SLTKRP 129

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAA 190
+G ++ L+++G V G D PV + G P ++ + S+Q SA+L+A

Sbjct: 130 MGRVLDPLREMGVQVKS AEG-DRLPVTLRG---PKTPNPITYRVPMASAQVKS AVLLAG 184

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR----FYIKGGQKYKSP 245
G +++ +++ + E ++++ FG A+ S DR ++G K +

Sbjct: 185 LNTPGIT--TVVEPVMTRDHT---KMLQGF--ADLSVETDRDGVRTIRLEGRGKLRG- 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGT-----VTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ V GD SS ++ L A + G+ V + T + + +E++ +++

Sbjct: 237 QVIDVPGDPSSTAFPLVAALLVPGSDLSIFNVLMNPTRTGLLITLQEMGARIEVLSSRLA 296

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASW 356
E + LK + V + P D LAV A FA+G T + +

Sbjct: 297 GGEDVADLR-----VRYSELKGVTVPEERAPSMIDEYPVLAVAAFAEGATVMNGLEEL 350

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEK----LNVTAIDTYDDHRMAMAF 410
RVKE++R+ A+ L G +EG ++ P K + + T+ DHR+AM+F

Sbjct: 351 RVKESDRLSA VA EGLKLN GVDCDEGEASLVVRGPRGGKGLGNDSGGQVKTHLDHRIAMSF 410

Query: 411 SLAACA-EVPVTIRDPGCTRKTFPDYFDVLS 440
+ A E PVT+ D +FP++ +++

Sbjct: 411 LVMGLASERPVTVDATMIATSFPEFMGLMT 441

>gb|ACB05431.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 53

Score = 70.9 bits (172), Expect = 4e-10, Method: Compositional matrix adjust.
Identities = 45/53 (84%), Positives = 48/53 (90%), Gaps = 1/53 (1%)

Query: 82 GGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
GG+F +E DAKEEV+LFLGNAG AMR LTA AV AAGGNATYVLDGVPRMRER

Sbjct: 1 GGRFQLEKDAKEEVKFLFLGNAGTAMRPLTAAVVAAGGNATYVLDGVPRMRER 53

>ref|ZP_03832182.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. carotovorum WPP14]
Length = 92

Score = 70.5 bits (171), Expect = 6e-10, Method: Composition-based stats.
Identities = 47/83 (56%), Positives = 59/83 (71%), Gaps = 4/83 (4%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPIK I+GT+ LPGSKS+SNR LLLAAL+EG T + NLL+S+DV +ML AL LG
Sbjct: 3 ESRTLQPIKLLINGTLNLPKSKSVSNRALLLAALAEKTRLNLLSDSDVRHMLTALTALG 62

Query: 65 LSVEADKAAKRAV--VVGCGGKF 85
VE ++ R V + G GG F
Sbjct: 63 --VEYHLSSDRTVCEITGLGGA 83

>ref|ZP_04126963.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar sotto str. T04001]
gb|EEM41409.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar sotto str. T04001]
Length = 236

Score = 69.7 bits (169), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 67/258 (25%), Positives = 123/258 (47%), Gaps = 35/258 (13%)

Query: 1 MAGAEEIVLQPIKE-ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGA 59
M +E +QP+ ++G + +PG KS+S+R ++ +++EG T + L+ D +
Sbjct: 1 MKNVKERTIQPVNGLNGNITIPGDKSISHRAVMFGSIAEGKTTIKGFLSGADCLSTISC 60

Query: 60 LRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGN 118
+ +G VE + VVG G +E +E + L +GN+G +R ++ + N
Sbjct: 61 FKEMG--VEITQNGDETVVVGK-----LEGLQEPKAVLDVGNSTTIRLMSGILA----N 110

Query: 119 ATY--VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK--- 173
+ + G + +RP+ + LKQ+GA++D P+ + GG +K
Sbjct: 111 TPFFSCVQGDESIKRPKRVTNPLKQMGANIDGREEGTFTPLTIR-----GGDLKAIE 164

Query: 174 -LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV--EMTLRLMERFGVKAHSDS 230
+S S+Q SA+L+A A G ++ P++ + T R++E FGK +
Sbjct: 165 YISPVASAQVKSAILLAGLRAEGVT-----AVTEPHISRDHTERMLEAFGVKV--TRE 215

Query: 231 WDRFYIKGGQKYKSPKNA 248
+ GGQK S K++
Sbjct: 216 GKTIVKLSGGQKINSNKHS 233

>ref|YP_001815138.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sibiricum 255-15]
gb|ACB62121.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sibiricum 255-15]
Length = 434

Score = 69.3 bits (168), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 106/377 (28%), Positives = 158/377 (41%), Gaps = 47/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+IV++ ++++GTVK+ G+K+ + L+ L SEGTV+V+ N+ DV+ + LR L
Sbjct: 2 EKIVVRGGRKLAGTVKVEGAKNVLTATLLASEGTSVLQNVPRADVYTINNVLRLN 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V D A V V + E E V R + A++ G G
Sbjct: 62 NAEVTFDAEAN-TVSVNAEAEKDEAPLEYV-----RKMRA SILVMGPLLARLG 109

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A + G + RPI + G + +GA +G V+ G L G K+ L
Sbjct: 110 RARVAMPGGCAIGSRPIDLHLKGFEAMGA--KTIIGNGFVEAHVD--GRLQAKIYLD 165

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G IE + K P + + G K + + + ++
Sbjct: 166 -SVGATENIMMAATLAEGTTVIENVAKE--PEIVDLANFLNAMGAKVRGAGT-ETIRVE 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K N YV D A F+ AAIT G V V G L+ +E MG K
Sbjct: 221 GVEKLHG-GNHVYIPDRIEAGTFMIAAAITEGDVEVIGAEREHLR---PLISKMEEMGVK 276

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
++ TE + V GP K L AIDV P DV + + L A+G + I +

Sbjct: 277 ISDTEEGLRVVGP-----KKLVAIDVKTMPHPGFPTDVQAQMMALVLKAEGTSVITET 329

Query: 354 A----SWRVKETERMVA 366
V+E RM A

Sbjct: 330 VFENRFMHVEEFRRMNA 346

>ref|ZP_01264335.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Pelagibacter ubique HTCC1002]
gb|EAS84822.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Pelagibacter ubique HTCC1002]
Length = 442

Score = 69.3 bits (168), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 102/452 (22%), Positives = 182/452 (40%), Gaps = 38/452 (8%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I+ IK+ + +++ G KSLR +LLA+ + G + NLL SEDV + +++ LG+
Sbjct: 6 IIKDKIKKFNKQIRVSGDKSLRIRVLLASQAIGKSKGYNLLMSDEVLAIDSIIKLGK 65

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V K +VG G + K L + + G
Sbjct: 66 VRIQKNY--CEIVGNG---INGFKYNKLTIDAKNSGTLGRLILGLLIKSTKKIKIIGD 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +R + L++ G + P+ + G G K S+Q S++
Sbjct: 120 KSLSKRDFSRVTTPLRKFVGFYSYKIKNKL-PLTILGTQSAKGIKY-FENKGSQAQCKSSV 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++AA A G I+ S + E+ + + + +K + +D IK +K +
Sbjct: 178 MLAALNASGTTSIKAKK---SRNHTELLFKYL-KIPIKVRKAKKFDIDIKPKKINAF- 232

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
N + GD SS+++F+ + + + ++ V +L+ MGA+T E
Sbjct: 233 NYQIPGDISSAFFMVLTTLADNSKLLIKNVNINP--SRVGVITILKMGAKIT-LENQK 289

Query: 306 TVTGGPPREF---GRKHLKAI--VNMNKMP-DVAMTLAVVALFADGPTAIRDVASWRVK 359
G K LKAI+ V +N D + + ++A A G + +D++ K
Sbjct: 290 NYRGEKISDILIKSSKKLKAINCPVELNSSAIDFLVIFLIAAKAGISYFKDLSELNQK 349

Query: 360 ETER-----MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
E+ R M+ I+T+LT + PD I P +T + DHR+ M
Sbjct: 350 ESPRLIWGSKILNMMGIKTDLTNDSIKIYGQPDLEIKKP-----ITVKNYLKDHVRVFMMS 404

Query: 411 SLAACAE-VPVTIRDPGCTRKTFPDYFDVLST 441
++AA I D +FP + ++
Sbjct: 405 TIAALTFGGKWKIYDKDSINTSFPSFLKIIKN 436

>ref|ZP_00051744.2| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase
[Magnetospirillum magnetotacticum MS-1]
Length = 398

Score = 69.3 bits (168), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 112/391 (28%), Positives = 155/391 (39%), Gaps = 49/391 (12%)

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R V VG GG ++D E L GNAG R + V G T DG +R+RP+
Sbjct: 24 RIVGVGIGG---MQDP--EGVLDFGNAGTGSRLMMGVV--GGQPVATFDGDASLRKRPM 76

Query: 135 GDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSI---SSQYLSALLMAAP 191
++ L Q+GA V P+ + G P + L + S+Q SA+L A
Sbjct: 77 RRILDPLLMQAQVVEAEAGGRVPLTLKG---PREAIPRYELPVASAIKSAVLFAGL 132

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFG---VKAHSDSWDRFYIKGGQKYKSPKN 247
A G + I+ S + E LRL FG V R GQ
Sbjct: 133 NAPGTTTV--IETAASRDHTEMLRL---FGAEVTVTPHGEHGRSVALTGQPVLRGTE 187

Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D SSA++ L A I G+ VT+ G L+ L MGA + +
Sbjct: 188 VIVPADPSSAAFPLVAALIVPGSEVTLRGVMMNPLR--TGLITTLIEMGAAIERLDE--- 242

Query: 307 VTGPPREPFGR-----KHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVA 354
RE G L +DV + P D LAV A FA+G T + +
Sbjct: 243 -----REEGGETVADLRVRASRLHGVDPVPAERAPSMIDEYPILAVAAFAEGTTRMNLH 297

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--PPEKLNVTATIDTYDDHRMAMAF-S 411
RVKE++R+ A+ L G S D I+T + T+ DHR+AMAF
Sbjct: 298 ELRVKESDRLLAAVAAGLAANGVSYAIEGDDLVGTGEGAPPAGGGTVATHLDHRIAMAFV 357

Query: 412 LAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ A PVT+ D +FP + +S
Sbjct: 358 MGLAARQPVTVDGAMIATSFPTFRPTMSAL 388

>ref|ZP_03634371.1| hypothetical protein HOLDEFILI_01664 [Holdemania filiformis DSM
12042]
gb|EEF68158.1| hypothetical protein HOLDEFILI_01664 [Holdemania filiformis DSM
12042]
Length = 156

Score = 68.9 bits (167), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 43/126 (34%), Positives = 66/126 (52%), Gaps = 4/126 (3%)

Query: 320 LKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWVRKETERMVAIRTELTKLGASVE 379
L +++M PD+ L V+A FA G T + + A R KE++R+ A+ TEL K+G +
Sbjct: 25 LSGCELMQNCPLDGPILMVLASFAQGETKMINAARLRYKESDRIEAMETELRKVGVPPIH 84

Query: 380 EGPDYCIITPPE--KLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYF 436
I P K VT +D + DHR+ MA ++ A A+ PVTI K++P +F
Sbjct: 85 SSEGEVWIQGPATAWKGGVT-LDGHKDHRIVMALAIGATMADAPVTIEGAEIAKSYPGFF 143

Query: 437 DVLSTF 442
L +
Sbjct: 144 RDLRSL 149

>ref|YP_088899.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
succiniciproducens MBEL55E]
sp|Q65RU6.1|MURA_MANS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAU38314.1| MurA protein [Mannheimia succiniciproducens MBEL55E]
Length = 421

Score = 67.8 bits (164), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 108/417 (25%), Positives = 177/417 (42%), Gaps = 42/417 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEVDHYMLGALRTLGLSVE-ADKAA 73
++GTV + G+K+ + IL + L+E ++ N+ + +DV LR LG++VE A++
Sbjct: 12 LTGTVDISGAKNAALPILFASILAEPPVILTNPDLKDVETTFKILRKLGVNVECAEPPG 71

Query: 74 KRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
K + G +F P E K A + R V+ GG +
Sbjct: 72 KVLIDAGNINQFVAPYELVKTMRASIWALAPLLSRFHEGQVSLPGGCT-----IGA 122

Query: 132 RPIGLDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+++GA ++ D V+ G L G ++ + +S +++MAA
Sbjct: 123 RPVDMHISGLEKMGAAIEL----DEGYVKATVNGRLKGARIYMD-KVSVGATLSIIMAAT 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G +I+ P V T + G K + + D I+G ++ ++ V
Sbjct: 178 LAEGKT---VIENAAREPEVVDTAIFLNAMGAKISGAGT-DTISIEGVERLAGCRHRIVP 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D FL AAI+GG +T G +L+ + E L G ++ TE S+T+
Sbjct: 234 -DRIETGTFLVAAAISGGRIITCRGTKADTLEAVI---EKLREAGMQIDITEDSITLDSL 289

Query: 312 REPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWVRKETERMVAIR--- 368
+ P KA VN+ MP + A F T + VA K TE + R
Sbjct: 290 QRP-----KA--VNIRTPHPGFPPTMQAQF---TLLNVVAEGTSKITETIFENRFMH 337

Query: 369 -TELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I E L+ + D R +++ LA C TI D
Sbjct: 338 IPELIRMGAKEIEGNTAICHGVEHLSGAQV-MATDLRASISLVLAGCIASGETIVD 393

>gb|ABZ10397.1| putative EPSP synthase (3-phosphoshikimate
1-carboxyvinyltransferase) [uncultured marine bacterium
HF4000_APKG3108]
Length = 443

Score = 67.8 bits (164), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 106/452 (23%), Positives = 189/452 (41%), Gaps = 40/452 (8%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++ I + + T+ + KS+S+R LL+A+ G + + +L SEDV + L+ LG
Sbjct: 8 LIKNKITKFNKTILVENDKSISHRALLIASQCIGPSNLKGVLESEDVKNTIICLKKLG-- 65

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V+ K K+ +V G G + + K L++GN+G R L A V A N + G
Sbjct: 66 VKILKKNKKYIVYGNGLRSFRKPHKN--LLYVGNSGTLARMLIALV-ATHPNLKVKVSGD 122

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ +R + ++ L ++G F D P+ + G +P + S+Q S
Sbjct: 123 NSLNKRDMKRIIEPLSKIGC---TFYPRDKTTLPLTIEG-TSMPLAQKHTETLGSQVKS 178

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+AA G +E +K IS + E L + GQ+ S
Sbjct: 179 AILLAAINTHGITTVE--EKKISRNHTENL--LTAIKASIKVKKIKNNLISLRGQENLS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
N + GD SSA+ F+ +T G+ + C T + F ++L+ M A +
Sbjct: 235 NFNLEIHGDPSSAAPFIVLTLLTAGSKLLIKNVNCNPTR----IGFIKILKKMNANIRIK 290

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMPDVAMT-----LAVVALFADGPTAIRDV 353
+ E G +K+ + P ++ L ++A G +
Sbjct: 291 ----NLKKKSGEHVGNIFVKSGLKPISCPKELVSSAIDEFPLLFIIASVIKGVCKFSGI 346

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKLNVTIAIDTY--DDHRMAMA 409
R KE++R+ +I L ++G + D I P K+ T ++ Y +DHR+A++
Sbjct: 347 NELRHKESDRIKSIEIGLNQIGIKTKSTIDSLKIFGNPNIKIKKT-LEVYPKNDHRIAVS 405

Query: 410 FS-LAACAEVPVTIRDPGCTRKTFPDYFDVLS 440
+ L E + I + +FP + + S
Sbjct: 406 YVILGLLLEGGIKIHNHCETINTSFPRFLKINS 437

>ref|NP_872847.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
ducreyi 35000HP]
sp|Q7VP51.1|MURA_HAEDU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAP95236.1| UDP-N-Acetylglucosamine- 1-carboxyvinyltransferase [Haemophilus
ducreyi 35000HP]
Length = 426

Score = 67.8 bits (164), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 104/417 (24%), Positives = 171/417 (41%), Gaps = 41/417 (9%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SGTV + G+K+ + IL L+E + N+ + +DV LR LG+ +E D
Sbjct: 11 KLSGTVDISGAKNAALPILFATILAEPISLTNVPLDKVDVDTTFKILRKLGVVIERDANG 70

Query: 74 KRAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + P E K A + R V+ GG +
Sbjct: 71 VVQIDASHIQHYVAPYELVKTMRAIWAAPLVARFHHQGVSLPGGCT-----IGA 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + L+++GA ++ D V+ G L G ++ + +S +++MAA
Sbjct: 122 RPVDMHITSLEKMGAIIEI----DEGYVKATANGRLQGARIYMD-KVSVGATLSVMMMAAT 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G II+ P + T + G + + + D IKG ++ ++ ++
Sbjct: 177 LAEGST---IIENAAREPEIVDTAHLNAMGAIEISGAGT-DTITIKGERLTGCQH-HIV 231

Query: 252 GDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D FL AAI+GG +T +G +L + E L G +VT TE S+T+
Sbjct: 232 ADRIETGTFLVAAAISGGKITCQGTAKDTLDAVI---EKLREAGMEVTVTENSITLDTKG 288

Query: 312 REPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR--- 368
+ P KA VN+ MP + A F T + VA + TE + R
Sbjct: 289 QRP-----KA--VNIRTPHPGFPPTDMAQF----TLLNAVAEGTSRITETIFENRFMH 336

Query: 369 -TELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRD 424
EL ++GA E + I E+L + D R +++ LA C TI D
Sbjct: 337 IPELNRMGAKEIEGNTAICQGEQLKPAEV-MATDLRASISLVLAGCIASGETIVD 392

>gb|ABZ06003.1| putative EPSP synthase (3-phosphoshikimate
1-carboxyvinyltransferase) [uncultured marine
microorganism HF4000_005D21]
Length = 446

Score = 67.0 bits (162), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 105/451 (23%), Positives = 189/451 (41%), Gaps = 40/451 (8%)

Query: 7 IVLQPIKEISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
++ I ++ + T+ + KS+S+R LL+A+ G + + +L SEDV + L+ LG
Sbjct: 8 LIKNKITKFNKTILVENDKSISHRALLIASQCIGPSNLKGVLESEDVKNITICLKKLG-- 65

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V+ K K+ +V G G + + K L++GN+G R L A V A N + G
Sbjct: 66 VKILKKNKKYIVYGNGLRSFRKPHKN--LLYVGNSTGLARMLIALV-ATHPNLKVKVS GD 122

Query: 127 PRMRERPIGDLVVLKQLGADVDCFLGTD--CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ +R + ++ L ++G F D P+ + G +P + S+Q S
Sbjct: 123 NSLNKRMKRIIEPLSKIGC---TFYPRDKTTLPLTIEGT-SMPLAQKHTETLGSQVKS 178

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A+L+AA G +E +K IS + E L + GQ+ S
Sbjct: 179 AILLAAINTHGITTVE--EKKISRNTENL--LTAIKASIKVKKIKNNLISLRGQENLS 234

Query: 245 PKNAYVEGDASSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
N + GD SSA+ F+ +T G+ + C T + F ++L+ M A +
Sbjct: 235 NFNLEIHGDPSSAAPFIVLTLLTAGSKLLIKNVNCPNTR----IGFIKILKKNANIRIK 290

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMT-----LAVVALFADGPTAIRDV 353
+ E G +K+ + P ++ L ++A G +
Sbjct: 291 ----NLKKKSGEHVGNIFVKSGLKPISCPKELVSSAIDEFPLLFIIASVIKGVCKFSGI 346

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTY--DDHRMAMA 409
R KE++R+ +I L ++G + D I P K+ T ++ Y +DHR+A++
Sbjct: 347 NELRHKESDRIKSIEIGLNQIGIKTKSTIDSLKIFGNPNIKIKKT-LEVYPKNDHRIAVS 405

Query: 410 FS-LAACAEVPTIRDPGCTRTKTFPDYFDVL 439
+ L E + I + +FP + ++
Sbjct: 406 YVILGLLLEGGIKIHNCETINTSFPGFLKLI 436

>ref|ZP_04978529.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica PHL213]
gb|EDN74925.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica PHL213]
Length = 426

Score = 67.0 bits (162), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 107/419 (25%), Positives = 172/419 (41%), Gaps = 46/419 (10%)

Query: 15 ISGTVKLPKSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV + G+K+ + IL A L+E T + N+ + +DV LR LG++VE K +
Sbjct: 12 LNGTVDISGAKNAALPILFAAILAEKTVTLKNVPDLKDVDTFKILRQLGVTV--KGSD 69

Query: 75 RAVVVGCGGKF-----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ VV K P E K A + R V+ GG +
Sbjct: 70 KGVVHIDASKINNYVAPYELVKTMRASIWALAPLVARFQLGQVSLPGGCT-----I 120

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL+++GA ++ D V+ G L G ++ + +S +++MA
Sbjct: 121 GARPVDMHISGLEKMGAKIEL----DEGYVKATSNRNLNGARIYMD-KVSVGATLSVMMA 175

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
LA G +I+ P + T + G K + + D I+G + +++
Sbjct: 176 GTLAKGTT---VIENAAREPEIVDTADFLNAMGAKISGAGT-DMITIEGVEHLGGCEHSV 231

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V D FL AAI+GG +T +L + E L G +V TE ++T+
Sbjct: 232 VP-DRIETGTFLVAAAISSGRITCRNTKADTLDAVI---EKLREAGMQVDVTENTITLDS 287

Query: 310 PPREFPGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR- 368
R P KA VN+ MP + A F T + VA + TE + R
Sbjct: 288 LGRRP-----KA--VNIRTMHPGPFPTDMQAQF----TLLNTVAEGTSRITETIFENRF 335

Query: 369 ---TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I E+L + D R +++ LA C TI D
Sbjct: 336 MHIPELIRMGAKEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLAGCIATGETIVD 393

>ref|ZP_07528285.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
ref|ZP_07537002.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 9 str. CVJ13261]
ref|ZP_07541346.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 11 str. 56153]
gb|EFM85037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
gb|EFM94033.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 9 str. CVJ13261]
gb|EFM98131.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 11 str. 56153]
Length = 424

Score = 67.0 bits (162), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 107/421 (25%), Positives = 175/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPGSKLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPLDKDVTTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++GA ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISGLEKMGALIEL----DEGYVKATSNRNLHGARIYMD-KVSVGATLSVMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG +T G +L+ + E L G +VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAISSGKITCRGKADTLEAVI---EKLREAGMEVTVTETITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNKMMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P KA VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RP-----KA--VNIRTMHPGPFPTDMQAQFTLLNVVAEGTS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLAGCIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>ref|ZP_05990592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. BOVINE]
ref|ZP_05992480.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. OVINE]
gb|EEY09613.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. OVINE]
gb|EEY11455.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mannheimia
haemolytica serotype A2 str. BOVINE]
Length = 426

Score = 67.0 bits (162), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 107/419 (25%), Positives = 172/419 (41%), Gaps = 46/419 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV + G+K+ + IL A L+E T + N+ + +DV LR LG++VE K +
Sbjct: 12 LNGTVDISGAKNAALPILFAAILAEKVTTLKNVPDLKDVDTTFKILRQLGVTVE--KGSD 69

Query: 75 RAVVVGCGGKF-----PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ VV K P E K A + R V+ GG +
Sbjct: 70 KGVVHIDASKINNYVAPYELVKTMRASIWALAPLVARFQLGQVSLPGGCT-----I 120

Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL+++GA ++ D V+ G L G ++ + +S +++MA
Sbjct: 121 GARPVDMHISGLEKMGAKIEL---DEGYVKATSNGLRLNGARIYMD-KVSVGATLSVMMA 175

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
LA G +I+ P + T + G K + + D I+G + +++
Sbjct: 176 GTLAKGTT--VIENAAREPEIVDTADFLNAMGAKISGAGT-DMITIEGVEHLGGCEHSV 231

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V D FL AAI+GG +T +L + E L G +V TE ++T+
Sbjct: 232 VP-DRIETGTFLVAAAISGGRITCRNKTADTLDAVI---EKLREAGMQVDVTENTITLDS 287

Query: 310 PPREFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR- 368
R P KA VN+ MP + A F T + VA + TE + R
Sbjct: 288 LGRPP-----KA--VNIRTMHPGPFPTDMQAQF---TLLNTVAEGTSRITETIFENRF 335

Query: 369 ---TELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTVIRD 424
EL ++GA E + I E+L + D R +++ LA C TI D
Sbjct: 336 MHIPELIRMGAKEIEGNTAICYGVEQLKSAEV-MATDLRASISLVLGCIATGETIVD 393

>gb|AAA81514.1| 5-enolpyruvylshikimate-3-phosphate-synthase [Escherichia coli str.
K-12 substr. MG1655]
Length = 48

Score = 66.6 bits (161), Expect = 7e-09, Method: Composition-based stats.
Identities = 28/41 (68%), Positives = 33/41 (80%)

Query: 400 TYDDHRMAMAFSLAACAEVPTVIRDPGCTRKTFPDYFDVLS 440
TY+DHRMAM FSL A ++ PVTI DP CT KTFPDYF+ L+
Sbjct: 2 TYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLA 42

>ref|ZP_05922164.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TC 6]
gb|EEW66074.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Enterococcus faecium
TC 6]
Length = 135

Score = 66.6 bits (161), Expect = 7e-09, Method: Compositional matrix adjust.
Identities = 38/108 (35%), Positives = 58/108 (53%), Gaps = 1/108 (0%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT 396
LA+VA A+G T I+D +VKET R+ A+ EL K+GA ++ D II P L+
Sbjct: 21 LALVATQAEGTITIKDAEELVKETNRIIDAVAEELQKMGAKIKATADGLIIHGPTPLHGA 80

Query: 397 AIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFV 443
+ + DHR+ M +AA A+ P + ++P +FD L+ V
Sbjct: 81 KVSSRGDHRIGMMLQVAALIADGPCELEGAEAVSISYPAFFDDLAEV 128

>emb|CBI77162.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella rochalimae
ATCC BAA-1498]
Length = 442

Score = 66.6 bits (161), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 103/449 (22%), Positives = 192/449 (42%), Gaps = 45/449 (10%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SGT+K+PG KS+S++ L+L L+ G + + LL ++ V + ++ +G + K
Sbjct: 14 NLSGTIKMPGDKSISHKALILGGLAHGESHIHGLLENDVSLRIATIMQAMG--AQCYYKN 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G G ++ + L GN+G + + V++ T++ G + P
Sbjct: 72 NLWIIHGTNGCLLQ---AQTPLNFGNSGSAHLIMGLVSSYHMKTTFL--GSASLSRYP 126

Query: 134 IGDVLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL-SALLMAAPL 192
+ ++ L+ +G + + LG P + G ++ ++S + SA+L+A
Sbjct: 127 MEHILNPLMGVETPTLGNHLP---LTLYGPKMANPIRYPIPMASAPVKSAILLAGLN 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G II++ ++ + E ++++ FG + + + RF GQ + + V
Sbjct: 184 TAGTT--TIIETLTQDHTTE---KMLQAFGAIEIDIKIDKTGTRFTSLKGQPHLIGQIINV 238

Query: 251 EGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVK--FAEVLEMMGAKV-----TW 300
GD S A++ +A + +T++ L D K F + L MGAK+ T
Sbjct: 239 PGDLSLAAFPPIAALLVENS DITLKNV----LVNDEKMEFIQTLWEMGAKIELLNQRKTG 294

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWR 357
E V + E LK + V + P D LA+ A FA G T I +
Sbjct: 295 IENIVDIRVKSSE-----LKGVTVPKERAPLIIDEYPALAIAAAFAGKGTIISGIEGLF 348

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTIADTYDDHRMAMAFSL-A 413
K ++R+ + L E G D+ II + L + T+ DH++AM F +
Sbjct: 349 YKISDRSLTAEGLKINHICENGKDFLIHGNSTKDLGGGRVTTTHFDHQIAMCFLIFG 408

Query: 414 ACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
+E PV I D P++ ++
Sbjct: 409 LVSEKPMIDDKQMIITNCPEFIPLMHQL 437

>emb|CBI78616.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella sp. AR
15-3]
Length = 442

Score = 66.2 bits (160), Expect = 8e-09, Method: Compositional matrix adjust.
Identities = 98/445 (22%), Positives = 189/445 (42%), Gaps = 37/445 (8%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SGT+K+PG KS+S+R L+L L+ G + + LL S++V ++ +G + K
Sbjct: 14 NLSGTIKMPGDKSISHRALILGGLAHGESYIHGLLESDNVLRATIMQAMG--AQCYYKN 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G G ++ ++ L GN+G + + V++ T++ G + +
Sbjct: 72 NLWIIIRGTNGCLLQ---AQIPLNFGNSGSAHLIMGLVSSYHIKTTFL--GHASLSKLS 126

Query: 134 IGDVLVVLKQLGADVDCFLGTDCCP-----PVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ ++ L+ +G +++ G P P N I + ++ + S+Q SA+L
Sbjct: 127 MEHILSPLRLMGVEIEPTRGNRLPLTFYGPKNMPI-----RYRIPMA-STQVKSAILF 179

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEE--HSDSWDRFYIKGGQKYKSPK 246
A G + + S P + T ++++ FG + + + R GQ + +
Sbjct: 180 AGLNTAGTTTV-----IESTPTRDHTKMLQAFGAELDIKTDKTGTRSTSLKGQPHLIGQ 234

Query: 247 NAYVEGDASSASY-FLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT-WTETS 304
V GD S A++ +A + +T+E + ++F + L MGAK+ +

Sbjct: 235 IINVPGLDLSAALFPIIAALLVEDSDITLNVNLINDFR--MEFIQTLWEMGAKIELLNQRK 292

Query: 305 VVTGPPREPFRGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V + LK + V ++P D LA+ A FA G T + + K +

Sbjct: 293 VNLENIVDIRIKSSELKGVTVPKERVPLMIDEYPALAIAAAFAGKGTIMSGIEEPCFKVS 352

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLVNTA---IDTYDDHRMAMAF-SLAACAE 417
R+ A+ L E G + II + + + TY DH++AM F +E

Sbjct: 353 NRLSALAEGKLKINHICESGKGLIIHGKNSIKSGGGHVTTYFDHQIAMCFLVFGGLISE 412

Query: 418 VPVTIRDPGCTRKTTPDYFDVLSTF 442
PV I + + P++ ++

Sbjct: 413 KPVIIDNKQIIATSCPEFIPLMHQL 437

>ref|YP_001053977.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae L20]
ref|ZP_07336829.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 6 str. Femo]
ref|ZP_07338253.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 2 str. 4226]
ref|ZP_07530336.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 2 str. S1536]
ref|ZP_07534809.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 6 str. Femo]
ref|ZP_07539122.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 10 str. D13039]
sp|A3N1T6.1|MURA_ACTP2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
gb|ABN74372.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 5b str. L20]
gb|EFL79253.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 2 str. 4226]
gb|EFL80779.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 6 str. Femo]
gb|EFM87359.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 2 str. S1536]
gb|EFM91584.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 6 str. Femo]
gb|EFM96115.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 10 str. D13039]
Length = 424

Score = 66.2 bits (160), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 106/421 (25%), Positives = 175/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPDLKDVTTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHEGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++GA ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISGLEKMGALIEL----DEGYVKATSNRHLHGARIYMD-KVSVGATLSVMMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L+ + E L G +VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAVSGGKITCRGKTADTLEAVI---EKLREAGMEVTVTETITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P KA VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RP-----KA--VNIRTPHPGFPTDMAQFLLNVVAEGTS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKGEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLAGCIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>ref|YP_002475331.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parasuis SH0165]
sp|B8F4Y1.1|MURA_HAEPS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACL32383.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parasuis SH0165]
Length = 424

Score = 66.2 bits (160), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 111/418 (26%), Positives = 173/418 (41%), Gaps = 45/418 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+E ++ N+ N +DV + LR LG+ VE +A
Sbjct: 12 LSGTVDISGAKNAALPILFAAILAEEPVILTNPVNLKDVETTVKILRKLGVVVE--RAEN 69

Query: 75 RAVVVGCGG----KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AV + P E K A + R V+ GG +
Sbjct: 70 NAVHIDASKIDHYVAPYELVKTMRASIWALAPLVARFHQQGVSLPGGCT-----IG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+++GA + D V+ G L G ++ L +S +++MAA
Sbjct: 121 ARPVDMMHIAGLEKMGATITL---DEGYVKAENVNGRLTGARI-LMDKVSVGATLSVMMAA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G IE P + T + + G K + + D I+G ++ ++ ++
Sbjct: 176 TLAKGTTTIE---NAAREPEIVDTAIFLNKMGAKITGAGT-DTITIEGVERLGGCEH-HI 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AAI+GG +T G +L + E L G +V TE S+T+
Sbjct: 231 VPDRIETGTFLVAAISGGRITCRGTKADTLDAVI---EKLREAGMQVDVTENSITLDSL 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR-- 368
P KA VN+ MP + A F T + VA+ K TE + R
Sbjct: 288 GMRP-----KA--VNIRTMHPGFPPTDMAQF---TLLNVVANGTSKITETIFENRFM 335

Query: 369 --TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I E L+ + D R +++ LA C TI D
Sbjct: 336 HIPELIRMGAKAEIEGNTAICHGVENLSGAEV-MATDLRASISLVLAGCIANGQTIVD 392

>ref|ZP_02868920.1| 3-phosphoshikimate 1-carboxyvinyltransferase [candidate division
TM7 single-cell isolate TM7a]
Length = 202

Score = 65.9 bits (159), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 60/206 (29%), Positives = 104/206 (50%), Gaps = 16/206 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALL--SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++G +++P SKS S+R ++ AAL SE + +DNL S D+ + G ++ ++
Sbjct: 10 LNGKIEIPPSKSYSHRAVIAAALAASEKKSTIDNLKFSVDITTTTIDIMENWGAKIKRFES 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT-AAVTAAGGNATYVLDGVPRMRE 131
A +VG GK +D + VQ +G +R L +T+ + DG ++ +
Sbjct: 70 ALE--IVGNDGKVVPKD--KYVQC--NESGSTIRFLIPVGITSSEN---ELIFDGKGKLVLD 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ ++ G + G P+ VNG L G ++ G+ISSQ+++ LL A P
Sbjct: 121 RPLDSYKIFEEQGLKYETTDGK--LPLTVNG--KLKAGNYEIDGNISSQFITGLLYALP 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRL 217
L GD ++ I L S Y+++TL +
Sbjct: 177 LLDGDSKLIINKNLESKGYIDLTLLEI 202

>ref|ZP_03366990.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. E98-0664]
Length = 83

Score = 65.9 bits (159), Expect = 1e-08, Method: Composition-based stats.
Identities = 40/79 (50%), Positives = 52/79 (65%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E + LQPI + G + LKSKS+SNR LLLAAL+ G TV+ NLL+S+DV +ML AL LG
Sbjct: 2 ESLTLQPIARVDGAINLPKSKSVSNRALLAALACGKTVLTNLLSDDDVRHMLNALSALG 61

Query: 65 LSVEADKAAKRAVVVVGCGG 83
++ R + G GG
Sbjct: 62 INYTLADRTRCDITGNNG 80

>emb|CBI80133.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Bartonella sp. 1-1C]
Length = 442

Score = 65.9 bits (159), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 106/449 (23%), Positives = 189/449 (42%), Gaps = 45/449 (10%)

Query: 14 EISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SGT+K+PG KS+S+R L+L L+ G + + LL SE V ++ +G + K
Sbjct: 14 NLSGTIKMPGDKSISHRALILGGLAHGESHIHGLLESESVLRTATIMQAMG--AQYKKN 71

Query: 74 KRAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
++ G G ++ + L GN+G + + V++ ++ G + P
Sbjct: 72 NLWIIHGTGNGCLLQ---AQTPLNFGNSGSAHLIMGLVSSYHMKTAFL--GGALLSRYP 126

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGKVKLSGSISSQYL-SALLMAAPL 192
+ ++ L+ +G + + LG P + G ++ ++S + SA+L+A
Sbjct: 127 MKHILNPLRLMGVETEPTLGNHLP---LTLYGPKMANPIRYPIPMASAPVKSAILLAGLN 183

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYV 250
G II+ ++ + E ++++ FG + + + RF GQ + + V
Sbjct: 184 TAGTT--TIIETPLTQDHT---KMLQAFGAIEDIKIDKTGRFTSLKGQPHLIGQIINV 238

Query: 251 EGDASSASY-FLAGAAITGGTVTEGCGTTSLQGDKV--FAEVLEMMGAKV-----TW 300
GD S A++ +A + +T+E L D K F + L MGAK+ T
Sbjct: 239 PGDLSLAAFPPIAALLVENS DITLENV---LVNDEKMGFIQTLWEMGAKIELLNQRKTG 294

Query: 301 TETSVTVTGPPREPFRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWR 357
E V + E LK + V + P D LA+ A FA G T I +
Sbjct: 295 IENIVDIRVKSSE-----LKGVTVPKERAPLIIDKYPALAIAAFAKGTIISGIEGLF 348

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKLNVTADTYDDHRMAMAFSL-A 413
K ++R+ + L E G D+ II + L + T+ DH++AM F +
Sbjct: 349 CKISDRLSILAEGKINHHCENGKDFLIHKGNSIKDLGGGRVTTTFDHQIAMCFLIFG 408

Query: 414 ACAEVPVTIRDPGCTRKTFFPDYFDVLSTF 442
+E PV I D P++ ++
Sbjct: 409 LVSEKPMIDDKQMIITNCPEFIPLMHQL 437

>ref|ZP_06552741.1| hypothetical protein AWRIB429_0131 [Oenococcus oeni AWRIB429]
gb|EFD89284.1| hypothetical protein AWRIB429_0131 [Oenococcus oeni AWRIB429]
Length = 165

Score = 65.5 bits (158), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 40/135 (29%), Positives = 69/135 (51%), Gaps = 8/135 (5%)

Query: 319 HLKAIDVNMNKMMPDVAMTLAVVAL---FADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
+L A+++ ++P+V L ++ L A G T I RVKET R+ + EL KLG
Sbjct: 26 NLHAVEITSKEIPNVIDELPILTLAASLAKGRTIISGAGELRVKETYRISVVAELKKG 85

Query: 376 ASVEEGPDYCIITPPEKLVN--TAIDTYDDHRMAMAFSLAAC---AEVPVTIRDPGCTRK 430
 A ++E D +I KL + + T+ DHR+ M ++AA +T+ +P +
 Sbjct: 86 ARIQEKSDGMVIDGCPKLQIPENNLAHGDHRIGMMLAVAALLVDTSTITLNNPEAIKI 145

Query: 431 TFPDYFDVLSTFVK 445
 ++P++F L + N
 Sbjct: 146 SYPNFFRDLDYLLNN 160

>ref|ZP_03148433.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
 G11MC16]
 gb|EDY05376.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
 G11MC16]
 Length = 458

Score = 65.5 bits (158), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 103/374 (27%), Positives = 156/374 (41%), Gaps = 43/374 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
 E+I+++ +SGTVK+ G+K+ ++ L S+GT+ + ++ DV+ + LR L
 Sbjct: 26 EKIIIVRGGNRLSGTVKVEGAKNAVLPIAATLLASKGTSTIHDVLPALSDVYTISEVRLYL 85

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
 G V + A AV+V G VE E V+ MR+ + + A G A
 Sbjct: 86 GADV---RIAGNAVMVDATGPLTVEAPFEYVR-----KMRASVLVMGP LLARNGRAR 134

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
 L G + RPI + G + +GA V +G +NG L G KV L S
 Sbjct: 135 VALPGGCAIGSRPIDQHLKGFEAMGASVK--VGNGFIDAEING--RLRGAKVYLDFF-SV 189

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 ++MAA LA G +I+ P + + G K + + I+G
 Sbjct: 190 GATENIMMAAVLAEGTT--VIENCAKEPEIVDLANFLNAMGAKIRGAGTGT-IRIEGVD 245

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
 + + + D A F+ AAITGG V V+G L LE MG V
 Sbjct: 246 ELVGTHTVIP-DRIEAGTFMVAAAITGGNVLVQGAPEHLS---SLIAKLEEMGVTVIE 301

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA-- 354
 ET V V GP + LKA+D+ P D+ + + L A+G + I +
 Sbjct: 302 EETGVRVIGP-----ETLKAVIDIKTMPYPGFPTMQSQMMALLLKAEGTSMITETVFE 354

Query: 355 --SWRVKETERMVA 366
 V+E RM A
 Sbjct: 355 NRFMHVEEFRRMNA 368

>ref|YP_001127373.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
 thermodenitrificans NG80-2]
 gb|ABO68628.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
 thermodenitrificans NG80-2]
 Length = 434

Score = 65.5 bits (158), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 103/374 (27%), Positives = 156/374 (41%), Gaps = 43/374 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
 E+I+++ +SGTVK+ G+K+ ++ L S+GT+ + ++ DV+ + LR L
 Sbjct: 2 EKIIIVRGGNRLSGTVKVEGAKNAVLPIAATLLASKGTSTIHDVLPALSDVYTISEVRLYL 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
 G V + A AV+V G VE E V+ MR+ + + A G A
 Sbjct: 62 GADV---RIAGNAVMVDATGPLTVEAPFEYVR-----KMRASVLVMGP LLARNGRAR 110

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
 L G + RPI + G + +GA V +G +NG L G KV L S
 Sbjct: 111 VALPGGCAIGSRPIDQHLKGFEAMGASVK--VGNGFIDAEING--RLRGAKVYLDFF-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 ++MAA LA G +I+ P + + G K + + I+G
 Sbjct: 166 GATENIMMAAVLAEGTT--VIENCAKEPEIVDLANFLNAMGAKIRGAGTGT-IRIEGVD 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + D A F+ AAITGG V V+G L LE MG V
Sbjct: 222 ELVGTHTVIP-DRIEAGTFMVAAAITGGNVLVQGAPEHLS---SLIAKLEEMGVTVIE 277

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA-- 354
ET V V GP + LKA+D+ P D+ + + L A+G + I +
Sbjct: 278 EETGVRVIGP-----ETLKAVDIKTMYPGFPPTMQSQMMALLLKAEGTSMITETVFE 330

Query: 355 --SWRVKETERMVA 366
V+E RM A
Sbjct: 331 NRFMHVEEFRRMNA 344

>ref|ZP_00135108.1| COG0766: UDP-N-acetylglucosamine enolpyruvyl transferase
[Actinobacillus pleuropneumoniae serovar 1 str. 4074]
Length = 424

Score = 65.1 bits (157), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 104/421 (24%), Positives = 173/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPLDKVDVDTTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++GA ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISGLEKMGALIEL----DEGYVKATSNRHLHGARIYMD-KVSVGATLSVMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L+ + E L G +VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAVSGGKITCRGKTADTLEAVI---EKLREAGMEVTVTEDTITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RPK-----PVNIRTMHPHGFPTDMQAQFTLLNVVAEGTS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKGEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLGACIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>ref|ZP_07532482.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
gb|EFM89543.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
Length = 424

Score = 64.7 bits (156), Expect = 2e-08, Method: Compositional matrix adjust.
Identities = 105/421 (24%), Positives = 174/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPLDKVDVDTTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++G+ ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISGLEKMGSVIEL----DEGYVKATSNRGLHGARIYMD-KVSVGATLSVMMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L+ + E L G VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAVSGGKITCRGTKADTLEAVI---EKLREAGMDVTVTEDTITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P KA VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RP-----KA--VNIRTMPHPGFPTDMAQAQFTLLNVVAEGTS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKGEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLAGCIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>ref|YP_001652299.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 3 str. JL03]
sp|B0BQM0.1|MURA_ACTPJ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABY69855.1| UDP-N-Acetylglucosamine-1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 3 str. JL03]
Length = 424

Score = 64.7 bits (156), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 105/421 (24%), Positives = 175/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPDLKDVDTTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++G+ ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISGLEKMGSVIEL----DEGYVKATSNRGLHGARIYMD-KVSVGATLSVMMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L+ + E L G +VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAVSGGKITCRGTKADTLEAVI---EKLREAGMEVTVTETITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P KA VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RP-----KA--VNIRTMPHPGFPTDMAQAQFTLLNVVAEGIS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKGEIEGNTAICHGVEKLKSAEV-MATDLRASISLVLAGCIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>ref|YP_265919.2| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Pelagibacter ubique HTCC1062]
Length = 442

Score = 64.7 bits (156), Expect = 3e-08, Method: Compositional matrix adjust.
Identities = 102/450 (22%), Positives = 187/450 (41%), Gaps = 38/450 (8%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I+ IK+ + +++ G KSLS R +LLA+ + G + NLL SEDV + +++ LG+
Sbjct: 6 IIKDKIKKFNKQIRVSGDKSLRIRVWLLASQAIGKSKGYNLLMSEDVLAIDSIIKKLGK 65

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
V K V G G +++ + + N+G R + + + + G
Sbjct: 66 VRIQKNYCEIVGNGINGFKYIKNLTIDAK----NSGTLGRLLILGLLIKSP--KKIKIIGD 119

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ +R + L++ G + + P+ + G G K S+Q S++
Sbjct: 120 KSLSKRDIFSRTVTPLRKFGVKF-FYKIKNKLPLTILGTQSAKGIKY-FENKGSQAQCKSSV 177

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++AA A G I+ S + E+ + + + +K + +D F K
Sbjct: 178 MLAALNASGTTSIKAKK---SRNHTELLFKYL-KIPIKVRKTKKFD-FIDIKKPKKIIAF 232

Query: 247 NAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
N + GD SS+++F+ + + + + V +L+ MGA+T E
Sbjct: 233 NYQIPGDISSAFFMVLTTLADNSKLLIKNVNINP--SRVGVTILKKMGAKIT-LENQK 289

Query: 306 TVTGPPREPF---GRKHLKAI--VNMNMKP-DVAMTLAVVALFADGPTAIRDVASWRVK 359
G K LKAI+ V +N D + + ++A A G + +D++ K
Sbjct: 290 NYRGEKISDILIKSSKKLKAINCPVELNSSAIDEFLVIFLIAAKAKGISYFKDLSELNQK 349

Query: 360 ETER-----MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
E+ R M+ I+T+LT + PD I P +T + DHR+ M
Sbjct: 350 ESPRLIWGSKILNMMGIKTDLTNDNSIKIYGQPDLEIKKP-----ITVKNYLKDHRVFMMS 404

Query: 411 SLAACAE-VPVTIRDPGCTRKTFFPDYFDVL 439
++AA I D +FP + ++
Sbjct: 405 TIAALTFGGKWKIYDKDSINTSFPSFLKII 434

>gb|ACB05432.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 47

Score = 64.3 bits (155), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 40/46 (86%), Positives = 43/46 (93%)

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+DAKEEV+LFLGNA AMR+LTAAV AAGGNATYVLDGVPRMRERP
Sbjct: 2 KDAKEEVKLFLGNAVAMRALTAAVVAAGGNATYVLDGVPRMRERP 47

>gb|AAD47362.2|AF038578_5 cyclohexadienyl dehydrogenase/5-enolpyruvylshikimate 3-P synthase
[Pseudomonas stutzeri]
Length = 505

Score = 64.3 bits (155), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 54/191 (28%), Positives = 92/191 (48%), Gaps = 10/191 (5%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
P ++G +++PG KS+S+R ++L +L+EGTT + L ED A R +G+ +E
Sbjct: 309 NPGGSLTGQLRVPGDKSISHRSIMLGSLAEGTTEXEGFLEGEDALATXQAFRXMGVVIEG 368

Query: 70 DKAACKRAVV-VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V VG G ++LGN+G +MR L + A + T L G
Sbjct: 369 PHQGRVTVHGVGLHGL-----QAPPGPYILGNSGTSMRLLAGLLAAQPFDDT--LSGDAS 421

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ +RP+ + L+++GA ++ PP+ + G L G + + S+Q S LL+
Sbjct: 422 LTKRPMNRVAKPLREMGAVIET-AAEGRPPLTIRGGKLSGMHYDMPMA-SAQVKSCLLL 479

Query: 189 AAPLALGDVEI 199
A A G +
Sbjct: 480 AGLYAAGKTSV 490

>ref|ZP_02477459.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parasuis 29755]
gb|EDS25450.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parasuis 29755]
Length = 424

Score = 63.9 bits (154), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 110/418 (26%), Positives = 173/418 (41%), Gaps = 45/418 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+E ++ N+ + +DV + LR LG+ VE +A
Sbjct: 12 LSGTVDISGAKNAALPILFAAILAEEPVILTNPDLKDVETTVKILRKLGVVVE--RAEN 69

Query: 75 RAVVVGCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AV + P E K A + R V+ GG +
Sbjct: 70 NAVHIDASKIDHYVAPYELVKTMRSIWAALPLVARFHHQGVSLPGGCT-----IG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+++GA + D V+ G L G ++ L +S +++MAA
Sbjct: 121 ARPVDMHIAGLEKMGATITL---DEGYVKAEVNRLTGARI-LMDKVSVGATLSVMMAA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G IE P + T + + G K + + D I+G ++ ++ ++
Sbjct: 176 TLAKGTTTIE---NAAREPEIVDTAIFLNKMGAKITGAGT-DTITIEGVERLGGCEH-HI 230

Query: 251 EGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AAI+GG +T G +L + E L G +V TE S+T+
Sbjct: 231 VPDRIETGTFLVAAAISGGITCRGTGKADTLDAVI---EKLREAGMQVDVTENSITLDSL 287

Query: 311 PREPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR-- 368
P KA VN+ MP + A F T + VA+ K TE + R
Sbjct: 288 GMRP-----KA--VNIRTMHPGFPPTMQAQF---TLLNVVANGTSKITETIFENRFM 335

Query: 369 --TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++GA E + I E L+ + D R +++ LA C TI D
Sbjct: 336 HIPELIRMGAKAEIEGNTAICHGVESLSGAEV-MATDLRASISLVLAGCIANGQTIVD 392

>ref|ZP_03437775.1| hypothetical protein HPB128_142g26 [Helicobacter pylori B128]
gb|EEC24657.1| hypothetical protein HPB128_142g26 [Helicobacter pylori B128]
Length = 168

Score = 63.9 bits (154), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 42/143 (29%), Positives = 69/143 (48%), Gaps = 25/143 (17%)

Query: 320 LKAIDVNMN--KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGAS 377
LKAI + N + D L+V LFA G + +++ R KE++R+ A+ + LG
Sbjct: 27 LKAISIEQNIASLIDEIPALSVAMLFAGKSMVKNKDLRSKESDRIKAVVSNFKALGIE 86

Query: 378 VEEGPD-----YCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPT 421
EE D + I PP I +++DHR+AM+F++ A +P+
Sbjct: 87 CEEFEDGFYIEGLEDISPLKQCFSRKPP-----LIKSFNDHRIAMSFVLTALA-LPLE 139

Query: 422 IRDPGCTRKTFPDYFDVLSTFVK 444
I + CT +FP + +L+ F K
Sbjct: 140 IDNLECTNISFPQFKRLNLNLFKK 162

>ref|YP_001969131.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 7 str. AP76]
ref|ZP_07543429.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 12 str. 1096]
ref|ZP_07545554.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
pleuropneumoniae serovar 13 str. N273]
sp|B3H259.1|MURA_ACTP7 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:

Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACE61989.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 7 str. AP76]
gb|EFN00392.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 12 str. 1096]
gb|EFN02454.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus pleuropneumoniae serovar 13 str. N273]
Length = 424

Score = 63.9 bits (154), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 105/421 (24%), Positives = 174/421 (41%), Gaps = 51/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D++
Sbjct: 12 LSGTVDISGAKNAALPILFAAVLATEPVTLTNVPDLKDVDVTFKILRKLGVVVERDESGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALPLVARFHEGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+++GA ++ D V+ G L G ++ + +S +++MAA L
Sbjct: 123 PVDMHISSEKMGALIEL----DEGYVKATSNRGLHGARIYMD-KVSVGATLSVMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + G K + + D I+G ++ ++ V
Sbjct: 178 AEGTTTIE---NAAREPEIVDTALFLNAMGAKISGAGT-DTITIEGVERLTGCQHRIV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVVKFAEVLEMMGAKVITWTETSVTVTGPPR 312
D FL AA++GG +T G +L+ + E L G +VT TE ++T+ +
Sbjct: 233 DRIETGTFLVAAAVSGGKITCRGKTADTLEAVI---EKLREAGMEVTVTETITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKET---ER 363
P KA VN+ MP D+ ++ + A+G + R+ ET R
Sbjct: 290 RP-----KA--VNIRTMPHPGFPTDMQAQFTLLNVVAEGTS-----RITETIFENR 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I EKL + D R +++ LA C TI
Sbjct: 334 FMHI-PELNRMGAKGEIEGNTAICHGVEKLSAEV-MATDLRASISLVLGACIASGETIV 391

Query: 424 D 424
D
Sbjct: 392 D 392

>gb|EFV96998.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Streptococcus agalactiae ATCC 13813]
Length = 154

Score = 63.5 bits (153), Expect = 5e-08, Method: Compositional matrix adjust.
Identities = 39/149 (26%), Positives = 77/149 (51%), Gaps = 7/149 (4%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++PG KS+S+R ++ ++S+G T + ++L EDV + A + +G+ +E D
Sbjct: 10 LKGTIRVPGDKSISHRAIIFGSISQGVTRIVDVLRGEDVLSTIEAFKQMGVLIEDD---- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ GK + L +GN+G +MR + + T V D + +RP+
Sbjct: 66 -GEIITIYGKGFAGLTQPNLLDMGNSGTSMRLIAGVLAGQEFVETMVGDN--SLSKRPM 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNG 163
+ + L ++GA + D PP+++ G
Sbjct: 123 DRIALPLSKMGARISGVTNRDLPLPLKLG 151

>gb|ABC00790.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 38

Score = 63.5 bits (153), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 31/38 (81%), Positives = 35/38 (92%), Gaps = 1/38 (2%)

Query: 78 VVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
VVGCGG+FP+E DAKEEV+LFLGNAG AMR+LTAAV A
Sbjct: 1 VVGCGGRFPKIEKDAKEEVKLFLGNAGTAMRTLTAAVVA 38

>ref|YP_004066395.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni ICDCJ07001]
gb|ADT66206.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni
subsp. jejuni ICDCJ07001]
Length = 182

Score = 63.5 bits (153), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 41/156 (26%), Positives = 74/156 (47%), Gaps = 3/156 (1%)

Query: 289 EVLEMMGAKVTW--TETSVTVTGPPREPFGGRKHLKVIDNMNKMPPDVAMTLAVVALFADG 346
++L+ MGAK+ T+ G R + + + N+ + D A LA+ A G
Sbjct: 22 KILQKMGAKLEMIITQDNFETIGEIRVESSKLNIEVKDNIWLIDEAPALAI AFALAKG 81

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406
+++ + RVKE++R+ + L G E D I +L + I +Y DHR+
Sbjct: 82 KSSLINAKELRVKESDRIVAMVENLKLKCGVEARELDDGFEIEGGCEKSSKIKSYGDHRI 141

Query: 407 AMAFSLAACAEVPVTIRDPGCTRKTFFDYFDVLSTF 442
AM+F++ + I D C + +FP++ ++LS
Sbjct: 142 AMSFAILGGLL-CGIEIDSDCIKTSFPNFIEILSNL 176

>ref|YP_004168093.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Nitratifactor
salsuginis DSM 16511]
gb|ADV46344.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Nitratifactor
salsuginis DSM 16511]
Length = 424

Score = 63.2 bits (152), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 107/417 (25%), Positives = 168/417 (40%), Gaps = 51/417 (12%)

Query: 13 KEISGTVKLPKSKSLNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG++++ G+K+ + ++ LS+ V++NL N D+ +L L LG VE +
Sbjct: 10 KRLSGSIRISGAKNAALPVIAATILSDQPVVLENLPNVVDIITLLKLEMLGAEVEHEGH 69

Query: 73 AKR---AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
R + + + L LG + A G L G +
Sbjct: 70 VARIDPGTITSTRAVYEIVAQMRASILVLG-----PLLARFGECEVSLPGGCAI 118

Query: 130 RERPIGDLVVLGKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+RPI + ++ +GA ++ ++ P GGL G KV +S
Sbjct: 119 GQRPIDLHLKAMEAMGAQIEIKGGYVRAIAPE-----GGLQGAKVVD-KVSVGATENT 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK--GGQKYKS 244
LMAA LA G E I P + +++ GV E + R I+ GG
Sbjct: 172 LMAAALAHGTTE---IINAAREPEIVQLCEMLQAGGVNIEGIGT-GRLTIEGTGGTLLHF 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW-TET 303
P++ + D A +L AIT +T+E LQ + + LE MG + +E
Sbjct: 228 PESIRIIPDRIEAGTYLCAGAITYSQITLAEVNIEHLQSTI---DKLEAMGCSFEYPSEE 284

Query: 304 SVTVTGPPREPFGGRKHLKVIDNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
SVT+ P R G K + + P D+ L VA A G + I + R+ E
Sbjct: 285 SVTIF-PAR--GGLKEVNIVTAEYPGFPTDMQAQLMAVATLAAGESLIEE----RLFENR 337

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTATIDTYDDHRMAMAFSLAAC 416
M +EL +LGA + + + P EKL +V A D R + A LA A
Sbjct: 338 FMHV--SELNRLGADIWLKGNVAARVPVEKLYGADVMTDL---RASSALVLAGLA 388

>ref|ZP_08068303.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
ureae ATCC 25976]
gb|EFX90894.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
ureae ATCC 25976]
Length = 439

Score = 62.4 bits (150), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 103/416 (24%), Positives = 169/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ + +DV LR LG+ VE D+
Sbjct: 26 LSGTVDISGAKNAALPILFAAILATEPVTLTNVPLDKVDVDTTFKILRKLGVVVERDETGA 85

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 86 VQIDASHIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 136

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++GA ++ D V+ G L G ++ + +S +++MA L
Sbjct: 137 PVDMHISGLEKMGALIEL---DEGYVKATSNGLRQGTIRIYMD-KVSVGATLSVMMAGTL 191

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + G K + + D ++G ++ ++ V
Sbjct: 192 AEGTT---VIENAREPEIVDTALFLNAMGAKISGAGT-DTITVEGVERLTGCQHRVV-A 246

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L + E L G +VT TE ++T+ +
Sbjct: 247 DRIETGTFVLAAAVSGGKITCRGKTADTLDAVI---EKLREAGMEVTVTETITLDSKGQ 303

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR---- 368
P KA VN+ MP + A F T + VA + TE + R
Sbjct: 304 RP-----KA--VNIRTMPHSGFPPTMQAQF---TLLNVVAEGTSRITETIFENRFMHI 351

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I EKL + D R +++ LA C TI D
Sbjct: 352 PELNRMGAKGEIEGNTVICHGVEKLKSAEV-MATDLRASISLVLAGCIASGETIVD 406

>ref|YP_004010930.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodocrobium
vannielii ATCC 17100]
gb|ADP69831.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodocrobium
vannielii ATCC 17100]
Length = 429

Score = 62.4 bits (150), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 97/375 (25%), Positives = 160/375 (42%), Gaps = 35/375 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD-K 71
+ ++GT+ + G+K+ + +++ + L+ T + N+ N DV ++ LR G D K
Sbjct: 10 RHLNGTIPISGAKNAALPLMIASLLTPETVTLKNVPLADVSLILIRLNHGTDAADFQK 69

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPR 128
A V G F D + + + MR+ + + A G A L G
Sbjct: 70 RANGHVHQGDTHFTARDIVDTTAPY--DLVRRMRASFVVLGPLLAREGKARVSLPGGCA 127

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+ LGAD+ D V + GGL GG V+ IS +LM
Sbjct: 128 IGTRPVDLHLTGLQALGADIKL----DGGYVASAPGGLKGGVVRFP-KISVGATHNVLM 182

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+V +I+ P V + + G K E + + +I+G + + +
Sbjct: 183 AATLAKGEV---VIENACEPEVVDVAACLSKMGAKIEGAGT-PTIHIQGVDELEGATHT 238

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ + +Y +A AA GG VT+EG L G ++L G ++ T + VT
Sbjct: 239 VLPDRIETGTYAMAVAA-AGGDVTLEGARGDLLPG---VLDLLRNAGVEIAETNRGIRVT 294

Query: 309 GPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
L+ + V P D+ L + ADG + IR+ + E M
Sbjct: 295 -----RNGAALRPVTVETEPFPGFPTDLQAQLMALMCRADGISEIRET-----IFENRFM 344

Query: 365 VAIRTELTKLGASVE 379
+ELT+LGA +E
Sbjct: 345 HV--SELTRLGADIE 357

>ref|YP_003426316.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
pseudofirmus OF4]
gb|ADC49424.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
pseudofirmus OF4]
Length = 438

Score = 62.0 bits (149), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 107/416 (25%), Positives = 172/416 (41%), Gaps = 65/416 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLS----EGTTVVDNLLNSEDVHYMLGAL 60
E+I+++ ++ GTVK+ G+K N +L + A S +GT+ + ++ DV+ M L
Sbjct: 2 EKIIIVRGGNKLEGTVKVEGAK---NAVLPVIAASILAGKGTSKLYDVPELADVVTMREVL 58

Query: 61 RTLGLSVE-----ADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAA 111
R L + VE A+K K + P E ++ FL M L A
Sbjct: 59 RNLNIDVEYVNNFTTVNAEKTTLKT-----EAPFEYVRKMRASFL-----VMGPLLAR 105

Query: 112 VTAAGGNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGK 171
V G A L G + RPI + G + +GA V+ +G R++G L G K
Sbjct: 106 V---GKARIALPGGCAIGSRPIDQHLKGFEAMGATVE--IGNGFIEARIDG--KLQGTK 157

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
+ L S ++MAA LA G II+ + P + + G K + +
Sbjct: 158 IYLDFFP-SVGATENIMMAAVLAEGTT---IENVAEEPEIVCLANYLNGMGAKVRGAGTG 213

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVL 291
I+G ++ K+ + GD A F+ AAITGG V VEG L+ +
Sbjct: 214 I-IRIEGVEELNGAKHTVI-GDRIEAGTFMVAAAITGGNVLVEGAVAHLR---PLIAKM 268

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNMKP----DVAMTLAVVALFADGP 347
MG ++ E + V GP + LKAID+ P D+ + + L A G
Sbjct: 269 REMGVEIKEEENGLRVIGP-----ETLKAIDIKTMPHPGFPTDMQAQMALLLKAKGT 321

Query: 348 TAIRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYD 402
+ I + V R E E ++ +++ II+ P L + + D
Sbjct: 322 SVITETVFENRFMHVE-----EFRRMNSNIKIEGRSAIISGPNNLQGAEVASTD 370

>ref|YP_660138.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Pseudoalteromonas atlantica T6c]
sp|Q15YF4.1|MURA_PSEA6 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABG39084.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Pseudoalteromonas atlantica T6c]
Length = 419

Score = 62.0 bits (149), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 79/329 (24%), Positives = 138/329 (41%), Gaps = 44/329 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLSSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ K + G+V++ G+K+ + IL+ + L++ T DN+ D++ L L LG
Sbjct: 2 DKLLIKASKPLQGSVRISGAKNAALPILMSSILADTTCYFDNVPELRDINTSLALLAELG 61

Query: 65 LSVEADKAAKRAV-----VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGN 118
+A + + AV + C + + L LG + A G
Sbjct: 62 --ADAKRVSGHAVEIDPSSINNCNASYDLVKTMRASILVLG-----PLLAKYGE 108

Query: 119 ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + GL+++GA +D G +R G L G + + +
Sbjct: 109 ANVSLPGGCAIGARPVNLHLQLGLEKMGAKIDVEAGY----IRAKVDGRLKGANIFMD-MV 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S L+MAA LA G+ +++ P + + G K H+ S D+ I+G
Sbjct: 164 SVGATENLMMAACLADGET---VLENAAREPEIVDLANCLNAMGAKVTHAGS-DKIRIQG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ + + A + D FL AA+TGG + E +L + L M GA +
Sbjct: 220 VERLQGCYAVLP-DRIETGTFLIAAAVTGGKIRCENAAPETLDA---VLDKLVMA GAVI 275

Query: 299 T----WTE-----TSVTVTGPPREPF 315
T W E TSV + P F
Sbjct: 276 TTGDDWIELDMQGHPLTSVNIKTAPHPGF 304

>emb|CAN79289.1| hypothetical protein VITISV_044036 [Vitis vinifera]
Length = 133

Score = 62.0 bits (149), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 32/38 (84%), Positives = 34/38 (89%), Gaps = 1/38 (2%)

Query: 93 EVQLFLGNAGIAMRSLTAAVTAAGGNATY-VLDGVPRM 129
EVQLFLGNAG AMR LTAAVTAAGGNA+Y V DGVPR+
Sbjct: 63 EVQLFLGNAGTAMRPLTAAVTAAGGNASYHVPDGVPRI 100

>ref|ZP_04858335.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
gb|EES75581.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39BFAA]
Length = 430

Score = 62.0 bits (149), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 105/424 (24%), Positives = 182/424 (42%), Gaps = 39/424 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + G V++ G+K+ + IL A +++ T +++NL + D++ +L A+ G
Sbjct: 2 EQYVIKGGNPLVGEVEIAGAKNAALAILAAAIMTDEILILNLPDVRDINVLEAI--AG 59

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D+ K V + V E ++ A L A+ +A L
Sbjct: 60 IGAQVDRIDKSTVKINGSTIGDVSVDYIYIKKIR-----ASYLLGALLGKYKHAEPPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGADVD G V L G + L +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGADVDIMHGA-----IVAKADELHGSHIFLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G I++ P+V + G + + + D IKG +K
Sbjct: 169 NIMMAASLAPGRT---ILENAAREPHVVDVANFLNSMGANIKGAGT-DVIRIKGVEKLHR 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ AA TGG VTV+ L+ LE +G +V + +
Sbjct: 225 TEYSIIP-DQIEAGTFMFAAAATGGDVTVKNVIPKHLEATTA---KLEEIGCEVEEFDDA 280

Query: 305 VTVTGPPEPFGRKHLKAI---DVNMNKMPPDVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V V P R R H+K + + P +A+TLA A+G + + + + R K
Sbjct: 281 VRVRAPKR--LHRTVKTLPYPGYPTMQPQIAVTLA----LAEGTSIVTESIFENRFKY 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPV 420
+ EL+++GA+++ + II +KL + + D R A +A A +
Sbjct: 335 AD-----ELSRMGANIKVEGNSAIIIDGVKKLTGARV-SAPDLRAGAALVIAGLAADGI 386

Query: 421 TIRD 424
T+ D
Sbjct: 387 TVVD 390

>gb|AAA97396.1| encodes EPSP synthase domain [Pneumocystis murina]
prf||2210353A AROM protein
Length = 108

Score = 61.6 bits (148), Expect = 2e-07, Method: Composition-based stats.
Identities = 40/105 (38%), Positives = 54/105 (51%), Gaps = 7/105 (6%)

Query: 334 AMTLAVVALFADGP--TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPE 391
A LA VA P T I +++ R+KE R+ A+ EL K G E PD +
Sbjct: 4 AAVLASVAYEESKPYYITKITGISNQRIKECNRIDAMICELKKFGIEAGELPDGIYVKAQN 63

Query: 392 KLN---VTAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
N V I+ Y+DHR+AM+FS+ AC ++ P TI D C KT
Sbjct: 64 ISNLSYPVEGINCYNDRHRIAMSFSVLACISQKPTTILDKACVNKT 108

```
>ref|YP_633066.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Myxococcus
xanthus DK 1622]
sp|Q1D2Q7.1|MURA_MYXXD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABF90980.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Myxococcus
xanthus DK 1622]
Length = 420
```

Score = 61.6 bits (148), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 98/386 (25%), Positives = 158/386 (40%), Gaps = 43/386 (11%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + + G V+ G+K+ + IL A L++GT+ N+ DV ML LRT+G
Sbjct: 2 DKIVIKGGQALHGEVQASGAKNAALPILASALLADGTSTYRNPALADVATMLKVLRTMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
E D VG G E + V+ MR+ + + A G A
Sbjct: 62 CDAERDSETTDCRVGVNGHITPEAPYDLVK-----TMRASVLVLGPLVARFGRARV 113

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ G + RPI + GLK LGAD+ G + L GG V I+
Sbjct: 114 SMPGGCAIGARPIDQHLKGLKALGADIHLTEGYVEATAK----QLKGGTVNFD-VITVT 167

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA LA G +++ P VE +++ + G + E + + I+G
Sbjct: 168 GTENVMAAVLAKGRT---LMENCAREPEVEELAKVLNKMGARIEGAGTSS-ITIEGVDG 223

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWT 301
K ++A + D A L AAI+GG V V+ + E L G +T
Sbjct: 224 LKPVEHAILP-DRIEAGTLLVAAAISGGDVLVVRVPEHMDA---LVEKLREAGCTITTE 279

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ + P R L A+++ + P D+ L + + G + I S
Sbjct: 280 GSGLRCKAPQR-----LDAVNITTEHPGFPTDMQAQLMALMSVSQGTSVI----SEN 328

Query: 358 VKETERMVAIRTELTKLGASVE-EGP 382
+ E M EL +LGA + +GP
Sbjct: 329 IFENRFMHV--PELHRLGADITIQQP 352
```

```
>ref|YP_980934.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polaromonas
naphthalenivorans CJ2]
sp|A1VK35.1|MURA_POLNA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABM36013.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polaromonas
naphthalenivorans CJ2]
Length = 424
```

Score = 61.2 bits (147), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 94/398 (23%), Positives = 163/398 (40%), Gaps = 56/398 (14%)

```
Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G+V + G+K+ + L A L+ T + N+ +DV ML +R +G+ E
Sbjct: 10 KSLAGSVDISGAKNAALPELCAALLTAETVTLQNVPLQDVATMLKLIRNMGVEAERSAH 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
A V++ G P+ + +L +++ A+V A G G AT L G
Sbjct: 70 APGTVILNAG---PLSSPEAPYEL-----VKTMRASVLALGPLLARFGEATVSLPGG 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-SISSQYLSA 185
+ RP+ + GL+ +GAD+ G + LP G+ +L G +I++ ++
Sbjct: 119 CAIGSRPVDQHIKGLQAMGADIIVEHGYM-----LARLPKGQTRLKGAAITTDMVTV 170

Query: 186 -----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LMAA LA G+ I++ P + + + G K E S R I+G +
Sbjct: 171 TGTFENFLMAATLAEGET---ILENAAQEPEIGDLAEMLIKMGAKIEGHGSR-RIRIQGVE 226
```

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + V D FL A GG V + L+ + E L GA VT
Sbjct: 227 RLHGCTHQVV-ADRIETGTFLCAVAAGGDVVLNHGRADHLEVVI---EKLREAGATVTA 282

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
E + + R +KA + P D+ + A G + + +
Sbjct: 283 GEGFIRIQASGR-----MKAQSFRTTEYPGFPTDMQAQFMALNAIAQGTSTVTET--- 332

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M E+ +LGA ++ C+I E+L+
Sbjct: 333 -IFENRFMHV--NEMVRLGAKIQIEGKVCVINGVEQLS 367

>gb|AAK64441.1|AF377339_2 UDP-GlcNAc 1-carboxyvinyl transferase MurA [Myxococcus xanthus]
Length = 420

Score = 61.2 bits (147), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 98/386 (25%), Positives = 157/386 (40%), Gaps = 43/386 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
++IV++ + + G V+ G+K+ + IL A L++GT+ N+ DV ML LRT+G
Sbjct: 2 DKIVIKGGQALHGEVQASGAKNAALPILASALLADGTSTYRNVLPALADVATMLKVLRTMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
E D VG G E + V+ MR+ + + A G A
Sbjct: 62 CDAERDSETTDCRVGVNGHITPEAPYDLVK-----TMRASVLVLGPLVARFGRARV 113

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ G + RPI + GLK LGAD+ G + L GG V I+
Sbjct: 114 SMPGGCAIGARPIDQHLKGLKALGADIHLTEGYVEATAK-----QLKGGTVNFD-VITVT 167

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA LA G +++ P VE +++ + G + E + + I+G
Sbjct: 168 GTENVMAAVLAQGRT---LMENCAREPEVEELAKVLNKMGARIEGAGTSS-ITIEGVGD 223

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K ++A + D A L AAI+GG V V + E L G +T
Sbjct: 224 LKPVEHAILP-DRIEAGTLLVAAAISGGDVLVRRVVEHMDA---LVEKLREAGCTITTE 279

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ + P R L A+++ + P D+ L + + G + I S
Sbjct: 280 GSGLRCKAPQR-----LDAVNITTEHPGFPTDMQAQLMALMSVSQGTSVI----SEN 328

Query: 358 VKETERMVAIRTELTKLGASVE-EGP 382
+ E M EL +LGA + +GP
Sbjct: 329 IFENRFMHV--PELHRLGADITIQQP 352

>ref|YP_003467663.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xenorhabdus bovienii
SS-2004]
ref|YP_003469654.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xenorhabdus bovienii
SS-2004]
emb|CBJ80883.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (fragment) [Xenorhabdus bovienii
SS-2004]
emb|CBJ82892.1| 3-phosphoshikimate 1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
synthase) (EPSPS) (fragment) [Xenorhabdus bovienii
SS-2004]
Length = 239

Score = 61.2 bits (147), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 59/237 (24%), Positives = 103/237 (43%), Gaps = 27/237 (11%)

Query: 211 VEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT 270
V T+ +++ G++ E+ + F++ G + + AS F G+
Sbjct: 2 VHTTINNLKKAGIRIEYDSDFREFFVHGRCLQ-----ASDFTVGS DPASTA 48

Query: 271 VTVEGCGTTSLQGDVKFAEVLEM---MGAKVTW---TETSVTVTGPPREPFGGRKHLKAI 323

+ CG SL+ +V+ E GA + + T T++ G G ++ +
Sbjct: 49 AIALCG--SLESEVQLNGFFEEELGNGAVIQYLIDTGTNIEFIGNETIIRGSTAIRPL 106

Query: 324 DVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD 383
 D + + PD LA A A G + ++ R KE++R+ R EL+KLG +E D
Sbjct: 107 DFDGS LAPDAVPALAAASLASGTSIFYNIEHIRYKESDRISDFRKELSKLGVKSEKHD 166

Query: 384 YCII--TPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYF 436
 II P +D + DH + M + C+E PV I++P +T+P+YF
Sbjct: 167 QLIIHGNPKGYKGRVVLDGHYDHGLIMGLTTIGLHCSE-PVIIKEPFHVQGTYPEYF 222

>gb|ACB05435.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 42

Score = 60.8 bits (146), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 37/42 (88%), Positives = 40/42 (95%)

Query: 92 EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
 EEV+LFLGNAG AMR+LTAAV AAGG+ATYVLDGVPRMRER
Sbjct: 1 EEVKLFLGNAGTAMRALTAAVVAAGGNATYVLDGVPRMRER 42

>gb|ACB05433.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 42

Score = 60.8 bits (146), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 38/42 (90%), Positives = 40/42 (95%)

Query: 92 EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
 EEV+LFLGNAG AMR+LTAAV AAGGNATYVLDGVPRMRER
Sbjct: 1 EEVKLFLGNAGTAMRALTAAVVAAGGNATYVLDGVPRMRER 42

>ref|ZP_04752696.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
minor NM305]
gb|EER47890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
minor NM305]
Length = 425

Score = 60.8 bits (146), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 105/416 (25%), Positives = 166/416 (39%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 +SGTV++ G+K+ + IL A L+E + N+ +DV LR LG+ VE D
Sbjct: 12 LSGTVEISGAKNAALPILFAAILAEKPVTLTNVPVLKDVETTFKILRKLGVVVERDANGA 71

Query: 75 RAVVVCGCGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
 + + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHEGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
 P+ + GL+++GA ++ D V+ G L G +V + +S +++MAA L
Sbjct: 123 PVDMHIAGLEKMGATIEL----DEGYVKATSNGRLKGARVYMD-KVSVGATLSVMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
 A G +I+ P + T + G K + + D ++G + ++ V
Sbjct: 178 AEGKT---VIENAREPEIVDTAIFLNAMGAKISGAGT-DMITVEGVEHLGGCEHRVV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
 D FL AA++GG +T G +L + E L G V TE ++T+ R
Sbjct: 233 DRIETGTFLIAAAVSGKITCRGTKADTLDAVI---EKLREAGMDVEVTEDTITLDSKGR 289

Query: 313 EPFGRKHLKAIDVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETERMVAIR---- 368
 P KA VN+ MP + A F T + VA + TE + R
Sbjct: 290 RP-----KA--VNIRTMPHPGFPTMQAQF---TLLNTVAEGTSRITETIFENRFMHI 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
 EL ++GA E + I E L + D R +++ LA C TI D

Sbjct: 338 PELNRMGAKGEIEGNTAICHGVESLKPAEV-MATDLRASISLVLAGCIANGETIVD 392

>ref|ZP_05297041.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J1-208]
Length = 160

Score = 60.8 bits (146), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 51/164 (31%), Positives = 80/164 (48%), Gaps = 13/164 (7%)

Query: 255 SSASYFLAGAAITGGT---VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
SSA++F+ IT G+ +T G T +V+E MG + ++S + TG
Sbjct: 2 SSAAFFIVAGLITPGSEIELTHVGLNPTR---TGIFDVVEQMGGSLVVKDSSRS-TGKL 56

Query: 312 REPFGRK--HLKAIDVNMNKMPPDVAMTLAVVALFA---DGPTAIRDVASWRVKETERMVA 366
K LK ++ + +P + + V+AL A +G T I+D A +VKET R+ A
Sbjct: 57 AGTVVVKTSDLKGTEIGGDIIPRLIDEIPVIALLATQAEGTTI IKDAAELKVKETNRIDA 116

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAF 410
+ TEL K+GA + D II L+ + +Y DHR+ M
Sbjct: 117 VATELNKMGADITPTEDGLIIRGKTPLHAANVTSYGDHRIGMML 160

>ref|ZP_07896341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
italicus DSM 15952]
gb|EFU73550.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
italicus DSM 15952]
Length = 431

Score = 60.8 bits (146), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 106/457 (23%), Positives = 181/457 (39%), Gaps = 84/457 (18%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
+EI+++ ++ GTVK+ G+K+ IL + L+ EGTT + N+ DV M +R L
Sbjct: 2 DEIIVKGGNQLKGTVKIEGAKNAVLPLAASLLADEGTTNLHNPILSDVFTMNEVIRQL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
V+ D+ K+ V + +E E V MR+ + + A G+A
Sbjct: 62 NAQVKFDEEQKQ-VTIDATADLNIEAPYEYVS-----QMRASIVVMGP LLARNGHAK 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADV-----DCFLGT---DCPPVRVNGIG 165
+ G + +RPI + G + LGA + D +GT D P V
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAQIIQKDG YIEAIDQLIGTNIYLD FPSV----- 166

Query: 166 GLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA 225
G+ + ++MAA A G +I + P + ++ + G K
Sbjct: 167 -----GATQN-----IMMAAVKAKGTT---VISNVAREPEIVDLANILNKMGA KI 208

Query: 226 EHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDV 285
+ I+G +K + ++A V+ D A F+ AA+T G V +E + +
Sbjct: 209 -FGVGTETMRIEGVEKLHAVEHAIVQ-DRIEAGTFMVAAAMTQGDVLIENA---IAEHN R 263

Query: 286 KFAEVLEMMGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNKM P---DVAMTLAVVA 341
L MGA+++ + + + GP K LKA D+ P D+ + +
Sbjct: 264 PLLSKLAEMGA EISENDEGIRIVGP-----KILKATDIKTLPHPGFPTDMQAQMTAIQ 316

Query: 342 LFADGPTAIRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDT 400
+ A G + + + V R + E MV ++ A V+ + +I P L + +
Sbjct: 317 MLAHGRSIVTETVFENRFQHLEEMV-----RMNAKVKIDGNVAVIDGPNDLQGSIVHA 369

Query: 401 YDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFD 437
D A + CAE G TR Y D
Sbjct: 370 TDLRAAALVLVGLCAE-----GITVRNLKYLD 398

>ref|YP_004062583.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Liberibacter solanacearum CLso-ZC1]
gb|ADR52095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Liberibacter solanacearum CLso-ZC1]
Length = 491

Score = 60.5 bits (145), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 100/439 (22%), Positives = 192/439 (43%), Gaps = 34/439 (7%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GT+ +PG +S+S+ ++L L+ G T + LL S+DV + ++ LG K
Sbjct: 64 LTGTICVPGDRSISHFSIILGGLASGETRISGLLESDDVLKTIKSMNCLG--AHFTKKNK 121

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
++ G G + E L N+ I LT + T+ G + ++ +
Sbjct: 122 EWIKGVGNGCLL---APESPLDFENSEIGCE-LTMGLVGVYDFQTFKKG--DLSKKAV 175

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++ L Q+G V +C ++G P V S +S++ S +L+A +L
Sbjct: 176 ERVLTPLIQMGTVQV-VPKKNCLEFSLHG-PKTPNPVYKSSMVSARMKSVLLAGLNSL 233

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIK-GGQKYKSPKNAYVEG 252
G ++I+ + + ++E+ L+ FGV SD + ++ G+K S + + G
Sbjct: 234 GVT--KVIESMKTQNHMEIMLK---EFGVDLLVKSDKIRGYSVQIEGRKKLSGCSLTIPG 288

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D S A + LA A + G+ V+ + +L+ MGA + + +
Sbjct: 289 DPSFAIFPLAAALLIPGS-NVQILNVLINPSRIGLINILQDMGADIVFVNHRIESGENIA 347

Query: 313 EPFGR-KHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
+ R +LK I ++ ++MP D LA+++ FA+G T I+ + + E++ I
Sbjct: 348 DIQVRFSNLKGITISEDRMPYMIDEYSILAIISAFAGRTVIKGMG-----KLEQLSTIL 402

Query: 369 TELTKLGASVEEGP-DYCIITPPEKLNVT-----IDTYDDHRMAMAFSLAACA-EVPVT 421
L+ E+G D ++ P + + + DHR+AM+F + A E V
Sbjct: 403 EGLSINNVCQCEQGENDLVVMGVPGGKGLGSRSGRMVQPKFDHRIAMSFLVMGLASEYSVI 462

Query: 422 IRDPGCTRKTFPDYFDVLS 440
+ D F D+ +++
Sbjct: 463 VDDCSMASTIFQDFINLMQ 481

>ref|YP_003495370.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Deferribacter
desulfuricans SSM1]
dbj|BAI79614.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Deferribacter
desulfuricans SSM1]
Length = 420

Score = 60.1 bits (144), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 103/404 (25%), Positives = 170/404 (42%), Gaps = 58/404 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
E++V++ +SG V++ GSK+ S I+ L+EG +DN+ N DV + L L
Sbjct: 2 EKLVEGGYRLSGEVEVSGSKNASLPMAATILAEVDYFIDNVPNLRDVRTLSKLLNLLN 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ E + + + G G F P E K L + R A V+ GG A
Sbjct: 62 IETEQQQNSLKIKNNG-GNSFEAPYELVKTMRASILVLGPLLGRRGKAKVSLPGGCA--- 117

Query: 123 LDGVPRMRERPIGDLVGLKQLGADVDC---FLGTDCPPVRVNGIGLPGGKVKLSGSIS 179
+ ERP+ + LK +GA ++ ++ +C R+ G + V ++G+
Sbjct: 118 -----IGERPVDQHIKALKAMGAKIEIEHGYIIAECE--RLKGT-DIYFDLVTVTGT-- 166

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKG 238
++MAA A G E I + I V++ + + GVK E + + Y
Sbjct: 167 ----ENIMMAACAAG--ETIYNAAIEPEVVDLG-NFLRKMGVKIEGLGKTVKIY--- 216

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG---CGTTSLQGDVKFAEVLEMM 294
G++ SP N V D A+ + AAITGG V + G C TT ++ KF E+
Sbjct: 217 GKETLSPTNRYVMNDRIEAAATLICAAITGGDVKILGVKNCLTTVIE---KFLEI---- 269

Query: 295 GAKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAI 350
G ++ + +K LKA D+ P D+ + A+G +
Sbjct: 270 GVEIEDIDNETV-----RILSKKKLKAADITTQVYPGFPTDLQAQFMALMTVAEGVS-- 321

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V + + E M EL ++GA++ I+T EKL+

Sbjct: 322 --VVTENIFENRFMHV--AELKRMGANIRLKDRSAIVTGVEKLS 361

>ref|YP_149194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
 kaustophilus HTA426]
 sp|Q5KUL0.1|MURAI_GEOKA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
 AltName: Full=Enoylpyruvate transferase 1; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
 Short=EPT 1
 dbj|BAD77626.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
 kaustophilus HTA426]
 Length = 434

Score = 60.1 bits (144), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 99/374 (26%), Positives = 153/374 (40%), Gaps = 43/374 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLAAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
 E+I+++ +SGTVK+ G+K+ ++ L ++GT+ + ++ DV+ + LR L
 Sbjct: 2 EKIIIVRGGNRLSGTVKVEGAKNAVLVPVIAATLLATKGTSTIHDVPALSDVYTISEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
 G V A V V G VE E V+ MR+ + + A G A
 Sbjct: 62 GADVHI---ADETVTVDATGPLTVEAPFEYVR-----KMRASVLVMGPELLARNGRAR 110

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
 L G + RPI + G + +GA V +G VNG L G K+ L S
 Sbjct: 111 VALPGGCAIGSRPIDQHLKGFAMGASVK--VGNGFIDAEVNG--RLRGAKIYLDFF-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 ++MAA LA G +I+ P + + G K + + I+G
 Sbjct: 166 GATENIMMAAVLAEGTT--VIENCAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIEGVD 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
 + + + D A F+ AAITGG V V+G L LE MG V
 Sbjct: 222 ELVGTTHTVIP-DRIEAGTFMVAAAITGGNVLVQGAPEHLG---SLIAKLEEMGVTVIE 277

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA-- 354
 E+ + V GP + LKA+D+ P D+ + + L A+G + I +
 Sbjct: 278 EESGLRVIGPEK-----LKAVDIKTMPYPGFPTMQSQMMALLLKAEGTSMITETVFE 330

Query: 355 --SWRVKETERMVA 366
 V+E RM A
 Sbjct: 331 NRFMHVEEFRMNA 344

>gb|EFR84087.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Listeria
 monocytogenes FSL F2-208]
 Length = 102

Score = 60.1 bits (144), Expect = 7e-07, Method: Compositional matrix adjust.
 Identities = 33/102 (32%), Positives = 53/102 (51%), Gaps = 2/102 (1%)

Query: 345 DGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDH 404
 +G T I+D A +VKET R+ A+ TEL K+GA + D II L+ + +Y DH
 Sbjct: 1 EGTTIKDAELKVKETNRIDAVATELNKMGADITPTEDGLIIRGKTPLHAANVTSYGDH 60

Query: 405 RMAMAFSLAA--CAEVPVTIRDPGCTRKTFPDYFDVLSTFVK 444
 R+ M +AA E V + ++P +F+ + + +K
 Sbjct: 61 RIGMMLQIAALLVEEGDVELERAEAVSVSYPTFFEDIRSLK 102

>ref|ZP_07399236.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
 duerdenii ATCC BAA-1640]
 gb|EFM25793.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Peptoniphilus
 duerdenii ATCC BAA-1640]
 Length = 238

Score = 59.7 bits (143), Expect = 8e-07, Method: Compositional matrix adjust.
 Identities = 66/236 (27%), Positives = 113/236 (47%), Gaps = 18/236 (7%)

Query: 15 ISGTVKLPKSGSKLSNRILLAAALSEG-TTVVDNLLN-SEDVHYMLGALRTLGLSVEADKA 72

I+G +K SKSL +R ++L+ +S+ T ++N+ S+D+ L + LG ++ +
Sbjct: 16 INGELKSIPSKSLLHRAILSGISKDRETKLENTISKDIEATLTCMEKLGAKIKVEGD 75

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 132
+ R +G K +V+L G +G +R L V+ AT +D +R+R
Sbjct: 76 SIRIASLG-----NIKKSKVELHCGESGTTLRLLPLVSTFSKTAT--VDCSEGLRKR 126

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI +L+ L++ G L + + G + ++SG ISSQY+S LL+ + L
Sbjct: 127 PIRELIETLEESG-----LYFEEKEFSIKISGNVNSDFFRISGDISSQYVSGLLLLSSSL 180

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQKYKSPKN 247
I + KL S YV +T++++ FG+ E + Y G KY KN
Sbjct: 181 LDQKSSIYLTTKLESRAVYNITIKVLRDFGIIFNELEEGVFIEYGGGETKYSRLKN 236

>ref|YP_003672818.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
C56-T3]
gb|ADI28241.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
C56-T3]
Length = 434

Score = 59.7 bits (143), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 99/374 (26%), Positives = 153/374 (40%), Gaps = 43/374 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
E+I+++ +SGTVK+ G+K+ ++ L ++GT+ + ++ DV+ + LR L
Sbjct: 2 EKIIIVRGGNRLSGTVKVEGAKNAVLPLVIAATLLATKTSTIHDVPALSDVYTISEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
G V A V V G VE E V+ MR+ + + A G A
Sbjct: 62 GADVHI---AGETVTVDATGPLTVEAPFEYVR-----KMRASVLVMGPPLLARNGRAR 110

Query: 121 YVLDGVPVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RPI + G + +GA V +G VNG L G K+ L S
Sbjct: 111 VALPGGCAIGSRPIDQHLKGFEAMGASVK--VGNGFIDAEVNG--RLRGAKIYLDFF-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G +I+ P + + G K + + I+G
Sbjct: 166 GATENIMMAAVLAEGTT--VIENCAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIEGVD 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + D A F+ AAITGG V V+G L LE MG V
Sbjct: 222 ELVGTTHTVIP-DRIEAGTFMVAIAITGGNVLVQGAPEHLG---SLIAKLEEMGVTVM 277

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVA-- 354
E+ + V GP + LKA+D+ P D+ + + L A+G + I +
Sbjct: 278 EESGLRVIGPEK-----LKAVDIKTMYPGFPPTMQSQMMALLLKAEGTSMITETVFE 330

Query: 355 --SWRVKETERMVA 366
V+E RM A
Sbjct: 331 NRFMHVEEFRRMNA 344

>ref|ZP_07956900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 5_1_63FAA]
gb|EFV16283.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 5_1_63FAA]
Length = 431

Score = 59.7 bits (143), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 103/436 (23%), Positives = 182/436 (41%), Gaps = 39/436 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + +L A +++G ++DN+ + D++ +L A++ +G
Sbjct: 2 EQYIIKGGNPLVGEVVGAKNAALPVLAAMVMTDGKCMIDNMPDVRDINVLQAMQEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D+ K V + G P D E F+ A L A+ A L
Sbjct: 62 ADV--DRTGKHEVTISGKGIHPECDVDNE---FIRKIR-ASYYLIGALLGKYKRARVALP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G K LGA ++ G L G + + +S
Sbjct: 116 GGCEIGSRPIDQHIGFKMLGAQIEIENGMIATAE-----ELKGAHIYMD-VVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ II+ P+V + G K + + D IKG +K+
Sbjct: 170 NVMMASLAKGNT---IENAAKEPHVVDVANFLNSMGAKIRGAGT-DVIRIKGVEKFGD 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMGAKVTWTET 303
+ + + D A F+ A T G + ++ L+ K E+ GA+V +
Sbjct: 226 CQYSIIP-DQIEAGTFMTAAVATKGDIMIKNVIPKHLAISAKLIEI---GAEVVEFDD 280

Query: 304 SVTVTGPPR-EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD-VASWRVKET 361
+V V+ R E K L + P +A+TLA ++G + I + + R +
Sbjct: 281 AVRVSATKRLESTNIKTLPYPGFPTDMQPQMAVTLA----LSNGTSVISESIFENRFRYV 336

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYD-DHRMAMAFSLAA-CAEVP 419
+ ELTK+GA+++ II+ E T D + D R A +A A+
Sbjct: 337 D-----ELTKMGATIQVDGRTAIISGVEGF--TGADVHAPDLRAGAALVIAGLSAKGF 387

Query: 420 VTIRDPGCTRKTFPDY 435
T+ D G + + +
Sbjct: 388 TTVSDIGYIYRGYEQF 403

>gb|ADU52755.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52760.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52770.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52771.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52772.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 59.7 bits (143), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 67/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYSRPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + K V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTAVVVGGSRLVGQK-VQVPGDISSAAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|YP_003254430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
ref|YP_004133919.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
gb|ACX79948.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
gb|ADU95776.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
Length = 434

Score = 59.7 bits (143), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 99/374 (26%), Positives = 153/374 (40%), Gaps = 43/374 (11%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      E+I+++ +SGTVK+ G+K+ ++ L ++GT+ + ++ DV+ + LR L
Sbjct: 2  EKIIVRGGNRLSGTVKVEGAKNAVLPIAATLLATKGTSTIHDVPALSDVYTISEVLYL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
      G V A V V G VE E V+ MR+ + + A G A
Sbjct: 62  GADVHI---AGETVTVDATGPLTVEAPFEYVR-----KMRASVLVMGPILLARNGRAR 110

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
      L G + RPI + G + +GA V +G VNG L G K+ L S
Sbjct: 111 VALPGGCAIGSRPIDQHLKGFEAMGASVK--VGNGFIDAEVNG--RLRGAKIYLDFF-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G +I+ P + + G K + + I+G
Sbjct: 166 GATENIMMAAVLAEGTT---VIENCAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIEGVD 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      + + + D A F+ AAITGG V V+G L LE MG V
Sbjct: 222 ELVGTHTVIP-DRIEAGTFMVAAAITGGNVLVQGA VPEHLG---SLIAKLEEMGVTVME 277

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPATIRDA-- 354
      E+ + V GP + LKA+D+ P D+ + + L A+G + I +
Sbjct: 278 EESGLRVIGPEK-----LKAVDIKTMPYPGFPTDMQSQMMALLLKAEGTSMITETVFE 330

Query: 355 --SWRVKETERMVA 366
      V+E RM A
Sbjct: 331 NRFMHVEEFRRMNA 344
```

>gb|ACO70904.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [uncultured
Verrucomicrobia bacterium]
Length = 419

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 85/313 (27%), Positives = 131/313 (41%), Gaps = 36/313 (11%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      ++I++ + +SGTVK+ GSK+ + IL L++ V+ ++ + D+HYML L LG
Sbjct: 2  DKILVHGGQSLSGTVKISGSKNSALPILATLLTKEPCVHHVDPDLSDIHYMLQILSHLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
      VE G + P E +R + A+V G
Sbjct: 62  AQVERASGVVTVQAEEKIGTEAPYE-----IVRKMRAVVCVLGPLLGREKE 106

Query: 119 ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      AT L G + +RPI + G + LGA G V+V G L GG V L G +
Sbjct: 107 ATVSLPGGCIVIGDRPIDLHLKGFEALGAMHRIEQGN---VKVFA-GQLVGVVNLRGKL 161

Query: 179 SSQYLSA--LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
      L ++MAA LA G +ID + P V + G K E + + R I
Sbjct: 162 GPTVLGTDNVMMAAVLAEGTT---VIDSAAAEPEVVDLANFLNAMGAKIEGAGTR-RIVI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGA 296
      +G ++ +++ + D A FL AI G VT++ + L + L G
Sbjct: 218 EGVKELHGAHSHVIP-DRIEAGTFLVAGAIAGKEVTLKRVDASHLTA--VTDALVRSGF 273

Query: 297 KVTWTETSVTVTG 309
      +T SVT+ G
Sbjct: 274 AITVNGDSVTIRG 286
```

>gb|ADU52729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 72/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSV-EADKAAKRAVVVCGCGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALILGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + K V GD SSA+++L A
Sbjct: 171 ALSRDHSE--RMLRAFGANIQVDPETKTVAVVGGSRVLVGQK-VQVPGDISSAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_02439591.1| hypothetical protein CLOSS21_02057 [Clostridium sp. SS2/1]
gb|EDS21409.1| hypothetical protein CLOSS21_02057 [Clostridium sp. SS2/1]
emb|CBL37302.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[butyrate-producing bacterium SSC/2]
Length = 431

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 103/436 (23%), Positives = 182/436 (41%), Gaps = 39/436 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
E+ +++ + G V + G+K+ + +L A +++G ++DN+ + D++ +L A++ +G
Sbjct: 2 EQYIIKGGNPLVGEVVGAKNAALPVLAAMVMTDGKCMIDNMPDVRDINVLLQAMQEIG 61

Query: 65 LSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D+ K V + G P D E F+ A L A+ A L
Sbjct: 62 ADV--DRTGKHEVTISGKGIHPECVDNE---FIRKIR-ASYYLIGALLGKYKRARVALP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G K LGA ++ G L G + + +S
Sbjct: 116 GGCEIGSRPIDQHIGFKMLGAQIEIENGMIATAE-----ELKGAHIYMD-VVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ II+ P+V + G K + + D IKG +K+
Sbjct: 170 NVMMASLAKGNT---IIEENAKEPHVVDVANFLNSMGAKIRGAGT-DVIRIKGVEKFGD 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMGAKVTWTET 303
+ + + D A F+ A T G + ++ L+ K E+ GA+V +
Sbjct: 226 CQYSIIP-DQIEAGTFMTAAVATKGDIMIKNVIPKHLAISAKLIEI----GAEVVEFDD 280

Query: 304 SVTVTGPPR-EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD-VASWRVKET 361
+V V+ R E K L + P +A+TLA ++G + I + + R +
Sbjct: 281 AVRVSATKRLESTNIKTLPPYGFPTMQPQMAVTLA----LSNGTSVISESIFENFRYV 336

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIDTYD-DHRMAMAFSLAA-CAEVP 419
+ ELTK+GA+++ II+ E T D + D R A +A A+
Sbjct: 337 D-----ELTKMGATIQVDGRTAIIISGVEGF--TGADVHAPDLRAGAALVIAGLSAKGF 387

Query: 420 VTIRDPGCTRKTFPDY 435
T+ D G + + +
Sbjct: 388 TTVSDIGYIYRGYEQF 403

>gb|ADU52752.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSV-EADKAAKRAVVVCGCGK 84

S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LNAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +

Sbjct: 115 GASIWGRAGGT LAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|YP_003701185.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
selenitireducens MLS10]
gb|ADI00620.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
selenitireducens MLS10]
Length = 438

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 98/377 (25%), Positives = 168/377 (44%), Gaps = 47/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILLLAALS----EGTTVVDNLLNSEDVHYMLGAL 60
E+I+++ + ++GTV++ G+K N +L + A S +GT+ + ++ + DV+ + L

Sbjct: 2 EKIIIVRGGQPLTGTVRIEGAK---NAVLPVIAASLLGGKGTSTIHDVPSLADVYTINEVL 58

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGG 117
R L +SV D+A+ ++ V +E E V+ MR+ + + A G

Sbjct: 59 RNLNVSVTYDEASG-SIEVDAQDDLIEAPFEFVR-----KMRASFLVMGP LLARKG 109

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + +GA V+ +G+ +V L GGKV L

Sbjct: 110 HARIALPGGCAIGSRPIDQHLKGF EAMGATVE--IGSGFIEAKVED--RLYGK VYLDFFP 165

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA +ALG +I+ P + + G K + + I+

Sbjct: 166 -SVGATENIMMAATMALGTT---VIENAAQEPEIVDLANYLNAMGAKVRGAGTGT- IKIE 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAK 297
G ++ + + D A F+ AAITGG V VE T ++ + A++ E MG

Sbjct: 221 GVEELNGAVHTIIP-DRIEAGTFMVA AAITGNNVLVENVLTEHIRPLI--AKMTE-MGVI 276

Query: 298 VTWTETSVTVTGPPREPFG RKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ T V V GP + LKA+D+ P D+ + + L A+G + I +

Sbjct: 277 IYEESTGVRVIGPEK-----LKAVDIKTMPHPGFPTDMQSQMMAMMLVAEGTSVITET 329

Query: 354 A----SWRVKETERMVA 366
V+E RM A

Sbjct: 330 VFENRFMHVEEFRRMNA 346

>ref|YP_003565556.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
megaterium QM B1551]
gb|ADE72122.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
megaterium QM B1551]
Length = 434

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 103/403 (25%), Positives = 166/403 (41%), Gaps = 55/403 (13%)

Query: 5 EEIVLQPIKEISGTVKLP GSKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ +SGTVK+ G+K+ I+ L SEG T+++++ DV + LR L

Sbjct: 2 EKIIIVRGGNRLSGTVKVEGAKNAVLPIITATLLASEGKTILNDVPALSDVFTIGEVLRLH 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-MRSLTAAVTAAG----- 116
+ E D R VV DA E++ +A +R + A+V G
Sbjct: 62 --NAEVDFTNRVVV-----DASRELKT---DAPFEYVRKMRASVLVMGPLLART 106

Query: 117 GNATYVLGDGVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G A L G + RPI + G + +GA V +G +V G L G K+ L
Sbjct: 107 GEARVALPGGCAIGSRPIDQHLKGFEAMGAKVQ--VNGGFIDAKVEG--RLKGAKIYLD 162

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA LA G I++ + P + + G K + + I
Sbjct: 163 P-SVGATENIMMAAALAEGETT---IMENVAKEPEIVDLANFLNAMGAKVRGAGTGT-IRI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G K ++A + D A F+ AAITGG V V G + +E MG
Sbjct: 218 EGVNKLYGAEHAIIIP-DRIEAGTFMVAAAITGGNVLVRGAVAEHIS---SLVAKMEEMGV 273

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD 352
++T + V GP + LK++D+ P D+ + + L A+G + I +
Sbjct: 274 EITEEGDGLRVVGPEK-----LKSVDIKTMPHPGFPTDMQSQMMALLLAAEGTSMITE 326

Query: 353 -VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E E ++ A ++ II P +L
Sbjct: 327 TVFENRFMHVE-----EFRRMNADIKIEGRSVIINGPSQLQ 362

>ref|YP_001354980.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Janthinobacterium sp. Marseille]
sp|A6T383.1|MURA_JANMA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABR88978.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Janthinobacterium sp. Marseille]
Length = 416

Score = 59.3 bits (142), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 107/425 (25%), Positives = 179/425 (42%), Gaps = 58/425 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++Q +SG + + G+K+ + IL L+ T + N+ N +DV +L LR +G
Sbjct: 2 DKLLIQGGHRLSGEIAISGAKNAALPILCAGLLTADTVQLSNVNLQDVTTLRLRLRQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
L E D VV G +A E+ +++++ A++ G G
Sbjct: 62 LRAEQDGDGK---VVLNGSAIDKLEAPYEM-----VKTMRASILVLGPLLARFGE 107

Query: 119 ATYVLGDGVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + GL+ +GA+V G + L G ++ ++ I
Sbjct: 108 AKVSLPGGCAIGSRPVDQHIKGLQAMGAEVTEIAGYIHAKAK-----KLKGTRI-VTDMI 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ LLMAA LA G+ I++ P V L+ G K E + DR I+G
Sbjct: 162 TVTGTEENLLMAATLADGET---ILENAAREPEVTDLANLLVAMGAKIEGIGT-DRLVIQG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D + F+ A GG VT+ T +L DV F ++ E GA +
Sbjct: 218 VERLHGATHAVI-ADRIETATFMCAVATVGGDVTLRNARTDTL--DVAFDKLRE-AGAIL 273

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA 354
T + + V R KA+ + P D+ + A+G
Sbjct: 274 TSGDDWIRVQMASRP-----KAVSFRTEYPGFPTDMQAQFMAMNCVAEG----- 318

Query: 355 SWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS 411
S RV ET R + ++ E+ +LGA++ II +KL V A D R + +
Sbjct: 319 SSRVIETIFENRFMHVQ-EMNRLGAAITIEGHTAIINGVDKL-VGAPVMATDLRASASLV 376

Query: 412 LAACA 416
+AA A
Sbjct: 377 IAALA 381

>gb|ADU52795.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.9 bits (141), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRRTAACFRALGADISELNSECVRIRGVGLGR 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRLVG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52732.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52746.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52749.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52750.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52751.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52753.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52754.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52758.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52759.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52761.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52762.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52764.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52766.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52767.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52769.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52775.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52777.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52782.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.9 bits (141), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>gb|ADU52784.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.9 bits (141), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVCGCGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTMVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|YP_003600279.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
megaterium DSM 319]
gb|ADF41929.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
megaterium DSM 319]
Length = 434

Score = 58.9 bits (141), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 103/403 (25%), Positives = 166/403 (41%), Gaps = 55/403 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ +SGTVK+ G+K+ I+ L SEG T+++++ DV + LR L

Sbjct: 2 EKIIVRGGNRLSGTVKVEGAKNAVLPIITATLLASEGKTILNDVPALSDVFTIGEVLRLHL 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIA-MRSLTAAVTAAG----- 116
+ E D R VV DA E++ +A +R + A+V G

Sbjct: 62 --NAEVDFTNRRVVV-----DASRELKT---DAPFEYVRKMRASVLVMGPPLART 106

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G A L G + RPI + G + +GA V +G +V G L G K+ L

Sbjct: 107 GEARVALPGGCAIGSRPIDQHLKGFEAMGAKVQ--VGNGFIDAKVEG--RLKGAKIYLDLF 162

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA LA G I++ + P + + G K + + I

Sbjct: 163 P-SVGATENIMMAAALAEGTT---IMENVAKEPEIVDLANFLNAMGAKVRGAGTGT-IRI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G K ++A + D A F+ AAITGG V V G + +E MG
Sbjct: 218 EGVNKLYGAHAIP-DRIEAGTFMVAAAITGGNVLVGAVAHEHIS---SLVAKMEEMGV 273

Query: 297 KVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD 352
++T + V GP + LK++D+ P D+ + + L A+G + I +
Sbjct: 274 EITEEGDGLRVVGPEK-----LKSDIKTMPHPGFPTDMQSQMALLLAAEGTSMITE 326

Query: 353 -VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E E ++ A ++ II P +L
Sbjct: 327 TVFENRFMHVE-----EFRMNADIKIEGRSVIINGPTQLQ 362

>ref|ZP_07921844.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
gb|EFV01146.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
Length = 427

Score = 58.9 bits (141), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 106/424 (25%), Positives = 174/424 (41%), Gaps = 77/424 (18%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+ G+K+ ++ A LS V+DN+ DV M+ LR LG+ +++
Sbjct: 12 LQGEVKITGAKNAVLGLIPAAILSRNVIVMDNVPQINDVQKMNILRKLGVRIIDSE---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQL----FLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127
G DA+E++ + G MR+ L A+ A L G
Sbjct: 68 -----GDVLTIDAREKISHDCSPYQDQTG-RMRASYLLGALLGRYHEAIVPLPGGC 118

Query: 128 RMRERPIGDLVVGLKQLGADV-----DCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
+ +RPI + G + LGA V D +GTD + V +
Sbjct: 119 NIGDRPIDQHIGKFEALGAKVVEHGVKMKADRLVGTD-----IYLDVVSVA 167

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+I+ +++AA LA G IE + K P++ + + G + + + D I
Sbjct: 168 TIN-----IMLA AVLAEKTVIENVAKE---PHIVDVANFLNKMGANIKGAGT-DTIRI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G +K S + V ++ +Y +A AA TGG V V G + +E + A
Sbjct: 218 RGVEKLGSCSYSVVPDQITAGTYMMAAAA-TGGNVLVSGV-----IPKHME SVTA 266

Query: 297 KVTWTETSVTVTGPP-REPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR 351
K+ VTV G R ++ LKA + P D+ +AV+ A+G + I+
Sbjct: 267 KLREMGAEVTVEGDGLRVKNNKERLKCRIKTLPPYGFPTDLQQPMAVLMAIAEGNSMIQ 326

Query: 352 D-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
+ + R K + EL K+GA++ IT KL+ T I D R A
Sbjct: 327 ESIFENRFKYVD-----ELRKMGANITISGRIANITGVPKLSGTKI-VSTD LRAGAAM 378

Query: 411 SLAA 414
+AA
Sbjct: 379 VIAA 382

>gb|ADU52763.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGGRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52785.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 107/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V GG P G S S++ S LL+A LA ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQ--GGSPKGIHYRSPVASARVKSCLLLAGLLAE--GTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + K V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLGQK-VQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52728.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALILGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_05649870.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
gallinarum EG2]

gb|EEV33203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus gallinarum EG2]
Length = 429

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 91/373 (24%), Positives = 157/373 (42%), Gaps = 47/373 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI++Q + GTVK+ G+K+ IL + L+ EGTT ++N+ DV M +R L
Sbjct: 2 EEIIVQGGNRLIGTVKVEGAKNAVLPLAASLLAEEGTTTLENVPILSDVLTMNEVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ + D+ +K + + + +E E V MR+ + + A G+A
Sbjct: 62 NVEIAPDQ-SKNTITMDASRELAIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIG-GLPGGKVKLSG 176
+ G + +RPI + G + LGA++ D ++ ++ N I P
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAEIIQKDGIEAIASELKNTIYLDLP----- 164

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA A G II+ + P + ++ + G K + I
Sbjct: 165 --SVGATQNIIMAAVAKAGTT---IIENVAREPEIVDLANILNKMGAKV-FGAGTETMRI 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G + +A V+ D A F+ AA+T G V ++ + + + L MGA
Sbjct: 219 EGVDDLHSHAVSHAIQV-DRIEAGTFMVAAAMTEGDVVIKDAIS---EHNRLISKLTETMGA 274

Query: 297 KVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD 352
K+T + V GP K +KA DV P D+ + + + ADG + + +
Sbjct: 275 KITEVPEGIRVVGPF-----KTIKATDVKTMPHPGFPTDMQAQMTAIQMLADGTSIVNE 327

Query: 353 -VASWRVKETERM 364
V R + E M
Sbjct: 328 TVFENRFQHLEEM 340

>gb|ADU52756.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLEILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_03612083.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus minor 202]
gb|EEF15738.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus minor 202]
Length = 425

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 104/416 (25%), Positives = 166/416 (39%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SGTV++ G+K+ + IL A L+E + N+ +DV LR LG+ VE D
Sbjct: 12 LSGTVEISGAKNAALPILFAAILAEKPVTLTNVPVLKDVETTFKILRKLGVVVERDANGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + P E K A + R V+ GG + R
Sbjct: 72 VQIDASKIDHYVAPYELVKTMRASIWALAPLVARFHGQVSLPGGCT-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+++GA ++ D V+ G L G +V + +S +++MAA L
Sbjct: 123 PVDMHIAGLEKMGATIEL---DEGYVKATSNRGLKGARVYMD-KVSVGATLSVMMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + G K + + D ++G + ++ V
Sbjct: 178 AEGTT--VIENAREPEIVDTAIFLNAMGAKISGAGT-DMITVEGVEHLGGCEHRVV-A 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA++GG +T G +L + E L G V TE ++T+ +
Sbjct: 233 DRIETGTFLIAAAVSGGKITCRGTKADTLDAVI---EKLREAGMDVEVTEDTITLDSKGQ 289

Query: 313 EPFGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR---- 368
P KA VN+ MP + A F T + VA + TE + R
Sbjct: 290 RP-----KA--VNIRTMPHPGFPTDMAQAF---TLLNAVAEGTSRITETIFENRFMHI 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++GA E + I E L + D R +++ LA C TI D
Sbjct: 338 PELNRMGAKGEIEGNTAICHGVESLKPAEV-MATDLRASISLVLGCIANGETIVD 392

>gb|ADU52776.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRLVG-QXVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52783.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144

Sbjct: 61 D L GN+G +R L + A + + G +R RP+G +V L+Q+
QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGASIQVDPETKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>gb|ADU52727.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGPGR 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYSRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|YP_003151592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cryptobacterium
curtum DSM 15641]
gb|ACU94910.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cryptobacterium
curtum DSM 15641]
Length = 425

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 114/458 (24%), Positives = 182/458 (39%), Gaps = 62/458 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E I+ + + ++GTV+ G+K+ + +++ + L +G + + N+ D++ M L L

Sbjct: 4 EVIIARESENLTGTVRASGAKNSALKLMAASLLGQKSTIRNVPLISDIYIMGRVLEAL- 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
D R V VE + +L + + A+++ G G

Sbjct: 63 -----DAQVTREDHVLITIDTTAVERYETPYEL-----VSKMRASISVLGPLIGRFGC 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLS 175
A + G ++ R I +VGL+QLG + FL P GL GG + L

Sbjct: 110 AHVAMPGGCQIGARRIDMHLVGLQGLGVHFEIDHGFLIATTP-----NGLHGGNITLE 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S +MAA A G ID P +E ++ G + E + S

Sbjct: 163 FP-SVGATENTMMAAVTAEGRT---TIDNAACEPEIEDLALMLNEMGAQIEGAGSSS-IT 217

Query: 236 IKG-GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMM 294
I+G P + GD A FL G A+ GG VTVEG + L+ + L M

Sbjct: 218 IEGVPLSALHPCDHATVGDRIEAGTFLVGGALLGGPVTVEGINPSYLRMALM---KLRAM 274

Query: 295 GAKVTWTETSVTVT--GPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPT 348
G V E SVTV GP L+A+D+ P D+ ++A A+G +

Sbjct: 275 GCIVEEGEQSVTVRRDGP-----LRAVDIQTLPHPGFPTDLQAQFMLLASLAEGNS 325

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
I + V E M A +EL ++GA V + ++ ++L + D R

Sbjct: 326 VI---TENVFENRFMFA--SELVRMGADVTIDDHHALVRGVKRLQGAPV-VSTDLRAGG 378

Query: 409 AFSLAA-CAEVPVTIRDPGCTRKTFPDYFDVLSTFVKN 445
A LA AE +R + + DY L++ N

Sbjct: 379 ALVLAGMAAEGETIVRKISHIDRGYEDYVGKLTSLGGN 416

>gb|ADU52757.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.5 bits (140), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSRLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRLVG-QRVQVPGDISSAAFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>emb|CBI20198.3| unnamed protein product [Vitis vinifera]
Length = 475

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 97/383 (25%), Positives = 152/383 (39%), Gaps = 31/383 (8%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V + GSK+ + IL GT+ + + N D M LR+LG+ +EA

Sbjct: 53 KLSGHVPISGSKNSALSILAATLCCSGTSKLHGVPNLSDTRTMASILRSLGVEIEACNGE 112

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
G G V+ E++ G + + A G A L G + RP

Sbjct: 113 MWVNADGVGS--VQPCPEDIGKIRGGFFV-----IGPLLARFGEAVVALPGGCDIGTRP 164

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + GL+ LGA V+ LG + GL GG+ KL S L+MAA +A

Sbjct: 165 VDLYIRGLRALGAIVE--LGDGKVRAQAANGRLVGGRFKLDHP-SVGATETLMAACMA 221

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + ++ + P V R + G E + S D YIKG + V D

Sbjct: 222 DG---VTVLSNVAKEPEVIDLARFLTGSACVEGAGS-DTLYIKGNQLHG-SECIVPPD 276

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTETSVTVTGP 313
A F+ AAIT +++ + + L G K+T ++ V+ P +

Sbjct: 277 RIEAGTFMLAAAITRSSISMSPVIPSHV---ACLIDKLLAAGCKITCAHDTLEVSAPVDD 333

Query: 314 PFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 369
+L+ DV P D+ V+ DG + + + RM +R

Sbjct: 334 V--GHNHQGFDVRTCPFPGFPTDLQPQTMVLLTTCDGLSIVEETVF-----ENRMGHVR- 385

Query: 370 ELTKLGASVEEGPDYCIITPPEK 392

EL KLGA + +I EK

Sbjct: 386 ELQKLGARIRVCGSTAVICGKEK 408

>gb|EFR92855.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria innocua
FSL J1-023]
Length = 430

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 99/404 (24%), Positives = 171/404 (42%), Gaps = 58/404 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63

E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L

Sbjct: 2 EKIIVRGGKQLNGSVKMEGAKNAVLPVIAATLLASKGTSVLKNVPLNSDVFTINEVLKYL 61

Query: 64 G--LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116

+S E D+ V V GK + E V R + A++ G

Sbjct: 62 NADVSEFENDE-----VTVDATGKITSDAPFEYV-----RKMRSIVVMGPLLAR 105

Query: 117 -GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS 175

G+A L G + RP+ + G + +GA V G L G KV L

Sbjct: 106 TGSARVALPGGCAIGSRPVDLHLKGFAMGAIVKIEGYIEATAE-----KLVGAKVYLD 160

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235

S ++MAA LA G +I+ + P + + + G + + + +

Sbjct: 161 FP-SVGATQNMMAATLAEGTT--VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIR 215

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295

I+G ++ + +++ + D A F+ AAITGG V +E + LE MG

Sbjct: 216 IEGVKELTATEHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS--SLIAKLEEMG 271

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR 351

++ E + V GP + LKA+DV P D+ + V+ + ++G + +

Sbjct: 272 VQIIIEENGIRVIGPDK-----LKAVDVKTMPHPGFPTMQSQMMVIQMLSEGTSIMT 324

Query: 352 D-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394

+ V R E M + ++ G SV II+ P KL

Sbjct: 325 ETVFENFRFMHVEEMRRNMADMKIEGHSV-----IISGPAKLQ 361

>gb|ADU52741.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 107/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84

S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLPGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144

D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204

GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYSRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264

+S + E R++ FG + GG + + V GD SSA++L A

Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266

+I

Sbjct: 227 SI 228

>gb|ADU52779.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 58.2 bits (139), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQELLLGEDPRSTAACFRALGADISELNGECVIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRVLG-QRVRVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADO96649.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae R2846]
Length = 424

Score = 58.2 bits (139), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 99/416 (23%), Positives = 171/416 (41%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNVPELKDIIETTLNLRQLGVIANRDETGA 71

Query: 75 RAVVVGCGGKFF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R A V+ GG + + R
Sbjct: 72 VLLDASININHTAPYELVKTMRASIWALAPLVARFHQAQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKITGAGS-DHITIEGVERLTGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|YP_872128.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
gb|ABK52142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
Length = 432

Score = 57.8 bits (138), Expect = 3e-06, Method: Compositional matrix adjust.

Identities = 82/318 (25%), Positives = 125/318 (39%), Gaps = 44/318 (13%)

```
Query: 4   AEEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
          A+ V++P + G V L GSK+ + ++ A L++ +V+DN+ + DV LR +
Sbjct: 2   ADTWVIEFSGPLRGDVVLRGSKNAVTKHMVAALLADEPSVIDNVPDVGDTVITTTDILRAV 61

Query: 64  GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
          G V + R VV P + V L L + G A
Sbjct: 62  GAEVLVED--DRVTVV-----PSREVNPHVPLSFSGLNRIPLVLLGPLLHRAGEAFVPK 113

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG----LPGGKVKLS---- 175
          G R+ RP+ V L+ GADV+ V +GI L G ++ L
Sbjct: 114 VGGDRIGSRPVDHFHVAALRAFADVE-----VSDDGIFAKATRLTGARIHLPYPSV 164

Query: 176 GSISSQYLSALLMAAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW-D 232
          G+ S L+A L L + E E++D + ++R G + E W D
Sbjct: 165 GATESVLLTATLAKGKTVLTNAATEPEVVDLAL-----FLQRMGARIEF---WPD 211

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLE 292
          R + G A + GD + A +L +T G V V GC L V L+
Sbjct: 212 RRVVIEGVPVAVHGARLAGDRNEAFSYLVAGLLTKGDVVRVIGCPQERL---VTAITTLQ 268

Query: 293 MMGAKVTWTETSVTVTGP 310
          MGA+V + +T T P
Sbjct: 269 RMGARVDIDYGITATAP 286
```

```
>gb|ADU52773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
               Synechococcus sp.]
gb|ADU52780.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
               Synechococcus sp.]
gb|ADU52781.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
               Synechococcus sp.]
Length = 232
```

Score = 57.8 bits (138), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

```
Query: 26  SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL-SVEADKAAKRAVVVCGGK 84
          S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1   SISHRALMLGSLAEGETTIQGLLLGEPDPRSTAACFRALGADTSELNSECVRIRGVGLGRL 60

Query: 85  FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
          D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61  QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
          GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
          +S + E R++ FG + + GG + + V GD SSA++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSLVG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
          +I
Sbjct: 227 SI 228
```

```
>ref|ZP_05657191.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
               casseliflavus EC20]
gb|EEV40524.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
               casseliflavus EC20]
Length = 430
```

Score = 57.8 bits (138), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 91/373 (24%), Positives = 159/373 (42%), Gaps = 47/373 (12%)

```
Query: 5   EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLS-EGTTVVDNLLNSEDVHYMLGALRTL 63
          EE+++Q ++GTVK+ G+K+ IL + L+ EGTT + N+ DV M +R L
Sbjct: 2   EEMIVQGGNRLTGTVKIEGAKNAVLPILAASLLAEEGTTTLTNVPILSDVLTMKEVIRHL 61
```

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
++++ K + + + +E E V MR+ + + A G+A
Sbjct: 62 NVAIDF-KEENNTMTIDASQELAIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIG-GLPGGKVKLSG 176
+ G + +RPI + G + LGA + D ++ ++ N I P
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAQIIQKDGIEAIADELKGNISYLDFF----- 164

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA A G I II+ + P + ++ + G K + I
Sbjct: 165 --SVGATQNIMMAAVKAKG---ITIIENVAREPEIVDLANILNKMGAKEV-FGAGTETMRI 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGA 296
+G + + ++ V+ D A F+ AA+T G V ++ S ++++E MGA
Sbjct: 219 EGVEHLHAVDSIVQ-DRIEAGTFMVAAAMTQGDVLIKDA--ISEHNRPLISKLIE-MGA 274

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP----DVAMTLAVVALFADGPTAIRD 352
+VT + V GP R LKA DV P D+ ++ + L A G + + +
Sbjct: 275 EVTEVAEGIRVVGPPE-----LKATDVKTMPHPGFPTDMQAQMSAIQLLAQGTSSVNE 327

Query: 353 -VASWRVKETERM 364
V R + E M
Sbjct: 328 TVFENRFQHLEEM 340

>gb|ADU52786.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52787.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52788.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52790.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52792.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52793.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.8 bits (138), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 67/242 (27%), Positives = 107/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLALSEGTTVVNDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGT LAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + K V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLVGQK-VQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52745.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.8 bits (138), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 109/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSKCVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52733.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52734.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52735.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52737.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52738.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52740.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52742.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
gb|ADU52743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.4 bits (137), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 109/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSKCVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|YP_002317025.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anoxybacillus
flavithermus WK1]
gb|ACJ35040.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anoxybacillus
flavithermus WK1]
Length = 439

Score = 57.4 bits (137), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 97/377 (25%), Positives = 151/377 (40%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDEVHYMLGALRTL 63
E+I+++ K +SGTVK+ G+K+ ++ L SEG +V+ ++ DV+ + LR L
Sbjct: 9 EKIIIVRGKKRLSGTVKVEGAKNAVLPIAATLLASEGKSVIYDVPELSDVYTISEVLRHL 68

Query: 64 GLSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V +VV G+ +E E V R + A+V G G
Sbjct: 69 QADV---TVGNKIVVDASGELSIEAPFEYV-----RKMRASVLVMGPELLARKG 114

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V +G VNG L G K+ L
Sbjct: 115 RARVALPGGCAIGSRPIDQHLKGFEAMGATVK--IGNGFIAAEVNG--KLRGAKIYLDFF 170

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G II+ P + + G K + + I
Sbjct: 171 -SVGATENIMMAAVLAEGTT---IIENCAKEPEIVDLANFLNAMGAKVRGAGTGT-IRID 225

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G ++ + D A F+ AAITGG V V+G L LE MG
Sbjct: 226 GVTTLYGAEHTVIP-DRIEAGTFMIAAAITGGNVLVQGAVPEHL---TSLIAKLEEMGVT 281

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDV 353
+ ++ + V P + LKA+DV P D+ + + + A+G + + +
Sbjct: 282 IVEEDSGLRVIAPDK-----LKAVDVKTMPHPGFPTDMQSQMMALLMKAEGTSMVTET 334

Query: 354 A----SWRVKETERMVA 366
V+E RM A
Sbjct: 335 VFENRFMHVEEFRRMNA 351

>gb|ADU52765.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.4 bits (137), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACSRLGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSLVG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|YP_001800982.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
urealyticum DSM 7109]
emb|CAQ05548.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
urealyticum DSM 7109]
Length = 413

Score = 57.4 bits (137), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 82/293 (27%), Positives = 121/293 (41%), Gaps = 22/293 (7%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ G VK+ G+K+ +++ A L+EG TV+ N DV YM LR LG VE D
Sbjct: 8 LQGAVKVSGAKNSVLKLSAAMLAEGRTVLKNCPQISDVPYMAVLRGLGCDVELDGG-- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V++ + + + V+ F + + +TA A L G + RP+
Sbjct: 66 -TVIIDVPAEINHDAFDFAVRQFRASVAV-----LGPLTARCHRARVALPGGDAIGSRPL 119

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
GL+ LGA G C + GL G ++KL S +L AA LA
Sbjct: 120 DMHQTGLETLGATTRIEHG--CVVAETD---GLHGAEIKLDFFP-SVGATENILTAAVLAN 173

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + ++D P + ++ G K E S + + G +K P V GD
Sbjct: 174 G---VTVLDNAAREPEIVDLCDMLNEMGAKVEGGGS-NVITVTGVEKLH-PVEHEVVGDR 228

Query: 255 SSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTV 307
A + AAIT G VTV G L + E L++ GA+V T V
Sbjct: 229 IVAGTWAYAAAITQGDVTVGIDPQHLHLPL---EKLKLAGARVETYPGTGRV 278

>ref|YP_004135636.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae F3031]
emb|CBY81312.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae F3031]
Length = 424

Score = 57.4 bits (137), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 99/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNPVELKDIETTLNLRQLGVIANRDEGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R A V+ GG + + R
Sbjct: 72 VLLDTSNINHFTAPYELVKTMRASIWALAPLVARFHQAQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G + +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKITGAGS-DHITIEGVEHLTGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|ZP_06062508.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
johnsonii SH046]
gb|EEY97895.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
johnsonii SH046]
Length = 419

Score = 57.4 bits (137), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 107/420 (25%), Positives = 178/420 (42%), Gaps = 46/420 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ ++Q ++ G V++ G+K+ + +L L E T + N+ + +DV+ ++ + LG
Sbjct: 2 DKFLIQGGTKLEGEVRISGAKNAALPLLAAMILPETPTKLTNPVPHLKDVTNLVQLIGGLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+++ + A +F P E K L + R +A V+ GG A
Sbjct: 62 ITMTYEGDVTADTSTLDNQFAPYELVKTMRASILVLGPLVARYGSAKVS LPGGCA---- 117

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RP+ + L+ LGA+++ G V G L GG+V + ++
Sbjct: 118 -----IGSRPVDQHLKALEALGAEIEVEAGY----VHAKVDGRLKGGEV-IFDMVTVGTT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+LMAA LA G + I P + +++ G K E D+ D + G +K
Sbjct: 168 ENILMAAALAEG---VTIRNAAREPEITDLAKMLIAMAKIEGLDT-DTLVVTGVEKLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVT---- 299
+ A V + SY LA AAITGG V T ++ E E MGA+VT
Sbjct: 224 GCEYAVVADRIETGSY-LAAAAITGGRVKTTHDPTLME---SVLEKFEEMGAEVTRGDD 279

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVA--MTLAVVALFADGPTAIRDVASWR 357
W E + P KA+ PD M ++A+ A G R A+
Sbjct: 280 WIELDMMGKRP-----KAVSFQTLPHDPFPTDMAQIMAVNAIG----RGFATIS 325

Query: 358 VKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
E EL+++GA+++ EG D ++T EKL+ + D R + + LAA A
Sbjct: 326 ETIFENRFMHVPELSRMGANIQVEGND-AVVTGVEKLSAAPV-MATDLRASFSVLVLAALA 383

>ref|YP_001617525.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sorangium cellulosum
'So ce 56']
emb|CAN97045.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Sorangium cellulosum
'So ce 56']
Length = 461

Score = 57.4 bits (137), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 118/468 (25%), Positives = 195/468 (41%), Gaps = 52/468 (11%)

Query: 6 EIVLQPI-KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++++ P + + G+V +P KS+++R LLLAAL+ G + + DV +GALR +G
Sbjct: 3 DLIVHPAERPLIGSVVPADKSIHRALLAALATGQSRIRGGTLGGDVLTSTVGALRAMG 62

Query: 65 LSVEADKAAKRAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ VE + + VV G G D + GN+G MR L + A A V
Sbjct: 63 VRVE-EPSPGDLVVHGAGLSGLRAPDGP----IDCGNSGTTMRLLAGILVAQRFAARLVG 117

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFL-----GTDCPPVRVNGIGGLPGGKVKLSGSI 178
D P + RP+ + L+ G ++ L G P+ V G LP + + SI
Sbjct: 118 D--PSLSRRPMEVAKPLRLRGRIEQLDPRKIGEITAPLDV---GPLP--EPHVLSSI 170

Query: 179 SS-----QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
Q SALL++ A G + + ++S + E R++ GV DS
Sbjct: 171 EHELPVPCDQVKSALLSGLYADGPTFVR--EPIVSRDHTE---RMLTALGVPI---DSV 222

Query: 232 DRFYIKGGQKYKSPKNAY---VEGDAS-----SASYFLAGAAITGGTVTVEGCGTSLQ 282
++ A+ V GD S +A+ + G+ +T V + T L+
Sbjct: 223 GAMVCLDAARFSGALPAFEIDVPGDLASAAFLVAAAQIVPGSRVTARRVGLNPTRTGLLE 282

Query: 283 -----GDVKFAEVLEMMGAKVWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTL 337
D+ + +E+ G + V V R ++ + ++ + L
Sbjct: 283 VLRDMDMDGSGVAVEIKGEALGEPTGDVHVASASSGAGLRAGRAGGELASRALDELPILL 342

Query: 338 AVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT--TPPEKLN 395
+ A A G T + D R +ET+R+ A+ + L G EE D ++ P L+
Sbjct: 343 GLGA-RARGLTEVFDARELRAQETDRIAAMASVLGAFGLRCEERTDGLLVEGRPDRLDA 401

Query: 396 TAIDTYDDHRMAM-AFSLAACAEPVPTIRDPGCTRKTFFPDYFDVLSTF 442
+D+ DHR+AM A L A P +RD GC +FP + L
Sbjct: 402 ADVDSRGDHRIAMTAAVLGLAAGGPTRVRDAGCIATSFPLFVGTLRAL 449

>gb|AAA97397.1| encodes EPSP synthase domain [Pneumocystis oryctolagi]
prf||2210353B AROM protein
Length = 108

Score = 57.0 bits (136), Expect = 5e-06, Method: Composition-based stats.
Identities = 33/93 (35%), Positives = 50/93 (53%), Gaps = 13/93 (13%)

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT-----PPEKLNVT AID 399
T I +++ RVKE R+ A+ EL K G V+E PD + PP+ ++
Sbjct: 20 TKITGISNQVRVKECNRIEAMVCELKKFGIQVKELPDGIYVKSINISNLLPPK----NGVN 75

Query: 400 TYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
Y+DHR+AM+FS+ AC + P+ I + C KT
Sbjct: 76 CYNDRHRIAMSFSVLACISPKPIVILNKTCVNKT 108

>gb|ADU52791.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.0 bits (136), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 107/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|YP_003064871.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Liberibacter asiaticus str. psy62]
gb|ACT56931.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Liberibacter asiaticus str. psy62]
Length = 449

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 109/445 (24%), Positives = 192/445 (43%), Gaps = 38/445 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ GT+ +PG +SLS+ ++L ++ G T + +L S+DV + + LG K +
Sbjct: 18 LQGTICIPGDRSLSHFSIILGGIAAGETQIRGVLESDVLTMRMMHYLG--ARFTKKDR 75

Query: 75 RAVVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+V G G G + + + F G+ M V T+ G + +
Sbjct: 76 EWIVQGVNGCCLLSPEYPLDFKGFDMGYGLMM-----GVVGVDYDFQTF-FKGRAEILQPT 129

Query: 134 IGDVVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I L+ L Q+G V P V ++G P V S S Q S +L+A
Sbjct: 130 IESLLAPLYQMGVQVKLPEDKRLPLV-LHG-PRTPNPVYKSPMDSVQSKSVVLLAGLNT 187

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-GGQKYKSPKNAYVE 251
G E+ I+ + + ++E+ L+ FGV SD+ + + ++ G+K S N +
Sbjct: 188 PGITEV---IEPVKTQDHMEIILK---EFGVDLLIKSDTIEDYSVRIEGRKRISGCNLKIP 242

Query: 252 GDASSASYFLAGA-AITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV--- 307
GD+S A + LA A I G + + T L+ V ++L MGA +T + + +
Sbjct: 243 GDSSIAFFPLAALLIPGSDIKLLNVLNPLR--VGIIDILREMGADITLSNRIESGEN 300

Query: 308 TGPPREPFPGRKHLKAIDVNMNMKMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERM 364
R F + +K I ++ N++ + L V++ FA+G T I+ +A V +++
Sbjct: 301 IADIRVRFSK--IKGITISDNRLRSIVDEYPILLVISAFAGETIIKGLA--EVMTSKQF 356

Query: 365 VAIRTELTKLGASVEEGPDYCIIT--TPPEK-LNVT---IDTYDDHRMAMAFSLAAC-AE 417

I E DY +I P K L + + + +R+AM+F + A E
Sbjct: 357 SGIIIECFNNINNIQYEREGDYLMIKGVPGGKGLGCSTGHMVQSKFGYRVAMSFLVMGLASE 416
Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
V + D FPD+ +++ T
Sbjct: 417 YSVVVDYTMISTIFPDFINLMKTL 441

>ref|NP_393762.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Thermoplasma
acidophilum DSM 1728]
sp|Q9HLE6.1|AROA_THEAC RecName: Full=Probable 3-phosphoshikimate
1-carboxyvinyltransferase; AltName:
Full=5-enolpyruvylshikimate-3-phosphate synthase;
Short=EPSP synthase; Short=EPSPS
emb|CAC11427.1| 3-phosphoshikimate 1-carboxyvinyltransferase related protein
[Thermoplasma acidophilum]
Length = 410

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 108/442 (24%), Positives = 184/442 (41%), Gaps = 64/442 (14%)

Query: 16 SGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-DEAKA 74
SGTV LP SKS + R +L + + ++ + + D L + G ++ D + K
Sbjct: 11 SGTVALPSSKSFTQRYILGSLNKSFTLNLYVTITGDDSIALDIAQRAGANITMNDSSIK 70
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
C V ++ ++ LG G A G T+V G P + +RP+
Sbjct: 71 IRTSFTCPSDIYVGESATSYRIALGGLGSA-----GCITHV-KGDPDLAKRPM 117
Query: 135 GDLVVGLK----QLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAA 190
LV L+ L + D F D + I ++ G +SSQ++S+++
Sbjct: 118 DPLVKALEANDVHLKLNEDGFYDVGSESKKRYI-----EVDG-VSSQFVSSMIFY 168
Query: 191 PLALGDVEIEIIDKLISIP-YVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKN 247
G E + K + P YV +T R++ G V E + I +K+ +
Sbjct: 169 ARKGGG---EFLVKNMRSPGYVYITKRVLYDLGYFVNIKT-----ITINPSGVWKTAK 220
Query: 248 AYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
VE D SS ++FL ++ V + +Q D + +L+M + ++
Sbjct: 221 --VEPDYSSLAFFLVGLLSENVDVRFNIKMSRIQPD---SVLLDMFKDNIAIDRDLR 275
Query: 307 VTGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
V R+ I V+ + PD+ ++V+ +F++ I + A + KE+ R
Sbjct: 276 VLPGIRD-----RITVDADHNPDLCPPIISVIGIFSEHGVEIDNYARLKTKESENRYEG 327
Query: 367 IRTELTKLGASVEE-GPDYCI----ITPPEKLNVTADTYDDHRMAMAFSLAACAE-VPV 420
I ++ GA VE+ G D I + P L +Y DHRM M+ ++AA A V
Sbjct: 328 IIDMASRFGAIVEDNGKDLFIKRGDLKDPGTL-----SYTDHRMIMSAAVAAAASGFV 381
Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
I + K+FP +F LS F
Sbjct: 382 ELENETKVSFSFGFFKELSKF 403

>gb|ADU52731.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 66/242 (27%), Positives = 106/242 (43%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRIGVGLGRL 60
Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114
Query: 145 GADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + + +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLAEGTTL-VTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|ZP_01796349.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
gb|EDK14555.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 22.4-21]
Length = 424

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNPVPELKDIETTLNLRQLGIANRDEGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHQGVVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKITGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTGTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMAQOFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGAIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>gb|ADU52774.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 109/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGKQL 144
D L GN+G +R L + A + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFLAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTAVVVG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>gb|ADU52794.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 67/242 (27%), Positives = 106/242 (43%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTTQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFVAFTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGTLAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + K V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFADIHVDPEAKTVAVVGGSRVLVGQK-VQVPGDISSAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_01783755.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 22.1-21]
ref|ZP_01785954.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
ref|ZP_01793715.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittII]
ref|ZP_05849662.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae NT127]
gb|EDJ89388.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 22.1-21]
gb|EDJ91876.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae R3021]
gb|EDK12341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittII]
gb|EEW78951.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae NT127]
gb|ADO81255.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae R2866]
Length = 424

Score = 57.0 bits (136), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNVPELKDIEITLNLRLQGLVIANRDEGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V

Sbjct: 178 AKGTT---VIENAAAREPEIVDTADFLNKMGAISGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+

Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I

Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D

Sbjct: 338 PELIRMGGAIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>gb|ADU52768.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 56.6 bits (135), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 109/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84

S+S+R L L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALTLGSLAEGETTIRGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144

D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204

GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264

+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGANIQVDPETKTVAVVGGSRLVG-QRVQVPGDISSAAFVLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>gb|ADU52747.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 56.6 bits (135), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 70/242 (28%), Positives = 110/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84

S+S+R L+L +L+EG T++ LL E+ R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIIQGLLLGENPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144

D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDGCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204

GA + G P+ V G G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264

+S + E R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRLVG-QRVQVPGDISSAAFVLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|ZP_02004393.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beggiatoa sp. PS]
gb|EDN65607.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beggiatoa sp. PS]
Length = 94

Score = 56.6 bits (135), Expect = 7e-06, Method: Composition-based stats.
Identities = 25/77 (32%), Positives = 51/77 (66%), Gaps = 3/77 (3%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 63
+++ ++ P ++ GT+++PG KS+S+R ++L AL+E TT ++ L ED L A +T+
Sbjct: 5 SQKFIINPGGKLGQTIRVPGDKSISHRAIMLGALAENTTTINGFLAGEDTLATLAAFQTM 64

Query: 64 GLSVE---ADKAAKRAV 77
G+ ++ DK++ +A+
Sbjct: 65 GVPIKNHNMDKSSYQAL 81

>ref|YP_001291058.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PitTEE]
sp|A5UD24.1|MURA_HAEIE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABQ98675.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PitTEE]
Length = 424

Score = 56.6 bits (135), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVLKTNVPELKDITTLNLRQLGVIANRDETGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHQQQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAAREPEIVDTADFLNKMGAKITGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLLIAAAISGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDMLGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGAIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|YP_001942592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
limicola DSM 245]
sp|B3EGH6.1|MURA_CHLL2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACD89613.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
limicola DSM 245]
Length = 424

Score = 56.6 bits (135), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 81/291 (27%), Positives = 122/291 (41%), Gaps = 31/291 (10%)

Query: 117 GNATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G AT L G RPI ++ +++LGA++ G R G L G ++
Sbjct: 107 GEATVSLPGGCAFGPRPIDLHLMAMEKLGAEITETGFIKARN---GKLQGARIDFPV 163

Query: 177 SSSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S +AL MAA LA G II + P +E R + G + E + + + I
Sbjct: 164 SSVGATGNAL-MAAVLAEGKT---IITNAAEPEIEALCRFLASMGARIEGTGTTE-LII 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDV-KFAEVLEMMG 295
+G + + V D A LA AAITGGTVTV+G L+ + KFA G
Sbjct: 219 EGVTSLSAVEFTNVF-DRIEAGTLLAAAAITGGTVTVDGVEPEQLKSVLKKFAHA----G 273

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIR 351
++ T S+T+ P + L D+ P D+ + A+G + I
Sbjct: 274 CTISQTPGSITLASPEK-----LIPTDITAKPYPSFPTDMAQWALTALMTQAEGTSRIT 326

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
D ER I EL +LGA +E + I+ P +L+ T + + D
Sbjct: 327 DKVYH-----ERFNHI-PELNRLGAHIEIRKNQAIVEGPRRLSGTKVMSTD 371

>ref|YP_004139154.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae F3047]
emb|CBY87491.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae F3047]
Length = 424

Score = 56.6 bits (135), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVLEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNVPELKDIETTLNLRQLGVIANRDEGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHTAPYELVKTMRASIWALAPLVARFHQGVVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKISGAGS-DHITIEGVERLTGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDMGN 289

Query: 313 EPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>gb|ADU52744.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 56.6 bits (135), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 71/242 (29%), Positives = 109/242 (45%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALTLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLGKQL 144

Sbjct: 61 D L GN+G +R L + A + + G +R RP+G +V L+Q+
QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V+G G L G + S S+Q S LL+A LA + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVHG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGG SRLVG-QRVQVPGDISA AFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|ZP_06810684.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus thermoglucosidasius C56-YS93]
ref|YP_003990915.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp. Y4.1MC1]
gb|EFG52889.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus thermoglucosidasius C56-YS93]
gb|ADP76304.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp. Y4.1MC1]
Length = 435

Score = 56.6 bits (135), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 93/371 (25%), Positives = 151/371 (40%), Gaps = 37/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
E+I+++ K +SGTVK+ G+K+ ++ L S+G +++ ++ DV+ + LR L

Sbjct: 2 EKLIIVRGKRLSGTVKVEGAKNAVLPVIAATLLASKGKSIHDPALSDVYTISEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G V K + V +E E V+ + + M SL A G A L

Sbjct: 62 GADV---KREGNTITVDASQDLKLEAPFEYVRKMRASV-LVMGSLAR---NGRARVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V+ G L G K+ L S

Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGASVKVGNFGIDAEVK---GKLRGAKIYLDFFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G +I+ P + + G K + + I+G +

Sbjct: 169 ENIMMAAVLAEGTT---VIENCAKEPIVDLANFLNAMGAKVRGAGTGT-IRIEGVDEL 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AAITGG V ++G L +E MG + E

Sbjct: 225 GTTHTVIP-DRIEAGTFMVAAAITGGNVFIQGA VPEHLS---SLIAKMEEMGVTTIEEN 280

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA----S 355
+ V GP + LKA+D+ P D+ + + L A+G + + +

Sbjct: 281 GLRVIGPEK-----LKAVIDIKTMPYPGFPDMQSQMMALLLKAEGTSMVTETVFENRF 333

Query: 356 WRVKETERMVA 366
V+E RM A

Sbjct: 334 MHVEEFRRMNA 344

>gb|AAV48979.1| hypothetical carboxyvinyltransferase [Weissella paramesenteroides]
Length = 202

Score = 56.6 bits (135), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 53/185 (28%), Positives = 90/185 (48%), Gaps = 24/185 (12%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ GT+ +PG KS+S+R ++L +++ G T V +LL+SEDV + A+ LG++ +

Sbjct: 11 KQLRGTLTMPGDKSISHRAVMLGSIASGDTRVQHLLDSEDVVRTVTAMSNLGVTFSTENH 70

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTA-----AVTAAGGNATYVLDG 125
+ GK E + + L +GN+G R L A+T G N+

Sbjct: 71 D-----LIHIGKSLNELVEPKQMLDMGNSGTTARLLMGLLANQPFAITFRGDNS----- 119

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RP ++ L+ +G V D PV G L G +L + S+Q SA
Sbjct: 120 ---LSKRPFARVIKPLRAMG--VSYSKNDHLPVTKLGTRYLEGLVYELPVA-SAQVKS 173

Query: 186 LLMAA 190
+++AA
Sbjct: 174 IILAA 178

>ref|ZP_01792135.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittHH]
gb|EDK10227.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittHH]
Length = 424

Score = 56.6 bits (135), Expect = 8e-06, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNPVELKDIETTLNLRQLGVIANRDETGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHRGQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAAAREPEIVDTADFLNKMGAISGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|YP_001095423.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
loihica PV-4]
sp|A3QI66.1|MURA_SHELP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABO25164.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
loihica PV-4]
Length = 419

Score = 56.2 bits (134), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 104/398 (26%), Positives = 159/398 (39%), Gaps = 44/398 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ +Q ++G V + G+K+ + IL+ L+E VV N+ N DV+ LR LG
Sbjct: 2 DKLTIQASGALAGDVVISGAKNAALPILMAGVLAETDFVVSNNPDLRDVNTSCCELLRCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V K + +F P E K L + R TA V+ GG A
Sbjct: 62 AEVSRSDGKITISTTHLNEFCAPYELVKTMRASILILGPLLARYGTADVSLPGGCA--- 118

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+Q+GA ++ G ++ G L G + + IS

Sbjct: 119 -----IGARPVNLHLHGLEQMGAKIEVKEGY----IKARVDGRLKGAHIFMD-MISVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LLMAA LA G+ +I+ P V + G K + S D I+G +

Sbjct: 168 TENLLMAALADGET---VIENAAREPEVIDLANCLNAMGAKISGAGS-DTIRIQGVESL 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
S V D FL AA+T G + +L+ LE GA +T E

Sbjct: 224 -SGCEYRVMPDRIETGSFLVAAAVTKGKIRCVDADPKTLEA---VLAKLEDAGASITTGE 279

Query: 303 TSVTVTGPPREPFGKHLKKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASW 356
+ + + P KA VN+ MP D+ V+ A+G I +

Sbjct: 280 DWIELDMQGR-----KA--VNIKTMPYPGFPTDMAQFCVLNALAEGTATITET--- 328

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL ++GA++E + CII E LN

Sbjct: 329 -IFENRFMHV--PELIRMGANMELEGNTCIKGCCELLN 363

>emb|CBW99666.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Legionella
pneumophila 130b]
Length = 161

Score = 56.2 bits (134), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 37/121 (30%), Positives = 63/121 (52%), Gaps = 5/121 (4%)

Query: 319 HLKAIIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLG 375
LK ID+ ++ +P D + + A A G T + R+KE++R+ A+ L +LG

Sbjct: 27 QLKGDIPVSMVPLAIDFPPVIFIAACAQKTTLHGAKELRLKESDRIGAMVDGLNQLG 86

Query: 376 ASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLA-ACAEPVPTIRDPGCTRKTFFPD 434
EG D I+ + +++ DHR+AM+F++A A A PVTI++ +FP

Sbjct: 87 VHA-EGFDDGILIEGGSIQGGEVNSRGDHRIAMSFAGAVASAPVTIKNCANVATSFPS 145

Query: 435 Y 435
+

Sbjct: 146 F 146

>gb|EFT44670.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0017]
gb|EFT87779.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX2141]
Length = 433

Score = 56.2 bits (134), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 103/438 (23%), Positives = 179/438 (40%), Gaps = 64/438 (14%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GTVK+ G+K+ IL L+ EG T + N+ DV M ++ L +++ D+

Sbjct: 12 KLEGTVKIEGAKNAVLPLAATLLAEEGVTTLKNVPILSDVFTMNQVIKHLNVAIDFDED 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A V + +E E V MR+ + + A G+A + G +

Sbjct: 72 ANE-VTIDATQPLGIEANYEYVS-----KMRASIVVMGPLLARNGHAKVAMPGGCAI 122

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGI-----GGLPGGKVKLSGSISSQYLS 184
+RPI + G + LGA + ++ NG L G + L S

Sbjct: 123 GKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLDFFP-SVGATQ 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G II+ + P + ++ + G + + + I+G K +

Sbjct: 172 NIMMAAVRAKGT---IENVAREPEIVDLANILNKMGANVIGAGT-ETMRIEGVDKLHA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+++ V+ D A F+ AA+T G V +E + + + L MGA + E

Sbjct: 228 VEHSIVQ-DRIEAGTFMVAAMTEGNVLEIEAIS---EHNRLISKLTEMGAIIIEEENG 283

Query: 305 VTVTGPPREPFGKHLKKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
+ V GP KHLK DV P D+ + + +FA+G + + + V R +

Sbjct: 284 IRVIGP-----KHLKPTDVKTMPHPGFPTDMAQMTAIQMFAGETSIVTETVFENRYQ 336

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVP 419
E E+ ++ A ++ + II +L A++ D AA A +
Sbjct: 337 HLE-----EMRRMNADLKIDGNIAIINGGNELQGAAVEATDLR-----AAAALIL 381

Query: 420 VTIRDPGCTRKTFPDYFD 437
V +R G TR + Y D
Sbjct: 382 VGLRANGITRVSNLKYLD 399

>ref|ZP_05593788.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis ARO1/DG]
gb|EEU88582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis ARO1/DG]
Length = 433

Score = 56.2 bits (134), Expect = 9e-06, Method: Compositional matrix adjust.
Identities = 102/438 (23%), Positives = 179/438 (40%), Gaps = 64/438 (14%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GTVK+ G+K+ IL L+ EG T + N+ DV M ++ L +++ D+
Sbjct: 12 KLEGTVKIEGAKNAVLPIAATLLAEEGVTTLKNVPILSDVFTMNQVIKHLNVAIDFDED 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A V + +E E V MR+ + + A G+A + G +
Sbjct: 72 ANE-VTIDATQPLGIEANYEYVS-----KMRASIVVMGPLLARNGHAKVAMPGGCAI 122

Query: 130 RERPIGLDVVLGKQLGADVDCFLGTDGPPVRVNGI-----GGLPGGKVKLSGSISSQYLS 184
+RPI + G + LGA + ++ NG L G + L S
Sbjct: 123 GKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLDFFP-SVGATQ 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G II+ + P + ++ + G + + + I+G K +
Sbjct: 172 NIMMAAVRAKGT---IENVAREPEIVDLANILNKMGANVIGAGT-ETMRIEGVDKLHA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+++ V+ D A F+ AA+T G V +E + + + L MGA + E
Sbjct: 228 VEHSIVQ-DRIEAGTFMVAAAMTEGNVLIEEAI---EHNRLPLISKLTMGALIEEEENG 283

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
+ V GP KHLK DV P D+ + + +FA+G + + + V R +
Sbjct: 284 IRVIGP-----KHLKPTDVKTMPHPGFPTDMQAQMTAIQMFAGETSIVTETVFENRYQ 336

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAACAEVP 419
E E+ ++ A ++ + +I +L A++ D AA A +
Sbjct: 337 HLE-----EMRRMNADLKIDGNIAVINGGNLQGAAVEATDLR-----AAAALIL 381

Query: 420 VTIRDPGCTRKTFPDYFD 437
V +R G TR + Y D
Sbjct: 382 VGLRANGITRVSNLKYLD 399

>ref|ZP_07547874.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermoanaerobacter wiegelii Rt8.B1]
gb|EFN48877.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermoanaerobacter wiegelii Rt8.B1]
Length = 417

Score = 56.2 bits (134), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 97/397 (24%), Positives = 160/397 (40%), Gaps = 47/397 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ K + G++++ G+K+ + IL A L++ +V+DNL + +D+ ++ +R LG
Sbjct: 2 EKFIKGGKPLKGSIQISGAKNSAVAILPAALLADTPSVIDNLPDIKDIELLVQMIRHLG 61

Query: 65 LSVEADKA AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K G +P D +++ G + AV A G
Sbjct: 62 GKVEKKKHEVVIAPEGLNSFYPPRDLASQMRASYYLIGALLSRFNEAVIAMPGGCNI--- 118

Query: 125 GVPRMRERPIGLDVVLGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RPI + G + LGA+ G +R+ L G + + ++

Sbjct: 119 GV-----RPIDQHIKGFALGAETTIEHGL----IRIKA-DKLVGNHIYFDVASVGATIN 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G + I++ P+V + G + + + D I G K

Sbjct: 169 -LMLAAVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDKLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTET 303
+ + +Y +A AA T G V ++G L+ V K AE MG V +

Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TKGDVYIKGVIPNHLEAIVAKLAE---MGVIVEEYDD 278

Query: 304 SVTV--TGPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI-RDVASW 356
+ V GP LK +D+ P D+ AV+ ADG + I ++

Sbjct: 279 VIRVRREGP-----LKHVDIKTLPYPGFPTDMQQPFAVLLALADGISVITENIYEN 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
R K EL K+GA V II EKL

Sbjct: 330 RPKYL-----NELKKMGAKVRVEGRTAIEGVEKL 359

>ref|YP_001951063.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
lovleyi SZ]
sp|B3E4X8.1|MURA_GEOLS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACD94543.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
lovleyi SZ]
Length = 419

Score = 56.2 bits (134), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 96/383 (25%), Positives = 158/383 (41%), Gaps = 48/383 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++++ + + + G V + GSK+ S I + A L+ G + + N+ D+ L +LG

Sbjct: 2 DKLIINGGRKLKGEVTVSGSKNASLPICIAAVLAPGASTITNVPRLRDITTTAKLLES 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
++E + R + G VE + V+ MR+ + + A G +

Sbjct: 62 ATIERHENTMR---IDAGTINTVEATYDLVK-----TMRASVLVLGPLLARFGRSRV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RPI + GLK LGA++ G V GL G ++ S

Sbjct: 111 SLPGGCAIGARPIDQHLKGLKALGAIEIRLEHGY----VEAIAKKGLKGARINFVDVSTVGG 166

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
L+MAA +A G+ I++ P + + R G K E + + D I+G +

Sbjct: 167 T-EHLMMAAAIAKGE---SILENAAREPEIADLADYLNRMGAKVEGAGT-DTIRIQGVSE 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+P V D A F+ AAITGG + + G L A ++M A V T

Sbjct: 222 L-TPAAEYVMPDRIEAGTFMCAAAITGGDIKINGMKLEHLD-----ALTFKLMDAGVEIT 275

Query: 302 ETS--VTVTGPPREPFGRKHLKAIDVNMNKMMPDVA--MTLAVVALF--ADGPTAIRDVAS 355
+ V V GP R +A+++ P A M +AL A+G + I S

Sbjct: 276 NRNGVVRVKGPKRP-----QAVNIKTRPYPGFATMQAQFMALMCVAEGASVI----S 324

Query: 356 WRVKETERMVAIRTELTKLGASV 378
+ E M +EL + GA +

Sbjct: 325 ENIFENRFMHV--SELLRFGADI 345

>gb|ADU52778.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 65/242 (26%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEGDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + + R++ FG + + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDH---SGRMLRAFGANIQVDPETKTVAVVGGSRLVG-QRVQVPGDISAFAFLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_01788180.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 3655]
ref|ZP_01789950.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittAA]
ref|ZP_04464021.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 6P18H1]
gb|EDJ93882.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 3655]
gb|EDK08676.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittAA]
gb|EEP48562.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 6P18H1]
Length = 424

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 169/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNVPELKDITETLNLRLQLGVIANRDETGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHTFAPYELVKTMRASIWALAPLVARFHQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G + +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAISGAGS-DHITIEGVEHLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|ZP_06444105.1| LOW QUALITY PROTEIN: UDP-N-acetylglucosamine
1-carboxyvinyltransferase MurA [Mycobacterium
tuberculosis KZN 605]
gb|EFD22020.1| LOW QUALITY PROTEIN: UDP-N-acetylglucosamine
1-carboxyvinyltransferase MurA [Mycobacterium
tuberculosis KZN 605]
Length = 420

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 102/395 (25%), Positives = 154/395 (38%), Gaps = 53/395 (13%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTGGNRLSGEVAVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R ++ K + A+R A+V G
Sbjct: 62 GATVELDGDVARITA-----PDEPKYDAF-----AAVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C R L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--HCNIEHGCVVAAE---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVVAEG--VTIHNAAAREPDVVDLCTMLNQMQAVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G ++V G LQ L GA
Sbjct: 218 GVPRLLH-PTEHRVIGDRIVAATWGIAAAMTRGDISVAGVDPAHLQ---LVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S VT R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDASFRVTQYERP-----KAVNVATLFPFGFPTDLQPMALASIASIDGTSMITEN 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCI 387
V R + E M+ +LGA + ++
Sbjct: 327 VFEARFRFVEEMI-----RLGADARTDGHHAVV 354

>ref|ZP_08148960.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parainfluenzae ATCC 33392]
gb|EGC71373.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parainfluenzae ATCC 33392]
Length = 426

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 101/418 (24%), Positives = 174/418 (41%), Gaps = 45/418 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SGTV + G+K+ + IL A L+ + N+ +D+ L LR LG+ E D A+
Sbjct: 13 LSGTVTISGAKNAALPILFAAILATEPVKLTNPVELKDIDTTLKILRKLGVVAERD--AE 70

Query: 75 RAVVVGCG--GKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGVPVRMR 130
AV++ C F P E K A + R V+ GG + +
Sbjct: 71 GAVLLDCSKIDHFVAPYELVKTMRASIWALAPLVARFNQGVVSLPGGCS-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL++LGA ++ D V+ L G ++ + +S +++MAA
Sbjct: 122 ARPVDLHISGLEKLGATIEL----DEGYVKAVVADRLVGTRIVME-KVSVGATLSIMMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G II+ P + T + + G K + + D I+G ++ +++ V
Sbjct: 177 TLAAGTT---IIEANAAREPEIVDTADFLNKMGAKITGAGT-DHIVIEGVERLTGCEHSIV 232

Query: 251 EGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTVTETSVTVTGP 310
+ ++ +AG AI+GG V C T + L GA+V TE S+T+
Sbjct: 233 PDRIETGTFLIAG-AISGGRVV---CKNTKADTMDAVIDKLEAGAQVEVTEDSITLDMH 288

Query: 311 PREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P KA+++ P D+ ++ + A+G + I + R +
Sbjct: 289 GNRP-----KAVNIRTAHPGFPPTMQAQFTLLNMVAEGTSIITETIF-----ENRFMH 337

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEPVPTIRD 424
I EL ++G E + + E L+ + D R +++ LA C TI D
Sbjct: 338 I-PELIRMGGAIEGNTAVCHGVEHLSGAEV-MATDLRASISLVLAGCISSETIVD 393


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>ref|YP_248750.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 86-028NP]
sp|Q4QLK7.1|MURA_HAEI8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAx88090.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 86-028NP]
Length = 424
```

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

```
Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGLEKNAALPILFAAILATEPVKLTNPVELKDIETTLNLRQLGVIANRDEGTGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R A V+ GG + + R
Sbjct: 72 VLLDASININHTAPYELVKTMRASIWALPLVARFHQAQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY----VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHESDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D +G ++ +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKITGAGS-DHITTEGVERLTGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVVKFAEVLEMMGAKVTTWTETSVTVTGP 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLGACIATGETIVD 392
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>ref|NP_816244.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecalis V583]
ref|ZP_03949760.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecalis TX0104]
ref|ZP_03984147.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecalis HH22]
ref|ZP_04433752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecalis TX1322]
ref|ZP_04437996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecalis ATCC 29200]
ref|ZP_05422569.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis T1]
ref|ZP_05425626.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis T2]
ref|ZP_05473729.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis ATCC 4200]
ref|ZP_05503823.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis T3]
ref|ZP_05559281.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 [Enterococcus
faecalis T8]
ref|ZP_05562015.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis DS5]
ref|ZP_05565328.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis Merz96]
ref|ZP_05567895.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis HIP11704]
ref|ZP_05574143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis JH1]
ref|ZP_05576233.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
```

faecalis ElSol]

ref|ZP_05578775.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis Fly1]

ref|ZP_05581948.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis D6]

ref|ZP_05585107.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis CH188]

ref|ZP_05597004.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis T11]

ref|ZP_05598801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis X98]

ref|ZP_06629997.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis R712]

ref|ZP_06631487.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis S613]

ref|ZP_06746737.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis PC1.1]

ref|ZP_07107362.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TUSoD Ef11]

ref|ZP_07551970.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX4248]

ref|ZP_07552942.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0855]

ref|ZP_07557964.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX2134]

ref|ZP_07565688.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0860]

ref|ZP_07567613.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0109]

ref|ZP_07570296.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0411]

ref|ZP_07761582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0635]

ref|ZP_07766929.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis DAPTO 512]

ref|ZP_07772473.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0102]

ref|ZP_07790264.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis DAPTO 516]

sp|Q831A8.1|MURA2_ENTFA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2; AltName: Full=Enoylpyruvate transferase 2; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2; Short=EPT 2

gb|AA082314.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus faecalis V583]

gb|EEI10762.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus faecalis TX0104]

gb|EEI57698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus faecalis HH22]

gb|EEN71504.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus faecalis ATCC 29200]

gb|EEN75906.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus faecalis TX1322]

gb|EET95477.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis T1]

gb|EET98534.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis T2]

gb|EEU15586.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis ATCC 4200]

gb|EEU24189.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis T3]

gb|EEU25902.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 [Enterococcus faecalis T8]

gb|EEU64972.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis DS5]

gb|EEU68285.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis Merz96]

gb|EEU70852.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis HIP11704]

gb|EEU75114.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis JH1]

gb|EEU77204.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis ElSol]

gb|EEU79746.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis Fly1]

gb|EEU82919.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis D6]

gb|EEU86078.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis CH188]

gb|EEU91798.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis T11]

gb|EEU93595.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis X98]

gb|EFE15947.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis R712]

gb|EFE20551.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis S613]

gb|EFG19982.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis PC1.1]

emb|CBL32222.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus sp.
7L76]

gb|EFK78064.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TUSoD Ef11]

gb|EFM68076.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0411]

gb|EFM70611.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0109]

gb|EFM72038.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0860]

gb|EFM75649.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX2134]

gb|EFM80548.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0855]

gb|EFM81630.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX4248]

gb|EFQ09320.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis DAPTO 512]

gb|EFQ11757.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0102]

gb|EFQ17329.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0635]

gb|EFQ67231.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis DAPTO 516]

gb|EFT37187.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX2137]

gb|EFT42270.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX4000]

gb|EFT47736.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0027]

gb|EFT92596.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX4244]

gb|EFT94027.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0012]

gb|EFT95919.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0031]

gb|EFT99503.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0043]

gb|EFU03233.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0312]

gb|EFU06862.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0645]

gb|EFU08984.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX1302]

gb|EFU12613.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX1341]

gb|EFU14161.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX1342]

gb|EFU17374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX1346]

gb|EFU88400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0309B]

gb|EFU91405.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus

faecalis TX0630]
gb|EFU95116.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis TX0309A]
gb|ADX80980.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecalis 62]
Length = 433

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 102/438 (23%), Positives = 179/438 (40%), Gaps = 64/438 (14%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GTVK+ G+K+ IL L+ EG T + N+ DV M ++ L ++++ D+
Sbjct: 12 KLEGTVKIEGAKNAVLPIAATLLAEEGVTTLKNVPILSDVFTMNQVIKHLNVAIDFDED 71

Query: 73 AKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A V + +E E V MR+ + + A G+A + G +
Sbjct: 72 ANE-VTIDATQPLGIEANYEYVS-----KMRASIVVMGPLLARNGHAKVAMPGGCAI 122

Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLSGSISSQYLS 184
+RPI + G + LGA + ++ NG L G + L S
Sbjct: 123 GKRPIDLHLKGFQALGAKI-----IQNGYIEAIADELIGNTIYLDFFP-SVGATQ 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G II+ + P + ++ + G + + + I+G K +
Sbjct: 172 NIMMAAVRAKGT---IENVAREPEIVDLANILNKMGANVIGAGT-ETMRIEGVDKLHA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+++ V+ D A F+ AA+T G V +E + + + L MGA + E
Sbjct: 228 VEHSIVQ-DRIEAGTFMVAAMTEGNVLIEEAI---EHNRLPLISKLTMGAIIEEEENG 283

Query: 305 VTVTGPMPREPFRGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
+ V GP KHLK DV P D+ + + +FA+G + + + V R +
Sbjct: 284 IRVIGP-----KHLKPTDVKTMPHPGFPTDMAQMTAIQMFAEGTSIVTETVFNRYQ 336

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
E ++ A ++ + +I +L A++ D AA A +
Sbjct: 337 HLE-----EMRRMNADLKIDGNIAVINGGNELGAAVEATDLR-----AAAALIL 381

Query: 420 VTIRDPGCTRKTFPDYFD 437
V +R G TR + Y D
Sbjct: 382 VGLRANGITRVSNLKYLD 399

>ref|NP_215831.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Rv]
ref|NP_335803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis CDC1551]
ref|NP_855002.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
bovis AF2122/97]
ref|YP_977468.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
bovis BCG str. Pasteur 1173P2]
ref|YP_001282626.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Ra]
ref|YP_001287287.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis F11]
ref|ZP_02549864.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Ra]
ref|ZP_03415338.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 02_1987]
ref|ZP_03419762.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 94_M4241A]
ref|ZP_03428119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis EAS054]
ref|ZP_03531820.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis GM 1503]
ref|YP_002644406.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
bovis BCG str. Tokyo 172]
ref|YP_003032640.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis KZN 1435]
ref|ZP_04924899.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium tuberculosis C]

ref|ZP_04980258.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium tuberculosis str. Haarlem]

ref|ZP_05220123.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis KZN 4207]

ref|ZP_05763729.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis CPHL_A]

ref|ZP_05772065.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis K85]

ref|ZP_06436654.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis CPHL_A]

ref|ZP_06454205.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis K85]

ref|ZP_06504439.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis 02_1987]

ref|ZP_06512770.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis EAS054]

ref|ZP_06520848.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis GM 1503]

ref|ZP_06800562.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 210]

ref|ZP_06951647.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis KZN 4207]

ref|ZP_06959972.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis KZN R506]

ref|ZP_07012228.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 94_M4241A]

ref|ZP_07413827.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu001]

ref|ZP_07419938.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu002]

ref|ZP_07422363.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu003]

ref|ZP_07426724.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu004]

ref|ZP_07431033.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu005]

ref|ZP_07435438.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu006]

ref|ZP_07439684.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu008]

ref|ZP_07443874.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu007]

ref|ZP_07480066.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu009]

ref|ZP_07484258.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu010]

ref|ZP_07488482.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu011]

ref|ZP_07492993.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu012]

ref|ZP_07815067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis KZN V2475]

sp|P0A5L2.1|MURA_MYCTU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|P0A5L3.1|MURA_MYCBO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

emb|CAA65472.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Mycobacterium
tuberculosis H37Rv]

emb|CAA97748.1| PROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE MURA
[Mycobacterium tuberculosis H37Rv]

gb|AAK45617.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis CDC1551]

emb|CAD94209.1| PROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE MURA
[Mycobacterium bovis AF2122/97]

emb|CAL71363.1| Probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium bovis BCG str. Pasteur 1173P2]

gb|EAY59641.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA

[Mycobacterium tuberculosis C]
gb|EBA41771.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium tuberculosis str. Haarlem]
gb|ABQ73064.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis H37Ra]
gb|ABR05685.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium tuberculosis F11]
dbj|BAH25638.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
bovis BCG str. Tokyo 172]
gb|ACT25745.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis KZN 1435]
gb|EFD17069.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis CPHL_A]
gb|EFD42987.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis K85]
gb|EFD53077.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis 02_1987]
gb|EFD61408.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis EAS054]
gb|EFD72992.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis GM 1503]
gb|EFI29907.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
tuberculosis 94_M4241A]
gb|EFO75408.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu001]
gb|EFP14491.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu002]
gb|EFP20045.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu003]
gb|EFP23860.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu004]
gb|EFP27669.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu005]
gb|EFP31338.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu006]
gb|EFP35219.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu007]
gb|EFP39142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu008]
gb|EFP43791.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu009]
gb|EFP47738.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu010]
gb|EFP51673.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu011]
gb|EFP55314.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Mycobacterium tuberculosis SUMu012]
gb|EGB29294.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA
[Mycobacterium tuberculosis CDC1551A]
Length = 418

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 101/373 (27%), Positives = 148/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTGGNRLSGEVAVGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLG 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R A +E + A A+R A+V G
Sbjct: 62 GATVELDGDVARIT-----APDEPKYDADFA--AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C R L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--HCNIEHGCVVARE---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGQDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMQAGVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297

Sbjct: 218 G V P R L H - P T E H R V I G D R I V A A T W G I A A M T R G D I S V A G V D P A H L Q --- L V L H K L H D A G A T 273

Query: 298 V T W T E T S V T V T G P P R E P F G R K H L K A I D V N M N K M P D V A M T L A V V A L --- F A D G P T A I - R D 352
V T T + S V T R K A ++ V P L + A + A D G + I +

Sbjct: 274 V T Q T D A S F R V T Q Y E R P ----- K A V N V A T L P F P G F P T D L Q P M A I A L A S I A D G T S M I T E N 326

Query: 353 V A S W R V K E T E R M V 365
V R + E M +

Sbjct: 327 V F E A R F R F V E E M I 339

>ref|NP_244616.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
halodurans C-125]
sp|Q9K6I0.1|MURAI_BACHD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
dbj|BAB07468.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
halodurans C-125]
Length = 440

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 101/415 (24%), Positives = 171/415 (41%), Gaps = 42/415 (10%)

Query: 5 E E I V L Q P I K E I S G T V K L P G S K S L S N R I L L A A L - S E G T T V V D N L N S E D V H Y M L G A L R T L 63
E + I + + + + + S G + V K + G + K + + + + L S G T + + + + D V + M L R L
Sbjct: 2 E K I I V R G G R Q L S G S V K V E G A K N A V L P V I A A S I L A S R G T S K I Y D V P K L A D V Y T M K E V L R N L 61

Query: 64 G L S V E A D K A A K R A V V V G C G G K F P V E D A K E E V Q L F L G N A G I A M R S L T A A V T A A G G N A T Y V L 123
++VE + V V E E V + + + M L A V G + A L
Sbjct: 62 N I N V E Y E N G E --- F V V N A T N P L K T E A P F E Y V R K M R A S F - L V M G P L L A R V --- G H A R I A L 113

Query: 124 D G V P R M R E R P I G D L V V G L K Q L G A D V D C F L G T D C P P V R V N G I G G L P G G K V K L S G S I S S Q Y L 183
G + R P I + G + + G A V + + G + V G L G K + L S
Sbjct: 114 P G G C A I G S R P I D Q H L K G F E A M G A T V E -- I G N G F I E A K V E G -- R L Q G T K I Y L D F P - S V G A T 168

Query: 184 S A L L M A A P L A L G D V E I E I I D K L I S I P Y V E M T L R L M E R F G V K A E H S D S W D R F Y I K G G Q K Y K 243
++MAA +A G I++ P + + G K + + I+G +
Sbjct: 169 E N I M M A A M A E G T T --- I L E N A A E E P I V C L A N Y L N A M G A K V R G A G T G - V I R I E G V D E L V 224

Query: 244 S P K N A Y V E G D A S S A S Y F L A G A A I T G G T V T V E G C G T T S L Q G D V K F A E V L E M M G A K V T W T E T 303
++ + D A F + A A I T G G V + E G L + + M G K +
Sbjct: 225 G A E H T V I S - D R I E A G T F M V A A A I T G G D V F I E G A V A E H L R --- P L I A K M H E M G V K T I E E D N 280

Query: 304 S V T V T G P P R E P F G R K H L K A I D V N M N K M P --- D V A M T L A V V A L F A D G P T A I R D - V A S W R V 358
+ V G P L K + D + P D + + + L A + G + I + V R
Sbjct: 281 G I R V I G P ----- D E L K P V D I K T M P H P G F P T D M Q S Q M M A L L R A N G T S V I T E T V F E N R F 333

Query: 359 K E T E R M V A I R T E L T K L G A S V E E G P D Y C I I T P P E K L N V T A I D Y D D H R M A M A F S L A 413
E E ++ +++ I I + P + L + T D R A L A
Sbjct: 334 M H V E ----- E F R R M N G N I K I E G R S A I I S G P C Q L Q G A E V - T A T D L R A G A A L V L A 380

>ref|YP_015087.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes str. 4b F2365]
ref|ZP_00231829.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes str. 4b H7858]
ref|YP_002759181.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes Clip81459]
ref|ZP_05230352.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J1-194]
ref|ZP_05243293.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL R2-503]
ref|ZP_05265591.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes HPB2262]
ref|ZP_05387015.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J1-175]
ref|ZP_07074962.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL N1-017]
sp|Q71WQ2.1|MURAI_LISMF RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;

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AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAT05264.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes serotype 4b str. F2365]
gb|EAL08321.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes str. 4b H7858]
emb|CAS06250.1| Putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Listeria monocytogenes serotype 4b str. CLIP 80459]
gb|EEW19942.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL R2-503]
gb|EFF95821.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes HPB2262]
gb|EFG02355.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J1-194]
gb|EFK41333.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL N1-017]
Length = 430

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 96/402 (23%), Positives = 167/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L
Sbjct: 2 EKIIVRGGKQLNGSVKMEGAKNAVLPVIAATLLASKGTSVLKNVPLNSDVFTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V G+ + E V R + A++ G G
Sbjct: 62 NADV---SFNDEVTVNATGEITSDAPFEYV-----RKMRSIVVMGPLLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V G L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFEAMGAIVKIENGYIEATAE-----KLVGAKVYLDFF 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 163 -SVGATQNIMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G ++ + +++ + D A F+ AAITGG V +E + LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD- 352
+ E + V GP + LKA+DV P D+ + V+ + +G + + +
Sbjct: 274 IIEEENGIRVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVIQMLSEGTSIMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 361

>gb|ACB05436.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
gb|ACB05441.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 38

Score = 55.8 bits (133), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 36/38 (94%), Positives = 36/38 (94%)

Query: 96 LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
LFLGNAG AMRSLTAAV AAGGNATYVLDGVPRMRER
Sbjct: 1 LFLGNAGTAMRSLTAAVVAAGGNATYVLDGVPRMRER 38

>ref|YP_004159437.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bartonella
clarridgeiae 73]
emb|CBI76867.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bartonella
clarridgeiae 73]
Length = 430

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Score = 55.5 bits (132), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 100/426 (23%), Positives = 174/426 (40%), Gaps = 55/426 (12%)

Query: 15 ISGTVKLLPGSKSLSNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRT--LGLSVEADKA 72
++G + + G+K+ + +++ A L+EGT +DN+ + DV ++L L +G +VE K+
Sbjct: 12 LNGVIPISGAKNATLPLMVAALLTEGTLTLDNIPHLVDVEFLLRILNHHGIGYAVEGRKS 71

Query: 73 -----AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
AK+ + P E K+ F + R A V+ GG A
Sbjct: 72 HQDSGYSRTIHFHTAKKITTINA----PYELVKMRASFWVIGPLLRARCREAYVSLPGGCA 127

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+ RP+ ++ GLK LGA + G V GL GG+ + ++
Sbjct: 128 -----IGTRPVDFILEGLKSLGAQIVIEQGY----VHAKAPEGLKGGRYRFP-KVT 173

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
LLMAA +A G I+D + P V ++ ++ G + I G
Sbjct: 174 VGGTHVLLMAAVMAKGT---ILDNIACEPEVINLIQALKAMGAHIS-GEQTQTLTIHGV 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+K K + + +Y +A A+TGG V ++ L + E L+ G ++
Sbjct: 230 EKLNGAKIQVIADRIEAGTYAMA-VAMTGGKVLLKNANPHHL---TQVLECLKKTGLEIE 285

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
++V R+P K + +D+ PD L A F T R + +
Sbjct: 286 IKPEGISVK---RDP--EKKIIPVDIKTGPFDPFPTDLQ--AQFMALMT--RAQGNAHIT 336

Query: 360 ET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACA 416
ET R + ++ EL +LGA + +I ++L + D R +++ +AA A
Sbjct: 337 ETIFENRFMHVQ-ELVRLGAQITLSGQTALIRGTDRLQGAQV-MATDLRASVSLVIAALA 394

Query: 417 EVPVTI 422
TI
Sbjct: 395 AQGKTI 400

>ref|ZP_05670034.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,410]
gb|EEV53367.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,410]
Length = 433

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 90/374 (24%), Positives = 158/374 (42%), Gaps = 49/374 (13%)

Query: 5 EEIVLQPIKEISGTVKLLPGSKSLSNRIILLALLS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ ++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEAGNAVLPLAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A
Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI----GGLPGGKVKLS 175
+ G + +RPI + G + LGA + ++ NG L G + L
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA A G II+ + P + ++ + G + + +
Sbjct: 163 FP-SVGATQNMMAAVKAKGT---IIENVAREPEIVDLANILNKMGAQV-YGAGTETMC 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + ++ V+ D A F+ AA+T G V + S ++++E MG
Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTQGNVLI--ADAISEHNRPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIR 351
A++ E V V GP KH+ DV P D+ + + L A+G + +
Sbjct: 274 AEIIIEEGGVRVIGP-----KHILPTDVKTMPHPGFPTDMAQMTAIQLVAEGTSVVT 326

Query: 352 D-VASWRVKETERM 364
+ V R + E M

Sbjct: 327 ETVFENRFQHLEEM 340

>ref|ZP_05647112.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus casseliflavus EC30]
ref|ZP_05653441.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus casseliflavus EC10]
gb|EEV30445.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus casseliflavus EC30]
gb|EEV36774.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus casseliflavus EC10]
Length = 430

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 89/373 (23%), Positives = 160/373 (42%), Gaps = 47/373 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EE+++Q ++GTVK+ G+K+ IL + L+ EGTT + N+ DV M +R L
Sbjct: 2 EEMIVQGGNRLTGTVKIEGAKNAVLPLAASLLAEEGTTTLTNVPILSDVLTMKVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
++++ ++ + + + +E E V MR+ + + A G+A
Sbjct: 62 NVAIDFEE-ENNTMTIDASQELAIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIG-GLPGGKVKLSG 176
+ G + +RPI + G + LGA + D ++ ++ N I P
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAQIIQKDGYLEIADELKGNISYLDLP----- 164

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA A G I II+ + P + ++ + G K + I
Sbjct: 165 --SVGATQNIIMAAVAKAG---ITIIENVAREPEIVDLANILNKMGAKV-FGAGTETMRI 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G + + ++ V+ D A F+ AA+T G V ++ S ++++E MGA
Sbjct: 219 EGVEHLHAVDHSIVQ-DRIEAGTFMVAAAMTQGDVVIKDA--ISEHNRPLISKLIE-MGA 274

Query: 297 KVTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD 352
+VT + V GP + LKA DV P D+ ++ + L A G + + +
Sbjct: 275 EVTEVARGIRVVGPF-----EQLKATDVKTMPHPGFPTDMQAQMSAIQLLAQGTSVVNE 327

Query: 353 -VASWRVKETERM 364
V R + E M
Sbjct: 328 TVFENRFQHLEEM 340

>gb|ADU52736.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured Synechococcus sp.]
Length = 232

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 70/242 (28%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L G++G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGDSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + S S+Q S LL+A LA ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLAE--GTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>emb|CBL20721.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ruminococcus sp.
SR1/5]
Length = 430

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 103/424 (24%), Positives = 176/424 (41%), Gaps = 39/424 (9%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + G V + G+K+ + IL A +++ T +++NL + D++ +L A+ +G
Sbjct: 2 EQYVIKGGNPLVGEVDIAGAKNAALAILSAAIMTDEILIEINLPDVRDINVLEAISEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE + + G V+ E ++ A L A+ +A L
Sbjct: 62 AQVERIDKSTVKINGSTIGNLSVD--YEFIKKIR----ASYLLGALLGKYKHAEPVLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGADV C V L G + L +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGADVDI-----CHGAIVAKAENLHGSHIFLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G II+ P+V + G + + + D I+G +
Sbjct: 169 NIMMAASMATGRT--IIENAAREPHVVDVANFLNSMGANIKGAGT-DVIRIRGVETLHR 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A FL AA T G VTV L+ LE +G +V + +
Sbjct: 225 TEYSIIP-DQIEAGTFLFAAAATRGDVTVRNVIPKHLEATTA--KLEEIGCEVEEFDDA 280

Query: 305 VTVTGPPEPFGGRKHLKAI---DVNMNMPDVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V V P R H+K + + P +A+TLA A+G + + + + R K
Sbjct: 281 VRVRAP--HVLHRTVKTLPYPGYPTDMQPQIAVTLA---LAEGTSIVTESIFENRFKY 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
+ EL+++GA+++ + II KL + + D R A +A A V
Sbjct: 335 AD-----ELSRMGANIKVEGNSAIDGVRKLTGARV-SAPDLRAGAAALVIAGLAAEGV 386

Query: 421 TIRD 424
T+ D
Sbjct: 387 TVVD 390

>gb|ADH42952.1| UDP-N-acetylglucosamine enolpyruvyl transferase [uncultured SAR11
cluster alpha proteobacterium H17925_23J24]
Length = 421

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 88/397 (22%), Positives = 166/397 (41%), Gaps = 41/397 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ K +SG VK+ GSK+ + IL + LS+ + N+ +DV M L+ +G
Sbjct: 2 QKLIVKGKKNLSGVVKISGSKNATLPILAASILSDKKIEIKNIPLVKDVITMSQLLKHIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+++ + K+ ++ KF V+ AG+ + + A A L
Sbjct: 62 SNIKVNFRDKKFLIHNKNKKFKTIAPYAFVKTM--RAGVI---VLGPLLAKFRKAKVSLP 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ + GLK+LGAD+ G + GL G ++ SIS
Sbjct: 117 GGCAIGTRPVNIHLFGLKKLGADIKIKDGYILAEAK----EGLIGTSIRFP-SISVGATE 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSW--DRFYIKGGQK 241
+++AA A G ++ P ++ +++ G+K +W + I G QK
Sbjct: 172 NVIIAASFAGTTTYLK---NCACEPEIKNLTDFLKKGMIKI---TWLSKRKIKIIGNQK 224

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K+ + V D A F+ A+ + + G T L ++K VL+ MG K
Sbjct: 225 LKAVSHN-VMFDRIEAGTFIIAGALASRNLIKIVGIETKILNKELK---VLKKMGVKFKIK 280

Query: 302 ETSVTVTGPPEPFGGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWR 357
+ + + K++++ + P D+ + V+ A G + I++

Sbjct: 281 KNEIKI-----LDSKNIRSAYIKTEPYPGFPTDLQAQIMVLMTKAKGISIKI-----N 329

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL ++GA + + I P+ LN

Sbjct: 330 IFENRFMHV--PELNRMGAKIRTSGNSSFIHGPNLN 364

>ref|ZP_07759297.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0470]
gb|EFQ71531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecalis TX0470]
Length = 433

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 102/438 (23%), Positives = 179/438 (40%), Gaps = 64/438 (14%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GTVK+ G+K+ IL L+ EG T + N+ DV M ++ L ++++ D+
Sbjct: 12 KLEGTVKIEGAKNAVLPIAATLLAEEGVTTLKNVPILSDVFTMNQVIKHLNVAIDFDED 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A V + +E E V MR+ + + A G+A + G +
Sbjct: 72 ANE-VTIDATQPLGIEANYEYVS-----KMRASIVVMGPELLARNGHAKVAMPGGCAI 122

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGI-----GGLPGGKVKLSGSISSQYLS 184
+RPI + G + LGA + ++ NG L G + L S
Sbjct: 123 GKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLDFFP-SVGATQ 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G II+ + P + ++ + G + + + I+G K +
Sbjct: 172 NIMMAAVRAKGT--IIENVAREPEIVDLANILNKMGANVIGAGT-ETMRIEGVDKLHA 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+++ V+ D A F+ AA+T G V +E + + + L MGA + E
Sbjct: 228 VEHSIVQ-DRIEAGTFMVAAAMTEGNVLIEEAIS---EHNRLPLISKITEMGAIIEEEENG 283

Query: 305 VTVTGPPREPFRGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVK 359
+ V GP KHLK DV P D+ + + +FA+G + + + V R +
Sbjct: 284 IRVIGP-----KHLKPTDVKTMPHPGFPTDMAQMTAIQMFAEGTSIVTETVFNERYQ 336

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
E E+ ++ A ++ + +I +L A++ D AA A +
Sbjct: 337 HLE-----EMRRMNADLKIDGNIAVINGGNEQLQGAATEATDLR-----AAAALIL 381

Query: 420 VTIRDPGCTRKTFPDYFD 437
V +R G TR + Y D
Sbjct: 382 VGLRANGITRVSNLKYLD 399

>ref|ZP_05069059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus Pelagibacter sp. HTCC7211]
gb|EDZ60058.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus Pelagibacter sp. HTCC7211]
Length = 417

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 69/292 (23%), Positives = 128/292 (43%), Gaps = 33/292 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G +K+ GSK+ S IL LS ++NL +D+ M+ +++LG V+ D
Sbjct: 11 KLKGQIKISGSKNASLPILAATLLSSKKIYLNLPKVKDIETMINLIQSLGSKVKFDNE- 69

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130
K ++++K++ ++ N MR+ + + A G+A L G +
Sbjct: 70 -----KLIIDNSKQKKIASYNLMKTMRAGILVLGPELLAKFGSAKVSPLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + L +LG G V GL G K++ IS L+AA
Sbjct: 120 TRPVDIHLKALSGLGVKYKIIIEGY---VHATAPKGLKGSKIRFP-KISVGATENLIIAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW---DRFYIKGGQKYKSPKN 247

LA G I+ P ++ + + + G K + W I+G K + N
 Sbjct: 175 SLAKGTT---ILSNCAIEPEIKDLINFLNKAGCKIK---WITKRSIKIQGVSKI-NETN 226

Query: 248 AYVEGDASSASYFLAGAAITGGTGTVEGCGTSLQGDVKFAEVLEMMGAKVT 299
 + D A +L AA+T G +T++ + +Q ++ ++L+ +GAK++

Sbjct: 227 YKIMFDRIEAGTYLVAAAVTEGNLTIKNVVPSIIQTEI---DILKKIGAKIS 275

>ref|ZP_00604477.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium DO]
 ref|ZP_05659519.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium 1,230,933]
 ref|ZP_05663677.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium 1,231,501]
 ref|ZP_05831804.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium C68]
 ref|ZP_05923126.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TC 6]
 ref|ZP_06446491.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium D344SRF]
 ref|ZP_06674995.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1039]
 ref|ZP_06676853.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1162]
 ref|ZP_06680037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1071]
 ref|ZP_07846837.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133a04]
 ref|ZP_07848132.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133C]
 ref|ZP_07853142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0082]
 ref|ZP_07856301.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133A]
 ref|ZP_07858819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133B]
 ref|ZP_07862289.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133a01]
 gb|EAN09183.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium DO]
 gb|EEV42852.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium 1,230,933]
 gb|EEV47010.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium 1,231,501]
 gb|EEW62614.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium C68]
 gb|EEW64911.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TC 6]
 gb|EFD10024.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium D344SRF]
 gb|EFF20515.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1071]
 gb|EFF31752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1039]
 gb|EFF35089.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium E1162]
 gb|EFR67460.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133a01]
 gb|EFR70964.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133B]
 gb|EFR73414.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133A]
 gb|EFR78803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133C]
 gb|EFS05730.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0133a04]
 gb|EFS08485.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
 faecium TX0082]
 Length = 433

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.

Identities = 90/374 (24%), Positives = 158/374 (42%), Gaps = 49/374 (13%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
      EEI+++  ++GTV++ G+K+  IL  + L+ EG T +DN+  DV  M  +R L
Sbjct: 2  EEIIVRGGNQLNGTIVRIEGAKNAVLPLAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
      + V+ D+  K  V  +  + +E  E  V  MR+  +  + A  G+A
Sbjct: 62  NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPVRMRERPIGLVVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLS 175
      + G  + +RPI  + G + LGA +  ++ NG  L G  + L
Sbjct: 113 VAMPGGCAIGKRPIDHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      S  ++MAA  A G  II+ +  P +  ++ + G +  +
Sbjct: 163 FP-SVGATQNMMAAVKAKGTT---IENVAREPEIVDLANILNKMAQV-YGAGTETMR 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
      I+G  +  ++ V+ D  A  F+  AA+T G V +  S  ++++E MG
Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTQGNVLI--ADAISEHNRPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIR 351
      A++  E  V V GP  KH+  DV  P  D+  +  + L A+G + +
Sbjct: 274 AEIIEEGGVVRVIGP-----KHILPTDVKTMHPGFPTDMAQMTAIQLVAEGTSVVT 326

Query: 352 D-VASWRVKETERM 364
      + V  R +  E M
Sbjct: 327 ETVFENRFQHLEEM 340
```

```
>ref|YP_001341704.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
      1-carboxyvinyltransferase [Marinomonas sp. MWYL1]
gb|ABR71769.1| Prephenate dehydrogenase., 3-phosphoshikimate
      1-carboxyvinyltransferase [Marinomonas sp. MWYL1]
Length = 748
```

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 95/393 (24%), Positives = 164/393 (41%), Gaps = 58/393 (14%)

```
Query: 11  PIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      P  I G + L G KSLs++++ +AALSEG + + N+  + DV  + A R +G+ +E +
Sbjct: 325 PASAIKGDISLGLDKSLSHKVITIAALSEGVEIKNVDLTGDVRITMQAFRDMGVVIE-E 383

Query: 71  KAAKRAVVVGCGGK-----FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +A  V G G +  P+  +  L+L  +A +S  +V A G
Sbjct: 384 VSADHLRVHGVGLRGLKAPIAPINVHQSRSLYLLLPVLAGQSFPVSVVAEGA----- 436

Query: 125 GVPRMRERPIGLVVGLKQLGADV-----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
      +  + + DL  ++++G V  DC  +  P V N  L G +L
Sbjct: 437 ----LLNQSMSDLFSLVRKMGGGVVSEVTDCLPVSLVPGVSSNVYIDLTAGSERLR---M 489

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKA-EHSDSWDRFYIKG 238
      S +L+AL  +P  VE ++  + + E+ LR  FGV  EH+D  F +
Sbjct: 490 SAFLAALY--SP-----VEGSVMTLSTGLSHCEVLLR---HFGVTILEHADG---FSVVP 536

Query: 239 GQKYKSPKNAYVEGDASSASYF-LAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      +  + + GD  A++  L + + G + +E G S+  F  L+ +GA
Sbjct: 537 ASLVGT--DIVLSGDEYEAALVLLASLLPGSELLIENAGLDSVS--YAFLSFLKSIGAN 592

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDV-----NMNKMPDVAMTLAVVALFADGPTAI 350
      +  E  +  G  LK+  +  N++P  L V A +A G + I
Sbjct: 593 ICIPEQGEFGLCEGKLQAGFAELKSFTLLPEQAYQFRNELP----LLCVAAAYAKGESCI 648

Query: 351 RDVASWRVKETERMVAI--RTELTKLGASVEEG 381
      + V S  +R++A+  E  K+  + E G
Sbjct: 649 QGVGSLPYCYCEDRVLALVDALEHVKICCAAYENG 681
```

```
>ref|ZP_05492794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
      [Thermoanaerobacter ethanolicus CCS1]
```

gb|EEU62261.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter ethanolicus CCSD1]
Length = 417

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 97/396 (24%), Positives = 160/396 (40%), Gaps = 45/396 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ K + G+V++ G+K+ + IL A L++ +V+DNL + +D+ + +R LG
Sbjct: 2 EKFEVIKGGKPLRGSVQISGAKNSAVAILPAALLADTPSVIDNLPDIKDIELLAQMIRNLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E K G +P D +++ G + AV A G
Sbjct: 62 GKIEKKKHEVVIAPGELNSFYPPRDLASQMRASYYLIGALLSRFNEAVIAMPGGCNI--- 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RPI + G + LGA+ G +R+ L G + +S
Sbjct: 119 GV-----RPIDQHIKGFALGAETTIEHGL----IRIKA-DKLVGNHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G + I++ P+V + G + + + D I G K
Sbjct: 168 NLMLAAVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDKLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + +Y +A AA T G V ++G L+ + A+++E MG V +
Sbjct: 224 CHYTIIIPDQIEAGTYMVAAAA-TKGDVYIKGVIPNHLEAII--AKLVE-MGVIVEEYDDM 279

Query: 305 VTV--TGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V GP LK +D+ P D+ AV+ ADG + I ++ R
Sbjct: 280 IRVRREGP-----LKHVDIRTLPPGFPPTMQPFVALLALADGISVITENIYENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
K EL K+GA V II EKL
Sbjct: 331 FKYL-----NELKKMGAKVRVEGRTAIEGVEKL 359

>emb|CBW29426.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 10810]
Length = 424

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 169/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D
Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNVPELKDIIETTLNIRQLGVIANRDGTGA 71

Query: 75 RAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHTAPYELVKTMRASIWALAPLVARFHRGQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAAREPEIVDTADFLNKMGAKITGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLMDLGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPPTMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|ZP_01911939.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Plesiocystis
pacificus SIR-1]
gb|EDM75138.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Plesiocystis
pacificus SIR-1]
Length = 434

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 100/399 (25%), Positives = 162/399 (40%), Gaps = 49/399 (12%)

Query: 17 GTVKLPGSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G + + G+K+ + I A L++G T + ++ DV M LR LG V AD +
Sbjct: 20 GRIPVRGAKNAALPIQCAALLADGKTRLRHVPRLTDVSTMNKLRLGCEVSADVDERRV 79

Query: 77 VVVGCG-GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRM 129
+ G G +E E V +++ A+VT G G A L G +
Sbjct: 80 EIDPTGVGSGSLEAPYEHV-----KTMRASVTVMGPLLGRYQARVSLPGGCAI 128

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGG-LPGGKVKLSGSISSQYLSALLM 188
RPI + GL+ LG +V G VR G L GG+ ++ ++M
Sbjct: 129 GARPIDQHLKGLLEALGGEVTTLEHG--VDVRKASHGRLEGGRFHFDP-KVTVGGTQNVMM 185

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +E + + P V+ L+ + G + + + D I+G + + +A
Sbjct: 186 AAVLAKGSSRLNENARE---PEVQELAVLLNKMGAQISGAGT-DAIEIEGVDRLEGIDHA 241

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTV 307
+ D A F AAIT G V +E ++ + K E G + + V
Sbjct: 242 IL-ADRIEAGTFAVAAAITRGDVLLEHAPVDHMRVIDKLEA----GVECRVEAEGLRV 296

Query: 308 TGPPREPFGGRKHLKAIDVNMNMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
GP R ++ IDV P D+ + V+A ADG + IR+ + E
Sbjct: 297 IGPER-----IRPIDVATRPHPGFPTDMQAQIMVLACMADGASVIRET----IFENRF 345

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYD 402
M EL +LGA + + ++ P + + T + D
Sbjct: 346 MHV--PELNRLGADIVVNGNTAVVRGPTRFSGTTVMATD 382

>ref|YP_001213408.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Pelotomaculum
thermopropionicum SI]
dbj|BAF61039.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Pelotomaculum
thermopropionicum SI]
Length = 418

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 96/387 (24%), Positives = 154/387 (39%), Gaps = 52/387 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLNRIILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++IV+ + + G +K+ G+K+ S IL LS TV++N+ + DV M+ + +LG
Sbjct: 2 DKIVIDGGRPLRGRIKISGAKNASLAILCATILSRKETVLENVDPDISDVRVMIEIVNSLG 61

Query: 65 LSVEADKAAKRAVV---VCGGKGFVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
S+ + A VV + G F + L LG + A G A
Sbjct: 62 ASITWEGAETLRVVPAAEKISAGPPFHLVKKLRASNLLG-----PMLARFGQAQ 110

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ GL LGA + G V+ + G L G ++ L S
Sbjct: 111 VALPGGKNIGVRPMDLHFKGLTGLGASLSLERGC---VQASAPGRLKGARIYLDFF-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF----- 234
++MAA LA G IE + K P V + G + + + D
Sbjct: 166 GATENIMMAACLAEGQTLIENVAKE---PEVVDLANFLNAMGARVRGAGT-DVIKIEGVP 221

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
Y++GG++Y + D A F+ AA TGG V ++ LE +
Sbjct: 222 YLEGGERYS-----IIPDRIEAGTFMVAATGGDVLDNVIPIH-----LEPL 265

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMMPDVA--MTLAVVALFADGPTAIRD 352
AK+ V G + K L+ ID+ P M ++A+ + P
Sbjct: 266 SAKLREAGVEVREEDTLQVRAEKPLRPIDIKTMPYPGFPTDMQPQLMAMLSTAPGT--S 323

Query: 353 VASWRVKETERMVAIRTELTKLGASVE 379
V + E MVA EL ++GA+++
Sbjct: 324 VIVENIFENRFMVA--DELKRMGANIK 348

>ref|YP_463577.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-C]
sp|Q2IMV5.1|MURA_ANADE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABC80140.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-C]
Length = 422

Score = 55.5 bits (132), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 97/386 (25%), Positives = 164/386 (42%), Gaps = 48/386 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + G+V + G+K+ + ++ A L+EG V N+ + DV + L +G
Sbjct: 2 DKIVIEGGVPLRGSDVSGAKNAALPVIAAALLAEGEHEVRNVPDLADVRTLGKLLGHMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + +R V + E E V+ + + + L A + G A L
Sbjct: 62 CEVVRGEGDRRTVRLRVPAAVTPEAPYELVKTMRASV-LVLGPLLARL----GRARVSLP 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLS-GSISQYL 183
G + RPI + L LGA++ G VN +PGG+++ + + +Q +
Sbjct: 117 GGCAIGARPIDQHLKALTALGAEIRLEHGY-----VN--ASVPGGRLRGTVFTFDAQT 168

Query: 184 SA---LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ ++MAA LA G+ ++ P V+ + G E + + D +I+G
Sbjct: 169 TGTENVMMMAALAEGEET---VLRNCAREPEVKDLGDALVAMGALVEGAGT-DEIWIEGVP 224

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ +A + D A FL A+ G VTV GC + E L +GA+VT
Sbjct: 225 SLRPLSHAVIP-DRIEAGTFLVAGALPGNDVTVRGCVAAHQEA---LVEKLRAVGAETVK 280

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASW 356
E + V G R + +DV P D+ L V+ ADG +
Sbjct: 281 VEGGLRVIGDGRP-----RPVDVRTAPHPGFPTDMQAQLMVLCLADG-----TS 325

Query: 357 RVKET---ERMVAIRTELTKLGASVE 379
R+ ET R + ++ EL +LGA VE
Sbjct: 326 RITETVFENRFMHVQ-ELIRLGAHVE 350

>ref|YP_561517.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
denitrificans OS217]
sp|Q12RY2.1|MURA_SHEDO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABE53794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
denitrificans OS217]
Length = 419

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 101/398 (25%), Positives = 162/398 (40%), Gaps = 44/398 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ +Q K ++G+V + G+K+ + IL+ L+E V+ N+ DV LR LG
Sbjct: 2 DKLTIQASKPLTGSVVISGAKNAALPILMAGVLAETDFVLSNVPELRDVSTSCKLLRCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V+ + + +F P + K L + R TA V+ GG A
Sbjct: 62 AEVDELGGGRIRISTTNLNEFCAPYDLVKTMRASILILGPLLARFGTADVSLPGGCA--- 118

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+Q+GA ++ G ++ G L G + + IS

Sbjct: 119 -----IGARPVNLHLHGLEQMGAKIEVKEGY----IKARVDGRLKGAHIFMD-MISVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LLMAA LA G I II+ P V + G K + I+G ++

Sbjct: 168 TENLLMAAALADG---ITIIENAAQEPEVTDLAHCLIAMGAKITGVGTAT-LKIEGVERL 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + V D FL AA+T G + E S++ + LE GA VT E

Sbjct: 224 QGCEY-RVMPDRIETGTFLVAAAVTRGRIRCENADPASMEAVLA---KLEDAGATVTSGE 279

Query: 303 TSVTVTGPPREPFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRV 358
+ + ++P KA+++ P D+ V+ A G + RV

Sbjct: 280 DWIELDMHGKQP-----KAVNIKTAPYPAPFTDMQAQFCVLNALAQG-----TGRV 325

Query: 359 KET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
ET E EL ++GA++E CII +KLN

Sbjct: 326 TETIFENRFMHVPELIRMGANMELEGHTCIIQGIDKLN 363

>gb|ABC00783.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 35

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 28/35 (80%), Positives = 31/35 (88%), Gaps = 1/35 (2%)

Query: 82 GGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAA 115

GG+FP+E DAKEEV+LFLGNAG AMR LTA AV AA

Sbjct: 1 GGRFPIEKDAKEEVKLFLGNAGTAMRPLTAAVVAA 35

>ref|NP_466049.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes EGD-e]
ref|ZP_00234525.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes str. 1/2a F6854]
ref|ZP_03668228.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes Finland 1988]
ref|ZP_03671541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL R2-561]
ref|ZP_05232788.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL N3-165]
ref|ZP_05235706.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes 10403S]
ref|ZP_05260260.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes J0161]
ref|ZP_05263437.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Listeria
monocytogenes J2818]
ref|ZP_05269503.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes F6900]
ref|YP_003414829.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Listeria
monocytogenes 08-5578]
ref|YP_003417873.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Listeria
monocytogenes 08-5923]
sp|Q8Y4C4.1|MURAL_LISMO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
emb|CAD00604.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes EGD-e]
gb|EAL05616.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes str. 1/2a F6854]
gb|EEW13811.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL N3-165]
gb|EEW23018.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes F6900]
gb|ADB69467.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Listeria
monocytogenes 08-5578]
gb|ADB72511.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Listeria
monocytogenes 08-5923]
gb|EFF99766.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Listeria
monocytogenes J2818]
Length = 430

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 96/402 (23%), Positives = 167/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L
Sbjct: 2 EKIIVRGGKQLNGSVKMEGAKNAVLPAIAATLLASKGTSVLKNVNLSDVFTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V V G+ + E V R + A++ G G
Sbjct: 62 NADV---SfVNDVTVDATGEITSDAPFEYV-----RKMRAISIVMGPLLARTG 107

Query: 118 NATYVLGDGVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V G L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFEAMGAVVKIENGIEATAE-----KLVGAKVYLDFF 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 163 -SVGATQNMMAATLAEGTT--VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G ++ + +++ + D A F+ AAITGG V +E + LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD- 352
+ E + V GP + LKA+DV P D+ + V+ + ++G + + +
Sbjct: 274 IIEEENGIRVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVIQMLSEGTSIMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 361

>ref|YP_003181465.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eggerthella lenta
DSM 2243]
ref|ZP_07946983.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eggerthella sp.
1_3_56FAA]
gb|ACV55076.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eggerthella lenta
DSM 2243]
gb|EFV34030.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eggerthella sp.
1_3_56FAA]
gb|EGC88671.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eggerthella sp.
HGA1]
Length = 429

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 117/446 (26%), Positives = 180/446 (40%), Gaps = 55/446 (12%)

Query: 4 AEEIVL-QPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
AEEI++ Q ++G V + G+K+ + +++ A L +G T + N+ D+ M LR
Sbjct: 2 AEEIIIVQGNNTLAGDVAVSGAKNSALKLIAAALLGQGETTIHNVPLISDISIMSDVLRC 61

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDA---KEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
LG VE D G V+ + K E L + A S+ + G A
Sbjct: 62 LGARVERD-----GHTLTVDTSADVKHETPYELVSKMRASISVLGPLVGRFGCA 110

Query: 120 TYVLGDGVRMRERPIGDLVVLGKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSG 176
+ G ++ R I +VGL+ +G + FL P GL G V L
Sbjct: 111 RVAMPGGCQIGARKIDMHLVGLAIGVEFSIDHGFLEASTP-----NGLHGAHVVLDF 163

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S LLMAA A G +I+ P + ++ G + + S D +
Sbjct: 164 P-SVGATENLLMAAVAAGST---VIENAAREPEIVDLANMLVSMGTRVTGAGS-DIIEV 218

Query: 237 KG-GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+G P GD A FLAG A+TGG VTV G + L+ V + L MG
Sbjct: 219 EGVPLSSLHPCEHTTVGDRIEAGTFLAGGALTGGPVTVHGIDPSYLR--VALMK-LRAMG 275

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
V + +TV GR + L ID+ P D+ ++A FADG + I
Sbjct: 276 CDVETGDDWITV-----GRTRPLAPIDLQTLPHPGFPTDLQAQFMLLAFAFGMSVI 327

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
+ V E M A +EL ++GA + ++ + L ++ D R A
Sbjct: 328 TE----NVFENRFMFA--SELMRMGADIAIEDHHALVRGVDVLQGADVSST-DLRAGAAL 380

Query: 411 SLAACA-EVPVTIRDPGCTRKTFPDY 435
LA A E ++ G ++ DY
Sbjct: 381 VLAGIAGEGETRVHNIGHIDRGYEDY 406

>ref|NP_471999.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria innocua
Clip11262]
sp|Q927W7.1|MURAl_LISIN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
emb|CAC97896.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria innocua
Clip11262]
Length = 430

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 96/402 (23%), Positives = 167/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L
Sbjct: 2 EKIIIVRGKQLNGSVKMEGAKNAVLPIAATLLASKGTSVLKNVPNLSDFVTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V V G+ + E V R + A++ G G
Sbjct: 62 NADV---SFVNDEVTVDATGEITSDAPFEYV-----RKMRAIVVMGPELLARTG 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V G L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFAMGAIVKIEGYIEATAE-----KLVGAKVYLDFFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 163 -SVGATQNIMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G ++ + +++ + D A F+ AAITGG V +E + LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGNNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPATIRD- 352
+ E + V GP + LKA+DV P D+ + V+ + ++G + + +
Sbjct: 274 IIEEENGIRVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVIQMLSEGTSIMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 361

>gb|ADU52730.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 70/242 (28%), Positives = 108/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLALLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGEITIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLGDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRSLRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G L G + S S+Q S LL+A LA + ++ +
Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKGIHYR-SPVASAQVKSCLLLAGLLA--EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|ZP_03439747.1| hypothetical protein HP9810_49lg24 [Helicobacter pylori 98-10]
gb|EEC22683.1| hypothetical protein HP9810_49lg24 [Helicobacter pylori 98-10]
Length = 353

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 70/289 (24%), Positives = 125/289 (43%), Gaps = 18/289 (6%)

Query: 99 GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
N+G +MR + ++A G +VL G + RP+ ++ LK GA++ LG +
Sbjct: 45 NNSGTSMLRYSGLLSAQKG--LFVLSGDNLSNARPMKRIIEPLKAFGANI---LGRENH 99

Query: 159 VRVNGIGGLPGGKVKLSGSISS-QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRL 217
I G P I+S Q SA +++A A G + + +S + E+ L+
Sbjct: 100 FAPLVILGSPKACDYESPISAAQVKSALFALSALQAQGSSTYK--ESELNRNHEIMLK- 156

Query: 218 MERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGT-VTVEGC 276
G ++ D I +K + + D SSA +F AIT + + ++
Sbjct: 157 --SLGANIQNQDGV--LMISPLEKPLEAFDFTIANDPSSAFFALACAITPKSRLLLKNV 212

Query: 277 GTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGKHLKVIDVNMN--KMPDVA 334
+ ++ E L+ MGA + + S + LKAI+++ N + D
Sbjct: 213 LLNPTR--IEAFEALKMGASIEYAIQSKDLEMIGDIYIEHAPLKAINIDQNIASLIDEI 270

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPD 383
L++ LFA G + +++ R KE++R+ A+ + LG EE D
Sbjct: 271 PALSIALMLFAKGKSMVKNKDLRSKESDRVKAVVSNFKALGIECEEFEED 319

>ref|ZP_05662363.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,502]
ref|ZP_05672642.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,408]
ref|ZP_06700541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium U0317]
gb|EEV45696.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,502]
gb|EEV55975.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,408]
gb|EFF30105.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium U0317]
Length = 433

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 90/374 (24%), Positives = 158/374 (42%), Gaps = 49/374 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ +++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEAKNAVLPIAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A
Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPPLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLS 175
+ G + +RPI + G + LGA + ++ NG L G + L
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA A G II+ + P + ++ + G + + +
Sbjct: 163 FP-SVGATQNIIMAAVKAKGTT---IIENVAREPEIVDLANILNKMGAQV-YGAGTETMR 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSQGDVKFAEVLEMMG 295

I+G + ++ V+ D A F+ AA+T G V + S +++++E MG
Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTQGNVLI--ADAISEHNCPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR 351
A++ E V V GP KH+ DV P D+ + + L A+G + +
Sbjct: 274 AEIIEEEGGVRVIGP-----KHILPTDVKTMPHPGFPTDMAQMTAIQLVAEGTSVVT 326

Query: 352 D-VASWRVKETERM 364
+ V R + E M
Sbjct: 327 ETVFENRFQHLEEM 340

>ref|YP_002349049.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes HCC23]
ref|ZP_06555681.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-071]
gb|ACK38435.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes HCC23]
gb|EFD91271.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-071]
emb|CAR85232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes L99]
Length = 430

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 96/402 (23%), Positives = 167/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L
Sbjct: 2 EKIIIVRGKQLNGSVKMEGAKNAVLPIAATLLASKGTSVLKNVPLNSDVFTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V V G+ + E V R + A++ G G
Sbjct: 62 NADV---SFVNDEVTVDATGEITSDAPFEYV-----RKMRSIVVMGPLLARTG 107

Query: 118 NATYVLGDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V G L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFEAMGAVVKIENGYLEATAE-----KLVGAKVYLDFFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDLKISIPVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 163 -SVGATQNMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTSLQGDVKFAEVLEMMGAK 297
G ++ + +++ + D A F+ AAITGG V +E + LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR- 352
+ E + V GP + LKA+DV P D+ + V+ + ++G + + +
Sbjct: 274 IIEEENGIRVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVIQMLSEGTSTMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 361

>ref|ZP_06683403.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E980]
gb|EFF36827.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E980]
Length = 433

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 89/374 (23%), Positives = 157/374 (41%), Gaps = 49/374 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAL-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ ++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEAKNAVLPIAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A

Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPILLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGI-----GGLPGGKVKLS 175
+ G + +RPI + G + LGA + ++ NG L G + L

Sbjct: 113 VAMPGGCAIGKRPINLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA A G II+ + P + ++ + G + +

Sbjct: 163 FP-SVGATQNMMAAVKAKGTT---IIEENVAREPEIVDLANILNKMGAHV-YGAGTETMR 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMG 295
I+G + ++ V+ D A F+ AA+T G V + S ++++E MG

Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTEGNVLI--ADAISEHNRPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGKRLKKAIDVNMNKMP---DVAMTLAVVALFADGPTAIR 351
A++ E + V GP KH+ DV P D+ + + L A+G + +

Sbjct: 274 AEIIEEGGIRVIGP-----KHILPTDVKTMPHPGFPTDMQAQMTAIQLVAEGTSVVT 326

Query: 352 D-VASWRVKETERM 364
+ V R + E M

Sbjct: 327 ETVFENRFQHLEEM 340

>ref|NP_439238.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae Rd KW20]
ref|ZP_05847996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae RdAW]
sp|P45025.1|MURA_HAEIN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
pdb|2RL1|A Chain A, Crystal Structure Of Udp-N-Acetylglucosamine Enolpyruvyl
Transferase From Haemophilus Influenzae In Complex With
Udp-N-Acetylglucosamine
pdb|2RL2|A Chain A, Crystal Structure Of Udp-N-Acetylglucosamine Enolpyruvyl
Transferase From Haemophilus Influenzae In Complex With
Udp-N-Acetylglucosamine And Fosfomycin
gb|AAC22737.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murZ)
[Haemophilus influenzae Rd KW20]
gb|EEW77383.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae RdAW]
Length = 424

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 98/416 (23%), Positives = 170/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ V+ D

Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNPVELKDIEITLTKILRQLGVVVDRLATGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R

Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHQQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ ++ L G ++ + +S ++MAA L

Sbjct: 123 PVDLHISGLEKLGADIVLEEGY----VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S I+G ++ +++ V

Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAKITGAGSA-HITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+

Sbjct: 233 DRIETGTFLIAAAISGGCVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDMLGN 289

Query: 313 EPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I

Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424

EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGAKEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>ref|YP_001292996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittGG]
sp|A5UIK7.1|MURA_HAEIG RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABR00613.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae PittGG]
Length = 424

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 97/416 (23%), Positives = 169/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL L+ + N+ +D+ L LR LG+ D+
Sbjct: 12 LSGSVNISGAKNAALPILFAVILATEPVKLTNPVELKDIETTLNLRQLGVIANRDETGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VLLDASNINHTAPYELVKTMRASIWALAPLVARFHQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L
Sbjct: 123 PVDLHISGLEKLGADIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAREPEIVDTADFLNKMGAISGAGS-DHITIEGVERLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTGTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+
Sbjct: 233 DRIETGTFLIAAAISGGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDMLGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + + E+L+ T + D R +++ LA C TI D
Sbjct: 338 PELIRMGGAKEIEGNTAVCHGVEQLSGTEV-IATDLRASISLVLAGCIATGETIVD 392

>gb|ADU52739.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 55.1 bits (131), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 65/242 (26%), Positives = 106/242 (43%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+ +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMPGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGTPLAVLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLVG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

```
>ref|YP_001344097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
succinogenes 130Z]
sp|A6VMG5.1|MURA_ACTSZ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABR74162.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Actinobacillus
succinogenes 130Z]
Length = 420
```

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 102/409 (24%), Positives = 170/409 (41%), Gaps = 45/409 (11%)

```
Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V++ G+K+ + IL L+E + N+ +DV LR LG+ VE + +
Sbjct: 12 LSGDVQISGAKNAALPILFATILAEPPVKLTNPVELKDVDTTFEILRKLGVVVE--RTDE 69

Query: 75 RAVVVGCG--GKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ V++ ++ P E K A + R V+ GG +
Sbjct: 70 QTVLIDASRIDRYVAPYELVKTMRASIWALAPLLTRFREGQVSLPGGCT-----IG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+++GA ++ D V+ G L G ++ + +S +L+MAA
Sbjct: 121 ARPVDMHISGLEKMGAAIEL---DEGYVKATVNGRLTGTRIYMD-KVSVGATLSLIMAA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G + I+ P + T + + G K + + D I+G + +++ V
Sbjct: 176 TLAEG---VTTIENAAREPEIVDTADFLNKMGAKISGAGT-DTISIEGVSRLAGCEHSIV 231

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AAI+GG +T +L + E L G +V TE ++T+
Sbjct: 232 P-DRIETGTFLIAAAISGGRITCHNTKADTLDAVI---EKLREAGMQVDVTENTITLDSL 287

Query: 311 PREPFGKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR-- 368
+ P KA VN+ MP + A F T + VA K TE + R
Sbjct: 288 GQRP-----KA--VNIRTMHPGFPPTDMQAQF----TLLNVVAEGTSKITETIFENRFM 335

Query: 369 --TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC 415
EL ++GA E + II E L+ + D R +++ LA C
Sbjct: 336 HYPELIRMGAKGEIEGNTAIIHGVESLSGAQV-MATDLRASISLVLAGC 383
```

```
>emb|CBL40942.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[butyrate-producing bacterium SS3/4]
Length = 430
```

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 88/382 (23%), Positives = 160/382 (41%), Gaps = 44/382 (11%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E+ +++ + G V + G+K+ + IL A +++ V+DNL + D++ +L A+ LG
Sbjct: 2 EQYIMKGGNPLVGEVTISGAKNAALGILAAAIMTDDDVVIDNLPDVSINALLEAISHLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE + + V + V E ++ A A+ +A L
Sbjct: 62 AKVE--RIDRHTVKINAENIHAVTVEDEHMRKIR-----ASYFIGALLGKYKSAEVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LG+DV G V + I L + L +S
Sbjct: 115 GGCTIGSRPIDQHLKGFALGSDVKIVRGA---VVAHAI-DLVASHIYLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G+ I++ + P+V + G + + + D IKG ++
Sbjct: 169 NIMMAATMAEGET---ILENVAKEPHVVDVANFLNSMGANIKGAGT-DVIRIKGVRRLLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N + D A F+ AAIT G +TV+ L+ + L MG +V +
Sbjct: 225 -TNYSIIPDQIEAGTFMCAAAITRGDITVKNVIPKHLEA---ISAKLTEMGCEVVEFDEE 280
```

Query: 305 VVTGPPREPFGRKHLKAIDVNMNKMP-----DVAMTLAVVALFADGPTAIRD-VASWR 357
+ V G PR+ +H+ N +P D+ + V ADG + + + + R
Sbjct: 281 IRVVGKPRQ----RHM-----NFKTLPPGFPPTMQPQMTVALALADGTSVVTESIFENR 331

Query: 358 VKETERMVAIRTELTKLGASVE 379
K + EL+++GA+++
Sbjct: 332 FKYVD-----ELSRMGANIK 346

>ref|ZP_01463041.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
ref|YP_003955287.1| UDP-n-acetylglucosamine 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
gb|EAU66160.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
gb|ADO73460.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stigmatella
aurantiaca DW4/3-1]
Length = 421

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 105/407 (25%), Positives = 165/407 (40%), Gaps = 66/407 (16%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + G VK G+K+ + IL + L++G + N+ + DV ML LRT+
Sbjct: 2 DKIVVKGPPALHGEVKASGAKNAALPILASSLLADGKSTYRNPDLVDVSTMLKVLRTM- 60

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG- 116
GCG + E AK+ ++ +G AGI +++++ A+V G
Sbjct: 61 -----GCGAERLSETAKDVCEVTVG-AGITPEAPYELVKTMRASVLVLGP 104

Query: 117 -----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGLPGG 170
G A L G + RPI + GLK LGAD+ G + R L G
Sbjct: 105 LVARYGRARVSLPGGCAIGARPIDQHLKGLKALGADITLTEGYVEARAER-----LRGA 158

Query: 171 KVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
V I+ ++MAA LA G +++ P VE R++ + G + E
Sbjct: 159 TVNFD-LITVTGTENVMAAVLAKGRT---VLENCAREPEVEELARVLNKMKGARIE-GGG 213

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAE 289
I G ++A + D A L AAI+GG V V+ ++ V K E
Sbjct: 214 TSVITIDGVDALHPVEHAILP-DRIEAGTLLVAAISGGDVLVKHAVPEHMEAVVLKLE 272

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFAD 345
G VT V P + L+ +DV + P D+ L V+ A
Sbjct: 273 A----GCTVTTENGVRCKAP-----QTLRPVDVTTTEHPGFPTDMQAQLMVLLSVAQ 321

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPE 391
G + I S + E M EL ++GA + +GP + P+
Sbjct: 322 GTSVI----SEHIFENRFMHV--AELHRMGADITIQTAVVKGVPK 362

>ref|ZP_08145248.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
casseliflavus ATCC 12755]
gb|EGC70149.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
casseliflavus ATCC 12755]
Length = 430

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 89/373 (23%), Positives = 159/373 (42%), Gaps = 47/373 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EE+++Q ++GTVK+ G+K+ IL + L+ EGTT + N+ DV M +R L
Sbjct: 2 EEMIVQGGNRLTGTVKIEGAKNAVLPLAASLLAEEGTTTLTNVPILSDVLTMKEVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+++ ++ + + + +E E V MR+ + + A G+A
Sbjct: 62 NFAIDFEE-ENNTMTIDASQELAIEAPYEVVS-----QMRASIVVMGPLLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIG-GLPGGKVKLSG 176
+ G + +RPI + G + LGA + D ++ ++ N I P

Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAQIIQKDGyIEAIADELKGNsIYLDFP----- 164

Query: 177 SISSQYLSALLMAAPLAGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA A G I II+ + P + ++ + G K + I

Sbjct: 165 --SVGATQNIIMMAAVKAKG---ITIIENVAREPEIVDLANILNKMGAkv-FGAGTETMRI 218

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G + +++ V+ D A F+ AA+T G V ++ S ++++E MGA

Sbjct: 219 EGVDDLHVAHEHSIVQ-DRIEAGTFMVAAAMTQGDVVIKDA--ISEHNRPLISKLIE-MGA 274

Query: 297 KVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
+VT + V GP + LKA DV P D+ ++ + L A G + + +

Sbjct: 275 EVTEVAEGIRVVGp-----EQLKATDVKTMPHPGFPTDMQAQMSAIQLLAAGTSVVNE 327

Query: 353 -VASWRVKETERM 364
V R + E M

Sbjct: 328 TVFENRFQHLEEM 340

>ref|YP_001675891.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
halifaxensis HAW-EB4]
sp|B0TUW5.1|MURA_SHEHH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABZ78232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
halifaxensis HAW-EB4]
Length = 420

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 99/386 (25%), Positives = 156/386 (40%), Gaps = 40/386 (10%)

Query: 15 ISGTVKLPgSKSLSNRILLALLSEGGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V + G+K+ + IL+ L+E V N+ N DV+ LR LG V K

Sbjct: 12 LAGNVVISGAKNAALPILMAGVLAETDFNVSNVpNLRDVNTSCeLLRCLGAeVTRSGTDK 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +F P E K L + R TA V+ GG A + R

Sbjct: 72 VCISTTNLNEFCAPYELVKTMRASILILGPLLARYGTADVSLPGGCA-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+Q+GA ++ G ++ G L G + + IS LLMAA L

Sbjct: 123 PVNLHLQGLEQMGAKIEVKEGY---IKARVDGRLKGAHIFMD-MISVGATENLLMAAAL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ II+ P V + G K E + + D I+G + + + V

Sbjct: 178 ADGET---IIENAAAREPEVVDLANCLIAMGAKIEGAGT-DTVRIQGVESLQGC-DYQVMP 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA+T G + +L+ LE GA +T + + + +

Sbjct: 233 DRIETGSFLVAAAVTRGKIRCTKADPKTLE---SVLAKLEDAGASITTGDDWIELDMQgK 289

Query: 313 EPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ V+ A+G I + + E M

Sbjct: 290 RP-----KAVNIKTVAYPGFPTDMQAQFCVLNALAEGTATITET----IFENRFMHV-- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLN 394
EL+++GA++E + CII EKLN

Sbjct: 338 PELSRMGATMELEGNTCIIHGIEKLN 363

>ref|ZP_08103692.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
sinaloensis DSM 21326]
gb|EGA69279.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
sinaloensis DSM 21326]
Length = 419

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 106/418 (25%), Positives = 170/418 (40%), Gaps = 51/418 (12%)

Query: 17 GTVKLPgSKSLSNRILLALLSEGGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76

Sbjct: 15 G V + G+K+ + IL + L+E V N+ + D+ + L+ LG VE + +
GEVTISGAKNAALPILFASILAEPEVEVANVPHLRDIDTTMELLKRLGAKVERNGS---- 70

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMR 130
V V GG +++ L ++++ A++ A G G L G +

Sbjct: 71 VHVDAGG---IDEYCAPYDL-----VKTMRASIWALGPLVARFQGQVSLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+QLGA + G V+ + G L G + + +S ++ AA

Sbjct: 120 ARPVDLHIHGLEQLGATITLEDGY----VKAHVDGRLKGAHIVMD-KVSVGATITVMCAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G ++D P + T + + G K + + D I+G ++ K+A V

Sbjct: 175 TLAEGKT---VLDNAAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVERLAGGKHAVV 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLGQDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AA++GG VT C TS LE GAKV E ++V

Sbjct: 231 -ADRIETGTFTLVAAAVSGGKVT---CRNTSAHLLEAVLAKLEEAGAKVDSGEDWISVDMT 286

Query: 311 PREPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
RE LKA+ V P D+ ++ L A G I + + E M

Sbjct: 287 DRE-----LKAVTVRTAPHPGFPTDMAQFTLLNLMAKGGGVITE----NIFENRFMHV 336

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
EL ++GA E + I E+L+ + D R + + +A C TI D

Sbjct: 337 --PELMRMGAKAEIEGNTVICGDVEELSGAQV-MATDLRASASLVIAGCIANGETIVD 391

>gb|ADU52748.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 65/242 (26%), Positives = 107/242 (44%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L++G T + LL ED + LG + E + R VG G

Sbjct: 1 SISHRALMLGSLAKGETTIQGLLLGEDPRSTAACFQALGADISELNSECVRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+G +R L + A + + G +R RP+G +V L+Q+

Sbjct: 61 QEPADV-----LDAGNSGTTLR-LMLGILAGQAGRFFAVTGDRLSRSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDGPPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +

Sbjct: 115 GASIWGRAGGTLAPLAVQG-GSLKG--IHYRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + K V GD SSA+++L A

Sbjct: 171 ALSRDHSE---RMLRAFADIHVDPEAKTVAVVGGSRVLVGQK-VQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I

Sbjct: 227 SI 228

>ref|ZP_05746581.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
antri DSM 16041]
gb|EEW52806.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
antri DSM 16041]
Length = 441

Score = 54.7 bits (130), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 106/458 (23%), Positives = 175/458 (38%), Gaps = 68/458 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALS---EGTTVDNLLNSEDVHYMLGAL 60
E+I+++ + + G V + GSK N +L L A + +GT ++N+ DV M L

Sbjct: 2 EKIIKGGRPQKGVAVEGSK---NAVLPLQAAAILAVQGTVTLNNVPPVTDVQVMNRLL 58

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R L L + ++ V+ G FP+ E N A + + A G

Sbjct: 59 RFLNLKTAYGEQQRQLVI---NGSFPL---SAEAPFEYVNQMRASLLVMGPILLARTGQVR 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGS 177
L G + RPI + GL++LGA + F+ C L G ++ L

Sbjct: 113 IALPGGCSIGARPIDLHLAGLRKLGASIKQDAGFIEARC-----DHLVGARITLDFP 164

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-----WD 232
S L+MAA +A G I I+ P V L+ + G + + S

Sbjct: 165 -SVGATENLMAATMAEG--ITTIENTAACEPEVVELANLLNKMGGRVHGAGSKVIRIQG 220

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLE 292
+Y+ G + +P D A ++ AA+T G V V+ + + LE

Sbjct: 221 VYYLHGAEYTVAP-----DRIEAGTWMLAAAVTNGDVIVQNA---VAEYNASLIAKLE 270

Query: 293 MMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPP-----DVAMTLAVVALFADG 346
MG V + + V G I N+ MP D+ + V+ L A+G

Sbjct: 271 EMGVTVIRQDDGIRVLGTA-----VLIPANVKAMPYPGFPTDLQPQMTVLQLLANG 321

Query: 347 PTAIRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHR 405
+ + + V R E EL ++ A + ++ P + + T D R

Sbjct: 322 TSTMEEHVFQRFNHL-----ELRRMNADFQVAGPVAVLDGPTHFSGAEV-TATDLR 373

Query: 406 MAMAFSLAACAEVPVT-IRDPGCTRKTFPDYFDVLSTF 442
A LA A +T +R+P C + + D++ L

Sbjct: 374 AGAALVLAGLAATGITQVRNPACLDRGYHDFYQKLRQL 411

>ref|YP_001647859.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
ref|ZP_04200236.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH603]
gb|ABY46231.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
weihenstephanensis KBAB4]
gb|EEL68053.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH603]
Length = 434

Score = 54.3 bits (129), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 91/371 (24%), Positives = 148/371 (39%), Gaps = 37/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K +SGTV++ G+K+ I+ A L S+G V+ + DV+ + LR L

Sbjct: 2 EKIIIVRGGKRLSGTVRVEGAKNAVLPIIAAALLASDGKNVLEVPVLSVYVTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V + V + + +E E V+ + + + A G A L

Sbjct: 62 NAEVVFE---NNQVTIDSSKELNIEAPFEYVRKMRASV-----QVMGPILLARNGRARIAL 113

Query: 124 DGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V + G L G K+ L S

Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAKVKVGNF---VEAHVEGELKGAKIYLDLP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++ AA LA G +++ P + + G K + + I+G +K

Sbjct: 169 ENIMSATLAKGTT---VLENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIEGVEKLY 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTET 303
+ + D A F+ AAITGG + +E L+ +E MG K+

Sbjct: 225 GANHPIIP-DRIEAGTFMVAAAITGGDILINAVPEHLR---SITAKMEEMGVKIIIEENE 280

Query: 304 SVTVTGPPREPFGKRHLKAIDVNMNKMPP-----DVAMTLAVVALFADGPTAIRDVA----S 355
V V GP + LKA+D+ P D+ + + L ADG + I +

Sbjct: 281 GVRVIGDPK-----LKAVDIKTMHPGFPPTMQSQMMALLLHADGTSMTITETVFENRF 333

Query: 356 WRVKETERMVA 366
V+E RM A

Sbjct: 334 MHVEEFRRMNA 344

>ref|YP_002951194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
WCH70]

gb|ACS25928.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
WCH70]
Length = 435

Score = 54.3 bits (129), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 94/371 (25%), Positives = 149/371 (40%), Gaps = 37/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ +SGTVK+ G+K+ ++ L S G +V+ ++ DV+ + LR L
Sbjct: 2 EKIIIVRGGNRLSGTVKVEGAKNAVLPIAATLLASNGKSVIHDVPALSDVYTISEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G V K + + V + E E V+ + + M SL A G A L
Sbjct: 62 GADV---KIEENTITVDASQELKFEAPFEYVRKMRASV-LVMGSLAR---NGRARVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V+ G L G K+ L S
Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAHVKGNGFIDAEVK----GRLRGAKIYLDFFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ P + + G K + + I+G +
Sbjct: 169 ENIMMAAVLAEGTT---IIENCAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIEGVDQLT 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AAITGG V V+G L +E MG +
Sbjct: 225 GTTHTVIP-DRIEAGTFMVAIAITGGNVLVQGAVPEHLS---SLIAKMEEMGVTTIEEGN 280

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
+ V GP + LKA+D+ P D+ + + L A+G + + +
Sbjct: 281 GLRVIGPEK-----LKAVDIKTMPYPGFPTDMQSQMMALLLKAEGTSMVTETVFENRF 333

Query: 356 WRVKETERMVA 366
V+E RM A
Sbjct: 334 MHVEEFRRMNA 344

>ref|ZP_03982092.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium TX1330]
ref|ZP_05666449.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,141,733]
ref|ZP_05675017.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium Com12]
ref|ZP_05677629.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium Com15]
ref|ZP_06624403.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium PC4.1]
gb|EEI59768.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium TX1330]
gb|EEV49782.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,141,733]
gb|EEV58350.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium Com12]
gb|EEV60962.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium Com15]
gb|EFF61239.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium PC4.1]
Length = 433

Score = 54.3 bits (129), Expect = 3e-05, Method: Compositional matrix adjust.
Identities = 89/374 (23%), Positives = 157/374 (41%), Gaps = 49/374 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ +++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEAKNAVLPIAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A
Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPLLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI----GGLPGGKVKLS 175
+ G + +RPI + G + LGA + ++ NG L G + L

Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA A G II+ + P + ++ + G + +

Sbjct: 163 FP-SVGATQINIMMAAVKAKGTT---IENVAREPEIVDLANILNKMGAHV-YGAGTETMR 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMG 295
I+G + ++ V+ D A F+ AA+T G V + S ++++E MG

Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTEGNVLI--ADAISEHNRPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGKRLKKAIDVNMNKMP---DVAMTLAVVALFADGPPTAIR 351
A++ E + V GP KH+ DV P D+ + + L A+G + +

Sbjct: 274 AEIIEEGGIRVIGP-----KHILPTDVKTMPHPGFPTDQMQMTAIQLVAEGTSVVT 326

Query: 352 D-VASWRVKETERM 364
+ V R + E M

Sbjct: 327 ETVFENRFQHLEEM 340

>ref|ZP_06488789.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Xanthomonas
campestris pv. musacearum NCPPB4381]
Length = 150

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 37/107 (34%), Positives = 54/107 (50%), Gaps = 2/107 (1%)

Query: 330 MPDVAMTLAVVALFADGPPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITP 389
M D L V A A G T + A RVKE++R+ A+ T L LG V+E PD I

Sbjct: 28 MIDEFPALFVAAAAASGQTVVTGAAELRVKESDRLAAMATGLRTLGVQVDETPDGATIH- 86

Query: 390 PEKLNVTADITYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDY 435
+ I+++ DHR+AMAF++A + V + D +FP +

Sbjct: 87 GGSIGSGVIESHGDHRIAMAFIAGQLSTGQSVQVNDVANVATSFPGF 133

>ref|ZP_03128341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chthoniobacter
flavus Ellin428]
gb|EDY21213.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chthoniobacter
flavus Ellin428]
Length = 419

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 75/278 (26%), Positives = 125/278 (44%), Gaps = 33/278 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTL 64
++I++ +SG+VK+ GSK+ + IL L++ V+ ++ + D+HYML L LG

Sbjct: 2 DKILVHGASLGSVKSISGKSNALPILAAATLLTKEPCVHHVVDLSIHMYLQILSHLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE + + VV + +A E+ +R + A+V G

Sbjct: 62 AQVE-----RASGVVTVQAENIRTEAPYEI-----VRKMRASVCVLGPLGREKE 106

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
AT L G + +RPI + G + LGA G V+V G L G + L G +

Sbjct: 107 ATVSLPGGCVIGDRPIDLHLKGFEALGAMHRIENG---VKVFA-GELKGSMSHLRGKL 161

Query: 179 SSQYLSA--LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
L ++MAA LA G + +ID + P VE + + G K E + + R I

Sbjct: 162 GPTVLGTDNVMAAVLAEG---VTVIDSAAAEPEVEDLANFLIKMGAKIEGAGTR-RIVI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
+G ++ +++ + D A FL AI G +T++

Sbjct: 218 EGVKELHGAHESVIP-DRIEAGTFLVAGAIAGKGITLK 254

>ref|YP_001503451.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
pealeana ATCC 700345]
sp|A8H8M9.1|MURA_SHEPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

gb|ABV88916.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
pealeana ATCC 700345]
Length = 420

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 100/386 (25%), Positives = 157/386 (40%), Gaps = 40/386 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V + G+K+ + IL+ L+E V N+ N DV+ LR LG V K
Sbjct: 12 LAGNVVISGAKNAALPILMAGVLAETDFNVSNNPDLRDVNTSCCELLRCLGAEVTRSGTDK 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +F P + K L + R TA V+ GG A + R
Sbjct: 72 VCISTTNLNEFCAPYDLVKTMRASILILGPLLARYGTADVSLPGGCA-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL+Q+GA ++ G RV+ G L G + + IS LLMAA L
Sbjct: 123 PVNLHLQGLEQMGAEVQEGY--IKARVD--GRLKGAHIFMD-MISVGATENLLMAASL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ II+ P V + G K E + + D I+G + + + V
Sbjct: 178 ADGET---IIEANAAREPEVVDLANCLIAMGAKIEGAGT-DTVRIQGVESLQGC-DYRVMP 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AA+T G + SL+ LE GA +T + + + +
Sbjct: 233 DRIETGSFLVAAVTRGKIRCTKADPKSLEA---VLAKLEDAGANITGDDWIELDMQGK 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ V+ A+G I + + E M
Sbjct: 290 RP-----KAVNIKTVAYPGFPTDMQAQFCVLNALAEGTATITET----IFENRFMHV-- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLN 394
EL+++GA++E + CII E+LN
Sbjct: 338 PELSRMGATMELEGNTCIIHGIERLN 363

>emb|CBW15237.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
parainfluenzae T3T1]
Length = 426

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 99/418 (23%), Positives = 174/418 (41%), Gaps = 45/418 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV + G+K+ + IL A L+ + N+ +D+ L LR LG+ E D A+
Sbjct: 13 LTGTVTISGAKNAALPILFAAILATEPVKLTNPVELKDIDTTLKILRKLGVVAERD--AE 70

Query: 75 RAVVVGCG--GKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
AV++ C F P E K A + R V+ GG + +
Sbjct: 71 GAVLLDCSKIDHFVAPYELVKTMRASIWALAPLVARFHQQGVSLPGGCS-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL++LGA ++ D V+ L G ++ + +S +++MAA
Sbjct: 122 ARPVDLHISGLEKLGATIEL----DEGYVKAADVADRLVGTRIVME-KVSVGATLSIMMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G II+ P + T + + G K + + D ++G ++ +++ V
Sbjct: 177 TLAAGTT---IIEANAAREPEIVDTADFLNKMGAKITGAGT-DHIVVEGVERLTGCEHSIV 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
+ ++ +AG AI+GG V C T + L GA+V TE S+T+
Sbjct: 233 PDRIETGTFLIAG-AISGGRVV--CKNTKADTMDAVIDKLEAGAEVEVTEDSITLDMH 288

Query: 311 PREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
P KA+++ P D+ ++ + A+G + I + R +
Sbjct: 289 GNRP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMH 337

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRD 424
I EL ++G E + + E L+ + D R +++ LA C TI D
Sbjct: 338 I-PELIRMGGKAEIEGNTAVCHGVEHLSGAEV-MATDLRASISLVLAGCIASGETIVD 393

>gb|ADU52789.1| 3-phosphoshikimate 1-carboxyvinyltransferase [uncultured
Synechococcus sp.]
Length = 232

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 65/242 (26%), Positives = 106/242 (43%), Gaps = 15/242 (6%)

Query: 26 SLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV-EADKAAKRAVVVGCGGK 84
S+S+R L+L +L+EG T + LL ED R LG + E + R VG G
Sbjct: 1 SISHRALMLGSLAEGETTIQGLLLGEDPRSTAACFRALGADISELNSECVIRIRGVGLGRL 60

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
D L GN+ +R L + A + + G +R RP+G +V L+Q+
Sbjct: 61 QEPADV-----LDAGNSDTTLR-LMLGILAGQAGRFFAVTGDRLSRPMGRVVEPLRQM 114

Query: 145 GADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDK 204
GA + G P+ V G G L G + ++S + + L+ A L + ++ +
Sbjct: 115 GASIWGRAGGT LAPLAVQG-GSLKG--IHHRSPVASAQVKSCLLLAGLLA-EGTTQVTEP 170

Query: 205 LISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGA 264
+S + E R++ FG + GG + + V GD SSA+++L A
Sbjct: 171 ALSRDHSE---RMLRAFGADIHVDPEAKTVAVVGGSRVLG-QRVQVPGDISAFAFWLVAA 226

Query: 265 AI 266
+I
Sbjct: 227 SI 228

>ref|YP_001664112.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter pseudethanolicus ATCC 33223]
ref|YP_004185125.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter brockii subsp. finnii Ako-1]
gb|ABY93776.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter pseudethanolicus ATCC 33223]
gb|ADV78742.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter brockii subsp. finnii Ako-1]
Length = 417

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 96/397 (24%), Positives = 158/397 (39%), Gaps = 47/397 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ K + G+++ G+K+ + IL A L++ +V+DNL + +D+ ++ +R LG
Sbjct: 2 EKFIKGGKPLKGSIQISGAKNSAVAILPAALLADTPSVIDNLPDIKDIELLVQMIRHLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K G +P D +++ G + AV A G
Sbjct: 62 GKVEKKKHEVVIAPGINSFYPPRDLASQMRASYYLIGALLSRFNEAVIAMPGCCNI--- 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RPI + G + LGA G +R+ L G + +S
Sbjct: 119 GV-----RPIDQHIKGFALGAKTTIEHGL----IRIKA-DKLVGNHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++A+ A G + I++ P+V + G + + + D I G K
Sbjct: 168 NLMLASVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDKLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDV-KFAEVLEMMGAKVTWTET 303
+ +Y +A AA T G V ++G L+ + K AE MG V +
Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TKGDVYIKGIIPNHLEAIIAKLAE----MGVIVEEYDD 278

Query: 304 SVTV--TGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAI-RDVASW 356
+ V GP LK +D+ P D+ AV+ ADG + I ++
Sbjct: 279 VIRVRREGP-----LKHVDIRTLPPYGFPTDMQQPFVLLALADGISVITENIYEN 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
R K EL K+GA V II EKL
Sbjct: 330 RFKYL-----NELKKMGAKVRVEGRTAIIIEGVEKL 359

>ref|YP_003007876.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
aphrophilus NJ8700]
gb|ACS97789.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
aphrophilus NJ8700]
Length = 425

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 97/416 (23%), Positives = 172/416 (41%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV++ G+K+ + IL A L+ + N+ + +D+ L LR LG+ VE ++
Sbjct: 12 LKGTVEVSGAKNAALPILFAAILATEPVTLTNVPDLKDIETTLKILRQLGVFVERNEQGI 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VHLDAKIDHVFAPYELVKTMRASIWALAPLVARFNQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGA + G V+ + G L G ++ + +S +++AA L
Sbjct: 123 PVDLHISGLERLGAQIALEDGY---VKAHVNGCLTGTRIVME-KVSVGATLSIMIAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S D I+G ++ +++ V
Sbjct: 178 AKGTT---VIENAAAREPEIADTAEFNLKMGAKISGAGS-DAITIEGVERLTGCQHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTSLQGDVVKFAEVLEMMGAKVTWTETSVTGTGPPR 312
D FL AAI+GG + + +L + + L GA+V TE +VT+
Sbjct: 233 DRIETGTFLVAAAISSGRILCKNTKAGTLDVI---DKLREAGAQVDVTEDVTLDMLGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----KAVNIRTAPYPGFPTDMQAQFTLLNMIANGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + I E L+ + D R +++ LA C TI D
Sbjct: 338 PELIRMGGKAEIEGNTAICHGVEHLSGAEV-MATDLRASISLVLAGCIATGETIVD 392

>ref|YP_727854.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
eutropha H16]
sp|Q0K685.1|MURA_RALEH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAJ94486.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Ralstonia eutropha
H16]
Length = 416

Score = 54.3 bits (129), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 96/403 (23%), Positives = 168/403 (41%), Gaps = 64/403 (15%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L+ T +DN+ N +DV L LR +G+ E D A
Sbjct: 12 LKGEIRVSGAKNAALPILCAGLLTADTVSLDNVPLQDVRTTLKLLRQMGMAELDGAR- 70

Query: 75 RAVVVGCGGKFVVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V G V +A E+ +++++ A++ G G A L G
Sbjct: 71 ---VTLNGADVNVLEAPYEL-----VKTMRASILVLGPLVARFGEARVSLPGGCG 117

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+ +GA++ G + L G +V ++ I+ LLM
Sbjct: 118 IGARPDVQHIGKLQAMGAIEITIEHGFHARAK-----RLKGARV-VTDMITVTGTENLLM 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ +++ P V +L+ + G K E + DR ++G ++ ++
Sbjct: 172 AATLAEGET---VLENAAREPEVTDLAQLLVKMGAKIEGIGT-DRLVVQGVRLHGHASHS 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDV--KFAEVLEMMGAKVTWTETSVT 306
+ D A FL AA T G + + G +Q D+ + L GAK+ +
Sbjct: 228 VI-ADRIEAGTFLCAAAATLGDLVLRG-----VQPDILDTVLDKLEAGAKLETGADWIR 281

Query: 307 VTGPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKET- 361
+ P R KA+ ++ P D+ + A+G + RV ET
Sbjct: 282 LAMPQRA-----KAVSFRTSEYPAPFTDMQAQFMALNAVAEG-----TARVTETI 326

Query: 362 --ERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVT AID 399
R + ++ EL +LGA + + ++ +L NV A D
Sbjct: 327 FENRFMHVQ-ELNRLGADIAVEGNTAVVNGVPRLSGANVMATD 368

>gb|ACB05440.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 37

Score = 53.9 bits (128), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 35/37 (94%), Positives = 35/37 (94%)

Query: 97 FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
FLGNAG AMRSLTAAV AAGGNATYVLDGVPRMRER
Sbjct: 1 FLGNAGTAMRSLTAAVVAAGGNATYVLDGVPRMRER 37

>ref|YP_795412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
brevis ATCC 367]
gb|ABJ64381.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
brevis ATCC 367]
Length = 435

Score = 53.9 bits (128), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 93/372 (25%), Positives = 158/372 (42%), Gaps = 38/372 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSE-GTTVVDNLLNSEDVHYMLGALRTL 63
E+I++ +SG V + G+K+ IL + L++ G T + N+ DV+ M LR L
Sbjct: 2 EKIIIVHGGNRLSGVVHIEGAKNAVLPILAASILAQDGITHLANVPVLSVDTMKNVLRFL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L V+ D+ AKR V + + E E V + + M L A + G+A L
Sbjct: 62 NLKVDVDE-AKREVTIDATKQVSSEAPFEYVSKMRASI-VVMGPELLARL----GHARVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + RPI + GL+ LGA ++ G + R L G + L S
Sbjct: 116 PGGCAIGTRPIDLHLKGLEALGARIEQHDGYIEAFADR-----LQGAHIYLDFFP-SVGA 168

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+LMAA LA G +ID + P + ++ + G + + + + G +
Sbjct: 169 TQNILMAACLAGTT---VIDNVAREPEIVDLANILNKMGANVRGAGT-ETIRVDGVDQM 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
+++ V+ D A F+ GAA+T G V ++ ++ + L+ MG +VT
Sbjct: 225 HGAEHVSVDQ-DRIEAGTFMVGAAALTHGNVLIQDG---IVEHNKPLISKLQEMGVQVTEEA 280

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA---- 354
+ V GP R L+ DV P D+ + ++ L A+G + + +
Sbjct: 281 AGIRVIGPDR-----LQPTDVKTLPYPGFPTDMQPMQMTILQLAAEGTSTMTETVFENR 333

Query: 355 SWRVKETERMVA 366
++E RM A
Sbjct: 334 FMHLEELRRMNA 345

>ref|YP_001197964.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis
05ZYH33]
gb|ABP89564.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis
05ZYH33]
Length = 151

Score = 53.9 bits (128), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 35/129 (27%), Positives = 64/129 (49%), Gaps = 5/129 (3%)

Query: 320 LKAIDVNMNKMPPDVAMTLAVVALFAD---GPTAIRDVASWRVKETERMVAIRTELTKLGA 376
LK ++ +P + L ++ L A+ G T I D +V ET+R+ + L +GA
Sbjct: 22 LKGTEIAGELIPRLIDELPIITLIANQAHGTIIICDAEELKVTETDRIQVADALNSMGA 81

Query: 377 SVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA--CAEVPVTIRDPGCTRKTTPD 434
++E D II P L+ I+T+ DHR+ M ++AA + V + ++P
Sbjct: 82 TIEPTEDGMIHGPITALHGAEINTFGDHRIGMMTAIAALLAKDGEVVLRAEAINTSYPA 141

Query: 435 YFDVLSTFV 443
+F+ L++ +
Sbjct: 142 FFEHLNSLM 150

>ref|YP_003555177.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
violacea DSS12]
dbj|BAJ00399.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
violacea DSS12]
Length = 422

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 100/404 (24%), Positives = 165/404 (40%), Gaps = 56/404 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ +Q K ++G V + G+K+ + IL+ L+E V+ N+ + DV+ LR LG
Sbjct: 2 DKLKIQAASKALAGEVVISGAKNAALPILMAGVLAETDFVISNVPDLRDVNTSCCELLRCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V ++ + F P + K L + R TA V+ GG A
Sbjct: 62 AEVSRNTNSEVRISTTSLDNFCAPYDLVKTMRASILILGPLLARFGTADVSLPGGCA--- 118

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+Q+GA ++ G ++ G L G + + +S
Sbjct: 119 -----IGARPVNLHLHGLEGQMGAKIEVKEGY----IKARVDGRLKGAHIFMD-MVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LLMAA LA G+ II+ P V + G K E + + D I+G +
Sbjct: 168 TENLLMAASLADGET---IIENAAREPEVVDLANCLIAMGAKIEGAGT-DSIRIQGVESL 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEV---LEMMGAKV 298
+ + V D FL AA+T G + ++ D K E LE GAK+
Sbjct: 224 QGC-HYRVMPDRIETGSFLIAAAVTRGKI-----RCVKADPKTLEAVLAKLEDAGAKI 275

Query: 299 T----WTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI 350
T W E + P KA+++ P D+ ++ A+G + I
Sbjct: 276 TTGNDWIELDMQGRP-----KAVNIKTVPYPGFPTDMQAQFCLLNALAEGTSTI 325

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ + E M EL ++GA++E + CII E+LN
Sbjct: 326 TET----IFENRFMHV--PELIRMGANMELEGNTCIIQGIERLN 363

>ref|YP_902699.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pelobacter
propionicus DSM 2379]
gb|ABL00642.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pelobacter
propionicus DSM 2379]
Length = 417

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 88/384 (22%), Positives = 157/384 (40%), Gaps = 51/384 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++Q ++SG V + GSK+ + IL+ L+ G + N+ D++ + L +LG
Sbjct: 2 DKLIIQGGTKLSGEVLVSGSKNAALPILISTVLAPGKNEISNVFPLRDINTTIKVLES LG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE + + G D +++++ A+V G G
Sbjct: 62 ARVEGNHVVVKVDTAGINSHEATYD-----LVKTMRASVLVLGPLLARFGK 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RPI + GL+ LGA++ G R L G ++ S
Sbjct: 108 ARVSLPGGCAIGARPINLHLKGLQALGAEIILEHGYVAAKAR-----QLKGSRINFVST 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
L+MAA A G+ +++ P + R++ R G + E + + D I+G

Sbjct: 163 VGGT-EHLMMAAATAKGE---SLENAAREPEIIDLARILNRMGARIEGAGT-DTIRIQG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ +P + V D A F+ AAITGG + ++G L V F L+ G ++

Sbjct: 218 VAEL-APVSYEVMPDRIEAGTFMIAAAITGGDIRIKGMKLEHLDALV-FK--LQDAGVEI 273

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
+ + V V GP + ++++++ P D+ + ADG + I

Sbjct: 274 SSRDNVVRVKGPP-----RKIRSVNIKTRPYPGFPTDMAQFMALMCKADGASVI---- 322

Query: 355 SWRVKETERMVAIRTELTKLGASV 378
S + E M EL + GA +

Sbjct: 323 SENIFENRFMHV--AELLRFGADI 344

>ref|YP_003590968.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus tusciae
DSM 2912]
gb|ADG07824.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus tusciae
DSM 2912]
Length = 420

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 98/404 (24%), Positives = 169/404 (41%), Gaps = 43/404 (10%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRIILLAAALS-EGTTVVDNLLNSEDVHYMLGALRTLGL 65
I++Q + + GTV++ G+K+ S IL + L+ EG VV+++ DV M ++ LG+

Sbjct: 4 ILVQGGRLPKGTVRVSGAKNASLPILAASLLAVEGRCVVEDVPILRDVDCMCDMIQALGV 63

Query: 66 SVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V+ + VV + +A E+ + + + M L A G+A L G

Sbjct: 64 DVQREPGG---VVRNAAEEVSHTAPYELVRRMRASFVVMGPELLARF---GHARVALPG 116

Query: 126 VPRMRERPIGDLVVGLKQLGADVDC---FLGTDPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + G + LGADV ++ P G L G +V L S

Sbjct: 117 GCAIGARPVDQHIKGFALGADVTVVEHGYVEARAPR-----GRLRGNRVYLDIP-SVGA 169

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA LA G + II+ P + + + G + + + D ++G +

Sbjct: 170 TQNMMAAALADG---LTIENAAKEPEIVDLANFINKMGGVRGAGT-DVIRVEGVDR 225

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ ++ + + ++ LAGA ITGG + VEG +T L+ L+ G V

Sbjct: 226 RGVEHTVIPDRIEAGTFLLAGA-ITGGEIYVEGAISTHLK---PLLAKLKETGVHVEDDV 281

Query: 303 TSVTVTGPPREPFRKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDVASWRVKE 360
+ V G P + +A+D+ + P M ++AL P S V E

Sbjct: 282 NGIFVAGGPGQ-----RALDIKTHYYPGFPTDMAQIMALLTIIP-----GSSMVTE 328

Query: 361 T--ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYD 402
T E EL ++GA + +I KL +++ D

Sbjct: 329 TVFENRFMHVLAELQRMGADIRVEGRTAVIEGVPKLTGARVNSTD 372

>ref|ZP_03936449.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
striatum ATCC 6940]
gb|EEI77099.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
striatum ATCC 6940]
Length = 422

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 110/437 (25%), Positives = 172/437 (39%), Gaps = 53/437 (12%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV + G+K+ +++ A L+EGTT + N DV M L LG VE D +

Sbjct: 13 LEGTVVVDGAKNSVLKMAAALLAEGTTTLTNCPIQILDVPLMCKVLEGLGCEVEIDGSVV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV-----TAAGGNATYVLDGVPR 128
V K P +A + A+R A+V TA G+A L G

Sbjct: 73 SITV-----PKKQSNADFD-----AVRQFRASVCVLGPLTARCGHAKVALPGGDA 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188

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      + RP+      GL+++GA      G      V      GL G +KL      S      +L
Sbjct: 119 IGSRPLDMHQSGLKMGARTRIEHGA-----VVAEADGLHGASIKLDFP-SVGATENILT 172

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      AA LA G+      ++      P +      +++ G E S      I+G +K P
Sbjct: 173 AAVLADGET---VLHNAAREPEIVDLCTMLKEMGANIEGEGS-STITIRGVEKLH-PTEH 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
      V GD A + A +T G +TV G      L + E L+ GA++ + V
Sbjct: 228 KVIGDRIVAGTWAYAAVMTQGDITVGGIAPRHLHLPL--EKLKSAGAEIEAYDNGFRVC 284

Query: 309 GPPREPFGFRKHLKAIDVNMNKMPPDVAMTLAVVAL----FADGPTAI-RDVASWRVKETER 363
      RK A+D      P      L +A+      ADG T I +V R + +
Sbjct: 285 -----MRKRPVAVDYQTLPPGFPTDLQPMAGLSAIADGTTIITENVFESRFRFVDE 337

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
      M+      +LGA +      + +I E+L+ T + + D A A CA+ T+
Sbjct: 338 ML-----RLGADAQVDGHVVRIGQERLSSTHVWSSDIRAGAGLVLSALCADEVTTVH 390

Query: 424 DPGCTRKTFFPDYFDVLS 440
      D      + +P++ + L+
Sbjct: 391 DVFHIDRGYPNFVENLT 407

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>ref|YP_002774913.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacillus
      brevis NBRC 100599]
dbj|BAH46409.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacillus
      brevis NBRC 100599]
      Length = 438

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Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 92/376 (24%), Positives = 158/376 (42%), Gaps = 47/376 (12%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEG-TTVVDNLLNSEDVHYMLGALRTL 63
      ++I+++ K ++G VK+ G+K+ I+ + L+E T V+ ++ +DV + L+++
Sbjct: 2 DKIIIVRGKALAGNVKVSAGAKNAVLPIIAASILAEETTCVISDVPLDDVRTICDLLKSM 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
      G+S+ D      + +      VE + E V+      MR+ + + A G A
Sbjct: 62 GISLTYDH---EVLTIIDASKLTSVEASYELVR-----KMRASFLVMGPLLARKGQAR 110

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
      L G + RPI + G + +GA ++ G V G L G K+ L + S
Sbjct: 111 VALPGGCAIGTRPIDQHLKGFEAMGAKIEIGQGFIEATVE----GRLKGAKIYLDIA-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G +I+ P + + R G K + + I+G +
Sbjct: 166 GATENINMAAALAEGTT---LIENAAEEPEIVDLANFLNRMGAKIRGAGTGS-IRIEGVE 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      K K + + D A F+ AAITGG V VEG L+ L MG +
Sbjct: 222 KMKGCTHCVIP-DRIEAGTFMVAAAITGGDVFEAGICDHLK---SVTAKLREMGVDIEE 277

Query: 301 TETSVTV--TGPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
      E + V TGP +KA+D+ P D+ + + L ++G + + +
Sbjct: 278 QENGIRVVRTGP-----MKAVDLKTLPYPGFPTDMQSQMMALLLVSEGTSTIVTETV 328

Query: 355 ----SWRVKETERMVA 366
      V+E RM A
Sbjct: 329 FENRFMHVEEFRMNA 344

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>ref|YP_001797038.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polynucleobacter
      necessarius subsp. necessarius STIR1]
sp|B1XSU7.1|MURA_POLNS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ACB43424.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polynucleobacter
      necessarius subsp. necessarius STIR1]
      Length = 424

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Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 103/417 (24%), Positives = 170/417 (40%), Gaps = 54/417 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL L++ V+ N+ + +DV ML L+ +G++++ A
Sbjct: 12 LKGEVVIAGAKNAALPILCACLLTDQPVVLRNVPDLQDVRTMLKLLQEIGVTIDFPSAGD 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R+ +V +A E+ L LG + R +A V+ GG A
Sbjct: 72 RSYMVLNAAVIKSSEATYEMVKTMRASILVLGP--LLARMHSAKVS LPPGCA----- 121

Query: 128 RMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ RP+ + GLK +GA + ++ + P L G + L+ I+
Sbjct: 122 -IGARPVDQHIKGLKAMGATIKIKSGYIQAETKPQSDR---LKGASI-LTDMITVTGTGTE 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAA LA G +++ P V L+ + G K S DR I+G K
Sbjct: 176 NLLMAATLASGTT--VLENAAREPEVGDLAELLVKMGAKISGIGS-DRLVIEGVDKLHG 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQG-DVKFAEVLEMMGAKVTWTET 303
+++ + D A FL TGG +TV+ C +L VK E W +
Sbjct: 232 AEHSVIP-DRIEAGTFLCAVVATGGEITVKHCRPDTLDAVIVKLKEAGLQTEIGPDWIK 290

Query: 304 SVTVTGPFPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
S + G P KA++ ++ P D+ L V A G + I +
Sbjct: 291 S--MQGRP-----KAVNFRITSEYPAPFTDMQAQLMTVNAIAAGSSMITETIF---- 335

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLAACA 416
R + ++ EL +LGA + + I EKL+ AI D R + + +A A
Sbjct: 336 -ENRFMHVQ-ELNRLGADIAIEGNTAIAQGVEKLS-GAIVMATDLRASASLVIAGLA 389

>ref|ZP_05788793.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synechococcus
sp. WH 8109]
gb|EEX05993.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synechococcus
sp. WH 8109]
Length = 432

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 100/409 (24%), Positives = 159/409 (38%), Gaps = 48/409 (11%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++ G+K+ + ++ + LSE T + N+ + D+ M L LG+ V
Sbjct: 23 LKGTLRVSGAKNASALVMTASLLSEETIELTNIPSLTDIDGMSAILEALGVQVNRQSDCI 82

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R G P + + + + G + L G+A L G R+ RP+
Sbjct: 83 RLTAAKLSGSAPPYELVNSLRASFFSIGPLLRL-----GHARVPLPGGCRIGARPV 134

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALLM 188
+ + GLK LGA V+ G V PG K +L+G+ S +LM
Sbjct: 135 VEHIRGLKTLGAVVNVEHGIVTASV-----PGSKRLTGAQIVLDCPSVGATETILM 186

Query: 189 AAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + I+ P V+ L+ G + + + G ++ + N
Sbjct: 187 AAVLADG---VSTIENAAQEPEVQDLANLLNTMGAQVSGA-GGPVITVNGVERLRGCTNY 242

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D A FL AAIT + VE L + + L G + +VT+T
Sbjct: 243 PVIPDRIEAGTFLMAAAITRSPLVVEPIPEHLSAVI---QKLRDCGCSIEIKGRVTIT 299

Query: 309 GPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P E + A+D+ P D+ V A G + I + K E
Sbjct: 300 --PGE-----ITAVDITTQFPFGFTDLQAPFMAVMCTAKGISVISE-----KIYENR 345

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVAIDTYDDHRMAMAFSLA 413
+ EL ++GAS+ II +L+ + T D R A A LA
Sbjct: 346 LQHVAELQRMGASIRLEGSTAIIEGVAQLSAAPV-TGTDLRAAAAMVLA 393

>ref|YP_002943080.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Variovorax paradoxus S110]
sp|C5CQI8.1|MURA_VARPS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACS17814.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Variovorax paradoxus S110]
Length = 429

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 69/280 (24%), Positives = 124/280 (44%), Gaps = 40/280 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ +++ G V + G+K+ + L A L++ + N+ +DV ML +R +G
Sbjct: 2 DKLLIRGGRQLRGEVLISGAKNAALPELCAALLTDQPVTLHNVPRLQDVSTMLKLVNMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
++ E D V G + +A E+ ++++ A+V A G G+
Sbjct: 62 VAAERD---DNGTVRLDAGDLSIPEAPYEL-----VKTMRASVLALGPPLARFGH 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS- 177
A L G + RP+ + GL+ +GA++ G I LP G+ +L G+
Sbjct: 109 AKVSLPGGCAIGSRPVDQHIKQLQAMGAIEIVVEHGY-----MIASLPAGRTRLKGAR 160

Query: 178 -----ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSW 231
++ LMAA LA G+ +++ P + ++ R G + E H S
Sbjct: 161 ILTDMVTVTGTENFLMAAALAEGET---LLENAAQEPEIVDLAEMLRMGARIEGHGTSH 217

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
R I+G +K ++A V D A FL A TGG V
Sbjct: 218 IR--IQGVEKLHGCEHAVV-ADRIEAGTFLCAVAATGGDV 254

>ref|ZP_03228143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus coahuilensis m4-4]
Length = 436

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 95/377 (25%), Positives = 156/377 (41%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
++I+++ ++++GTVK+ G+K+ ++ L SEG +V+ ++ DV+ + LR L
Sbjct: 2 DKIIVRGGQKLNLTGTVKVEGAKNAVLPIAATLLASEGKSVIKDVPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + G+ V+ +E L + +R + A+V G G
Sbjct: 62 NADVSEFEN-----GEITVDATRE---LLVEAPFEYVRKMRASVLVMGSLLGRLG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V G + G L G KV L
Sbjct: 108 KARVALPGGCAIGSRPIDQHLKGFEAMGAKVKVGNF---IEAEVAGKLQAKVYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G I I+D + P + L+ + G + + + I+
Sbjct: 164 -SVGATENIMMAAVLAEG---ITILDNVAKEPEIIDLANLLNKMGANVKGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ +V D A F+ AAIT G V V G L ++ MG +
Sbjct: 219 GVDKLHGVEH-HVIPDRIEAGTFMVAIAITEGNVLVRGAVPEHLS---SLIAKMKEMGVE 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNKMMP---DVAMTLAVVALFADGPTAIRDV 353
+ + V GP K LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 IQEEDGLRVIGP-----KELKAVIDIKTMPHPGFPTDMAQMMSSLLLKADGTSMITET 327

Query: 354 A----SWRVKETERMVA 366
V+E RM A
Sbjct: 328 VFENRFMHVEEFRMNA 344

>ref|YP_003338602.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptosporangium

roseum DSM 43021]
gb|ACZ85859.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptosporangium
roseum DSM 43021]
Length = 438

Score = 53.9 bits (128), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 84/310 (27%), Positives = 137/310 (44%), Gaps = 29/310 (9%)

Query: 5 EEI-VLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
EE+ +++P + G V++ GSK+ ++ ++ A L G + + N + +V LR L
Sbjct: 3 EEVWLIEPSGPLRGDVEVRGSKNGVSKHMAAMLGTGESTIHNAPDVGEVGITAQMLRAL 62

Query: 64 GLSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+ VE R + + G + P A F G I + L + AG +
Sbjct: 63 GIDVE---ITPREIRIAQGPQINPHVPAA-----FTGLNRIPILMLGPLLHLAGEAFVPL 114

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCF-LGTDPPVRVNGIG-GLPGGKVKLSGSISS 180
+ G P R RP+ V L+ +GA+V+ G R+ G LP V + +I
Sbjct: 115 VGGDPIGR-RPVDHFVEALRAMGAEEVSDTGVYAKAKRLRGTRLELPYPSVGATETI-- 171

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LM+A LA G ++ + VE+ L ++R G + E S R I+G +
Sbjct: 172 -----LMSAVLAEGKTVLK--GAAMEPEVVELAL-FLQRMGARIELSPD-RRIVIEGVE 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + ++ GD A +LA ITGG V V GC L V L MGA++
Sbjct: 222 RLRG-ASTWLNDRIEAFSYLAAGLITGGEVRVHGCPQDRL---VTAITTLARMGAEMDI 277

Query: 301 TETSVTVTGP 310
T+ V+ + P
Sbjct: 278 TDDYVSASAP 287

>ref|YP_003465659.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
seeligeri serovar 1/2b str. SLCC3954]
emb|CBH28577.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
seeligeri serovar 1/2b str. SLCC3954]
gb|EFS02106.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
seeligeri FSL S4-171]
Length = 430

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 95/402 (23%), Positives = 167/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+V+ N+ N DV + L+ L
Sbjct: 2 EKIIIVRGGKQLNGSVKMEGAKNAVLPIAATLLASKGTSVLKNVPLNSDVFTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V V G+ + E V R + A++ G G
Sbjct: 62 NADV---SfVNDVTVDATGEITSDAPFEYV-----RKMRASIVVMGPELLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFGLTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V G L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFEAMGAIVKIEGYIEATAE-----KLVGAKVYLDFFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 163 -SVGATQNIMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G ++ + +++ + D A F+ AAITGG V +E + LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGNNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPATIRD- 352
+ + + V GP + LKA+DV P D+ + V+ + ++G + + +
Sbjct: 274 IIEEDNGIRVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVQMLSEGTSIMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHVS-----IISGPAKLQ 361

>ref|YP_001939082.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Methylobacterium
infernorum V4]
sp|B3DYW2.1|MURA_MET14 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACD82484.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Methylobacterium
infernorum V4]
Length = 421

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 102/424 (24%), Positives = 169/424 (39%), Gaps = 60/424 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G + + GSK+ + IL L+ V+ + N D+ YML L+ LG
Sbjct: 2 EKFIKGGNPLEGKITISGSKNSALPILAAATLLTPEECVIHRVNPNSDIRYMLEILKFLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V +K R K + + L +R + A++ G G
Sbjct: 62 AQVHYEKGTVRI-----KSKIVHSTAPYDL-----VRKMRASICILGPLIARCGQ 106

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + +RPI + GL++LGAD++ G V +G G L G + L G
Sbjct: 107 ARVSLPGGCVIGDRPIDLHITGLQKLADIEIIGKD---VVAHG-GILRGTSINLKGY 161

Query: 179 SSQYLSA--LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S L ++MAA A G II+ P VE + G K + + I
Sbjct: 162 GSTVLGTDNVMMAACQAEGETT---IEGAACEPEVEDLAHFLSSMGAKISGMT-QQLII 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G ++ + + D A F AA+T G + +E + G V E L+ GA
Sbjct: 218 EGVKELHGCEYTIIT-DRIEAGTFAVAAAMTKGNLLLEHAPVEHM-GSV--LEKLKDCGA 273

Query: 297 KVTWTETSVTV--TGPPREPFGGRKHLKAIDVMNMKMP---DVAMTLAVVALFADGPTAI 350
+ + V +GP L+A ++ P D+ +A A+G + I
Sbjct: 274 SIEIESQGIRVSRSGP-----LRAFEIVTAAYPGFPTDMQAQFCAMATVAEGTSKI 324

Query: 351 -RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMA 409
++ R +EL +LGA +E + +I E+L+ + D R + A
Sbjct: 325 VENIFPNRNFMI-----SELKRLGAMIELSQNQALIHGTERLSGAPV-MASDLRASAA 376

Query: 410 FSLA 413
LA
Sbjct: 377 LVLA 380

>ref|ZP_06697214.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1679]
gb|EFF27453.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1679]
Length = 433

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 89/374 (23%), Positives = 157/374 (41%), Gaps = 49/374 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ ++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEAGAKNAVLPLAASLLAEEGITTLDNVPILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A
Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEVVS-----QMRASIVVMGPLLARNGHAK 112

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVKLS 175
+ G + +RPI + G + LGA + ++ NG L G + L
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAKI-----IQKNGYIEAIADELIGNTIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA A G II+ + P + ++ + G + +

Sbjct: 163 FP-SVGATQNIMMAAVKAKGTT---IIENVAREPEIVDLANILNKMGAHV-YGAGTETMR 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + ++ V+ D A F+ AA+T G V + S ++++E MG

Sbjct: 218 IEGVDHLHAVNHSIVQ-DRIEAGTFMVAAAMTEGNVLI--ADAISEHNRPLISKLIE-MG 273

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIR 351
A++ E + V GP KH+ DV P D+ + + L A+G + +

Sbjct: 274 AEIIKEEGGIRVIGP-----KHILPTDVKTMPHPGFPTDMAQMTAIQLVAEGISVVT 326

Query: 352 D-VASWRVKETERM 364
+ V R + E M

Sbjct: 327 ETVFENRFQHLEEM 340

>ref|ZP_08142636.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas sp. TJI-51]
gb|EGB96073.1| bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate
1-carboxyvinyltransferase [Pseudomonas sp. TJI-51]
Length = 409

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 32/94 (34%), Positives = 52/94 (55%), Gaps = 6/94 (6%)

Query: 10 QPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP ++G +++PG KS+S+R ++L +L+EGTT V+ L ED L A R +G+ +E

Sbjct: 321 QPGGRLNGRIRVPGDKSISHSIMLSLAEGTTEVEGFLEGEDALATLQAFRDMGVVIEG 380

Query: 70 DKAARKRAVV-VGCGGKFPVEDAKEEVQLFLGNAG 102
+ + VG G P L++GN+G

Sbjct: 381 PNHGRVTIHGVLHGLKPPPGP-----LYVGNNG 409

>ref|ZP_05359516.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
radioresistens SK82]
ref|ZP_06072183.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
radioresistens SH164]
gb|EET83775.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
radioresistens SK82]
gb|EEY86397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
radioresistens SH164]
Length = 419

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 103/411 (25%), Positives = 170/411 (41%), Gaps = 46/411 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L+E + N+ N +DV+ ++ + LG+S+

Sbjct: 11 KLQGEVRISGAKNAALPLLAATILAETPITLTNPVNLKDVNTLVELIAGLGISISYSGDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+A +F P E K L + R +A V+ GG A + R

Sbjct: 71 VKADTSTLNNQFAPYELVKTMRASILVLGPLVARYGSAQVSLPGGCA-----IGSR 121

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + L+ LGA ++ G V G L G + ++ +LMAA L

Sbjct: 122 PVDQHLKALEALGAHIEVENGY----VNAKVDGRLKGADITFD-MVTVGGENILMAAVL 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G + + P + ++ + G K E D+ D I G + + + A V

Sbjct: 177 AEG---VTTLRNAACEPEITDLANMLIKMGAKIEGVD-TLTVITGVESLQGCYAVVAD 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGPP 311
+ SY LA AAITGG V T L+ + KF E MGA+VT + + +

Sbjct: 233 RIETGSY-LAAAAITGGKVKTTHTDPTLLEAVLDKFEE----MGAEVTRGDDWIELDMQD 287

Query: 312 REPFGKHLKAIDVNMNKMPPDV-----AMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ PD A +AV A+ T + R

Sbjct: 288 KRP-----KAVSFRTLPHPDFPTDMAQLMAVNAIGHGFATISETIFENRFMHV----- 336

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDHRMAMAFSLAACA 416

EL+++GA+++ EG D ++T EKL+ + D R + + LAA A
Sbjct: 337 --PELSRMGANIQVEGND-AVVTGVEKLSAAPV-MATDLRASFSLVLAALA 383

>ref|ZP_06347761.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
M62/1]
gb|EFE10955.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
M62/1]
emb|CBK76743.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium cf.
saccharolyticum K10]
Length = 430

Score = 53.5 bits (127), Expect = 6e-05, Method: Compositional matrix adjust.
Identities = 96/438 (21%), Positives = 186/438 (42%), Gaps = 36/438 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + IL + +++ +++NL + D++ +L A+ +G
Sbjct: 2 EQYIMKGGNPLVGEVTISGAKNAALGILAAASIMTDEEVIIENLPDVRDINVILLEAIEEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D+ + + V E ++ A A+ +A L
Sbjct: 62 ARV--DRIDRHTARINARHIKEVSVDEYIRKIR-----ASYFIGALLGKYKSAEVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA+V+ G V + I L G + L +S
Sbjct: 115 GGCNIGSRPIDQHKGFRALGAEVEVKRGA---VVAHAI-DLVGSHIYLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ II+ P+V + G + + + D I+G +K
Sbjct: 169 NVMMATLAEGET---IENAAKEPHVVDVANFLNSMGANVKGAGT-DIIRIRGVRKLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ AAIT G + V+ L+ A+++E MG +VT + +
Sbjct: 225 TEYSIIP-DQIEAGTFMCAAAITRGDIMVQNVIPKHLEAIT--AKLIE-MGCEVTEFDEA 280

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMP-DVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
V V G PR+ KH+ + P D+ + V A+G + + + + R K +
Sbjct: 281 VRVVGKPRQ---KHMDIKTLPPPGFPTDMQPQITVTLALAEGTSVVTESIFENRFKYVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
EL+++G +++ + II + ++ D R A +A A T+
Sbjct: 337 -----ELSRMGNIKVEGNVAIIDGVKGFTGATVNA-PDLRAGAALVIAGLAAEGYTV 388

Query: 423 RDP-GCTRKTFFPDYFDVL 439
D G ++ + ++ + L
Sbjct: 389 VDEIGYIQRGYENFEEKL 406

>ref|ZP_08080242.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Lactobacillus
ruminis ATCC 25644]
gb|EFZ35222.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Lactobacillus
ruminis ATCC 25644]
Length = 434

Score = 53.5 bits (127), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 94/397 (23%), Positives = 164/397 (41%), Gaps = 51/397 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I++ + GTV++ G+K+ IL + L SEG T + N+ DV+ M +R L
Sbjct: 2 EKIIIVHGGHRLGTVIEGAKNAVLPLAASILASEGRTFLSNVPILSDVYTMSNVIRFL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V D++ K +V+ G E + V MR+ + + A G+A
Sbjct: 62 NVQVGLDESTK-TMVLDATGNLSYEAPFKYVS-----KMRASIVVLGPILLARLGHAK 112

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLS 175
+ G + RPI + GL+ +G +++ G TDC L G + L
Sbjct: 113 VAMPGGCAIGSRPIDLHLKGLEAMGVEIERHDGYIEARTDC-----LKGANIYLD 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++MAA LA G II+ + P + ++ + G K + +

Sbjct: 163 FP-SVGATQNIMMAATLAKGTT---IIENVAREPEIVDLANVLNKMGAHV-YGAGTETIK 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMG 295
+ G ++ ++ D A F+ AA+T G V ++ ++ + LE MG

Sbjct: 218 VVGVDHLHGTEHTIIQ-DRIEAGTFMVAAALTKGNVLIKDA---IVEHNKPLISKLEEMG 273

Query: 296 AKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPATIR 351
+V E V + GP + LK + P D+ ++++ L ADG + +

Sbjct: 274 VEVIDEEKGVRIIGPEK-----LKPTTIKTLPHPGFPTDMQPQMSILQLSADGTSILT 326

Query: 352 D-VASWRVKETERMVAIRTELTKLGASV-EEGP-DYC 385
+ V R E + + + G SV GP D+C

Sbjct: 327 ETVFENRFMHLEELRRMNADFKEGNSVILYGPTDFC 363

>ref|ZP_06008579.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter fetus
subsp. venerealis str. Azul-94]
Length = 261

Score = 53.5 bits (127), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 69/257 (26%), Positives = 109/257 (42%), Gaps = 30/257 (11%)

Query: 20 KLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVV 79
K+ KS+S+R + + LS+ + + N L +ED L + LG VE

Sbjct: 16 KVSSDKSISHRCAIFSLSDKVSISNYLEAEDTMNSLKIIEKLGAKVEFK----- 66

Query: 80 GCGGKFPVEDAKEEVQ---LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
G + + K+ V L GN+G AMR + AG + +VL G + ERP+

Sbjct: 67 --NGVYLITPPKKIVSPNAILECGNSGTAMRIFMGLL--AGCDGFFVLSGDKYLNERPMK 122

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-SSQYLSALLMAAPLAL 194
+ L Q+GA +D G DC I G + S+ S+Q +AL++A +

Sbjct: 123 RVASPLMQIGAKID---GRDCANKAPLAIRGGELNYFAYNSSVASAQVKTALILAGLCSA 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ-KYKSPKNAYVEGD 253
G + + +S + E L G+ A+ S S +K + Y P V D

Sbjct: 180 G---CKFKEPELSRDHSERML-----LGMGAQISQSGLEIEVKPLKGAYLKLILDVPND 231

Query: 254 ASSASYFLAGAAITGGT 270
SS ++ AAI G+

Sbjct: 232 PSSCFFYAVAAAIIPGS 248

>ref|YP_381189.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synechococcus
sp. CC9605]
sp|Q3AL98.1|MURA_SYNSC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABB34634.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synechococcus
sp. CC9605]
Length = 433

Score = 53.5 bits (127), Expect = 7e-05, Method: Compositional matrix adjust.
Identities = 98/409 (23%), Positives = 162/409 (39%), Gaps = 48/409 (11%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+++ G+K+ + + + LSE T + N+ + D+ M L +LG+ V+

Sbjct: 24 LKGTLRVSGAKNSALVMTASLLSEETIELTNIPSLTDIDGMSAILES LGVQVDRQSDCI 83

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R G P + ++ + G + L G+A L G R+ RP+

Sbjct: 84 RLTAELSGSAPPYELVNSLRASFFSIGPLLGR-----GHAQVPLPGGCRIGARPV 135

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSALLM 188
+ + GLK LGA V+ G V PG K +L+G+ S +LM

Sbjct: 136 VEHIRGLKALGAVNVVEHGIIVTASV-----PGSKRLTGAQIVLDCPSVGATETILM 187

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + I+ P V+ L+ G + + ++G ++ + N

Sbjct: 188 AAVLADG---VSTIENAAQEPEVQDLANLLNSMGGQVSGA-GGPLITVQGVVERLRGCSNY 243

Query: 249 YVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D A FL AAIT + VE L ++ L G + +VT+T
Sbjct: 244 PVIPDRIEAGTFLMAAAITRSPLVVEPVIPEHLSAVIQK---LRDCGCSIQIKGRAVTIT 300

Query: 309 GPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
P E + A+D+ P D+ + A G + I + K E
Sbjct: 301 --PGE-----ITAVDITTQPPGFPPTDLQAPFMAIMCTAKGTSVISE-----KIYENR 346

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ EL ++GAS+ I+ +L+ + T D R A A LA
Sbjct: 347 LQHVAELQRMGASIRLEGSTAIVEGVAQLSAAPV-TGTDLRAAAAMVLA 394

>ref|ZP_05215869.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
avium subsp. avium ATCC 25291]
Length = 417

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 100/373 (26%), Positives = 147/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTTGGNRLSGEVAVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLGL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVARIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + + L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--TCNIEHGCVVQAQAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVVAEG---VTIHNAAAREPDVMDLCTMLNQMQAQVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G ++V G LQ L GA
Sbjct: 218 GVPRLY-PTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAHLQ---VVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPEPFGRKHLKAIDVNMNKMMPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S VT R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDSSFRVTQYERP-----KAVNVATLPFPGFPTDLQPMALIASIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+
Sbjct: 327 VFEARFRFVEEMI 339

>ref|ZP_05085293.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudovibrio sp.
JE062]
gb|EEA94293.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudovibrio sp.
JE062]
Length = 429

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 75/308 (24%), Positives = 131/308 (42%), Gaps = 37/308 (12%)

Query: 13 KEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD-K 71
+++G + + G+K+ + +++ + L E T ++N+ DV + L G+ D K
Sbjct: 10 NQLNGVIPISGAKNAALPLMIASLLCEDTLTLENVPRLRDVALLTQLLSNHGVDYSVDGK 69

Query: 72 AAKRAVVVG-----CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
A + + G P E + F + R +A V+ GG A
Sbjct: 70 RAGQDTMTGQTIHLNASNIVDTTAPYELVSKMRASFWVIGPLLARMHSARVSLPGGCA-- 127

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ RP+ + GLK LGAD++ D V+ GGL GG+V +S
Sbjct: 128 -----IGTRPVDFIDGLKALGADIEM---DRGYVQAEAKGGLKGRVVFV-KVSVG 175

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA LA G+ +I+ P V + G K E + + D +I+G
Sbjct: 176 ATHTVMMAATLAKGE---SVIENAAQPEVTDLANCLIGMGAKIEGAGT-DTIHIQGVDS 231

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV--KFAEVLEMMGAKVT 299
+ ++ + +Y +A A+TGG VT+EG +GD+ +VL G ++T
Sbjct: 232 LGAHRHPVIPDRIETGTYAMA-VAMTGGEVTLGA-----RGDLLESALDVLRTGTGTEIT 285

Query: 300 WTETSVTV 307
T + V
Sbjct: 286 ETNMG LKV 293

>ref|ZP_05077320.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacterales
bacterium Y4I]
gb|EDZ45299.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacterales
bacterium Y4I]
Length = 422

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 98/409 (23%), Positives = 170/409 (41%), Gaps = 42/409 (10%)

Query: 15 ISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + + G+K+ ++ LSE + N D+ M L++LG V + + +
Sbjct: 12 LNGQIPIAGAKNACLTLPATLLSEEPLTLTNAPRLSDIKMTLLQLSLGAEVSSLQDQG 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ A E+ + + + + A + G A L G + RP+
Sbjct: 72 --VLALSSHDLTSHVADYEIVRKMRASNLVLGPMLARL----GQAVVSLPGGCAIGARPM 125

Query: 135 GDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ GL+ LGA++ D +L P GGL G V+LS + S ++MAA
Sbjct: 126 DLHIHGLEALGAEIELKDGYLHAKAP-----GGLKGAVVELSFA-SVGATENIMMAAT 177

Query: 192 LALGDVEIEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G +I P + + + G + E D I+G + + V
Sbjct: 178 LAKGTT---VIKNAAREPEIVDLADCLRKMGAEIE-GDGSNITIQGVDRHLGHATHQVVT 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
+Y LA AI GG V + G + L+ F + LE G ++T E S+TV+
Sbjct: 234 DRIELGTYMLA-PAICGGEVELLGGRRSLLE---SFCDKLEAAGIEITEHENS LTVS--- 286

Query: 312 REPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GR ++A+DV P D+ + + A+G + + + ++ E M A
Sbjct: 287 -RKNGR--VRAVDVVTEPFGFPTDLQAQMMALMCTAEGTSVLEE----KIFENRFMHA- 338

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACA 416
EL ++GA +E + +T EKL + D R +++ LA A
Sbjct: 339 -PELVRMGAQIEVHGGHATVTGVEKLGAPV-MATDLRASVSLILAGMA 385

>ref|ZP_04153908.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
pseudomycoides DSM 12442]
ref|ZP_04159645.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
mycoides Rock3-17]
gb|EEM08588.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
mycoides Rock3-17]
gb|EEM14456.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
pseudomycoides DSM 12442]
Length = 434

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 150/377 (39%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKLIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVYTVINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFE---NNQVTIDASKELNIEAPFEYV-----RKMRASVQVMGP LLARNG 107

Query: 118 NATYVLGDVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V +G V+ G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFEAMGAKVK--VGNGFVEAYVD--GQLQGAKIYLDLP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G +++ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAAATLAKGTT---VLENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGAHHSIIP-DRIEAGTFMVAAAITGGDILIEHAVPEHLR---SITAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
V V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 VIEENEGVRVIGPSK-----LKAVDIKTMHPGFPPTMQSQMALLLHADGTSMTET 327

Query: 354 A---SWRVKETERMVA 366
V+E RM A
Sbjct: 328 VFENRFMHVEEFRMNA 344

>ref|YP_002132763.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
sp. K]
sp|B4UAY6.1|MURA_ANASK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACG71634.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
sp. K]
Length = 422

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 96/386 (24%), Positives = 163/386 (42%), Gaps = 48/386 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + G+V + G+K+ + ++ A L+EG V N+ + DV + L +G
Sbjct: 2 DKIVIEGGVPLRGSDVSGAKNAALPVIAAALLAEGEHEVRNVPLDADVRLGKLLGHMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + +R V + E E V+ + + + L A + G A L
Sbjct: 62 CEVARGEEDRRTVRLRVPAVAPEAPYELVKTMRASV-LVLGPLLARL---GRARVSLP 116

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS-GSISQYL 183
G + RPI + L LGA++ G VN +P G+++ + + +Q +
Sbjct: 117 GGCAIGARPIDQHLKALTALGAEIRIEHGY-----VNAT--VPRGRLRGTVFTFDAQTV 168

Query: 184 SA---LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ ++MAA LA G+ ++ P V+ + G E + + D +I+G
Sbjct: 169 TGTENVMMAAALAEGET---VLRNCAREPEVKDLGDALVAMGALVEGAGT-DEIWIEGVP 224

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ +A + D A FL A+ G VTV GC + E L +GA+VT
Sbjct: 225 SLRPLSHAVIP-DRIEAGTFLVAGALPGNDVTVRGCVAAHQEA---LVEKLRAVGAEVTK 280

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASW 356
E + V G R + +DV P D+ L V+ ADG +
Sbjct: 281 VEGGLRVVGDGRP-----RPVDVRTAPHPGFPPTMQAQLMVLLCLADG-----TS 325

Query: 357 RVKET---ERMVAIRTELTKLGASVE 379
R+ ET R + ++ EL +LGA VE
Sbjct: 326 RITETVFENRFMHVQ-ELIRLGAHVE 350

>ref|ZP_05826488.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter sp.
RUH2624]
gb|EEW98154.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter sp.
RUH2624]
Length = 418

Score = 53.1 bits (126), Expect = 8e-05, Method: Compositional matrix adjust.

Identities = 104/413 (25%), Positives = 175/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPITLTNPVNLKDVNTLVKLIGGLGVTISYENDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSPLGGCAI 118

Query: 130 RERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVNGY----VHATVDGRLKGGEVVD-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G I I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AALADG---ITTIRNAAREPEITDLAQMLIKMAKIEGIDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V + L+ + KF E MGA+VT + + +
Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPSLLESVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E
Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPTDMAQIMAVNAIG---RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T EKL + D + +FSL A V
Sbjct: 335 HVPELSRMGANIQVEGHD-AVVTGVEKLQAAPVMATD---LRASFSLVLAALV 383

>ref|YP_003800152.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Olsenella uli
DSM 7084]
gb|ADK67272.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Olsenella uli
DSM 7084]
Length = 426

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 94/378 (24%), Positives = 148/378 (39%), Gaps = 38/378 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
I G V + G+K+ + +++ L+ GTT + N+ N DVH M L+ LG +E +
Sbjct: 12 IGGEVTVGAKNSALKLMAATILAPGTTTLANVPNISDVHVMGKVLKYLGAHIEVENEHT 71

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V K+ E L A ++ + G A + G + R I
Sbjct: 72 LKVDTSVVDKW-----ETPYHLVAQMRASAVLGPLLRGFGKAIVAMPGGCNIGARKI 124

Query: 135 GDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
++GL+ LG + D + GL GG V L + S L+MAA A
Sbjct: 125 DMHILGLEALGVRFEV---DHGNIHATTTPNGLTGGMVTLDFASVGATENLMMAAVRAR 179

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + ID P + L+ G K + S I+G + + + V GD
Sbjct: 180 G---VTTIDNAAREPEIVDLANLLNEMGAKVRGAGS-PVIEIEGVDELRLPLETHAVVGDR 235

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPEP 314
A F+A A I G VTV+G L +K E+MG V VTV
Sbjct: 236 IEAGTFIAMAGICGPVTVKGFEPALHGLVLK---KYELMGLDVERGAHKVTV----- 286

Query: 315 FGRKHLKAIDVNMNKMPPDV-----AMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
+ +++ D+ P A T+ ++AL D + + V E M A +
Sbjct: 287 -RSRPIRSTDIQTLPPFGFPTDMAQTMCLLALGDDSC-----IVTENVFENRFMFMA--S 338

Query: 370 ELTKLGASVEEGPDYCI 387
EL ++GA + + I+
Sbjct: 339 ELQRMGAIEIRIEGHHAIV 356

>ref|ZP_04165189.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
mycoides Rock1-4]

gb|EEM03175.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus mycoides Rock1-4]
Length = 434

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 150/377 (39%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFEE---NNQVTIDASKELNIEAPFEYV-----RKMRAVSVQVMGPPLLARNG 107

Query: 118 NATYVLGDVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V +G V+ G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFAMGAKVK--VGNFVEAYVD--GQLQGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G +++ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAATLAKGTT---VLENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGAHHSIIP-DRIEAGTFMVAIAITGGDILINAVPEHLR---SITAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREFPGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
V V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 VIEENEGVRVIGPSK-----LKAVDIKTMHPGFPPTDMQSQMALLLHADGTSMITET 327

Query: 354 A----SWRVKETERMVA 366
V+E RM A
Sbjct: 328 VFENRFMHVEEFRRMNA 344

>ref|XP_002371877.1| AROM polypeptide/ shikimate-quininate 5-dehydrogenase [Toxoplasma gondii ME49]
gb|EEB04737.1| AROM polypeptide/ shikimate-quininate 5-dehydrogenase [Toxoplasma gondii ME49]
gb|EEE27216.1| AROM polypeptide/ shikimate-quininate 5-dehydrogenase, putative [Toxoplasma gondii VEG]
Length = 3332

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 26/50 (52%), Positives = 35/50 (70%)

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVT 299
VE DA++ASYF+A AA+ GG V + +TSLQGD+ FAE+L G V+
Sbjct: 1236 VEADATAASYFMMAAAVAGGRVHMNVDRSTSLQGDIAFAEMLPHFGCSVS 1285

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 29/46 (63%)

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYF 436
++L + A+++ DHR+AM+F++ V IRD C KTF D++
Sbjct: 1612 QQLELVAVESESDHRVAMSFALLGLVRTDVGIRDWQCVDKTFADFW 1657

>gb|AAQ83833.1| AROM polypeptide [Toxoplasma gondii]
Length = 3332

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 26/50 (52%), Positives = 35/50 (70%)

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVT 299
VE DA++ASYF+A AA+ GG V + +TSLQGD+ FAE+L G V+
Sbjct: 1236 VEADATAASYFMMAAAVAGGRVHMNVDRSTSLQGDIAFAEMLPHFGCSVS 1285

Score = 42.0 bits (97), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 29/46 (63%)

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYF 436
++L + A+++ DHR+AM+F++ V IRD C KTF D++
Sbjct: 1612 QQLKLVAVESEDHRVAMSFALGLVVRTDVGIRDWQCVDKTFADFW 1657

>gb|EEE19204.1| AROM polypeptide/ shikimate-quinase 5-dehydrogenase, putative
[Toxoplasma gondii GT1]
Length = 3332

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 26/50 (52%), Positives = 35/50 (70%)

Query: 250 VEGDASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKAFAEVLEMMGAKVT 299
VE DA++ASYF+A AA+ GG V + +TSLQGD+ FAE+L G V+
Sbjct: 1236 VEADATAASYFMAMAAVAGGRVHMNVDRSTSLQGDIAFAEMLPHFGCSVS 1285

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 29/46 (63%)

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFFPDYF 436
++L + A+++ DHR+AM+F++ V IRD C KTF D++
Sbjct: 1612 QQLKLVAVESEDHRVAMSFALGLVVRTDVGIRDWQCVDKTFADFW 1657

>ref|YP_002490817.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-1]
sp|B8JAU0.1|MURA_ANAD2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACL63751.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
dehalogenans 2CP-1]
Length = 422

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 96/386 (24%), Positives = 163/386 (42%), Gaps = 48/386 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
++IV++ + G+V + G+K+ + ++ A L+EG V N+ + DV + L +G
Sbjct: 2 DKIVIEGGVPLRGSDVSGAKNAALPVIAAALLAEGEHEVRNVPDLADVRLGKLLGHMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + +R V + E E V+ + + + L A + G A L
Sbjct: 62 CEVARGEEDRRTVRLRVPAVAPEAPYELVKTMRASV-LVLGPLLARL----GRARVSLP 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLS-GSISQYL 183
G + RPI + L LGA++ G VN +P G+++ + + +Q +
Sbjct: 117 GGCAIGARPIDQHLKALTALGAEIRLEHY-----VN--ASVPRGRLRGTVFTFDAQTV 168

Query: 184 SA---LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+ ++MAA LA G+ ++ P V+ + G E + + D +I+G
Sbjct: 169 TGTENVMAAALADGET---VLRNCAREPEVKDLGDALVAMGALVEGAGT-DEIWIIEGVP 224

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLSQGDVKAFAEVLEMMGAKVTW 300
+ +A + D A FL A+ G VTV GC + E L +GA+VT
Sbjct: 225 SLRPLSHAVIP-DRIEAGTFLVAGALPGNDVTVRGCVAAHQEA---LVEKLRAVGAEVTK 280

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPATAIRDVASW 356
E + V G R + +DV P D+ L V+ ADG +
Sbjct: 281 VEGGLRVVGDGRP-----RPVDVRTAPHPGFPTDMAQLMVLCLADG-----TS 325

Query: 357 RVKET---ERMVAIRTELTKLGASVE 379
R+ ET R + ++ EL +LGA VE
Sbjct: 326 RITETVFENRFMHVQ-ELIRLGAHVE 350

>ref|YP_547656.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polaromonas sp.
JS666]
sp|Q12FD4.1|MURA_POLSJ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABE42758.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polaromonas sp.
JS666]
Length = 424

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 93/407 (22%), Positives = 161/407 (39%), Gaps = 58/407 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ + ++GTV + G+K+ + L A L+ T ++N+ +DV ML +R +G
Sbjct: 2 DKLLIKGGRSLAGTVDISGAKNAALPELCAALLTADTVTLENVPRQLQDVATMLKLIRNMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ E A V + G E E V +++ A+V A G G
Sbjct: 62 VEAERGTHAPGTVTLHAGALSSPEAPYELV-----KTMRASVLALGPLLARFGE 110

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-S 177
AT L G + RP+ + GL+ +GA++ G I LP G+ +L G S
Sbjct: 111 ATVSLPGGCAIGSRPVDQHIKGLQAMGAEIVVEHGYM-----IAKLPAQKQRLKGV 162

Query: 178 ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
I++ ++ LMAA LA G+ I++ P + ++ + G K E
Sbjct: 163 ITTDMVTVTGTENFLMAASLAEGET---ILENAAQEPEIGDLADMLIKMGAKIE-GHGTR 218

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLE 292
R I+G ++ + V D FL A GG V + L + + L
Sbjct: 219 RIRIQGVERLHGCTHQVV-ADRIETGTFLCAVAAAGGDVVLRHGRADHLDAVI---DKLR 274

Query: 293 MMGAKVTWTETSVTVTGPPEPFRKHLKAIDVNMNMKMPDV-----AMTLAVVALFADGP 347
GA +T E + + R +KA + P A +A+ A+
Sbjct: 275 EAGATITAGEGFIRIQAQGR-----MKAQSFRTTEYPGFPTDMQAQFMALNAIAQGSS 327

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
T + R MV +LGA ++ ++ EKL+
Sbjct: 328 TVTETIFENRFMHVNEMV-----RLGAKIQIEGKAAMVEGVEKLS 367

>ref|ZP_06066705.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
junii SH205]
gb|EEY94536.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
junii SH205]
Length = 419

Score = 53.1 bits (126), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 104/413 (25%), Positives = 175/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ T + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPPTLTNPVNLKDVNTLVKLIAGLGITMTYEGNT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
RA +F P E K MR+ + + A GNA L G +
Sbjct: 71 VRADASTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V + G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGY----VHASVDGRLKGGVEVVD-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AVLADG---VTTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG + L+ + KF E MGA+VT + + +

Sbjct: 230 VADRIETGSY-LAAAAITGGRIKTTHTDPPALLEAVLDKFEE----MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E

Sbjct: 285 MQGKRP-----KAVSFRTLPHPEFPTDMQAQIMAVNAIG----RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D I+T E L + D + +FSL A V

Sbjct: 335 HVPFLSRMGANIQVEGHD-AIVTGVETLQAAPVMATD---LRASFSLVLAALV 383

>ref|ZP_03753048.1| hypothetical protein ROSEINA2194_01459 [Roseburia inulinivorans DSM 16841]
gb|EEG94616.1| hypothetical protein ROSEINA2194_01459 [Roseburia inulinivorans DSM 16841]
Length = 430

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 101/422 (23%), Positives = 176/422 (41%), Gaps = 35/422 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + G V++ G+K+ + IL A +++ T ++NL N D++ +L A++ +G
Sbjct: 2 EQYVIKGGNPLVGEVEIGGAKNAALAILSAAVMTDETVTIENLPNVRDINVLLNAIQEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V+ A V G F + D + + A L A+ A L
Sbjct: 62 AKVDRIDAH---TVKINGSF-IRDFNVDEYI--RKIRASYYLIGALLGKYKRAEVALP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G LGA+VD G L G + L +S
Sbjct: 115 GGCNIGSRPIDLHLKGFSAAGANVDIKHGLVLASAE-----KLTGTHIYLD-KVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G II+ P+V + G + + + D I G +K
Sbjct: 169 NIMMAASMAEGKT--IIENAAKEPHVVDVANFLNSMGAQIRGAGT-DVIRIVGVEKLHK 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ AA T G VTV+ L+ A++LE +G +V + +
Sbjct: 225 TEYSIIP-DQIEAGTFMFAAAATKGDVTVKNVIPKHLEATT--AKLLE-IGCEVEEFDDA 280

Query: 305 VTVTGPPEPFGKHLKAIDVNMNMP-DVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
V V +P H + + P D+ +AVV ++G + + + + R K +
Sbjct: 281 VRVVAS--KPL--HHTQVTTLPYPGFPPTDMQPMVAVLGISEGTSTVTESIFENRFKYVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
ELT++GA+++ + II EK ++ D R A +A A +T+
Sbjct: 337 -----ELTRMGANIKVESNIAIINGTEKYTGARVNA-PDLRAGAALVIAGLAAEGITV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|YP_850671.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria welshimeri serovar 6b str. SLCC5334]
emb|CAK21892.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria welshimeri serovar 6b str. SLCC5334]
Length = 430

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 94/402 (23%), Positives = 166/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++G+VK+ G+K+ ++ L S+GT+++ N+ DV + L+ L
Sbjct: 2 EKLIIVRGKQLNGSVKMEGAKNAVLPIAATLLASKGTSILKNVPLNSDVFTINEVLKYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V V V G + E V R + A++ G G
Sbjct: 62 NADV---SFVNDEVTVDATGSDAPFEYV-----RKMRASIVVMGPELLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177

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      +A  L G  +  RP+  + G + +GA V  G  L G KV L
Sbjct: 108 SARVALPGGCAIGSRPVDLHLKGFAMGAIVKIENGYIEATAE-----KLVGAKVYLDFF 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      S      ++MAA LA G      +I+ +  P +      + + G +  + + +  I+
Sbjct: 163 -SVGATQNMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G ++  + +++ +  D  A F+  AAITGG V +E      +      LE MG +
Sbjct: 218 GVKELTATEHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQ 273

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD- 352
      +  +  + V GP +      LKA+DV  P  D+  + V+ + ++G + + +
Sbjct: 274 IIEEDNGIRVIGPDK-----LKAVDVKTMHPGPFPTDMQSQMMVIQMLSEGTSIMTET 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
      V  R  E M +  ++  G SV      II+ P KL
Sbjct: 327 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 361

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>ref|NP_961381.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
      avium subsp. paratuberculosis K-10]
ref|YP_880770.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
      avium 104]
sp|Q73X63.1|MURA_MYCPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|AAS04764.1| MurA [Mycobacterium avium subsp. paratuberculosis K-10]
gb|ABK65084.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
      avium 104]
      Length = 417

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Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 100/373 (26%), Positives = 147/373 (39%), Gaps = 46/373 (12%)

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Query: 4  AEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVNDLNLNSEDVHYMLGALRTL 63
      AE  V+      +SG V + G+K+      +++  L+EGT+ + N +  DV  M  LR L
Sbjct: 2  AERFVVTGGNRLSGEVAVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLGL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      G +VE D      R      P  DA      A+R  A+V  G
Sbjct: 62  GATVELDGDVARIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      A  L G  +  RP+      GL+QLGA  C +  C  + +  L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--TCNIEHGCVVAQAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      S      +LMAA +A G  +  I      P V      ++ + G + E + S  I
Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMQGAQVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G +  P  V GD  A+ +  AA+T G ++V G  LQ      L  GA
Sbjct: 218 GVPRLY-PTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAHLQ---VVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVAL----FADGPTAI-RD 352
      VT T+ S  VT  R      KA++V  P  L  +A+      ADG + I  +
Sbjct: 274 VTQTDDSFRTVQYERP-----KAVNVATLPFPGFPTDLQPMALASIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
      V  R  +  E M+
Sbjct: 327 VFEARFRFVEEMI 339

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>ref|YP_001708014.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
      baumannii SDF]
emb|CAP02137.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate
      transferase) (UDP-N-acetylglucosamine enolpyruvyl
      transferase) (EPT) [Acinetobacter baumannii]
      Length = 418

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Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 103/413 (24%), Positives = 175/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPITLTNPVNLKDVNTLVKLIGGLGVTISYENDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLAHYGNKAVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGY----VHATVDGRLKGGEVVFDMVTGVTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AALADG---VTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTTWTETSVTVT 308
V + SY LA AAITGG V + L+ + KF E MGA+VT + + +
Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPSLLEAVLDKFEE----MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E
Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPTDMQAQIMAVNAIG----RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T EKL + D + +FSL A V
Sbjct: 335 HVPESLRMGANIQVEGHD-AVVTGVEKLQAAPVMATD---LRASFSLVLAALV 383

>emb|CBL22590.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ruminococcus
obeum A2-162]
Length = 430

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 99/424 (23%), Positives = 178/424 (41%), Gaps = 39/424 (9%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGL 64
E+ V++ + G V++ G+K+ + IL A +++ T +++NL + D++ +L A+ G
Sbjct: 2 EQYVIKGGNPLVGEVEIGGAKNAALAILSAAIMTDEILILNLPDVRDINVLEAI--AG 59

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + D+ + V + + E ++ A L A+ +A L
Sbjct: 60 IGAQVDRIDRSTVTKINGSTIADISVDYIYIKIR-----ASYLLGALLGKYKHAEPVLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA V G L G + L +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGASVKILHGAIVAETE-----NLHGSHIFLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G II+ P+V + G + + + D IKG +K
Sbjct: 169 NIMMAAAMASGRT---IENAAREPHVVDVANFLNSMGANIKGAGT-DVIRIKGVEKLHR 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
+ + + D A F+ AA TGG VTV+ L+ LE +G +V + +
Sbjct: 225 TEYSIIP-DQIEAGTFMFAAAATGGDVTVKNVIPKHLEATTA---KLEEIGCEVEEFDDA 280

Query: 305 VTVTGPPEPFGKHLKAI---DVNMNMPDVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V V R R H+K + + P +A+TLA A+G + + + + R K
Sbjct: 281 VRVRAGKR--LHRTVKTLPYPGYPTMQPQIAVTLA----LAEGTSIVTESIFENRFKY 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPV 420
+ EL+++GA+++ + II +KL + + D R A +A A +
Sbjct: 335 AD-----ELSRMGANIKVEGNSAIDGVKKLTGARV-SAPDLRAGAALVIAGLAADGI 386

Query: 421 TIRD 424
T+ D
Sbjct: 387 TVVD 390

```
>ref|YP_001101301.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Herminiimonas
arsenicoydans]
sp|A4G9J3.1|MURA_HERAR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAL63180.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate
transferase) (UDP-N-acetylglucosamine enolpyruvyl
transferase) (EPT) [Herminiimonas arsenicoydans]
Length = 416
```

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 104/433 (24%), Positives = 183/433 (42%), Gaps = 58/433 (13%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++Q +SG + + G+K+ + IL L+ + N+ + +DV ML LR +G
Sbjct: 2 DKLLIQGGHRLSGEIAISGAKNAALPILCAGLLTADALQLSNVPHLQDVATMLKLLRQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
L +E D V + G +E E V +++ A++ G G
Sbjct: 62 LQIEQD---GDQVTLNLSGVDKLEAPYEMV-----KTMRASILVLGPLLTRFGE 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + GL+ +GA++ G + L G ++ ++ I
Sbjct: 108 ARVSLPGGCAIGTRPVDQHIKGLQAMGAEITIEAGYIHAKAK-----RLKGARI-VTDMI 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ LLMAA LA G+ I++ P V L+ G + + DR I+G
Sbjct: 162 TVTGTENLLMAAVLADGET---ILENAAREPEVTDLANLLVAMGAQIAGIGT-DRLVIQG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + +A++ A AA+ GG VT+ T +L DV F ++ E GA +
Sbjct: 218 VERLHGASHAVIADRIETATFLCAVA AV-GGDVTLRKARTDTL--DVAFDKLRE-AGAIL 273

Query: 299 TWTETSVTVTGPPREPFGFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA 354
T + + V R KA+ + P D+ + A+G
Sbjct: 274 TAGDDWIRVQMSRP-----KAVSFRTTTEYPGFPTDMQAQFMAMNCIAEG----- 318

Query: 355 SWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
S +V ET R + ++ E+ +LGA++ I+ +KL V A D R + +
Sbjct: 319 SSQVVFETIFENRFMHVQ-EMNRLGAAITIEGHTAIVNGVDKL-VGAPVMATDLRASASLV 376

Query: 412 LAACAEVPVTIRD 424
+AA A T+ D
Sbjct: 377 IAALAAEGETLID 389
```

```
>ref|ZP_07205703.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius ACS-116-V-Col5a]
gb|EFK80565.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius ACS-116-V-Col5a]
Length = 441
```

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 77/312 (24%), Positives = 136/312 (43%), Gaps = 26/312 (8%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+IV++ ++ G V++ G+K+ IL A L SEG T++ N+ DV+ M +R L
Sbjct: 2 EKIVVRGGNKLEGEVEIEGAKNAVLPIAAAILPSEGRTILTNPVPLSDVYTMNNVIRFL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V D+ K +V + GK + + V MR+ + + A G A
Sbjct: 62 NVKVGFDENEK-SVEIDATGKLSYDAPFKYVS-----KMRASIVVLGPLLARLKGAR 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ G + G+ RPI + GL+ LGA ++ G + + G L G + L S
Sbjct: 113 VAMPGGCAIGSRPIDLHLKGLELLGAKIEQHNGY----IDAHTDGRVLVGANIYLDLDFP-SV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
```



```

      ++MAA LA G      II+ +   P +      ++ + G K +      ++ I G +
Sbjct: 168 GATQNMMAATLAKGTT---IIENVAREPEIVDLANVLNKMGAkv-YGAGTEKIKIIGVE 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      ++A ++ D   A F+  +A+T G V ++      + ++      LE MG KV
Sbjct: 224 SLHGTEHAI IQ-DRIEAGTFMVASALTQGNVLIK---EAIAEHNIPILISKLEEMGVK VIE 279

Query: 301 TETSVTVTGPPR 312
      + + GP +
Sbjct: 280 ENEGIQIIGPEK 291

```

>ref|ZP_01964667.1| hypothetical protein RUMOBE_02392 [Ruminococcus obeum ATCC 29174]
gb|EDM86984.1| hypothetical protein RUMOBE_02392 [Ruminococcus obeum ATCC 29174]
Length = 430

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 100/424 (23%), Positives = 178/424 (41%), Gaps = 39/424 (9%)

```

Query: 5   EEIVLQPIKEISGTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64
      E+ V++      + G V++ G+K+ +   IL A +++ T +++NL +   D++ +L A+  +G
Sbjct: 2   EQYVIKGGNPLVGEVEIGGAKNAALAILSAAIMTDEIL IENLPDVRDINVILLEAIAGIG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      VE  +  + V +      +   E ++      A L A+  +A L
Sbjct: 62  AQVE--RIDRSTVKINGSTINDISVDY EYIKIR-----ASYLLGALLGKYKHA EVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G  + RPI  + G + LGA V+   G      L G  + L  +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGASVNILHGAIVAETE-----NLHGSHIFLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ++MAA +A G      II+      P+V      +   G  + + + D   IKG +K
Sbjct: 169 NIMMAASMASGRT---IIENAAREPHVVDVANFLNSMGANIKGAGT-DVIRIKGVEKLHR 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + + + D   A F+  AA TGG VTV+      L+      LE +G +V  + +
Sbjct: 225 TEYSIIP-DQIEAGTFMFAAAATGGDVT VKNVIPKHLEATTA---KLEEIGCEVEEFDDA 280

Query: 305 VTVTGP PREPFGRKHLKAI---DVNMNKM P DVAMTLAVVALFADGP TAIRD-VASWRVKE 360
      V V      R      R H+K +      + P +A+TLA      A+G + + + +   R K
Sbjct: 281 VRVRAGKR--LHRTHVKTLPYPGYPTMQPQIAVTLA---LAEGTSIVTESIFENRFKY 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPV 420
      +      EL+++GA ++  +   II  +KL  + + D R   A +A A  +
Sbjct: 335 AD-----ELSRMGACIKVEGNSAIIIDGVKKLTGARV-SAPDLRAGAALVIAGLAADGI 386

Query: 421 TIRD 424
      T+ D
Sbjct: 387 TVVD 390

```

>ref|YP_003193454.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Desulfotomaculum acetoxidans DSM 771]
gb|ACV64831.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Desulfotomaculum acetoxidans DSM 771]
Length = 417

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 95/381 (24%), Positives = 161/381 (42%), Gaps = 41/381 (10%)

```

Query: 6   EIVLQPIKEISGTVKLP GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      ++++Q  + +SGTVK+ G+K+      I+ A L+  T+V+  + + DV+ +  + +LG
Sbjct: 3   KLIVQGGRRLSGTVKISGAKNVLPPIIAAALLTGETSVLHEVPDLSDVYTICSVIESLGA 62

Query: 66  -SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      +V DK  + V      + P + +      FL      +  + A G A L
Sbjct: 63  KAVRKDKTLQIQVSNIASNEAPYDFVRRMRASFL-----IIGPLLARTGEARIPLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G  + RPI  + GLK LGA +   G      +R      L G ++ L   S

```

Sbjct: 114 GGCAIGARPIDLHLKGLKALGAKITSEHGY----IRATA-AELHGAQIYLDFF-SVGATE 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+MAA LA G +++ P + + G K + + + I+G K

Sbjct: 168 NIMMAATLAKGRT--VLENCAEEPEIVDLANFLNGMGAKIKGAGT-KVIRIEGVNKLGS 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + D A FLA AA+TG +TVE L+ + A++LE G K+T E S

Sbjct: 224 TTHVIIP-DRIEAGTFLAAAVTGSEITVENIIFDHLKPVI--AKLLE-AGVKLTENEGS 279

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ VT P L+A+D+ P D+ + + A G + + + V E

Sbjct: 280 IKVTCPC-----SLRAVDIKTMPYPGFPTDMQAQIMALMTVAKGTS----ILTETVFE 328

Query: 361 TERMVAIRTELTKLGASVEEG 381
M EL ++GA ++ G

Sbjct: 329 NRFMHV--AELKRMGARIKTG 347

>ref|YP_003782309.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
ljungdahlii DSM 13528]
gb|ADK17207.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
ljungdahlii DSM 13528]
Length = 420

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 105/425 (24%), Positives = 177/425 (41%), Gaps = 63/425 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
+++V+ + +SG +++ G+K+ + IL + + S+G +DN+ N EDVH + L +L

Sbjct: 2 DKLIVINGGRPLSGFIEINGAKNAAVAILPASIMASKGLCSIDNIPNIEDVHCIERILESL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
G + K K +VV+ ++ ++V+ MR+ L A+ A

Sbjct: 62 GCEI---KTGKNSVVIDSTTINSIDANTDDVR-----KMRASYLIGALLGRFKKAR 110

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGS--- 177
L G + RPI + G + LGA V G C V KL G+

Sbjct: 111 VELPGGCPIGVRPIDQHIKGFALGAQVKIKHG--CVLVEAK-----KLIGTSIF 158

Query: 178 ---ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
+S +++AA LA G +E + K P+V + G + + + D

Sbjct: 159 FDVVSVGATINVLAASLAEGVTTLENVAKE---PHVVDVANFLNSMGANIKGAGT-DII 214

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMM 294
I G ++ K + + + +Y +A AA GG V V+ L+ + L M

Sbjct: 215 RIVGVKELKGCSSVIPDQIEAGTYMIAAAA-CGGEVVVQNVIPKHE---SISAKLIEM 270

Query: 295 GAKVTWTETSVTVTGPPEPFGGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAI 350
GA+V SVTV + LK +++ P DV L+ + A+G + I

Sbjct: 271 GAEVIEDGDSVTVKSSGK-----LKGVNIKTQPYPGFPTDVQQPLSTLLTVAEGRSII 323

Query: 351 RDVASW--RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAM 408
+ + W R K + EL K+GA+++ II KL+ AI D R

Sbjct: 324 NE-SIWESRFKHVD-----ELKKMGANIKVEGRTAIDGVSKLS-GAIVKATDLRAGA 374

Query: 409 AFSLA 413
A +A

Sbjct: 375 AMVIA 379

>ref|ZP_05113520.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Labrenzia
alexandrii DFL-11]
gb|EEE44119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Labrenzia
alexandrii DFL-11]
Length = 429

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 74/298 (24%), Positives = 136/298 (45%), Gaps = 19/298 (6%)

Query: 14 EISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTGLSVEADKAA 73

Sbjct: 11 E++G + + G+K+ + +++ + L++ T + N+ DV ++ L G+ +
ELNGIIPISGAKNAALPLMIASLLTDETLTSLNVPRLRDVAQLMQILSNHGVDYSVN--G 68

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-MRS---LTAAVTAAGGNATYVLDGVPRM 129
KR+ G+ A+E V ++ MR+ + + A A L G +

Sbjct: 69 KRSGQDDLAGQTLNLTAREIVDTTAPYELVSKMRASFVWVGPLVARMHEARVSLPGGCAI 128

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL+ LGAD++ G V V GGL GG+V+ +S ++MA

Sbjct: 129 GTRPVDFFIQGLEALGADIEIEGGY----VVKAPGGLTGGRVEFP-RVSVGATHTIMMA 183

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G E EI++ V++ R ++ G K E + I+G + +A

Sbjct: 184 ATLAKG--ETEIVNAAREPEVVDLA-RCLKAMGAKIE-GEGETSTIRIQGVPRHLGAAHHA 239

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V + +Y +A A+TGG V ++G T L+ + + L GA++T T+ + +

Sbjct: 240 VPDRIETGTGYAMA-VAMTGGDVFLQGARTELLESA---DTRLRQTGAIEITATDEGLRI 293

>ref|YP_001663939.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X514]
ref|ZP_07131152.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X561]
ref|YP_003905230.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X513]
gb|ABY93603.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X514]
gb|EFK85665.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X561]
gb|ADN55939.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X513]
Length = 417

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 93/396 (23%), Positives = 160/396 (40%), Gaps = 45/396 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ K + G+V++ G+K+ + IL A L++ +V+DNL + +D+ + +R LG

Sbjct: 2 EKFKVIGKPKLRGSGVQISGAKNSAVAILPAALLADTPSVIDNLPDIKDIELLAQMIRNLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E K +G +P D +++ A L A+ + A +

Sbjct: 62 GKIEKKKHEVVIDPIGLNSFYPPRDLASQMR-----ASYYLIGALLSKFNEAVIAMP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA G +R+ L G + +S

Sbjct: 114 GGCNIGVRPIDQHIKGFALGAKTTIEHGL----IRIKA-DKLVGNHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++A+ A G + I++ P+V + G + + + D I G K

Sbjct: 168 NLMLASVKAEG---VTILENCAKEPHVVDVANFLNANGANIKGAGT-DTIKITGVDKLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + +Y +A AA T G V ++G L+ + A+++E MG V +

Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TKGDVYIKGIIPNHLEAII--AKLVE-MGVIVEEYDDV 279

Query: 305 VTV--TGPPREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V GP LK +D+ P D+ AV+ ADG + I ++ R

Sbjct: 280 IRVRREGP-----LKHVDIRTLPPYGFPTDMQQPFVALLALADGISVITENIYENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
K EL K+GA V I EKL

Sbjct: 331 FKYL-----NELEKMGAKVRIEGRNAIFEGVEKL 359

>ref|YP_001393545.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
kluverii DSM 555]
ref|YP_002470567.1| hypothetical protein CKR_0102 [Clostridium kluverii NBRC 12016]
gb|EDK32197.1| MurA1 [Clostridium kluverii DSM 555]
dbj|BAH05153.1| hypothetical protein [Clostridium kluverii NBRC 12016]

Length = 420

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 103/415 (24%), Positives = 172/415 (41%), Gaps = 63/415 (15%)

```
Query: 15  ISGTVKLPGSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      +SG+++ G+K+ + IL + L S G +DN+ + EDVH + L++LG V K
Sbjct: 12  LSGSIEINGAKNAAVAILPASILASSGICSIDNIPDIEDVHCIEKILKSLGCKV---KTG 68

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130
      K VV+ ++ ++V+ MR+ L A+ A A L G +
Sbjct: 69  KNLVVIDSTTINKIDADTDDVR-----KMRASYYLIGALLARFKKARVELPGGCPIG 120

Query: 131  ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS-----ISSQYLS 184
      RPI + G LGA V+ G C V KL G+ +S
Sbjct: 121  VRPIDQHIGFGALGAKVEIKHG--CVSVSAE-----KLVGTSIFFDVVSVGATI 168

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      +++AA LA G +E + K P+V + G + + + + + G ++ K
Sbjct: 169  NVMLAATLAEGITTLENVAKE---PHVVDVANFLNSMGANIKGAGT-EIIRVVGKELKG 224

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + + + +Y +A AA GG V +E L+ + L MG ++ S
Sbjct: 225  CSYSVIPDQIEAGTYMIAAAA-CGGEVIEIENVIPKHLE---SISAKLIEMGVEIIEENGDS 280

Query: 305  VTVTGPPEPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASW--RV 358
      +TV R LK I++ P DV L+ + A+G + I + + W R
Sbjct: 281  ITVKSAGR-----LKGINKTQPYPGFPTDVQQLSALLTVAEGRSIINE-SIWESRF 332

Query: 359  KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
      K + EL K+GA+++ II +KL+ AI D R A +A
Sbjct: 333  KHID-----ELKKMGANIKVEGRIAIIDGVDKLS-GAIVKATDLRAGAAMVIA 379
```

>ref|ZP_06636240.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D7S-1]
gb|EFE02559.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
actinomycetemcomitans D7S-1]
Length = 425

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 96/416 (23%), Positives = 169/416 (40%), Gaps = 41/416 (9%)

```
Query: 15  ISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + GTV++ G+K+ + IL A L+ + N+ + +D+ L LR LG+ VE +K
Sbjct: 12  LKGTVEISGAKNAALPILFAAILATEPVTLTNPDLKDIETTLKILRQLGVVVEQNKPGT 71

Query: 75  RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
      + F P E K A + R V+ GG + + R
Sbjct: 72  VRLDASKIDHFIAPYELVKTMRASIWALAPLVARFNQGVSLPGGCS-----IGAR 122

Query: 133  PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
      P+ + GL++LGA + G V+ G L G ++ + +S ++++AA L
Sbjct: 123  PVDLHISGLERLGAKIALEDGY---VKAYVDGRLNGTRIVME-KVSVGATLSIMIAATL 177

Query: 193  ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
      A G +I+ P + T + + G K + S D I+G + +++ V
Sbjct: 178  AKGTT---VIENAAREPEIADTAEFNLKMGAKISGAGS-DAITIEGVNRLTGCEHSIVP- 232

Query: 253  DASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 312
      D FL AAI+GG + + +L + + L GA+V TE ++T+
Sbjct: 233  DRIETGTFLVAAISGGRIVCKNTKANTLDAVI---DKLREAGAQVDVTEDITLDMWGN 289

Query: 313  EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 290  RP-----KAVNIRTAPYPGFPTDMQAQFTLLNMVANGTSIITETIF-----ENRFMHI- 337

Query: 369  TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
      EL ++G E + I L+ + D R +++ LA C TI D
Sbjct: 338  PELIRMGGKAEIEGNTAICHGVSHLSGAEV-MATDLRASISLVLAGCIATGETIVD 392
```

>ref|XP_002283120.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 466

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 71/261 (27%), Positives = 108/261 (41%), Gaps = 16/261 (6%)

Query: 14 EISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V + GSK+ + IL GT+ + + N D M LR+LG+ +EA
Sbjct: 53 KLSGHVPISGSKNSALSILAATLCCSGTSKLHGVPNLSDTTRTMASILRSLGVEIEACNGE 112

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
G G V+ E++ G + + A G A L G + RP
Sbjct: 113 MWVNADGVGS---VQPCPEDIGKIRGGFFV-----IGPLLARFGEAVVALPGGCDIGTRP 164

Query: 134 IGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + GL+ LGA V+ LG + GL GG+ KL S L+MAA +A
Sbjct: 165 VDLYIRGLRALGAIVE--LGDGKVRAQAANGRLVGGRFKLDHP-SVGATETLMMAACMA 221

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + ++ + P V R + G E + S D YIKG + V D
Sbjct: 222 DG---VTVLSNVAKEPEVIDLARFLTGSGACVEGAGS-DTLYIKGKNQLHG-SECIVPPD 276

Query: 254 ASSASYFLAGAAITGGTVTVE 274
A F+ AAIT ++++
Sbjct: 277 RIEAGTFMLAAAITRSSISMS 297

>ref|YP_001714915.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AYE]
ref|YP_001845289.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter
baumannii ACICU]
ref|YP_002318133.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB0057]
ref|YP_002326819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB307-0294]
ref|YP_001083731.2| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii ATCC 17978]
ref|ZP_04660691.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB900]
ref|ZP_06782945.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. 6013113]
ref|ZP_06788333.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. 6014059]
ref|ZP_06795370.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. 6013150]
ref|ZP_07229394.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB056]
ref|ZP_07237134.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB058]
ref|ZP_07242344.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB059]
emb|CAM87943.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate
transferase) (UDP-N-acetylglucosamine enolpyruvyl
transferase) (EPT) [Acinetobacter baumannii AYE]
gb|ACC55942.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter
baumannii ACICU]
gb|ABO11129.2| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii ATCC 17978]
gb|ACJ40150.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB0057]
gb|ACJ56404.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii AB307-0294]
gb|ADX02301.1| murA [Acinetobacter baumannii 1656-2]
gb|ADX91097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
baumannii TCDC-AB0715]
Length = 418

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 103/413 (24%), Positives = 175/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPITLTNPVNLKDVNTLVKLIGGLGVTISYENDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LG+ ++ G V G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGY----VHATVDGRLKGGVEVVD-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AALADG---VTTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V + L+ + KF E MGA+VT + + +
Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPSLLEAVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E
Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPTDMQAQIMAVNAIG---RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T EKL + D + +FSL A V
Sbjct: 335 HVPESLRMGANIQVEGHD-AVVTGVEKLQAAPVMATD--LRASFSLVLAALV 383

>ref|YP_001376991.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
subsp. cytotoxis NVH 391-98]
gb|ABS23996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
cytotoxicus NVH 391-98]
Length = 434

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 95/377 (25%), Positives = 148/377 (39%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLEVPVLSVDTYINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + + V + +E E V R + A+V G G
Sbjct: 62 NAEVVVFEN---NQVTIDASKELKIEAPFEYV-----RKMRASVQVMGPLLARNG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFEAMGAKVKVGNFVEAYVE---GELKGAKIYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G II+ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAAALAKGTT---IENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGTHHSIIP-DRIEAGTFMVAAAITGNNILINAVPEHLR---SVTAKMEEMGVK 274

Query: 298 VWTETSVTVTGPPEPFGGRKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDV 353
V + V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 VIEENEGLRVIGPDK-----LKAVDIKTMPHPGFPTDMQSQMMALLLQADGTSMITET 327

Query: 354 A----SWRVKETERMVA 366
V+E RM A
Sbjct: 328 VFENRFMHVEEFRRMNA 344

>ref|ZP_08004986.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
2_A_57_CT2]
gb|EFV78148.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
2_A_57_CT2]

Length = 436

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 93/374 (24%), Positives = 152/374 (40%), Gaps = 42/374 (11%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      ++I+++ +SGTVK+ G+K+ ++ L S+G +V+ ++ DV+ + LR L
Sbjct: 2  DKIIIVRGGNRLSGTVKVEGAKNAVLPIAATLLASDGKSVIRDVPTLSDVYTINEVLRYL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
      VE + V V + VE E V+ + + M SL A G A L
Sbjct: 62  NAEVEFEN---NTVTVNASRELKVEAPFEYVRKMRAVS-LVMGSLLAR----NGRARVAL 113

Query: 124  DGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
      G + RPI + G + +GA V + F+ + P G L G K+ L S
Sbjct: 114  PGGCAIGSRPIDQHLKGFEAMGAKVKVNGFIEAEAPE-----GRLHGAKIYLDFF-SV 166

Query: 181  QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G I++ + P + + + G K + + + I+G
Sbjct: 167  GATENIMMAATLAKGTT---ILENVAKEPEIVDLANFLNKGAKVKAGAGTGT-IRIEGVD 222

Query: 241  KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      ++ + D A F+ AAITGG V V+G + +E MG
Sbjct: 223  VLFGAETHNIIP-DRIEAGTFMVAAAITGGDVLVKGA---VPEHSASLIAKMEEMGVTFIE 278

Query: 301  TETSVTVTGPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA-- 354
      + V GP + LKA D+ P D+ + + L A G + I +
Sbjct: 279  EAEGIRVLGDPK-----LKAADIKTMPHPGFPTDMQSQMMALLLHAQGTSVITETVFE 331

Query: 355  --SWRVKETERMVA 366
      V+E RM A
Sbjct: 332  NRFMHVEEFRRMNA 345
```

>ref|ZP_02927317.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Verrucomicrobium spinosum DSM 4136]
Length = 421

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 97/392 (24%), Positives = 163/392 (41%), Gaps = 31/392 (7%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 64
      E++++ + G V + GSK+ S IL L++ V+ + + D +YML LR LG
Sbjct: 2  EKLIVHGGNRLRGKVLISGSKNSSLPIAATLLTKDDCVIRQVDPDSDTNMYMLQILRALG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      VE + + V + + D ++ + + M LT + A +
Sbjct: 62  AEVE-----RASGTVNIKAEKIIPDTPYDLVRKMRAVICVMGPLTGRLR----KAVVSMP 112

Query: 125  GVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G + +RP+ + GL+ LGA V D + + L G + L G S L
Sbjct: 113  GGCIVIGDRPVDLHLKGLEYLGAQVQ---MDGGNIHIEAKKPLKGCTMNLGKFGSTVLG 168

Query: 185  A--LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
      +LMAA L G II+ + P VE + + G K E + + R ++G ++
Sbjct: 169  TDNVLMMAAVLTKGTT---IIEGAAAEPEVEDLANFLIKMGAKIEGAGTT-RIVVEGVKEL 224

Query: 243  KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      ++ + D A FL AI G V V+ L+ + L G +VT T+
Sbjct: 225  HGAHTVIP-DRIEAGTFLVAGAIFGDGVVMKRVVPAHLK---NVTDTLLASGYEVTSTK 280

Query: 303  TSVTVTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      SVT+ P G HL V D+ +A G ++I++ +
Sbjct: 281  DSVTIMP GSGAPKGF-HLTT-RVYPGFPTDMQAQFCALACLIPGLSSIKETIF-----PQ 333

Query: 363  RMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
      R + + +EL ++GA++E D IT E L+
Sbjct: 334  RFMHV-SELKRMGANIELDGDGTARITGVETLS 364
```

>ref|ZP_06752546.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parascardovia

denticolens F0305]
ref|ZP_07868935.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parascardovia
denticolens DSM 10105]
gb|EFG32284.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parascardovia
denticolens F0305]
gb|EFT82731.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parascardovia
denticolens DSM 10105]
Length = 443

Score = 52.8 bits (125), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 101/386 (26%), Positives = 164/386 (42%), Gaps = 44/386 (11%)

Query: 5 EEIVL--QPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
EE VL Q K ++GT+K+ G+K+L ++ ++ A L+ GT+V+ N+ DV + LR
Sbjct: 7 EEDVLRVQGGKPLNGTIKVRGAKNLVSKAMVAALLAPGTSVLKNVPEIRDVQVVDLLRL 66

Query: 63 LGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
G+SV+ + VV K A +V+ G + I + + + G A
Sbjct: 67 HGVSDVNDGETG--VVTIDAKHVEMPAVSDVETLSGASRIPIL-FSGPLLHRLGEAFIP 122

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS---GSI 178
G R+ +RPI + L++LGADV + + GL G K+ L G+
Sbjct: 123 TLGGCRIGDRPIDFHLETLRKLADVD--KEHEDGIHITAPNGLHGAKIHLPPYPSVGAT 179

Query: 179 SSQYLSALLMAAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FY 235
L+A+L L VE EI+D LI+I +++ G A S DR
Sbjct: 180 EQTVLAAVLADGKTELSGAAVEPEIMD-LIAI-----LQKMG--AIISVDVDRITIR 227

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G ++ K + + AS+ A A T G V ++G + + F V +G
Sbjct: 228 IEGVKELKGYTHALTDRIEVASWASAALA-TRGDVFIKATQPEM---MTFLNVYRKVG 283

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAI--DVNMNMPDVAMTLAVVALFADGPTAIRDV 353
T+ + P G H AI DV+ M D L V A+G + + +
Sbjct: 284 GAFDVTDEGIHFW---HPGGDLHPVAIETDVHPGFMTDQQPLVVALTQANGLSIVHET 339

Query: 354 ASWRVKETERMVAIRTELTKLGASVE 379
E L ++GA+++
Sbjct: 340 VY-----ENRFGFTKPLVQMGATIQ 359

>ref|YP_004059547.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfuricurvum
kujiense DSM 16994]
gb|ADR33347.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfuricurvum
kujiense DSM 16994]
Length = 420

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 100/419 (23%), Positives = 169/419 (40%), Gaps = 51/419 (12%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++SGTV + G+K+ + ++ LA L+ V N+ D+ +L L+ LG S
Sbjct: 6 IQGPTKLSGTVTISGAKNAALPLITLALLAHNPLKVTNMPEVADIKTLKLLQNLGASCT 65

Query: 69 ADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ + V + N I ++++ A++ G G+
Sbjct: 66 LENHV-----LNIDTSTVNHTMANYDI-VKTMRASILVLGPLLARFGHCEVS 111

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + +RPI + L+Q+GA + G V GL G + + I+
Sbjct: 112 LPPGCAIGQRPIDLHLKALEQMGAIQITIAGY----VHAQAPEGLKGAHI-IFDKITVTG 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+ ++MAA LA G ++ P V ++ G+ + + + G K
Sbjct: 167 TANIVMAAALAHGKT---VLVNCAKEPEVVQLCEILRDSGIDITGIGTSELVIVGTGGKT 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ V D A +L AIT +T+E L D A+ LE MG ++ TE
Sbjct: 224 IDMVDVEVIPDRIEAGTYLCAGAITNSVITLERVRPDHL--DAVTAK-LEQMGCRIESTE 280

Query: 303 TSVTVTGPPREPFGKHLKAIQDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRV 358

++T+ P E LK +D+ + P D+ +A A G + I + R+
Sbjct: 281 NTMTIY-PATE-----LKHVDIITQEYPAFPTDMAQFLALATLAKGASTIDE----RL 329

Query: 359 KETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
E M +EL +LGA ++ G +I P E + T D R + A LAA A

Sbjct: 330 FENRFMHV--SELQRLGADIKLSGHVATVIGPCELFADVMAT--DLRASSALVLAAMA 384

>ref|YP_535495.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius UCC118]
ref|ZP_04008470.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius ATCC 11741]
gb|ABD99412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius UCC118]
gb|EEJ75024.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius ATCC 11741]
gb|ADJ78817.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
salivarius CECT 5713]
Length = 441

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 77/312 (24%), Positives = 136/312 (43%), Gaps = 26/312 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+IV++ ++ G V++ G+K+ IL A L SEG T++ N+ DV+ M +R L
Sbjct: 2 EKIVVRGGNKLEGEVEIEGAKNAVLPIAAAILPSEGRTILTNPMLSDVYTMNNVIRFL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V D+ K +V + GK + + V MR+ + + A G A
Sbjct: 62 NVKVGFDENEK-SVEIDATGKLSYDAPFKYVS-----KMRASIVVLGPLLARLGKAR 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS 180
+ G + RPI + GL+ LGA ++ G + + G L G + L S
Sbjct: 113 VAMPGGCAIGSRPIDLHLKGLLELGAKIEQHNGY----IDAHTDGRLVGANIYLDFF-SV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G II+ + P + ++ + G K + ++ I G +
Sbjct: 168 GATQINIMMAATLAKGTT---IENVAREPEIVDLANVLNKMGAQV-YGAGTEKIKIIGVE 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
++A ++ D A F+ +A+T G V ++ + ++ LE MG KV
Sbjct: 224 SLHGTEHAIQ-DRIEAGTFMVASALTQGNVLIK---EAIAEHNIPLISKLEEMGVKVIE 279

Query: 301 TETSVTVTGPPR 312
+ + GP +
Sbjct: 280 ENEGIRIIGPEK 291

>ref|YP_907486.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
ulcerans Agy99]
gb|ABL06015.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase MurA
[Mycobacterium ulcerans Agy99]
Length = 417

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 99/373 (26%), Positives = 147/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTGGNRLSGEVAVGGAQNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLG 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVARIT---SPDEPKYDADF-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + + L G +++L
Sbjct: 108 RAKVALPGGDAIGSRPLDMHQAGLRQLGA--QCNIHGCVVAQAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I

Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMGAIQEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G +TV G + LQ L GA

Sbjct: 218 GVPRLH-PTEHRVIGDRIVAATWGIAAAMTRGDITVTGIDPSHLQ---LVLHKLYDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S + R KA++V P L +A+ ADG + I +

Sbjct: 274 VTQTDDSFRIVQYERP-----KAVNVATLPFPGFPTDLQPMALASIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+

Sbjct: 327 VFEARFRFVEEMI 339

>ref|YP_004153576.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Variovorax paradoxus EPS]
gb|ADU35465.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Variovorax paradoxus EPS]
Length = 429

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 122/280 (43%), Gaps = 40/280 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ +++ G V + G+K+ + L A L++ + N+ +DV ML +R +G

Sbjct: 2 DKLLIRGGRQLRGEVLISGAKNAALPELCAALLTDQPVTLHNVPRLQDVSTMLKLVNMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ E D V G +A E+ +++++ A+V A G G+

Sbjct: 62 VVAERD---DNGTVQLNAGDLTNPEAPYEL-----VKTMRASVLALGPLLARFGH 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS- 177
A L G + RP+ + GL+ +GA++ G I LP G+ +L G+

Sbjct: 109 AKVSLPGGCAIGSRPVDQHIKGLQAMGAEIVVEHGYM-----IASLPAGRTRLKGAR 160

Query: 178 -----ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-HSDSW 231
++ LMAA LA G+ +++ P + ++ R G K E H S

Sbjct: 161 ILTDMVTVTGTENFLMAAALAEGET---LLENAAQEPEIVDLAEMLIRMGAKIEGHGTS 217

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
R I+G +K ++A V D A FL A TGG V

Sbjct: 218 IR--IQGVEKLHGCEHAVV-ADRIEAGTFLCAVAATGGEV 254

>ref|YP_001852345.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase MurA
[Mycobacterium marinum M]
gb|ACC42490.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase MurA
[Mycobacterium marinum M]
Length = 417

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 99/373 (26%), Positives = 147/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L

Sbjct: 2 AERFVVTGGNRLSGEVAVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLGL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G

Sbjct: 62 GATVELDGDVARIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L

Sbjct: 108 RAKVALPGGDAIGSRPLDMHQAGLRQLGA--QCNIHGCVVQAQAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I

Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMGAIQEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAK 297

G + P V GD A+ + AA+T G +TV G + LQ L GA
Sbjct: 218 GVPR LH-PTEHRVIGDRIVAATWGIAAAMTRGDITVTGIDPSHLQ---LVLHKLYDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMPDVAMTLAVVAL----FADGPTAI-RD 352

VT T+ S + R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDSSFRIVQYERP-----KAVNVATLFPFGFPTDLQPMALALASIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365

V R + E M+
Sbjct: 327 VFEARFRFVEEMI 339

>ref|YP_001197962.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis
05ZYH33]
gb|ABP89562.1| 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus suis
05ZYH33]
Length = 101

Score = 52.4 bits (124), Expect = 1e-04, Method: Composition-based stats.
Identities = 30/102 (29%), Positives = 57/102 (55%), Gaps = 7/102 (6%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEA 69

+ +++++ GT+++PG KS+S+R ++ +L++G T N+L EDV + R LG+ +E
Sbjct: 5 RSVEKLKGTIRVPGDKSISHRSIIFGSLAKGVTRFHNILRGEDVLSMQLVFRDLGVKIED 64

Query: 70 DKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTA 110

+ VG G + P D L +GN+G ++R ++
Sbjct: 65 NGDIVEVHVGFDGLQAPKND-----LDMGNSGTSIRLISG 100

>ref|ZP_07931459.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerostipes sp.
3_2_56FAA]
gb|EFV22513.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerostipes sp.
3_2_56FAA]
Length = 431

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 102/434 (23%), Positives = 180/434 (41%), Gaps = 35/434 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64

E+ +++ + G V + G+K+ + IL A +++GT ++N+ + D + +L A+ +G
Sbjct: 2 EQYIIKGGNPLVGEVIGGAKNAALPILAAVMTDGTCTIENMPDVRDNTNVLQAMEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

+V ++ K VV+ G D E + A L A+ A L
Sbjct: 62 ATV--NRLGKHEVVISGSGMNADCDVDNEYIRKIR----ASYYLIGALLGKYKRARVALP 115

Query: 125 GVPRMRERPIGDLVVLGKQLGADVDCFLGTDGPPVRVNGIGLPGGKVKLSGSISSQYLS 184

G + RPI + G K LGA ++ G L G + + +S
Sbjct: 116 GGCEIGSRPIDQHIGFKALGARIEIENGMITATAD-----ELIGCHIYMD-VVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

++MAA LA G+ IE + K P+V + G + + D IKG +K +
Sbjct: 170 NVMMAAALAKGNTTIENVAKE---PHVVDVANFLNSMGASIRGAGT-DVIKIKGVEKLG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTVTETS 304

+ + + D A F+ A T G +TV+ L+ + LE +GA+V + +
Sbjct: 226 CEYSIIP-DQIEAGTFMTAAVATKGDITVKNVIPKHLEA---ISAKLEEIGAQVDEFDDA 281

Query: 305 VTVTGPPR-EPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRD-VASWRVKETE 362

V V R + K L + P +A++LA ++G + + + + R + +
Sbjct: 282 VRVVATKRLDSTQIKTLPPYGFPTDMQPMASVLA---LSNGTSIVSESIFENFRFYVD 337

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAA-CAEVPVT 421

ELTK+GA ++ IIT KL A + D R A +A A+ T
Sbjct: 338 -----ELTKMGARIQVDGRTAITITGV-KLFTGADVSAAPDLRAGAALVIAGLAADGYTT 389

Query: 422 IRDPGCTRKTFPDY 435

+ D G + + +
Sbjct: 390 VSDIGIYRGYEGF 403

```
>ref|ZP_00742764.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar israelensis ATCC 35646]
ref|YP_002448824.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus G9842]
gb|EAO52960.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar israelensis ATCC 35646]
gb|ACK94177.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus G9842]
Length = 434
```

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 148/377 (39%), Gaps = 49/377 (12%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVYTYINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFE---NNQVTIDSSKELNIEAPFEYV-----RKMRAVQVMGPLLARNG 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVNGGFVEAYVE---GELKGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G I++ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGEGCCTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGANHSIIP-DRIEAGTFMVAAAATGGDILIEAVPEHLR---SITAKMEEMGVK 274

Query: 298 VTWTETSVTVTPPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
+ V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 IIEENEGVRVIGPDK-----LKAVDIKTMPHPGFPTDMQSQMMALLLQADGTSMTET 327

Query: 354 A----SWRVKETERMVA 366
V+E RM A
Sbjct: 328 VFENRFMHVEEFRMNA 344
```

```
>ref|ZP_04188873.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH1271]
ref|ZP_04303457.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus MM3]
gb|EEK64879.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus MM3]
gb|EEL79484.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH1271]
Length = 434
```

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 97/384 (25%), Positives = 147/384 (38%), Gaps = 63/384 (16%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVYTYINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFE---NNQVTIDASKELNIEAPFEYV-----RKMRAVQVMGPLLARNG 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVNGGFVEAYVE---GELKGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS-----DS 230
S ++ AA LA G I++ P + + G K + +
Sbjct: 164 -SVGATENIMSAAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGTIRIEG 219
```

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
D+ Y GG P D A F+ AAITGG + +E L+
Sbjct: 220 VDKLY--GGNHSIIP-----DRIEAGTFMVAAAITGGDILIENAVPEHLR---SITAK 267

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADG 346
+E MG KV V V GP + LKA+D+ P D+ + + L ADG
Sbjct: 268 MEEMGVKVEENEGVRVIGDPK-----LKAVDIKTMPHPGFPTMQSQMMALLLQADG 320

Query: 347 PTAIRDVA---SWRVKETERMVA 366
+ I + V+E RM A
Sbjct: 321 TSMITETVFENRFMHVEEFRMNA 344

>ref|YP_177339.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
sp|Q5WB82.1|MURAl_BACSK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
dbj|BAD66378.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus clausii
KSM-K16]
Length = 432

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 90/376 (23%), Positives = 156/376 (41%), Gaps = 51/376 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALAE--GTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++ G+VK+ G+K+ ++ + L+E G +++++ + + DV+ M L L
Sbjct: 2 EKIIIVRGGNKLHGSVKVEGAKNAVLPIVIAASILAERGASIIIEEVPSTLDVYTMKEVLANL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVE-----DAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
+ VE + G+F V +A E + + + M L A V
Sbjct: 62 NVGVEYEN-----GRFAVRADRPLKTEAPFEYVRKMRASFLVMGPLLARV---- 106

Query: 117 GNATYVLGDGVPFRMRERPIGDLVVLGLQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSG 176
G A L G + RPI + G + +GA V+ +G R++G L G K+ L
Sbjct: 107 GRARIALPGGCAIGSRPIEQHLKGFEAMGATVE--IGNGFIEARIDG--KLQGTKIYLDL 162

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
S ++MAA LA G II+ + P + + G K + + I
Sbjct: 163 P-SVGATENIMMAAVLAEGTT---IENVAEEPEIVDLANYLNAMGAKVRGAGTG-VIRI 217

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G + ++ + D A F+ AAITGG V VEG ++ + MG
Sbjct: 218 DGVDALQGAVHSVIP-DRIEAGTFMVAAAITGGNVFVEGAIAEHMR---PLVAKMREMGV 273

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD 352
+ E + V GP + LKA+D+ P D+ + + L A+G + + +
Sbjct: 274 DIIEEEAGLRVIGP-----EQLKAVDIKTMPHPGFPTMQAQMMALLLRAEGTSVVTE 326

Query: 353 VA---SWRVKETERM 364
V+E RM
Sbjct: 327 TVFENRFMHVEEFRM 342

>gb|ABC00781.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 33

Score = 52.4 bits (124), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 27/33 (81%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 85 FPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
FP+E DAKEEV+LFLGNAG AMR LTAAG AAG
Sbjct: 1 FPIEKDAKEEVKLFLGNAGTAMRPLTAAVVAAG 33

>ref|YP_001154891.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. asymbioticus QLW-P1DMWA-1]
sp|A4SV13.1|MURA_POLSQ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:

Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABP33327.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Polynucleobacter
necessarius subsp. asymbioticus QLW-P1DMWA-1]
Length = 424

Score = 52.4 bits (124), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 105/417 (25%), Positives = 168/417 (40%), Gaps = 54/417 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V + G+K+ + IL L++ V+ NL + +DV ML L+ +G+ V A
Sbjct: 12 LNGEVTIAGAKNAALPILCACLLTDQPVVLRNLPDLQDVRTMLKLLQEIGVVVSFPDANN 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
V+ +A E+ L LG + R +A V+ GG A
Sbjct: 72 PNHVILNAAVIKSSSEATYEMVKTMRASILVLP--LLARMHSAKVSPLPGGCA----- 121

Query: 128 RMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ RP+ + GLK +GA + ++ + P L G + L+ I+
Sbjct: 122 -IGARPVDQHIGLKGAMGASIKSIQAETKPTTER----LKGASI-LTDMITVTGTE 175

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAA LA G I++ P V L+ + G K S DR I+G +K
Sbjct: 176 NLLMAATLASGTT---ILENAAREPEVGDLELLVKGAKITGIGS-DRLVIEGVEKLHG 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMGAKVTWTET 303
+++ + D A FL A GG V V+ C +L VK E M W +
Sbjct: 232 AEHSVIP-DRIEAGTFLCAVAAAGGEVLVKHCRPDTLDAVIVKLKEAGLKMEIGPDWIK 290

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
S + G P KA+ ++ P D+ L V A+G + I +
Sbjct: 291 S--MQGRP-----KAVSFRTSEYPAFPDTMQQLMAVNAVANGNSTITETIF---- 335

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACA 416
R + ++ EL +LGA + + I E+L+ AI D R + + +A A
Sbjct: 336 -ENRFMHVQ-ELNRLGADIAIEGNTAIAQGVERLS-GAIVMATDLRASASLVIAGLA 389

>ref|NP_739053.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
sp|Q8FMR0.1|MURA_COREF RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
dbj|BAC19253.1| putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Corynebacterium efficiens YS-314]
Length = 421

Score = 52.4 bits (124), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 109/429 (25%), Positives = 164/429 (38%), Gaps = 33/429 (7%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ +++ A L+EGTT + N DV M L LG VE D
Sbjct: 16 LQGSVRVDGAKNSVLKLMMAAALLAEGTTTLTNCPEILDVPLMRDVLVGLGCEVEID---G 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + + + V F + + +TA G A L G + RP+
Sbjct: 73 HTVTIHTPAELKSDADFPVAVTQFRASV-----CVLGPLTARCGRAVVSPLPGGDAIGSRPL 127

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
GL+QLGA G V L G ++ L S +LMA+ +A
Sbjct: 128 DMHQSGLEQLGATTTRTQHGA-----VVAEADKLVGAEISLDFP-SVGATENILMASVMAE 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G +D P + R++ G E S + I G +K P + V GD
Sbjct: 182 GQT---TLDNAAREPEIVDLCRMLRSMGADIEGEGS-PKITEINGVEKLH-PTSHEVIGDR 236

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A + AA+T G VTV G L + E L++ GA+V E V
Sbjct: 237 IVAGTWAFAAAMTRGDVTVGGIAPRYLHLPL---EKLKLAGAQVDTFENGFRVV----- 287

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRD-VASWRVKETERMVAIRTELTK 373
K K+ D P L +A+ G AI D VA E E+ +
Sbjct: 288 -MNRKPKSTDYQTLFPFGFPTDLQPMAL---GLNAIADGVAVVTENVFESRFRFVDEMQR 343

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFF 433
LGA + +I E+L+ T + + D A A CAE +RD + +P
Sbjct: 344 LGADTSVDGHHVVIRGIEELSSTTVWSSDIRAGAGLVIAALCAEGTTEVRDVFHIDRGYP 403

Query: 434 DYFDVLSTF 442
++ + L
Sbjct: 404 NFVENLQAL 412

>ref|ZP_05748914.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
gb|EEW51047.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
efficiens YS-314]
Length = 418

Score = 52.4 bits (124), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 109/429 (25%), Positives = 164/429 (38%), Gaps = 33/429 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ +++ A L+EGTT + N DV M L LG VE D
Sbjct: 13 LQGSVRVDGAKNSVLKLMMAALLAEGTTTLTNCPEILDVPLMRDVLVGLGCEVEID---G 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V + + + V F + + +TA G A L G + RP+
Sbjct: 70 HTVTIHTPAELKSDADFAVTFQFRASV-----CVLGPLTARCGRAVVSPLPGGDAIGSRPL 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
GL+QLGA G V L G ++ L S +LMA+ +A
Sbjct: 125 DMHQSGLEQLGATTTRTQHGA-----VVAEADKLVGAEISLDFP-SVGATENILMASVMAE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G +D P + R++ G E S + I G +K P + V GD
Sbjct: 179 GQT---TLDNAAREPEIVDLRMLRSMGADIEGEGS-PKITINGVEKLH-PTSHEVIGDR 233

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A + AA+T G VTV G L + E L++ GA+V E V
Sbjct: 234 IVAGTWAFAAAMTRGDVTVGGIAPRYLHLPL---EKLKLAGAQVDTFENGFRVV----- 284

Query: 315 FGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRD-VASWRVKETERMVAIRTELTK 373
K K+ D P L +A+ G AI D VA E E+ +
Sbjct: 285 -MNRKPKSTDYQTLFPFGFPTDLQPMAL---GLNAIADGVAVVTENVFESRFRFVDEMQR 340

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTRKTFF 433
LGA + +I E+L+ T + + D A A CAE +RD + +P
Sbjct: 341 LGADTSVDGHHVVIRGIEELSSTTVWSSDIRAGAGLVIAALCAEGTTEVRDVFHIDRGYP 400

Query: 434 DYFDVLSTF 442
++ + L
Sbjct: 401 NFVENLQAL 409

>ref|YP_001666059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter pseudethanolicus ATCC 33223]
ref|YP_001661761.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X514]
ref|ZP_05492226.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter ethanolicus CCSD1]
ref|ZP_07130956.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X561]
ref|YP_003903097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X513]
ref|YP_004187035.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter brockii subsp. finnii Ako-1]
gb|ABY91425.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X514]
gb|ABY95723.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter pseudethanolicus ATCC 33223]

gb|EEU62754.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter ethanolicus CCSD1]
gb|EFK85469.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X561]
gb|ADN53806.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter sp. X513]
gb|ADV80652.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter brockii subsp. finnii Ako-1]
Length = 416

Score = 52.4 bits (124), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 88/371 (23%), Positives = 153/371 (41%), Gaps = 44/371 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+VK+ G+K+ I+ + LS G V+D++ EDV+ M+ ++ G E +
Sbjct: 14 LKGSVKISGAKNSVLPPIAASLLSSGEIVLDDIPTLEDVNMIELIKHFGAICEFENEKL 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V + P + K+ FL I R A ++ GG A + RPI
Sbjct: 74 KIKVDIKDVEAPYDLVKMRASFLVMGPILARLGHAKISMPGGCA-----IGSRPI 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGAD+ +G R L G K+ L S ++MAA A
Sbjct: 125 DLHLKGFQTLGADIT--IGHGYVEARAK---KLTGKKIYLDLDFP-SVGATENIMMAAVFAE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + II+ P + + + G + + + D I+G ++ K ++ + D
Sbjct: 179 G---VTIIENAAEPEIVDLANFLNKMGANIKGAGT-DTIRIEGVKELKGAHTVIP-DR 233

Query: 255 SSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSTVVTGPPR-- 312
A F+ AA+TGG V +E ++ + TE + +T P+
Sbjct: 234 IEAGTFMVAAAMTGGNVLIIENVIVDHYRSII-----AKLTECGIKITEEPKGL 281

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
G K+ KA+D+ P D+ + V+ A G + I + V E M
Sbjct: 282 RVKGIKNYKAVDIKTLPPGFPTDMQAQMMVMTVAKGTSVIIET----VFENRFMHV-- 335

Query: 369 TELTKLGASVE 379
EL ++GA+++
Sbjct: 336 DELKRMGANIK 346

>ref|NP_847687.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
anthracis str. Ames]
ref|YP_022197.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
anthracis str. 'Ames Ancestor']
ref|ZP_00240453.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
G9241]
ref|YP_031376.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
anthracis str. Sterne]
ref|YP_086556.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
E33L]
ref|ZP_00390222.1| COG0766: UDP-N-acetylglucosamine enolpyruvyl transferase [Bacillus
anthracis str. A2012]
ref|YP_897481.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis str. Al Hakam]
ref|ZP_02214600.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0488]
ref|ZP_02394693.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0442]
ref|ZP_02399945.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0193]
ref|ZP_02880540.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0465]
ref|ZP_02899276.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0389]
ref|ZP_02936121.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis str. A0174]
ref|ZP_03020620.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
anthracis Tsiankovskii-I]
ref|ZP_03103721.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus

cereus W]

ref|ZP_03106794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus NVH0597-99]

ref|ZP_03112981.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 03BB108]

ref|YP_002454298.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus AH820]

ref|YP_002752642.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 03BB102]

ref|YP_002818059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. CDC 684]

ref|ZP_04111280.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]

ref|ZP_04253969.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 95/8201]

ref|ZP_04314653.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus BGSC 6E1]

ref|YP_002869502.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0248]

ref|ZP_05150149.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. CNEVA-9066]

ref|ZP_05186070.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. A1055]

ref|ZP_05192924.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. Western North America USA6153]

ref|ZP_05202099.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. Kruger B]

ref|ZP_05207756.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. Vollum]

ref|ZP_05211569.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis str. Australia 94]

ref|YP_003794965.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus anthracis CI]

sp|Q630W1.1|MURAI_BACCZ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1; AltName: Full=Enoylpyruvate transferase 1; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1; Short=EPT 1

sp|Q81K13.1|MURAI_BACAN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1; AltName: Full=Enoylpyruvate transferase 1; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1; Short=EPT 1

gb|AAP29173.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. Ames]

gb|AAT34672.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. 'Ames Ancestor']

gb|EAL11904.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus G9241]

gb|AAT57426.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. Sterne]

gb|AAU15293.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus E33L]

gb|ABK87974.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus thuringiensis str. Al Hakam]

gb|EDR19786.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0488]

gb|EDR85728.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0193]

gb|EDR91009.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0442]

gb|EDS95133.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0389]

gb|EDT17483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0465]

gb|EDT66073.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0174]

gb|EDV15097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis Tsiankovskii-I]

gb|EDX55085.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus W]

gb|EDX62259.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 03BB108]

gb|EDX68251.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus NVH0597-99]
gb|ACK88263.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus AH820]
gb|ACO27782.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 03BB102]
gb|ACP14702.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. CDC 684]
gb|EEK53630.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus BGSC 6E1]
gb|EEL14326.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 95/8201]
gb|EEM57111.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]
gb|ACQ47259.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus anthracis str. A0248]
gb|ADK07827.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus biovar anthracis str. CI]
Length = 434

Score = 52.4 bits (124), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 91/371 (24%), Positives = 147/371 (39%), Gaps = 37/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V + V + + +E E V+ + + + A G A L
Sbjct: 62 NAEVVFEE---NNQVTIDASKELNIEAPFEYVRKMRAV-----QVMGPLLARNRGRARIAL 113

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V G L G K+ L S
Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAYVE----GELKGAKIYLDFFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++ AA LA G I++ P + + G K + + I+G K
Sbjct: 169 ENIMSAATLAKGTT---ILENAAKEPIVDLANFLNAMGAKVRGAGTGT-IRIEGVDKLY 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLSQGDVKFAEVLEMMGAKVTWTET 303
++ + D A F+ AAITGG + +E L+ +E MG K+
Sbjct: 225 GANHSIIP-DRIEAGTFMVAAAITGGDILIEHAVPEHLR---SITAKMEEMGVKIIIEENE 280

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 281 GVRVIGPDK-----LKAVIDIKTMPHPGFPTMQSQMMALLLQADGTSMITETVFENRF 333

Query: 356 WRVKETERMVA 366
V+E RM A
Sbjct: 334 MHVEEFRRMNA 344

>ref|ZP_05827805.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter baumannii ATCC 19606]
gb|EEX03794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter baumannii ATCC 19606]
Length = 418

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 103/413 (24%), Positives = 175/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPITLTNPNLKDVTNLVKKLIGGLGVTISYENDT 70

Query: 74 KRAVVVCGCGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPFRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V G L GG+V ++ +LMA

Sbjct: 119 GSRPVDQHLKALEVLGAHIEVENGY----VHATVDGRLKGGEVVD-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + + + + G K E D+ D + G + + A

Sbjct: 174 AALADG---VTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V + L+ + KF E MGA+VT + + +

Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPSLLEAVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGGRKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E

Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPTDMQAQIMAVNAIG---RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T EKL + D + +FSL A V

Sbjct: 335 HVPELSRMGANIQVEGHD-AVVTGVEKLQAAPVMATD---LRASFSLVLAALV 383

>ref|YP_002774968.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacillus
brevis NBRC 100599]
dbj|BAH46464.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacillus
brevis NBRC 100599]
Length = 427

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 94/421 (22%), Positives = 175/421 (41%), Gaps = 48/421 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ K ++GTV + G+K+ + ++ A L++G V++NL +DV L+ +G

Sbjct: 2 DKLIINGGKPLAGTVTISGAKNSAVALIPAALLADGPVVIENLPRIQDVGIYHELLQEMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI---AMRSLTAAVTAAGGNAT 120
V ++ + D + + + N I A L A+ A G A

Sbjct: 62 ADVLFEE-----DWMEVDGRSMRLMLPNGRIKKLRASYLWGALLAKFGEAQ 109

Query: 121 YVLGDVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + G + +GA+V+ G +R G L G ++ L +S

Sbjct: 110 VGLPGGCDLGRPVLDLHIKGFAMGA EVENKNG--VMTIRAQN-GRLQGARIYLD-LVSV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+++AA A G + II+ P + L+ G + + + D I+G +

Sbjct: 166 GATINIMLAAAKADG---VTIENAAREPEIVDVATLLNNMGANIKAGT-DMIRIQGVE 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + ++ + + +Y +A AA T G V VE L+ L +GA+V

Sbjct: 222 RLRGCRHTIIPDRIEAGTYMIAAAA-TNGNVLVENVIPKHLE---SVTAKLREIGAQVVE 277

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRD-VAS 355
+ S+ V G ++IDV + P D+ + + A G + + D + S

Sbjct: 278 QDDSIQV-----IGHDSYRSIDVKTSPYPGFPTDLQQPITLLTLAKGSSIVTDNIYS 330

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAAC 415
R + + EL ++GAS++ +I KLN + D R A +A

Sbjct: 331 SRFRHVD-----ELRRMGASLKIEGRSAVIEGGSKLNGAKV-IASDLRAGAALFIAGL 382

Query: 416 A 416
A

Sbjct: 383 A 383

>ref|ZP_02420461.1| hypothetical protein ANACAC_03078 [Anaerostipes caccae DSM 14662]
gb|EDR96455.1| hypothetical protein ANACAC_03078 [Anaerostipes caccae DSM 14662]
Length = 432

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 101/434 (23%), Positives = 180/434 (41%), Gaps = 35/434 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + IL A +++GT ++N+ + D + +L A+ +G

Sbjct: 3 EQYIIKGGNPLVGEVVGAKNAALPILAAAVMTDGTCTIENMPDVRDNTNVLQAMEGIG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V ++ K VV+ G D E + A L A+ A L
Sbjct: 63 ATV--NRLGKHEVVISGSGMNADCDVDNEYIRKIR----ASYYLIGALLGKYKRARVALP 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G K LGA ++ G L G + + +S
Sbjct: 117 GGCEIGSRPIDQHIGKFKALGARIEIENGMITATAD-----ELIGCHIYMD-VVSVGATI 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ IE + K P+V + G + + D IKG +K +
Sbjct: 171 NVMMAAALAKGNTTIENVAKE---PHVVDVANFLNSMGASIRGAGT-DVIKIKGVEKLG 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ A T G +T++ L+ + LE +GA+V + +
Sbjct: 227 CEYSIIP-DQIEAGTFMTAAVATKGDITIKNVIPKHLEA---ISAKLEEIGAQVDEFDDA 282

Query: 305 VVTGTGPPR-EPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
V V R + K L + P +A++LA ++G + + + R + +
Sbjct: 283 VRVATKRLDSTQIKTLPPYGFPTDMPQMAVSLA----LSNGTSIVSESIFENRFRYVD 338

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA-CAEVPVT 421
ELTK+GA ++ IIT KL A + D R A +A A+ T
Sbjct: 339 -----ELTKMGARIQVDGRTAIITGV-KLFTGADV SAPDLRAGAALVIAGLAADGYTT 390

Query: 422 IRDPGCTRKTFPDY 435
+ D G + + +
Sbjct: 391 VSDIGYIRGYEGF 404

>ref|NP_981704.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
ATCC 10987]
sp|Q72XG6.1|MURAI_BACCI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAS44312.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus ATCC 10987]
gb|ADY24495.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar finitimus YBT-020]
Length = 434

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 148/377 (39%), Gaps = 49/377 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSSEVPVLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFEE---NNQVTIDASKELNIEAPFEYV-----RKMRAVSVQVMGPLLRNG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFAMGAKVQVGNFVEAYVE----GELKGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G I++ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGANHSIIP-DRIEAGTFMVAIAITGGDILINAVPEHLR---SITAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNMPD---DVAMTLAVVALFADGPTAIRDV 353
+ V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 IIEENEGVRVIGPDK-----LKAVDIKTMPHPGFPTDMQSQMMALLLQADGTSMITET 327

Query: 354 A----SWRVKETERMVA 366
V+E RM A

Sbjct: 328 VFENRFMHVEEFRRMNA 344

>ref|ZP_05092906.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
gb|EEB75234.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
Length = 419

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 91/381 (23%), Positives = 158/381 (41%), Gaps = 45/381 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ K + GTV++ G+K+ + +L A L++ +V+DNL + +D+ + ++ LG
Sbjct: 4 EK FVIRGGKPLRGTVQISGAKNSAVAVLP AALLADSPSVIDNLPDIKDIETLAEIIRKL 63

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K + G P + ++ A L A+ + A +
Sbjct: 64 GKVEKGKHEIKIDPTGLNSFHPPRELASRM-----ASYYLIGALLSKFNEAIIPMP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA+ G +R+ L G + +S
Sbjct: 116 GGCNIGVRPIDQHIKGFALGAETTIEHGF----IRIKA-EKLRGAHIYFD-VVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G + I++ P+V + G + + + D I G K +
Sbjct: 170 NLMLAAVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDKLEG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + +Y +A AA TGG V V+G T L+ + A+++E MG V +
Sbjct: 226 CHYTIIPDQIEAGTYMVAAAA-TGGDVYVKGVIPTHTLESII--AKLVE-MGVIVEEYDDV 281

Query: 305 VTV--TGPPREPFGKHLKADVNMMNKMP---DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V GP LK +D+ P D+ AV+ ADG + I ++ R
Sbjct: 282 IRVRREGP-----LKRVDIKTLPPYGFPTDMQQPFVALLALADGISVITENIYENR 332

Query: 358 VKETERMVAIRTELTKLGASV 378
+ E EL K+G V
Sbjct: 333 FRYLE-----ELKKMGMKV 346

>ref|YP_039278.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar konkukian str. 97-27]
sp|Q6HAZ8.1|MURAI_BACHK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enolpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAT63457.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
thuringiensis serovar konkukian str. 97-27]
Length = 434

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 91/371 (24%), Positives = 147/371 (39%), Gaps = 37/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVYVTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V + + +E E V+ + + A G A L
Sbjct: 62 NAEVVFE---NNQVTIDASKELNIEAPFEYVRKMRASV-----QVMGPLLARNGRARIAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V G L G K+ L S
Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAYVE----GELKGAKIYLDLDFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++ AA LA G I++ P + + G K + + I+G K
Sbjct: 169 ENIMSAAATLAKGTT---ILENAAKEPEIVDLANFLNMGAKVRGAGTG-IRIEGVDKLY 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303

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      ++ + D A F+ AAITGG + +E L+ +E MG K+
Sbjct: 225 GANHSIIP-DRIEAGTFMVAAAITGGDILIENAVPEHLR---SITAKMEEMGVKIIIEENE 280

Query: 304 SVTVTGPPEPFGFRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
      V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 281 GVRVIGDPK-----LKAVDIKTMHPGFPPTDMQSQMMALLLQADGTSMITETVFENRF 333

Query: 356 WRVKETERMVA 366
      V+E RM A
Sbjct: 334 MHVEEFRRMNA 344

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>ref|ZP_05367026.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
tuberculoostearicum SK141]
ref|ZP_07714067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
gb|EET76471.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
tuberculoostearicum SK141]
gb|EFQ80861.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
Length = 422

```

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 106/438 (24%), Positives = 169/438 (38%), Gaps = 55/438 (12%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + GTVK+ G+K+ +++ + L+EGTT + N DV M L LG V + +
Sbjct: 13 LEGTVKVDGAKNSVLKLAASLLAEGTTTLTNCPEILDVPLMKKVLEGLGCEVVEGSEV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAG-----GNATYVLDGVP 127
      R P + NA A+R A+V G G+A L G
Sbjct: 73 RITT-----PAQPQS-----NADFDAVRQFRASVCVLGPLTSRCGHAKVALPGGD 117

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      + RP+ GL++LGA G V L G ++L S +L
Sbjct: 118 AIGSRPLDMHQGLEKLGATTTRIEHG-----AVVAEATHLRGANIRLDFP-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      AA LA G+ ++ P + +++ G E S I+G K + P
Sbjct: 172 TAAVLAEGET---VLHNAAREPEIVDLCTMLKSMGADIEGEGS-SVVTIRGVDKLQ-PTQ 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      V GD A + AA+T G +TV G L + E L+ GA++ E V
Sbjct: 227 HEVIGDRIVAGTWAYAAAMTQGDITVGGISPRHLHLPL---EKLKSAGAELETYENGFRV 283

Query: 308 TGPPPREPFGFRKHLKAIDVNMNKMPDVAMTLAVVAL----FADGPTAI-RDVASWRVKETE 362
      R +A+D P L +A+ ADG T I +V R + +
Sbjct: 284 RMDQRP-----QAVDYQTLFPFGFPTDLQPMAIGISAIADGTTVITENVFESRFRFVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
      M+ +LGA + + ++ E+L+ T + + D A A CA+ T+
Sbjct: 337 EML-----RLGADAQVDGHHVVVRGKERLSSTHVWSSDIRAGAGLVLSALCADETTTV 389

Query: 423 RDPGCTRKTFPDYFDVLS 440
      D + +P++ + L
Sbjct: 390 HDVFHIDRGYPNFVENLQ 407

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>ref|YP_001762578.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
woodyi ATCC 51908]
sp|B1KII7.1|MURA_SHEWM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACA88483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
woodyi ATCC 51908]
Length = 419

```

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 97/400 (24%), Positives = 163/400 (40%), Gaps = 48/400 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ ++ + ++G V + G+K+ + IL+ L+E VV N+ N DV+ LR LG
Sbjct: 2 DKLKIEASEALAGNVVISGAKNAALPILMAGVLAETDFVVTNPNLRDVNTSCCELLRCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V ++ + F P + K L + R TA V+ GG A
Sbjct: 62 AEVTRSDNSEVRISTSSLDHFCAPYDLVKTMRASILILGPLLARFGTADVSLPGGCA--- 118

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+Q+GA ++ G ++ G L G + + +S
Sbjct: 119 -----IGARPVNLHLHGLQMGAKIEVEEGY---IKARVDGRLLKGAHIFMD-MVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LLMAA LA G+ II+ P V + G K E + + D I+G +
Sbjct: 168 TENLLMAATLADGET---IIENAAREPEVIDLANCLIAMGAKIEGAGT-DSIRIQGVESL 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVT--- 299
+ V D FL AA+T G + ++L+ LE GA +T
Sbjct: 224 NGC-HYRVMPDRIETGSFLIAAAVTRGKIRCVDADPSTLEA---VLAKLEDAGATITTTGS 279

Query: 300 -WTETSVTVTGPPREPFGKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
W E + P KA+++ P D+ ++ + A+G + I +
Sbjct: 280 DWIELDMQGKRP-----KAVNIKTVPYPGFPTDMQAQFCLLNVLAEGTSTITET- 328

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL ++GA++E + CII E+LN
Sbjct: 329 ---IFENRFMHV--PELIRMGANMELEGNTCIIQGIERLN 363

>gb|AAA97398.1| encodes EPSP synthase domain [Pneumocystis jirovecii]
prf||2210353C AROM protein
Length = 108

Score = 52.0 bits (123), Expect = 2e-04, Method: Composition-based stats.
Identities = 36/102 (35%), Positives = 51/102 (50%), Gaps = 7/102 (6%)

Query: 337 LAVVALFADGP--TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
LA VA P T I +++ R+KE R+ A+ EL K G E PD + + N
Sbjct: 7 LASVAYKESKPCITKITGISNQLKECNRIKAMVIELAKFGIEAGELPDGIYVKSLEISN 66

Query: 395 V----TAIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
+ I+ Y+DHR+AM+FS+ AC + P I C KT
Sbjct: 67 LLSPKNGINCYNDRHRIAMSFSLACISPKPTIILGKTCVNKT 108

>ref|ZP_03928220.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
urogenitalis DSM 15434]
gb|EEH64938.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces
urogenitalis DSM 15434]
Length = 212

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 53/196 (27%), Positives = 89/196 (45%), Gaps = 14/196 (7%)

Query: 257 ASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVT---WTETSVTVTGPPRE 313
A FLA A + GG V V + Q + +L +G +V+ S+ +T
Sbjct: 1 AGPFLAAALVAGGRVVRVPDWAETTQAGDAWRSLLPRLGGQVSAEPQNGSLVLTA---- 56

Query: 314 PFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGP---TAIRDVASWRVKETERMVAIRTE 370
G L ID +++ + ++A ++A +AL A + +R +A R ET R+ A+ TE
Sbjct: 57 -SGTGLQCGIDADLSAVGELAPSVAALALLASAQGHASRLRGIAHLRGHETNRLEALVTE 115

Query: 371 LTKLGA---SVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTIRDPGC 427
+ ++G E+G + + L+ + Y DHRMA +L T+ D C
Sbjct: 116 MRRVGGRRARQTEDGIEIEALPAGASLHPAELHAYADHRMATFAALVGLGVPGTTLDDVAC 175

Query: 428 TRKTFPDYFDVLSTFV 443
T KT PD+ + S +
Sbjct: 176 TSKTLPDFPAMWSRLL 191

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>ref|NP_834951.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
      ATCC 14579]
ref|ZP_03231294.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus AH1134]
ref|YP_002370062.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
      B4264]
ref|ZP_04194508.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus AH676]
ref|ZP_04259494.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus BDRD-Cer4]
ref|ZP_04276169.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus BDRD-ST24]
ref|YP_003667415.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      thuringiensis BMB171]
sp|Q814X9.1|MURAl_BACCR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
      AltName: Full=Enoylpyruvate transferase 1; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
      Short=EPT 1
gb|AAP12152.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
      ATCC 14579]
gb|EDZ52087.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus AH1134]
gb|ACK60046.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus B4264]
gb|EEK92143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus BDRD-ST24]
gb|EEL08759.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus BDRD-Cer4]
gb|EEL73811.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
      cereus AH676]
gb|ADH09695.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      thuringiensis BMB171]
      Length = 434
```

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 148/377 (39%), Gaps = 49/377 (12%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
      E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSVPLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFEE---NNQVTIDSSKELNIEAPFEYV-----RKMRAVSVQVMGPLLARNG 107

Query: 118 NATYVLGDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFAMGAKVQVGNFVEAYVE----GELKGAKIYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      S ++ AA LA G I++ P + + G K + + I+
Sbjct: 164 -SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 219 GVDKLYGANHSIIP-DRIEAGTFMVAIAITGGDILIEHAVPEHLR---SITAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
      + V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 275 IIEENEGVRVIGPDK-----LKAVIDIKTMPHPGFPTDMQSQMMALLLQADGTSMTITET 327

Query: 354 A----SWRVKETERMVA 366
      V+E RM A
Sbjct: 328 VFENRFMHVEEFRRMNA 344
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>ref|NP_624199.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
      [Thermoanaerobacter tengcongensis MB4]
sp|Q8R6V0.1|MURAl3_THETN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 3;
      AltName: Full=Enoylpyruvate transferase 3; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase 3;
```


Short=EPT 3
gb|AAM25803.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Thermoanaerobacter tengcongensis MB4]
Length = 417

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 91/381 (23%), Positives = 158/381 (41%), Gaps = 45/381 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ K + GTV++ G+K+ + +L A L++ +V+DNL + +D+ + ++ LG
Sbjct: 2 EKFBVIRGGKPLRGTVQISGAKNSAVAVLPAALLADSPSVIDNLPDIKDIETLAEIIRLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K + G P + ++ A L A+ + A +
Sbjct: 62 GKVEKGKHEIKIDPTGLNSFHPPRELASMR-----ASYYLIGALLSKFNEAIIPMP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA+ G +R+ L G + +S
Sbjct: 114 GGCNIGVRPIDQHIKGFALGAETTIEHGF----IRIKA-EKLRGAHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G + I++ P+V + G + + + D I G K +
Sbjct: 168 NLMLAAVKAEG---VTILENCAKEPHVVDVANFLNANIKGAGT-DTIKITGVDKLEG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
+ + +Y +A AA TGG V V+G T L+ + A+++E MG V +
Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TGGDVYVKGVIPTHELESII--AKLVE-MGVIVEEYDDV 279

Query: 305 VTV--TGPPREPFGKHLKADVNMMKMP---DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V GP LK +D+ P D+ AV+ ADG + I ++ R
Sbjct: 280 IRVRREGP-----LKRVDIKTLPPYGFPTDMQPPFAVLLALADGISVITENIYENR 330

Query: 358 VKETERMVAIRTELTKLGASV 378
+ E EL K+G V
Sbjct: 331 FRYLE-----ELKKMGMKV 344

>ref|ZP_04946771.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Burkholderia dolosa AU0158]
gb|EAY69942.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Burkholderia dolosa AU0158]
Length = 449

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 68/278 (24%), Positives = 122/278 (43%), Gaps = 27/278 (9%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G E++V++ + +SG + + G+K+ + IL L+ V+DN+ N +DV L L
Sbjct: 29 GMEKLVIEGGRRLSGEIVVSGAKNAALPILCAGLLTADPVVDNVPNLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNA 119
+G+ + D G + ++ ++ + + MR+ + + A G A
Sbjct: 89 MGVKSDTD-----GSRVQLDASRVNDLVAPYELVKTMRASILVLGPLLARFGEA 137

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + RP+ + GL+ +GA++ G + R L G ++ ++ I
Sbjct: 138 KVSPLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIEARAKR-----LKGARI-VTDMI 190

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ LLMAA LA G+ +I+ P V L+ G K + + DR I+G
Sbjct: 191 TVTGTEENLLMAATLADGET---VIENAAREPEVSDLAHLLVEMGAKIDGIGT-DRLVIQG 246

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC 276
++ ++A + D A FL A GG VT+ G
Sbjct: 247 VERLHGARHAVIP-DRIEAGTFLCAVAAAGDVTLTGV 283

>ref|YP_002006863.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase [Cupriavidus taiwanensis LMG 19424]
sp|B3R7A2.1|MURA_CUPTR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:

Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAQ70802.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cupriavidus taiwanensis LMG 19424]
Length = 416

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 94/397 (23%), Positives = 164/397 (41%), Gaps = 52/397 (13%)

Query: 15 ISGTVKLPGSKSLSNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L+ T +DN+ N +DV L LR +G+ E D A
Sbjct: 12 LKGEIRVSGAKNAALPILCAGLLTADTVALDNVPLQDVRTTLKLLRLMGMQAEFDGAR- 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V G V +A E+ + + + L A G A L G + RP+
Sbjct: 71 ---VTNLGADVNVLEAPYELVKTMRASILVLGPLVARF----GEARVSLPGGCGIGARPV 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ GL+ +GA++ G + L G +V ++ I+ LLMAA LA
Sbjct: 124 DQHIKGLQAMGAETIEHGFHARAK-----RLKGARV-VTDMITVTGTENLLMAATLAE 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G+ +++ P V L+ + G K + DR + G ++ ++ + D
Sbjct: 178 GET---VLENAAREPEVTDLAHLLVKMGAKID-GIGTDRLVVHGVERLHGASHSVI-ADR 232

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDV--KFAEVLEMMGAKVTWTETSVTVTGPPR 312
A FL AA T G + + G +Q D+ + L GA++ + + + P R
Sbjct: 233 IEAGTFLCAAAATLGDVLVRG-----VQPDILDTVLDKLREAGARLETGDDWIRLAMPHR 287

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKET---ERMV 365
KA+ ++ P D+ + A+G + RV ET R +
Sbjct: 288 A-----KAVSFRSTSEYPAFPTDMQAQFMALNAVAEG-----TARVTETIFENRFM 332

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL---NVT AID 399
++ EL +LGA + + ++ +L NV A D
Sbjct: 333 HVQ-ELNRLGADITVEGNTAVVNGVPRLSGANVMATD 368

>ref|ZP_07991679.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
variable DSM 44702]
Length = 403

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 104/428 (24%), Positives = 166/428 (38%), Gaps = 53/428 (12%)

Query: 23 GSKSLSNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVCG 82
G+K+ +++ A L+EGTTV+ N+ + DV YM+ L LG + D G
Sbjct: 4 GAKNSVLKLSAALLAEGTTVLHNIPDISDVRVMKVLEGLGCEAQID-----G 52

Query: 83 GKFPVEDAKEEVQLFLGNAGI-AMRSLTAAV-----TAAGGNATYVLDGVPRMRERPIG 135
G + E NA I ++R A+V TA +A L G + RP+
Sbjct: 53 GSVTITVP AE----ISWNADIDSVRQFRASCVLGPLTARCHHAVVALPGGDAIGSRPLD 108

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
GL+++GA G C V L G ++ L S +LMAA LA G
Sbjct: 109 MHQSGLEKMGAVTRIEHG--CVVAEVE---ALHGAEISLDFP-SVGATENILMAAVLAEG 162

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
+ ++D P + +++ G + E S + + G K +P V GD
Sbjct: 163 ET---VLDNAAREPEIVDLCHMLKQMGAIEGEGS-NTITVNGVPKL-NPVEHRVVGDR I 217

Query: 256 SASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 315
A + AA+T G +TV G L E L++ GA V T V
Sbjct: 218 VAGTWAYAAAMTRGDITVGGIDPVHLH---LVLEKLAGATVETPTGFRV-----I 267

Query: 316 GRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR----TEL 371
+ A+D P L +A+ A+ V+ TE + R EL
Sbjct: 268 QERRATAVDYQTLPPFGFPTDLQPLAI-----ALCTVSEGSVITENIFESRFRFVDEL 321

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
T++GA + +I E+L+ + + D A CA+ + D +

Sbjct: 322 TRMGADATIDGHHVVIRGREQLSYAPVWSSDIRAGAGLVLAGLCADGVTQVNDVHHIDRG 381

Query: 432 FPDYFDVL 439
+P + + L

Sbjct: 382 YPGFVENL 389

>ref|ZP_04748159.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
kansasii ATCC 12478]
Length = 418

Score = 52.0 bits (123), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 99/373 (26%), Positives = 146/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE ++ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFMVTGGNRLSGEAVVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVARIT---SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L
Sbjct: 108 RAKVALPGGDAIGSRPLDMHQAGLRQLGA--RCNIEHGCVVAQAE---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA LA G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVLAEG---VTTIHNAAREPDVVDLCTMLNQMGAVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G +TV G + LQ L GA
Sbjct: 218 GVPRLY-PTEHRVIGDRIVAATWGIAAAMTRGDITVTGIDPSHLQ---LVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S + R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDSDFRIVQYERP-----KAVNVATLPFPGFPTDLQPMALASIAADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+
Sbjct: 327 VFARFRFVEEMI 339

>ref|YP_002885677.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sp. AT1b]
gb|ACQ70232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sp. AT1b]
Length = 433

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 92/375 (24%), Positives = 151/375 (40%), Gaps = 47/375 (12%)

Query: 7 IVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTLGL 65
IV++ +++SGTV++ G+K+ + L+ L SEG +++ N+ DV+ + LR LG
Sbjct: 5 IVVRGGRKLSGTVRVEGAKNAVLKTLVATLLASEGKSILQNVPRADVYTINKVLRHLGA 64

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNA 119
V ++ V G D K+E L +R + A++ G G+A
Sbjct: 65 EVSFNEEKNEVTVDASG-----DIKDEAPLEY-----VRKMRASILVMGPILLARLGA 112

Query: 120 TYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSIS 179
+ G + RPI + G + +GA +G V G L G K+ L S
Sbjct: 113 RVAMPGGCSIGSRPIDLHLKGFEAMGA--KTVIGNGFVEASVE--GRLQGAKIYLDFF-S 167

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
++MAA LA G II+ + P + + G + + + I+G
Sbjct: 168 VGATENIMMAAVLAEGTT---IENVAKEPEIVDLANFLNGMAHVRGAGT-ETIRIEGV 223

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ + +++ + D A FL AITG + V G L+ +E MG
Sbjct: 224 ETLRGAEHSIIP-DRIEAGTFLVAGAITGSDIEVIGAEREHLR---PLISKMEEMGVHFE 279

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA- 354
T + VT P LK +DV P D+ + + L A G + I +
Sbjct: 280 DTAEGMRVTAP-----DELKPVDVKTMPHPGFPTMQSQMMALVLKAGGTSVITETVF 332

Query: 355 ---SWRVKETERMVA 366
V+E RM A
Sbjct: 333 ENRFMHVEEFRMNA 347

>gb|ABC00786.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 33

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 27/33 (81%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 86 PVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGG 117
P+E DAKEEV+LFLGNAG AMR LTA AV AAGG
Sbjct: 1 PIEKDAKEEVKLFLGNAGTAMRPLTAAVVAAGG 33

>ref|ZP_07711396.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
m3-13]
Length = 434

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 100/399 (25%), Positives = 163/399 (40%), Gaps = 47/399 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ + + GTVK+ G+K+ ++ L S+G + ++ DV+ + LR L
Sbjct: 2 EKIIIVRGQRLKGTVEGAKNAVLPIAATLLASKGKCEILDVPELSDVYTINEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE + ++V + E E V+ + + M SL A G A L
Sbjct: 62 NADVEFEN---NRIIVDATRELHTEAPFEYVRKMRASV-LVMGSELLAR---NGKAQIAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V +G V+G L G K+ L S
Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAKVK--VGNGYIDAEVDG--RLQGAKIYLDFFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G I++ + P + + G K + + I+G +
Sbjct: 169 ENIMMAATLAEGTT---IMENVAKEPEIVDLANFLNSMGAKVRGAGTGT-LRIEGVSELH 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGC---GTTSLQGDVKFAEVLEMMGAKVTW 300
++ + D A F+ AAITGG V VEG ++SL +E MG K
Sbjct: 225 GCQHNIIP-DRIEAGTFMVAIAITGGDVIVEGAVPEHSSSLIAK-----MEEMGVKFEE 277

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VAS 355
E + V GP + LK+ID+ P D+ + + L A+G + I + V
Sbjct: 278 VENGLRVIGPEK-----LKSIDIKTMPHPGFPTMQSQMMSLLLAAGTSMITETVFE 330

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
R E + ++ G SV +I P KL
Sbjct: 331 NRFMHVEEFRMNGDIKIEGRSV-----VINGPSKLQ 362

>ref|ZP_03943118.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
buchneri ATCC 11577]
ref|ZP_03954333.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
hilgardii ATCC 8290]
gb|EEI18956.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
buchneri ATCC 11577]
gb|EEI23827.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
hilgardii ATCC 8290]
Length = 439

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 97/390 (24%), Positives = 158/390 (40%), Gaps = 52/390 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL----SEGTTVVDNLLNSEDVHYMLGAL 60

Sbjct: 2 E+I++ + G V + G+K N +L + A SEG T + N+ DV+ M L
EKIIVHGGNPLKGRVHIDGAK---NAVLPIQAATILASEGHTSISNVPLLSDVYTMNNVL 58

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R L + V+ D+ + + E E V + + M L A + G A

Sbjct: 59 RFLNVKVDDELHNE-ITFDASSEISSEAPFEYVSKMRASI-VVMGPLLARL----GRAK 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISS 180
L G + RPI + G + LGA ++ G V GL G + L S

Sbjct: 113 VALPGGCAIGSRPIDLHLKGFEALGATIEQHDGY----VEATAPNGLVGTDIYLDLDFP-SV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G II P + ++ + G K + + ++ I+G

Sbjct: 168 GATQNMMAATLATGKT---IIQNAAREPEIVDLANVLNKMGAQVVGAGT-EQIRIQGVSS 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAE-----VLEM-- 293
+ ++ V+ D A F+ AA+T G V +E AE +L+M

Sbjct: 224 ELHGTDHSHVQ-DRIEAGTFMIAAAVTKGDVLIEDA-----IAEHNKPLILKMRE 272

Query: 294 MGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTA 349
MG VT ++ + V GP HLK +DV P D+ + ++ L ADG ++

Sbjct: 273 MGVSVTESDAGIRVIGP-----DHLKPVDVKTLPHPGFPTDMQPMQMTILQLAADGNSS 325

Query: 350 IRD-VASWRVKETERMVAIRTELTKLGASV 378
+ + V R E + + + T G +V

Sbjct: 326 MTETVFENRFMHMEELRRMNAKYTISGRTV 355

>ref|YP_528639.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Saccharophagus
degradans 2-40]
sp|Q21FV2.1|MURA_SACD2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABD82427.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Saccharophagus
degradans 2-40]
Length = 420

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 92/410 (22%), Positives = 169/410 (41%), Gaps = 52/410 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ I+G +++ GSK+ IL L+ G + NL + D+ ML LR +G

Sbjct: 2 DKLIIEGGSRINGEIRISGSKNSGLPILAAATLLASGPMHICNLPHLNDITTMLALLRCMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ V D+ K VE + F + +R++ A++ G G

Sbjct: 62 VGVITIDE-----KMCVEVDPTSITEFEAPYEL-VRTMRASILVLGPMLARFGK 108

Query: 119 ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI 178
A G + RP+ + GL+ +GA+++ D +R GL G + L ++

Sbjct: 109 ADVSFPGGCAIGSRPVDIHLRGLAMGAIE---VDGGYIRAKAPNGLKGARY-LMDTV 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ LLMAA LA G I++ P + + G K + + DR I+G

Sbjct: 164 TVGGTENLLMAAVLAEGTT---ILENAAREPEIVDLAECLIAMGAKIKGVGT-DRLEIEG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEV--LEMMGA 296
+ + + +Y +A AA TGG V + + D+ A + LE GA

Sbjct: 220 VKTLNGCTYEVMPDRIETGYLVAAAA-TGGWVKLR-----DTRADILEAVLLKLEEAGA 273

Query: 297 KVTWTETSVTVTGPPREPFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD 352
++T E ++ + + P KA+ P D+ + A+G +++ +

Sbjct: 274 EITVGEGTIELAMHGKRP-----KAVSFKTAPYPAFPTDMQAQFTAMNAIAEGTSSVVE 327

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
R++ + EL ++GA++ + IIT EKL + D

Sbjct: 328 TIF-----ENRLIQVH-ELNRMGANIRLEGNTAIITGVEKLKAAPVMASD 371

>ref|ZP_07053722.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria grayi

DSM 20601]
gb|EFI84735.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria grayi
DSM 20601]
Length = 433

Score = 51.6 bits (122), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 98/411 (23%), Positives = 165/411 (40%), Gaps = 50/411 (12%)

Query: 13 KEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ GTV++ G+K+ + ++ A L+E +D L + DVH + + LG +V+ DK
Sbjct: 20 KKLKGTQIDGAKNSAVALIPAAILAESQVSIDGLPDISDVHTLYRIIEELGGTVQEDK- 78

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVLDGVP---R 128
AV+ D V + L N + +R+ + A G + G+P
Sbjct: 79 -HTAVI-----DPSHLVAMPLPNGNVKKLRASYLLMGAMLGRFKAIVIGLPGGCY 127

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RPI + G LGA+V G +R L G ++ L +S +++
Sbjct: 128 LGFRPIDQHIKGFVALGAEVNEQGAIY--LRAE---KLTGARIYLD-VVSVGATINIML 181

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G +I+ P + L+ G + + + D I G +K K+
Sbjct: 182 AAVKAEGKT---VIENAAKEPEIIDVATLLNMGANIKGAGT-DTIRINGVEKLHGCKHT 237

Query: 249 YVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D A F+ AA G VT++ L+G L MG + + E SV +
Sbjct: 238 IIP-DRIEAGTFMTLAAACGDGVTIQNIPEHLEG---ITAKLHEMGVPIEFGEDSVYIG 293

Query: 309 GPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVKETER 363
K+LK +D+ P D+ L + + A+G + I D + R K
Sbjct: 294 QA-----KNLKKVDIKTYSYPGFPTDLQQPLTALMMAHAGSSVITDITIYPDRFKHI-- 344

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA 414
EL ++G + +IT P L ++ D R A +AA
Sbjct: 345 -----AELERMGGFRKLDGRSAVITGPVSLKGASVKA-SDLRAGAALVIAA 389

>emb|CAN76209.1| hypothetical protein VITISV_041624 [Vitis vinifera]
Length = 208

Score = 51.6 bits (122), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 35/48 (72%), Positives = 37/48 (77%), Gaps = 6/48 (12%)

Query: 88 EDAKE--EVQLFLGNAGIAMRSLTAAVTAA---GGNATYVLDGVPRM 129
ED E EVQLFLGNAG AMR LTA VTAA GGNA+YVLDGVPR+
Sbjct: 116 EDTGEVGEVQLFLGNAGTAMRPLTAVVTAAVTAAGGNASYVLDGVPRI 163

>ref|YP_001086592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile 630]
ref|YP_003213186.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile CD196]
ref|YP_003216632.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile R20291]
emb|CAJ66943.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Clostridium
difficile 630]
emb|CBA60286.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Clostridium
difficile CD196]
emb|CBE01674.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Clostridium
difficile R20291]
Length = 423

Score = 51.2 bits (121), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 94/405 (23%), Positives = 164/405 (40%), Gaps = 47/405 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I+++ + G+VK+ G+K+ I+ L+ G + ++ + N DVH + LR +G
Sbjct: 9 KIIVKKSNPLKGSVKIDGAKNAVLPIIAATLLANGKSTLNGVPNLRDVHVISDLLRHVGA 68

Query: 66 SVEADK---AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE + + + C + P E ++ FL + R + ++ GG A

Sbjct: 69 EVEYKENTLTVDASNIKTC--EAPYELVRKMRASFLVMGPLLARFNSTKISMPGGCA--- 123

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RPI + G K LGA ++ G L G K+ L S

Sbjct: 124 -----IGTRPIDLHLKGFKALGAKIEMDHGFVEAATE-----KLVGNKLYLDFF-SVGA 171

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA LA G II+ P + + G + + + + IKG ++

Sbjct: 172 TENIMMAASLAEGTT---IENAAEPEIVDLANFLNEMGADVKGAGT-NTIKIKGVKEL 227

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
K ++ + +A+Y +A AA+T G +TVE L+ V L G ++T +

Sbjct: 228 KGAENHVIPDRIEAATYMVVA-AAMTKGDITVENVLMHKLKPVVA---KLREAGCEITEMD 283

Query: 303 TSVTVTGPPREPFGKHLKKAIDVNMNMKMP---DVAMTLAVVALFADGP-TAIRDVASWR 357
SV V GP K LK ID+ P DV + A+G I V R

Sbjct: 284 NSVRVVGPF-----KVLKPIDIKTLPHPGFPTDVQAQFMAMLTVANGTGVVIETVFENR 336

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
E ++GA+++ ++ ++L+ A++ D

Sbjct: 337 FMHV-----AEFNRMGANIKIDGRSAVVNGVDELHGAAVNATD 374

>ref|ZP_04466225.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 7P49H1]
gb|EFP46834.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Haemophilus
influenzae 7P49H1]
Length = 421

Score = 51.2 bits (121), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 96/414 (23%), Positives = 167/414 (40%), Gaps = 41/414 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG+V + G+K+ + IL A L+ + N+ +D+ L LR LG+ D+

Sbjct: 12 LSGSVNISGAKNAALPILFAAILATEPVKLTNPVELKDIETTLNLRQLGVIANRDEGA 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R

Sbjct: 72 VLLDASNINHFTAPYELVKTMRASIWALAPLVARFHQGVVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGAD+ G V+ L G ++ + +S +++MAA L

Sbjct: 123 PVDLHISGLEKLGAIVLEEGY---VKAQVSDRLVGTRIVIE-KVSVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G +I+ P + T + + G K + S I+G + +++ V

Sbjct: 178 AKGTT---VIENAAAREPEIVDTADFLNKMGAKITGAGSA-HITIEGVEHLTGCEHSVVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG V + +L + + L GA+V TE S+T+

Sbjct: 233 DRIETGTFLIAAASISGRVVCQNTKADTLDAVI---DKLREAGAQVDVTENSITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I

Sbjct: 290 RP-----KAVNIRTAPHPGFPTDMQAQFTLLNMVAEGTSIITETIF-----ENRFMH I- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
EL ++G E + + E+L+ T + D R +++ LA C TI

Sbjct: 338 PELIRMGGAIEGNTAVCHGVEQLSGTEV-MATDLRASISLVLAGCIATGETI 390

>ref|NP_693894.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanobacillus
ihayensis HTE831]
sp|Q8EM86.1|MURAI_OCEIH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
dbj|BAC14928.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanobacillus
ihayensis HTE831]
Length = 443

Score = 51.2 bits (121), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 100/380 (26%), Positives = 153/380 (40%), Gaps = 53/380 (13%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLNRII--LLAAL--SEGTTVVDNLLNSEDVHYMLGAL 60
      E+I++   +++GTV+L G+K   N+L L A+L SEG +V+ +   DV+ +   L
Sbjct: 2  EKIIIVSGGHQLNGTVRLEGAK---NAVLPVLAASLIASEGESVIKEVPVLADVYTINEVL 58

Query: 61  RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---- 116
      R L   VE D   K V +   +   E   E V               R + A+V   G
Sbjct: 59  RNLNAEVEFDSTTK-TVNINASQQLETEAPFEYV-----RKMRAVVLVLGPLLA 106

Query: 117 --GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKL 174
      G+A   + G   + RPI   + G + +GA++   G   V N G L G K+ L
Sbjct: 107 RYGHAKVAMPGGCAIGSRPIDLHLKGFEAMGAEIHVNGY----VEANVNGRLQGAKIYL 162

Query: 175  SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
      S   ++MAA LA G   IE   K   I +   L M   V A   +
Sbjct: 163 DMP-SVGATENIMMAAALAEGKTVIENAAKEPEIVDLANYLNKMGANIVGA---GTETI 217

Query: 235  YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMM 294
      I G +K +   ++   + D   A F+   +AITGG V +E   L+   +   LE M
Sbjct: 218 RIIGVEKLRGTETHIIP-DRIEAGTFMVASAITGGNVFIENAMREHLRSVISK---LEEM 273

Query: 295  GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI 350
      V   + + GP +   LK+ D+   P   D+   +   + L A+G   I
Sbjct: 274 NVDVIDENGGLRIIGPEK-----LKSTDIKTLPHPGFPTMQSQMMSLMLRAEGTGVI 326

Query: 351  RDVA----SWRVKETERMVA 366
      +   V+E   RM A
Sbjct: 327 TETVFENRFMHVEEFRRMNA 346

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>ref|ZP_03784314.1| hypothetical protein RUMHYD_03797 [Blautia hydrogenotrophica DSM 10507]
gb|EEG47330.1| hypothetical protein RUMHYD_03797 [Blautia hydrogenotrophica DSM 10507]
Length = 430

Score = 51.2 bits (121), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 99/424 (23%), Positives = 176/424 (41%), Gaps = 39/424 (9%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E+ V++   + G V++ G+K+ +   IL A +++ T +++NL +   D++ +L A+ +G
Sbjct: 2  EQYVIKGGNPLVGEVEIAGAKNAALGILSAAIMTDETLIENLPDVRDINVLLAISGIG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      VE   ++   V   G   + D   + +   A   L A+   +A   L
Sbjct: 62  AQVERINSS----TVKINGS-TISDVSVDEYI--KKIRASYLLGALLGKYKHAEPVLP 114

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G   + RPI   + G + LGA V+   G   + G + L   +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGATVEIKHGAIVARAE-----NMHGSHIFLD-MVSVGATI 168

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      ++MAA +A G   II+   P+V   +   G   + + + D   IKG +K
Sbjct: 169 NIMMAAAMAPGRT--IIENAAREPHVVDVANFLNSMGANIKGAGT-DIIRIKGVEKLHR 224

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      + A +   D   A F+   AA T G VTV+   L+   LE +G +V   + +
Sbjct: 225 TEYAIIP-DQIEAGTFMFAAAATKGDVTVKNVIPKHLEATTA---KLEEIGCQVEEFDDA 280

Query: 305  VTVTGPPREPFGGRKHLKAI---DVNMNKMPDVAMTLAVVALFADGPTAIRD-VASWRVKE 360
      V +   R   R H+K +   +   P +A+TLA   A G + + + +   R K
Sbjct: 281 VRIVANKR--LTRTHVKTLPPGYPTDMQPQIAVTLA---LAKGTSIVTESIFENRFKY 334

Query: 361  TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIIDTYDDHRMAMAFSLAACAEVPV 420
      +   EL+++GA+++   + II   E L   + + D R   A +A A   +
Sbjct: 335 VD-----ELSRMGANIKVEGNSAIIIDGVEGLTGARV-SAPDLRAGAALVIAGLAAEGI 386

Query: 421  TIRD 424
      T+ D

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Sbjct: 387 TVVD 390

>gb|ACB05443.1| chloroplast 5-enolpyruvylshikimate 3-phosphate synthase [Lolium
rigidum]
Length = 30

Score = 51.2 bits (121), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 24/30 (80%), Positives = 26/30 (86%)

Query: 104 AMRSLTAAVTAAGGNATYVLDGVPRMRERP 133

AMR+LTAAV+ NATYVLDGVPRMRERP

Sbjct: 1 AMRALTAAVSDKENATYVLDGVPRMRERP 30

>ref|ZP_05270254.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-66c26]
ref|ZP_05320650.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile CIP 107932]
ref|ZP_05328260.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-63q42]
ref|ZP_05349241.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile ATCC 43255]
ref|ZP_05354409.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-76w55]
ref|ZP_05383261.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-97b34]
ref|ZP_05399623.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-23m63]
ref|ZP_06894194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile NAP08]
ref|ZP_06905033.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile NAP07]
ref|ZP_07405148.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile QCD-32g58]
gb|EFH05566.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile NAP08]
gb|EFH13860.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
difficile NAP07]
Length = 417

Score = 50.8 bits (120), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 94/405 (23%), Positives = 164/405 (40%), Gaps = 47/405 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65

+I+++ + G+VK+ G+K+ I+ L+ G + ++ + N DVH + LR +G

Sbjct: 3 KIIVKKSNPLKGSVKIDGAKNAVLPIIAATLLANGKSTLNGVPNLRDVHVISDLLRHVGA 62

Query: 66 SVEADK---AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122

VE + + + C + P E ++ FL + R + ++ GG A

Sbjct: 63 EVEYKENTLTVDASNIKTC--EAPYELVRKMRASFLVMGPLLARFNSTKISMPGGCA-- 117

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQY 182

+ RPI + G K LGA ++ G L G K+ L S

Sbjct: 118 -----IGTRPIDLHLKGFKALGAKIEMDHGFVEAATE-----KLVGNKLYLDFP-SVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242

++MAA LA G II+ P + + G + + + + IKG ++

Sbjct: 166 TENIMMAASLAEGTT---IENAAEEPEIVDLANFLNEMGADVKGAGT-NTIKIKGVKEL 221

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302

K ++ + +A+Y +A AA+T G +TVE L+ V L G ++T +

Sbjct: 222 KGAEHNVIPDRIEAAATYMAA-AAMTKGDITVENVLEHLKPVA---KLREAGCEITEMD 277

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGP-TAIRDVASWR 357

SV V GP K LK ID+ P DV + A+G I V R

Sbjct: 278 NSVRVVGPP-----KVLKPIDIKTLPHPGFPTDVQAQFMAMLTVANGTGVVIETVFENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402

E ++GA+++ ++ ++L+ A++ D

Sbjct: 331 FMHV-----AEFNRMGANIKIDGRSAVVNGVDELHGAAVNATD 368

>ref|ZP_04219897.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-44]
gb|EEL48397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-44]
Length = 433

Score = 50.8 bits (120), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 149/377 (39%), Gaps = 50/377 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIVRGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSVYITINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V + + +E E V R + A+V G G
Sbjct: 62 NAEVVFEE--NNQVTIDASKELNIEAPFEYV-----RKMRAVQVMGPLLARNG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V +G V+ L G K+ L
Sbjct: 108 RARIALPGGCAIGSRPIDQHLKGFEAMGAKVK--VGNGFVEAYVD---ELKGAKIYLDFF 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++ AA LA G I++ P + + G K + + I+
Sbjct: 163 -SVGATENIMSAAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IRIE 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + D A F+ AAITGG + +E L+ +E MG K
Sbjct: 218 GVDKLYGANHSIIP-DRIEAGTFMVAAAITGGDILIEHAVPEHLR---SITAKMEEMGVK 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
V V V GP + LKA+D+ P D+ + + L ADG + I +
Sbjct: 274 VIEENEGVRVIGPSK-----LKAVDIKTMPHPGFPTMQSQMMALLLHADGTSMTITET 326

Query: 354 A---SWRVKETERMVA 366
V+E RM A
Sbjct: 327 VFENRFMHVEEFRRMNA 343

>ref|YP_003256074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter actinomycetemcomitans D11S-1]
gb|ACX82855.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter actinomycetemcomitans D11S-1]
Length = 425

Score = 50.8 bits (120), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 95/416 (22%), Positives = 168/416 (40%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV++ G+K+ + IL A L+ + N+ + +D+ L LR LG+ VE +K
Sbjct: 12 LKGTVEISGAKNAALPILFAAILATEPVTLTNVPDLKDIETTLKILRQLGVVVEQNKPGT 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VRLDASKIDHFIAPYELVKTMRASIALAPLVARFNQGVVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGA + G V+ G L G ++ + +S ++++AA L
Sbjct: 123 PVDLHISGLERLGAKIALEDGY---VKAYVDGRLNGTRIVME-KVSVGATLSIMIAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G +I+ P + T + + G K + S D I+G + +++ V
Sbjct: 178 TKGTT---VIENAAAREPEIADTAEFNLKMGAKISGAGS-DAITIEGVNRLTGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG + + +L + + L GA+V TE ++T+
Sbjct: 233 DRIETGTFLVAAAISGGRIVCKNTKANTLDAVI---DKLREAGAQVDVTEDTITLDMWGN 289

Query: 313 EPFGRKHLKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P KA+++ P D+ ++ + A+G + I + R + I

Sbjct: 290 RP-----KAVNIRTAPYPGFPTDMQAQFTLLNMVANGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424

EL ++G E + I L+ + D R +++ LA C TI D

Sbjct: 338 PELIRMGGKAEIEGNTAICHGVSHLSGAEV-MATDLRASISLVLAGCIATGETIVD 392

>ref|ZP_03940189.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
brevis subsp. gravesensis ATCC 27305]
gb|EEI70412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
brevis subsp. gravesensis ATCC 27305]
Length = 439

Score = 50.8 bits (120), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 96/390 (24%), Positives = 158/390 (40%), Gaps = 52/390 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLAL----SEGTTVVDNLLNSEDVHYMLGAL 60

E+I++ + G V + G+K N +L + A SEG T + N+ DV+ M L

Sbjct: 2 EKIIIVHGGNPLKGRVHIDGAK---NAVLPPIQAATILASEGQTSISNVPLLSDVYTMNNVL 58

Query: 61 RTLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120

R L + V+ D+ + + E E V + + M L A + G A

Sbjct: 59 RFLNVKVDDELHNE-ITFDASSEISSEAPFEYVSKMRASI-VVMGPELLARL---GRAK 112

Query: 121 YVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180

L G + RPI + G + LGA ++ G V GL G + L S

Sbjct: 113 VALPGGCAIGSRPIDLHLKGFEALGATIEQHDGY---VEATAPNGLVGTDIYLDFF-SV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240

++MAA LA G +I P + ++ + G K + + ++ I+G

Sbjct: 168 GATQNMMAATLATGKT--VIQNAAREPEIVDLANVLNKMGAKEVVGAGT-EQIRIQGVS 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAE-----VLEM-- 293

+ ++ V+ D A F+ AA+T G V +E AE +L+M

Sbjct: 224 ELHGTDHSSVQ-DRIEAGTFMIAAAVTRGDVLIEDA-----IAEHNKPLILKMR 272

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTA 349

MG VT ++ + V GP HLK +DV P D+ + ++ L ADG ++

Sbjct: 273 MGVSVTESDAGIRVIGP-----DHLKPVDVKTLPHPGFPTDMQPQMTILQLAADGNSS 325

Query: 350 IRD-VASWRVKETERMVAIRTELTKLGASV 378

+ + V R E + + + T G +V

Sbjct: 326 MTETVFENRFMHMEELRRMNAKYTISGRTV 355

>ref|ZP_03824066.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. ATCC 27244]
ref|ZP_06726834.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
haemolyticus ATCC 19194]
gb|EEH68039.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. ATCC 27244]
gb|EFF83475.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
haemolyticus ATCC 19194]
Length = 419

Score = 50.8 bits (120), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 103/413 (24%), Positives = 176/413 (42%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73

++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +

Sbjct: 11 KLEGEVRISGAKNAALPLLAAMILADSPITLTNPVNLKDVNTLVKLIAGLVGVTMSYEGET 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129

A +F P E K MR+ + + A GNA L G +

Sbjct: 71 VCADASTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189

RP+ + L+ LGA ++ G V + G L GG+V + ++ +LMA

Sbjct: 119 GSRPVDQHLKALEALGAQIEVNGY----VHASVDGRLKGGEV-IFDMVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249

A L A G + I P + + + + G K E D + D + G + + A
 Sbjct: 174 AALAEG---VTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229
 Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
 V + SY LA AAITGG V + L+ + K F E MGA+VT + + +
 Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPSLLEAVLDKFEE---MGAEVTRGDDWIELD 284
 Query: 309 GPPREPFGFRKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
 + P KA+ P+ M ++A+ A G R A+ E
 Sbjct: 285 MQGKRP-----KAVSFRTLPHPEFPPTDQQAQIMAVNAIG---RGFATISSETIFENRFM 334
 Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEV 418
 EL+++GA+++ EG D ++T EKL + D + +FSL A V
 Sbjct: 335 HVPESLRMGANIQVEGHD-AVVTGVEKLQAAPVMATD--LRASFSLVLAALV 383

>gb|AAB32920.1| enolpyruvylshikimate-3-phosphate synthase type B [Pneumocystis
 carinii]
 gb|AAA97400.1| encodes EPSP synthase domain [Pneumocystis carinii f. sp. mustelae]
 prf||2210353E AROM protein
 Length = 108

Score = 50.8 bits (120), Expect = 4e-04, Method: Composition-based stats.
 Identities = 31/92 (33%), Positives = 46/92 (50%), Gaps = 11/92 (11%)

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT-----AIDT 400
 T I + + + R+KE R+ A+ E K G E PD + LN++ ID
 Sbjct: 20 TEITGISNQRIKECNINAMVCEFKFGIEAGELPDGIYV---RALNISDLLSPTNGIDC 76
 Query: 401 YDDHRMAMAFSLAACAEV-PVTIRDPGCTRKT 431
 ++DHR+AM+FS+ AC P I + C KT
 Sbjct: 77 HNDHRIAMSFSVLACVSPNPTIILNKTCVNKT 108

>emb|CBL28304.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synergistetes
 bacterium SGP1]
 Length = 420

Score = 50.8 bits (120), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 98/395 (24%), Positives = 166/395 (42%), Gaps = 43/395 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALALSEGTTV-VDNLLNSEDVHYMLGALRTLGLSVEADK 71
 + + GTV+ G+K+ + ++ L +G + + N+ DV M+ L LG++ +
 Sbjct: 10 RPLQGTVRTQGAKNALPVMAACLLKGGALTLANVPELYDVSTMMELLTALGVTARREG 69
 Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
 + V +G + E + V+ ++ + + A G A L G +
 Sbjct: 70 ---KEVTLGVADSVWEAPESLVRKMRASSLV-----LGPLLARCGRALPLPGGCSIGS 121
 Query: 132 RPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
 RPI + GL Q+GA ++ G C L G ++ L S L+MAA
 Sbjct: 122 RPIDLHLKGLVQMGAKIEIRNGVVCAQA-----DRLRGRIYLDFFP-SVGATENLMMAAA 175
 Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
 LA G+ IE I + I + LR M GV + + IKG ++ +S + +
 Sbjct: 176 LAQGETIIEIENIAREPEIDNLA AVLRS--GVPIDMEGTGC-VRIKGVVEVRSCRERVIP 231
 Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGP 311
 + +Y LAG +TGG VTVE + D A+ LE G + ++VTV
 Sbjct: 232 DRIEACTYLLAG-VMTGGRVTVEDAIPAHI--DSLLAK-LEEAGVRFAVNGSAVTV---- 283
 Query: 312 REPFGRKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
 F L+++ + P D+ +A A+G + I + V + + A
 Sbjct: 284 ---FPADRLQSVSLKTMFPFGFPTDLQPQMAAALSLAEGTSVIEE---SVFQARFLYA- 335
 Query: 368 RTELTKLGASVEEGPDYCIITPPEKL---NVT AID 399
 EL ++GA + D +I+ E+L NV A D
 Sbjct: 336 -AELNRMGADIRVKGDTAVISGVERLSGANVKATD 369

>ref|YP_001381377.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter

sp. Fw109-5]
sp|A7HI47.1|MURA_ANADF RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABS28393.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaeromyxobacter
sp. Fw109-5]
Length = 422

Score = 50.8 bits (120), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 94/391 (24%), Positives = 155/391 (39%), Gaps = 60/391 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV+ + G+V G+K+ + I+ A L+EG +V N+ + DV + L +G
Sbjct: 2 DKIVIDGGVPLRGSVATSGAKNAALPIIAGALLAEGDHLVRNVPDLADVRTLGRLLVHMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
E + K A+ + E E V+ + + + A G A L
Sbjct: 62 CQAERNAGEKGALWIRVPAAVQPEAPYELVKTMRASV-----VVLGPLVARWGKARVSLP 116

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
G + RPI + GL LGA++ ++ P R+ G + + +Q
Sbjct: 117 GGCAIGARPIDQHLKGLSALGAEIRLEHGYVEATAPRGRLRGA-----TFTFDAQ 166

Query: 182 YLSA---LLMAAPLALGDV-----EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
++ ++MAA LA G+ E EI+D ++ V M R+
Sbjct: 167 TVTGTENVMMAALAEGETLLRNCAREPEIVD--LAAALVRMGARI-----SGAGA 215

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 291
D I+G + + P + V D A FLA A+ G VTV+GC ++ E L
Sbjct: 216 DEIRIEGVETLR-PLDHVVIADRIEAGTFLAAGALPGNDVTVQGCVLHVEA--LVEKL 271

Query: 292 EMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGP 347
GA+V + + V G R + +DV P D+ + + ADG
Sbjct: 272 RAAGAELVLPVDGGLRVVGDGRP-----RPVDVRTAPHPGFPTDMQAQMMALLCLADGS 324

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASV 378
+ I + V E M EL +LGA +
Sbjct: 325 SKITET---VFENRFMHV--QELQRLGAEI 349

>ref|ZP_07729106.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
oris PB013-T2-3]
gb|EFQ53806.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactobacillus
oris PB013-T2-3]
Length = 441

Score = 50.4 bits (119), Expect = 5e-04, Method: Compositional matrix adjust.
Identities = 101/457 (22%), Positives = 168/457 (36%), Gaps = 66/457 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALS----EGTTVVDNLLNSEDVHYMLGAL 60
E+I+++ + + G V + GSK N +L L A + +GT ++N+ DV M L
Sbjct: 2 EKIIIKGGRPLRGQVTVESK---NAVLPLQAAAILAVQGTVTLNNVPPVTDVQLMNRL 58

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
R L L + ++ V+ G P+ E N A + + A G A
Sbjct: 59 RFLNLKTAYGEKQRQLVI---NGSVPLSS---EAPFEYVNQMRASLLVMGPILLARTGQAR 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGS 177
L G + RPI + GL++LGA + F+ C L G ++ L
Sbjct: 113 IALPGGCSIGARPIDLHLAAGLRKLKLGATIKQDAGFIDARC-----DHLVGSRITLDFP 164

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS-----WD 232
S L+MAA +A G I I+ P + L+ + G + + S
Sbjct: 165 -SVGATENLMAATMAEG---ITTIENAAEPEIVELANLLNKMGGRVHAGSKVIRIQG 220

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 292
+Y+ G + +P D A ++ AA+T G V V + LE
Sbjct: 221 VYILHGAEYTVAP-----DRIEAGTWMLAAAVTNGDVIVRNAAAAY---NTSLIAKLE 270

Query: 293 MMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKP-----DVAMTLAVVALFADG 346

MG V E + V G I ++ MP D+ + V+ L A+G
Sbjct: 271 EMGVTVIKQEDGIRVLGTS-----VLIPASVKAMPYPGFPTDLQPQMTVLQLLANG 321
Query: 347 PTAIRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHR 405
+ + + V R E EL ++ A + I+ P + + T + D
Sbjct: 322 TSTMEEHVFQERFNHLE-----ELRRMNADFQIAGSVAILDGPTRFSQTEVAATDLRA 374
Query: 406 MAMAFSLAACAEVPTTIRDPGCTRKTFPDYFDVLSTF 442
A A + +P C + + D++ L
Sbjct: 375 GAALVLAGLAATGITQVCNPQCLDRGYDFYQKLHQL 411

>ref|NP_871332.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Wigglesworthia
glossinidia endosymbiont of Glossina brevipalpis]
sp|Q8D2M5.1|MURA_WIGBR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
dbj|BAC24475.1| murA [Wigglesworthia glossinidia endosymbiont of Glossina
brevipalpis]
Length = 418

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 90/394 (22%), Positives = 164/394 (41%), Gaps = 54/394 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ V++ +++G V + GSK+ S IL LSE + N+ +D + + LR LG
Sbjct: 2 NQFVIKSGSNKLTGDFVIFSGSKNASLPILFATILSEEEIEIQNVPKIKDTEFAIKLLRYLG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+VE +K+ + + + + + + + + + A++ A G G
Sbjct: 62 ATVEENKS-----IYINAKNISYHAPCNL-VKTMRASIWALGPLLARFGE 106
Query: 119 ATYVLDGVPFRMRPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ L G + RP+ + GLK+LGA + G V+ N G L ++ ++ I
Sbjct: 107 GSISLPGGCEIGNRPVDLHLYGLKKGAKIYKLDGY----VKANVKGRLHSARIVMN-KI 161
Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++ AA LA+G I II+ P + T + G K + + +IKG
Sbjct: 162 SVGATLTIMSAATLAIG---ITIIENAAREPEIIDTANFLISLGAKINGVGT-NTIFIKG 217
Query: 239 GQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+K K Y + D FL AAI+ G +T +L +K L GA+
Sbjct: 218 VKKLKG--GVYKILPDRIETGTFLVAAAIISRGKITCYDTNPNTLNIVLK---KLHESGAR 272
Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + + + + P KA+ + + P D+ V+ L + G + I +
Sbjct: 273 IEIGKDWIKLDMIDKRP-----KAVKIETSPYPGFPTDMQAQFTVLNLISYGSSIITE- 325
Query: 354 ASWRVKETERMVAIRTELTKLG--ASVEEGPDYC 385
+ E M +EL K+G A ++ +C
Sbjct: 326 ---NIFENRFMHI--SELIKMGGRAIIKNNNIFC 354

>ref|YP_003839890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor obsidiansis OB47]
gb|ADL41904.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor obsidiansis OB47]
Length = 419

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 78/303 (25%), Positives = 131/303 (43%), Gaps = 22/303 (7%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+IV++ + G V + G+K+ + ++ A +SEG +V++NL EDV M L LG
Sbjct: 6 EKIVIEGGYPLEGEVINGAKNAAVAVIPAALMSEGESVIENLPLIEDVVFAMDDILLKLG 65
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ + + + A L A+ G A +
Sbjct: 66 AKIEYDNHSLKIDARNLHSYIAPYESVKKIR-----ASYYLIGALLTRFGKAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RPI + G + LGADV G ++ L G K+ L +S
Sbjct: 118 GGCNFGSRPIDQHIKGFRLGADVRIENGM----IKAYA-DRLVGTKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G I II+ P+V T + G K + + + D I+G +
Sbjct: 172 NLMLAAVKAKG---ITIIENAAKEPHVVDANFLNSMGAKIKGAGT-DVIRIEGVDRLYP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K A + + +Y +A A T G + V+ L+ A+++E MGA+V E S
Sbjct: 228 TKYAIIPDQIEAGTYMIAACA-TKGHIVVKNVIPKHLESLT--AKLVE-MGAEVITYEDS 283

Query: 305 VTV 307
+ V
Sbjct: 284 IEV 286

>ref|ZP_05345049.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]
gb|EET62164.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]
Length = 429

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 96/427 (22%), Positives = 176/427 (41%), Gaps = 46/427 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T V++NL + +D+H +LGA+R +G
Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALGILAAAIMTDDTVVIEINLPDVQDIHALLGAIRGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VEA + V + V E ++ A L A+ A L
Sbjct: 62 ATVEAH---GKTQVINGSSIGSVSDVEYIKKIR----ASYLLGALLGKYKRAEVPLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G K LGA G+ L G + L ++S
Sbjct: 114 GGCNIGSRPIDLHLKGFKALGAKTRISHGSIIAEAC-----LRGNHIYLD-TVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G +I+ P+V + G + + + D I+G ++ +
Sbjct: 168 NIMMAASMAEGRT---VIENAAKEPHVVDVANFLNSMGANIKGAGT-DIIRIRGVERLHA 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ AA+T G V V+ L+ A+++E +G +V + +
Sbjct: 224 TEYSIIP-DQIEAGTFMFAAAVTKGDVIVKNVIPKHLEATT--AKLVE-IGCQVEEFDDA 279

Query: 305 VVTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASWR 357
V V R + N+ +P D+ + V A+G + + + + R
Sbjct: 280 VRVVKRLN-----NTNVKTLPPYGPYPTDMQPQIGVALALANGTSLVTESIFENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
K + EL ++GA + + +I EK + D R A +A A
Sbjct: 331 FKYVD-----ELMRMGADIRVEGNTAVIYGTEKFTGARVSA-PDLRAGALVIAGLAA 382

Query: 418 VPVTIRD 424
+TI D
Sbjct: 383 EGITIVD 389

>ref|YP_045400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
sp. ADP1]
sp|Q6FED0.1|MURA_ACIAD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAG67578.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate
transferase) (UDP-N-acetylglucosamine enolpyruvyl
transferase) (EPT) [Acinetobacter sp. ADP1]
Length = 418

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.

Identities = 103/415 (24%), Positives = 172/415 (41%), Gaps = 52/415 (12%)

```
Query: 14  EISGTVKLPGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ ++N+ N +DV+ ++ + LG++++ +
Sbjct: 11  KLEGEVRISGAKNAALPLLAAMILADSPITLNNVPLNKDVNTLVKLIAGLGITMDYEGET 70

Query: 74  KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71  VKADTSTLSNQFAPYELVK-----TMRASILVLGPLLARYGNAQVSLPGGCAI 118

Query: 130  RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V G L G + ++ +LMA
Sbjct: 119  GSRPVDQHLKALEALGAHIEVENGY----VHATVDGRLKGADITFD-MVTVGGTENILMA 173

Query: 190  APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G I P + +++ G K E D+ D + G + + +
Sbjct: 174  AVLAEGTTTIR---NAAREPEITDLAQMLIEMGAKIEGLDT-DTLVVTGVESLHGCEYSV 229

Query: 250  VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V + L+ + KF E MGA+VT E + +
Sbjct: 230  VADRIETGSY-LAAAAITGGRVKTTHTDPSLLESVLDKFEE---MGAEVTRGEDWIELD 284

Query: 309  GPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ P D+ L V + G I S + E M
Sbjct: 285  MMGKRP-----KAVSFRTLPHPEFPTDMQAQLMAVNVIGRGFATI---SETIFENRFM 334

Query: 365  VAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D I+T EKL + D + +FSL A V
Sbjct: 335  HV--PELSRMGANIQVEGND-AIVTGVEKLQAAPVMATD---LRASFSLVLAALV 383
```

```
>ref|ZP_05116642.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
superfamily [Labrenzia alexandrii DFL-11]
gb|EEE47241.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
superfamily [Labrenzia alexandrii DFL-11]
Length = 289
```

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 65/249 (26%), Positives = 111/249 (44%), Gaps = 20/249 (8%)

```
Query: 33  LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAAKRAVVVGCGGKFPVEDAK 91
+ AL+ G T V LL SEDV A+R +G +E D + +G G +
Sbjct: 1  MFGALAVGRTTVQGLLESEDVLATADAMRAVGAKIEKQDDGSYTVDGIGLGSLL-----E 55

Query: 92  EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCF 151
+ + GNAG +R + AT+V D + +RP+G ++ L+++G +V
Sbjct: 56  PQGVIDFGNAGTGVRLTMGIFGSHNIAATFVGDA--SLSKRPMGRVLNPLREMGNTNVIAR 113

Query: 152  LGTDCPPVRVNGIGGLP-GGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPY 210
G P LP +V + S+Q SA+L+A A G + + I
Sbjct: 114  DGDRLPASIRGAEQALPITYRVPM---SAQVKSAVLLAGLNAPG-----VTTVIEPIAT 165

Query: 211  VEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITG 268
+ T ++++ FG + +++ +R GQ P++ V D SSA++ + A I
Sbjct: 166  RDHTEKMLKGFADISVSLNEAGERVIKLTGQPELKPQDIDVPADPSSAAFPIVAALIVP 225

Query: 269  GT-VTVEGC 276
G+ VT+E
Sbjct: 226  GSDVTIENV 234
```

```
>ref|ZP_03237826.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus H3081.97]
ref|YP_002341352.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
AH187]
ref|YP_002532816.1| udp-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus cereus
Q1]
gb|EDZ56295.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus H3081.97]
gb|ACJ78082.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH187]
```


gb|ACM15527.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Q1]
Length = 434

Score = 50.4 bits (119), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 95/379 (25%), Positives = 150/379 (39%), Gaps = 53/379 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K ++GTV++ G+K+ I+ A L S+G V+ + DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVRVEGAKNAVLPIIAAALLASDGKNVLSEVPVLSDVYTINEVLRHL 61

Query: 64 GLSV--EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
V E +K V + + +E E V R + A+V G
Sbjct: 62 NAEVVFENNK-----VTIDASKELNIEAPFEYV-----RKMRASVQVMGPILLAR 105

Query: 117 -GNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLS 175
G A L G + RPI + G + +GA V G V G L G K+ L
Sbjct: 106 NGRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNFVEAYVE----GELKGAKIYLD 161

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S ++ AA LA G I++ P + + G K + +
Sbjct: 162 FP-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFLNAMGAKVRGAGTGT-IR 216

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMG 295
I+G K ++ + D A F+ AAITGG + +E L+ +E MG
Sbjct: 217 IEGVDKLYGANHSIIP-DRIEAGTFMVAAAITGGDILIENAVPEHLR---SITAKMEEMG 272

Query: 296 AKVTWTETSVTVTGPPREPFGRKHLKVIDNMNKMP----DVAMTLAVVALFADGPTAIR 351
K+ V V GP + LKA+D+ P D+ + + L A+G + I
Sbjct: 273 VKIIIEENEGVRVIGPDK-----LKAVIDIKTMPHPGFPTDMQSQMMALLLQAEGTSMIT 325

Query: 352 DVA----SWRVKETERMVA 366
+ V+E RM A
Sbjct: 326 ETVFENRFMHVEEFRMNA 344

>ref|ZP_03292078.1| hypothetical protein CLOHIR_00021 [Clostridium hiranonis DSM 13275]
gb|EEA86318.1| hypothetical protein CLOHIR_00021 [Clostridium hiranonis DSM 13275]
Length = 408

Score = 50.1 bits (118), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 95/395 (24%), Positives = 155/395 (39%), Gaps = 45/395 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+ GTVK+ G+K+ I+ L+EG +V+ + N DVH + LR LG V +
Sbjct: 4 LRGTVKIDGAKNAVLPIIAATLLAEGKSVLKGVPNLRDVHVISDLLRHLGAEVTYEGTTL 63

Query: 74 --KRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
+ + C + P E ++ FL + R ++ GG A +
Sbjct: 64 TVDASNITTC--EAPYELVRKMRASFLVMGPILLARFNHTKISMPPGCA-----IGT 112

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RPI + G K LGA+V+ G L G K+ L S ++MAA
Sbjct: 113 RPIDLHLKGFKSLGAEVEIDHGFVEAKTE-----KLTGNKLYLDFP-SVGATENIMMAAA 166

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G II+ P + + G + + + + IKG + K ++ +
Sbjct: 167 LAEGTT---IENAAEEPEIVDLANFLNEMGANVKGAGT-NTIKIKGVESLKGAEHTVIP 222

Query: 252 GDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
+A+Y +A AA+T G +TVE L+ L G ++ E +V V GP
Sbjct: 223 DRIEAATYMAA-AAMTKGDITVENVMEHLK---PIIAKLRETGCEIEMENAVRVIGP- 277

Query: 312 REPFGRKHLKVIDNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ LK ID+ P DV + A+G + + V E M
Sbjct: 278 -----EVLKPIDIKTLPHPGFPTDVQAQFMAMLTIANGTAVVIET---VFENRFMHV- 326

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
E ++GA ++ I+ +KL ++ D
Sbjct: 327 -AEFNRMGADIKIEGRSAIVNGVDKLYGAKVNATD 360

>ref|YP_002905746.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
kroppenstedtii DSM 44385]
gb|ACR17203.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Corynebacterium
kroppenstedtii DSM 44385]
Length = 425

Score = 50.1 bits (118), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 109/431 (25%), Positives = 168/431 (38%), Gaps = 41/431 (9%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V++ G+K+ +++ A L+EGTTV+ N DV YM LR LG V D
Sbjct: 16 LQGQVRVAGAKNSVLKLMGAALLAEGTTVLTNCPEIADVPYMAVLRGLGCRVVLDGPTV 75

Query: 75 RAVV---VCGCGKFPVEDAKEEVQLFLGNAG-IAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V V F DA + + + G + RS A V GG+A +
Sbjct: 76 YITVPEHVTSDADF---DAVRKFRASVCVLGPLTARSHRAVVALPGGDA-----IG 123

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ GL++LGA G V+ L G +KL S +L AA
Sbjct: 124 SRPLDMHQSGLEKLGATTKIEHG----CVVSEAESLHGASIKLDFP-SVGATENILTAA 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G ++D P + ++ G K + S + ++G + P V
Sbjct: 178 VLAEGTT--VLDNAAREPEIVDLCTMLSEMGAKISGAGS-NTITVEGVPRP-DPVRHEV 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD A + AAIT G +TV G + L E ++ GA+V T V
Sbjct: 233 IGDRIVAGTWYAAAATQGDITVGGIDPSFLH---LVLEKVKGAGAEVETATGFRVVQN 289

Query: 311 PREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETE-RMVAIRT 369
R KA+D P L +A+ + V + V E+ R V
Sbjct: 290 HRP-----KAVDYQTLPPFGFPTDLQPMIALCSVSEGSTVITENVFESRFRFV---D 339

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E+T+LGA + +I E+L+ + + D A CA+ + D
Sbjct: 340 EMTRLGADAYIDGHVMIRGVEQLSSAPVWSSDIRAGAGLVLAGLCADGMTEVNDVYHID 399

Query: 430 KTFPDYFDVLS 440
+ +PD+ + L+
Sbjct: 400 RGYPDFVETLT 410

>ref|ZP_05226314.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
intracellulare ATCC 13950]
Length = 417

Score = 50.1 bits (118), Expect = 6e-04, Method: Compositional matrix adjust.
Identities = 101/373 (27%), Positives = 148/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ A L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTGGNRLSGEVAVGGAKNSVLKMAAALLAEGTSTITNCPDILDVPLMAEVLRLG 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVARIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + + L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--QCNIHGCVVQAQAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMGAVVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G ++V G LQ L GA
Sbjct: 218 GVPRLH-PTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAHLQ---VVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVAL----FADGPTAI-RD 352

VT TE+S V R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTESSFRVAQYERP-----KAVNVATLFPFGFPTDLQPMALASIAADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+

Sbjct: 327 VFEARFRFVEEMI 339

>ref|ZP_05852759.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Granulicatella
elegans ATCC 700633]
gb|EEW92395.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Granulicatella
elegans ATCC 700633]
Length = 437

Score = 50.1 bits (118), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 91/379 (24%), Positives = 152/379 (40%), Gaps = 45/379 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSE--GTTVVDNLLNSEDVHYMLGALRTL 63
E+++Q ++GTVK+ G+K+ IL + L+E G T + N+ N DVH ML L +L
Sbjct: 2 EKMIVQGGTRLNGTVKVEGAKNAVLPIAASILAEYGVTHLTNPVNLSDVHTMLAVLNSL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
++ D+ K A+ + A E V MR+ + + A G+A
Sbjct: 62 NVTSTFDEEEK-AITLNATKDVQTTAAFEFVS-----KMRASIVVMGPILLARFGHAR 112

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+ G + RPI + G + +GA + D ++ L G ++ +
Sbjct: 113 VAMPGGCAIGTRPIDLHLKGFEAMGATITQADGYVEAHADQ-----LVGARIYMDFP 164

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +++ + P + ++ + G K + + + I+
Sbjct: 165 -SVGATQNLMAATLAKGTT---LLENVAREPEIVDLANILNKMGAIIAGT-ENIRIE 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAK 297
G + ++ + D A F+ AA+TGG V VE Q L MG +
Sbjct: 220 GVDHLEGTIHSIIP-DRIEAGTFMVAADVGGDVFEADIAEHNQ---PLISKLSEMGVQ 275

Query: 298 VTWTETSVTVTGPPREPFRGRHLKAIDVNMNMKMP---DVAMTLAVVALFADG-PTAIRD 352
E + V GP + LK DV P D+ + +V L A G T
Sbjct: 276 FIEEENGIRVIGP-----ETLKPTDVKTLPHPGFPTDMQAQMTIVQLLASGVSTMTET 328

Query: 353 VASWRVKETERMVAIRTEL 371
V R E + + E
Sbjct: 329 VFENRFNHLEELRRMNAEF 347

>ref|YP_002885719.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sp. ATlb]
gb|ACQ70274.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Exiguobacterium
sp. ATlb]
Length = 418

Score = 50.1 bits (118), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 96/372 (25%), Positives = 159/372 (42%), Gaps = 40/372 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++ GTV++ G+K + L+ A L+E + ++N+ EDV M+ L+ LG+ VE D
Sbjct: 10 QKLEGTVEISGAKQSALPCLVAALLTEESVTIENVPMIEDVEVMVNLLKELGVRVERD-- 67

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G+ + E V + L G R + AAV G L G
Sbjct: 68 -----GERTTIHSNEAVAMPL--LGSETRKVRAAVYLLGVFAARFGKGAVGLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RPI + L++LG V+ G VRV+ L G ++ L +SA+
Sbjct: 116 YAIGPRPIDLHLKALERLGIHVENESG--LYHVRVD---ELVGNRIYLDLRSFGATVSAM 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
L AA LA G +I+ P V ++ G + + D IKG ++
Sbjct: 171 L-AAVLATGTT---VIENACDPEVVDVATMLTSMGAHVSGAGT-DEIRIKGVERLHGCT 225

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTETSVT 306
+ + + + + GA G VTV+ T L+G ++ ++L+ GA V E S+T
Sbjct: 226 HTLIPDRLEAGTFMMFGA--VSGHVTVPVPIPTHLEGVIIQ--KLLD-FGADVEVGEESIT 280

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
VT P + + P MT A+ L ADG + + D + + R + M
Sbjct: 281 VTANQFMPTDIRVFHYSGYPSDLQP--VMTAAL--LKADGTSVVTDKLYAQRFRHIAEMR 336

Query: 366 AIRTELTKLGAS 377
+ ++T AS
Sbjct: 337 RMNAQTILEDAS 348

>ref|ZP_06804882.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacterium
mcbrellneri ATCC 49030]
gb|EFG48412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brevibacterium
mcbrellneri ATCC 49030]
Length = 426

Score = 50.1 bits (118), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 99/409 (24%), Positives = 163/409 (39%), Gaps = 70/409 (17%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V + G+K+ +++ L+ GT+V++N+ DV M+ L +LG SV+ D A
Sbjct: 12 LRGSVDVRGAKNSVLKMAATLLAPGTSVIENVPAILDVKIMVKLLMSLGCSVDYDSDA- 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
VV + P + + + +L +R++ A+++ G A L G
Sbjct: 71 -GVVAITVPETP--EVRADYKL-----VRAMRASISVLGSLMGRVNEAHVALPGGDA 119

Query: 129 MRERPIGDLVVLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ R + GL+ +GA V + P GL G ++L+ S
Sbjct: 120 IGSRGDLHEAGLRAMGAQVSLDHGYFIARAPQ-----GLHGADIRLAFP-SVGATEN 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+MAA LA G + ID P + ++ G E + + G +
Sbjct: 172 LVMAATLANG---VTTIDNAAREPEIVDICSMLVAMGANIEGIGT-STLTVTGVESLHPV 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV--KFAEVLEMMGAKVTWTET 303
++ V GD A + AAITGG + + G G GD+ + L GA+VT E
Sbjct: 228 RHVCV-GDRIVAGTWAFAAAITGGDIQINGVG-----GDLLPVVLDKLRSAQAQVTELEG 281

Query: 304 SVTVTGPPRE-----PFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDV 353
+ V+GP R P L+ + +N + D L LF
Sbjct: 282 GIHVSGPERPRPVRISTLPFPGFPTDLQPFATLNAISD-GQGLLTENLFE----- 331

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
A WR EL +LGA VE ++ +I E L+ ++ D
Sbjct: 332 ARWRFVR-----ELARLGAQVELDGNHALINGVESLSGAEVEASD 371

>ref|YP_001997332.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chloroherpeton
thalassium ATCC 35110]
sp|B3QX75.1|MURA_CHLT3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACF14885.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chloroherpeton
thalassium ATCC 35110]
Length = 429

Score = 50.1 bits (118), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 82/322 (25%), Positives = 126/322 (39%), Gaps = 51/322 (15%)

Query: 5 EEIVLQPIKEISGTVKLPGSK-SLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
E++V++ K +SGTV + GSK S + + G TV+ + N DVH + LR +
Sbjct: 2 EKLIVIRGGKPLSGTVSVSGSKNSALAMAAALLPASGKTVIHRVPLRDVHTLSNLLRII 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V+ + + + G E E V + + A++ G G
Sbjct: 62 GAKVDFE---AHTLSIASGDISHYEAPYELV-----KKMRASIYVLGPLLGRFG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G RP+ + +K+LGAD+ G + G+ G K+
Sbjct: 108 RAKVSLPGGCAFGPRPVDLHIESMKKLGADIKLEDGYIIAKTKRKLGS-----AKIDFR 162

Query: 178 ISSQYLSA-LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE-----HSD 229
ISS + LMAA LA G + P + +E+ G K +
Sbjct: 163 ISSVGATGNTLMAAALAKGTT---CLTNAALEPEIIVYLCEFLKMGAKISGIGTTTTLEIE 219

Query: 230 SWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFA 288
D Y P A D A LA AAIT G +T+ L + KF
Sbjct: 220 GVDELY-----PIRADNICDRIEAGTLLAAAAITHGNITLTDVDPDLTAILEKFK 270

Query: 289 EVLEMMGAKVTWTETSVTVTGP 310
E+ G +V+ TET++T++ P
Sbjct: 271 EI----GCEVSTTETAITLSAP 288

>ref|ZP_05888320.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
coralliilyticus ATCC BAA-450]
gb|EEX30819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
coralliilyticus ATCC BAA-450]
Length = 421

Score = 50.1 bits (118), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 102/418 (24%), Positives = 166/418 (39%), Gaps = 51/418 (12%)

Query: 17 GTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V + G+K+ + IL + L+E V N+ + D+ + L+ LG VE +
Sbjct: 15 GEVTISGAKNAALPILFASILAEEPVEVANVPHLRDIDTTMELLKRLGAKVERN----- 68

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMR 130
G V+ + + + + +++++ A++ A G G L G +
Sbjct: 69 -----GSHVDPSS--INEYCAPYDL-VKTMRAI WALGPLVARFGQGQVSLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+QLGA + G V+ N G L G + + +S ++ AA
Sbjct: 120 ARPVDLHIHGLEQLGATITLEDGY----VKANVDGRLGAHIVMD-KVSVGATITIMCAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G ++D P + T + G K + + D I+G ++ ++A V
Sbjct: 175 TLAEGKT---VLDNAAREPEIVDTAEFLNTLGAKISGAGT-DTITIEGVERLGGGQHAVV 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AA++GG V C T Q LE GAKV E ++V
Sbjct: 231 -ADRIETGTFLVAAVSGGKV---CRNTKAQLLEAVLAKLEEAGAKVETGEDWISVDMT 286

Query: 311 PREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
RE LKA+ V P D+ ++ L A G I + + E M
Sbjct: 287 DRE-----LKAVTVRTAPHPGFPTDMAQAQFTLLNLMAKGGGVITET----IFENRFMHV 336

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I E+L+ + D R + + +A C TI D
Sbjct: 337 --PELMRMGAKAEIEGNTVICGDVEELSGAQV-MATDLRASASLVIAGCIANGETIVD 391

>ref|ZP_00990836.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
splendidus 12B01]
gb|EAP94204.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
splendidus 12B01]
Length = 421

Score = 50.1 bits (118), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 99/422 (23%), Positives = 169/422 (40%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 11 KPLSGEVTISGAKNAALPILFASILAEEPVEVSNVPHLRDIDTTMELLKRLGAKVSRN-- 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ + E+ F + +++++ A++ A G G L G

Sbjct: 69 -----GSVHVDGS--EINEFCAPYDL-VKTMRASIWALGPLVARFGEGQVSLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ + G L G + + +S +

Sbjct: 116 CAIGARPVDLHIHGLEQLGATIKLEDGY---VKASVDGRLKGAHIVMD-KVSVGATITI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G ++D P + T + + G K + + D I+G ++

Sbjct: 171 MCAATLAEGTT---VLDNSAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVERLGGGH 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
++ V D FL AA++GG V L+ + LE GAKV E ++

Sbjct: 227 HSVV-ADRIETGTFLVAAVSGGKVCRNTNAHLLEAALA---KLEEAGAKVETGEDWIS 282

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ RE LKA+ + P D+ ++ + A G I +

Sbjct: 283 LDMTDRE-----LKAVKIVTAPHPGFPTDMQAQFTLLNMMAKGSGVITETIF-----EN 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
R + I EL ++GA E + I EKL+ + D R + + +A C TI

Sbjct: 332 RFMHI-PELQRMGAKEIEGNTAICGETEKLGAQV-MATDLRASASLVIAGCIAQGETI 389

Query: 423 RD 424
D

Sbjct: 390 VD 391

>ref|ZP_01168542.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
NRRL B-14911]
gb|EAR68501.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
NRRL B-14911]
Length = 435

Score = 49.7 bits (117), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 100/383 (26%), Positives = 153/383 (39%), Gaps = 40/383 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K +SGTVK+ G+K+ ++ L S+G +V+ ++ DV+ + LR L

Sbjct: 2 EKIIIVRGGKRLSGTVKVEGAKNAVLPIAATLLASDGKSVIRDVPTLSDVYTINEVLRYL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE V+V + VE E V+ + + M SL A G A L

Sbjct: 62 NAEVEFK---NNEVIVDASRELKVEAPFEYVRKMRASV-LVMGSL---LARNGRARVAL 113

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA V G V L G K+ L S

Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGAKVKVGNGFIEAEVEDR---LQGAKIYLDLP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ + P + + + G K + + + I+G

Sbjct: 169 ENIMMAATLAKGTT---IIENVAKEPEIVDLANFLNKMGAQVKGAGTGT-IEGVDMLF 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTIVTVEGC---GTTSLQGDVKFAEVLEMMGAKVTW 300
+ + D A F+ AAITGG V V+ TSL +E MG

Sbjct: 225 GAVHNIIP-DRIEAGTFMVAAAITGGDVLVQNAVPEHMTSLIAK-----MEEMGVTFIE 277

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD-VAS 355
V V GP + LKA+D+ P D+ + + L A G + I + V

Sbjct: 278 EGEGVRVIGDPK-----LKAVDIKTMPHPGFPTMQSQMMALLLRAKGTSMITETVFE 330

Query: 356 WRVKETERMVAIRTELTKLGASV 378
R E + E+ G SV

Sbjct: 331 NRFMHVEEFRMNAEVKIEGRSV 353

>ref|YP_001578518.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
ref|YP_001947349.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
multivorans ATCC 17616]
ref|ZP_03574682.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
multivorans CGD2M]

ref|ZP_03580291.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans CGD2]
ref|ZP_03586394.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans CGD1]
gb|ABX14021.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans ATCC 17616]
dbj|BAG44813.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans ATCC 17616]
gb|EED99342.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans CGD1]
gb|EEE05306.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans CGD2]
gb|EEE10869.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia multivorans CGD2M]
Length = 449

Score = 49.7 bits (117), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 68/280 (24%), Positives = 118/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEIEVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++V++ + ++G + + G+K+ + IL LS +DN+ N +DV L L
Sbjct: 29 GMDKLVIEGGRRLAGEIVVSGAKNAALPILCAGLLSAEPVHLNDVNPQLQDVRTTLKVLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + +++++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVSDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGAHHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|YP_002936386.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium rectale ATCC 33656]
gb|ACR74252.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium rectale ATCC 33656]
emb|CBK89357.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium rectale DSM 17629]
emb|CBK94351.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium rectale M104/1]
Length = 430

Score = 49.7 bits (117), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 100/427 (23%), Positives = 176/427 (41%), Gaps = 45/427 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + G V++ G+K+ + IL A +++ T +DNL N D++ +L A+ +G
Sbjct: 2 EQYVIKGGNPLYGEVEIGGAKNAALAILAAAIMTDETVTIDNLPNVRDINVLLQAIEEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE K V G F V E ++ A L A+ +A
Sbjct: 62 AHVERVDIHK----VKINGSFIRGVNVDNEFIRIR-----ASYYLIGALLGKYKHAEVA 112

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RPI + G + +GAD+D G + + KV + +I+
Sbjct: 113 LPGGCDIGSRPIDLHMKGFRSMGADIDIAHGLVIARAKELKGTHIYMDKVSVGATIN--- 169

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA +A G +I+ P+V + G + + D I G +K
Sbjct: 170 ---IMMAAMADGKT---VIENAAKEPHVVDVANFLNSMGANIRGAGT-DVIRIVGVEKL 222

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + + + D A F+ A GG V V+ L+ A++LE +G +V +

Sbjct: 223 HATEYSVIP-DQIEAGTFMFAVAAAGGNVLVKNVIPKHLEATT--AKLLE-VGCQVEEFD 278

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWR 357
SV V HLK V P D+ +AV+ A+G + + + + R

Sbjct: 279 DSVRV-----ISDGLKHTQVTTLPYPGFPTDMQPMVAVLGLAEGTSTVTESIFENR 331

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
K + ELT++GA ++ + II+ ++ ++ D R A +A A

Sbjct: 332 FKYVD-----ELTRMGADIKVESNIAIISGVKRYTGARVNA-PDLRAGAALVIAGLAA 383

Query: 418 VPVTIRD 424

+T+ D

Sbjct: 384 EGITVVD 390

>ref|YP_003822651.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
saccharolyticum WM1]
gb|ADL05028.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
saccharolyticum WM1]
Length = 416

Score = 49.7 bits (117), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 73/305 (23%), Positives = 120/305 (39%), Gaps = 28/305 (9%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I +Q ++ + G +K+ GSK+ ++ A L +GTTV+ N+ +DV MLG L +G

Sbjct: 4 IQVQGLRSLKGEIKIQGSKNAVLPMMAAVLHKGTTVIHNPRIQDVFCLGILEHIGCI 63

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVL 123
D ++ + E +E ++ +MRS L+ + GNA

Sbjct: 64 CTFD---GHSLTIDASTVTQAEIPEEYIK-----SMRSSIMLSGPLLGRGTGNAVTSF 112

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + ERPI + ++LGA ++ + V L G +

Sbjct: 113 PGGCSIGERPIDLHLSAFRKLGAIE-----EKGDKLVASANRLMGADIYFPFSPVGATE 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+A LMAA A G + +I P + + G K H R + G K

Sbjct: 168 NA-LMAAVYAQG---VTVIHGAAKEPEIITLCEFLNMGAKI-HGTGTSRLAVT-GVKAL 221

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V GD A +L G + ++G L + A E MGA++ W E+

Sbjct: 222 WDSEFTVAGDRIVAGTYLMAVMAAEGNIVIQGIRPGHLTAALYLA---EKMGAIEIKWYES 278

Query: 304 SVTVT 308

+ V+

Sbjct: 279 QLEVS 283

>gb|EFV87840.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis FRI909]
Length = 421

Score = 49.7 bits (117), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 81/305 (26%), Positives = 126/305 (41%), Gaps = 20/305 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G V + G+K+ +L + L SEG + + N+ DV + L TL

Sbjct: 2 DKIVINGGNRLTGEVNVEGAKNAVLPLVLTASLLASEGQSKLVNPVELSDVETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+VE DK K AV V E E V + + M L A + G+A L

Sbjct: 62 NANVEYDKD-KNAVKVDATKTLNEEAPYEYVSKMRASI-LVMGPLLRL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGAD+ G + N GL G + L S

Sbjct: 116 PGGCAIGTRPIEQHIKGFALGADIHLENGN----IYANAKDGLKGAGIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ + P + + G K + + D I G +K

Sbjct: 171 QNIIMAASLASGK---SIIENVAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVEKLY 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++A + + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHAIIPDRIEAGTLLIAG-AITRGDIFVRGAIKEHM---ASLIYKLEEMGVLDLEYNEE 282

Query: 304 SVTVT 308
+ VT
Sbjct: 283 GIRVT 287

>ref|YP_002572527.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor bescii DSM 6725]
gb|ACM59754.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor bescii DSM 6725]
Length = 419

Score = 49.7 bits (117), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 100/408 (24%), Positives = 167/408 (40%), Gaps = 54/408 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++V++ + G V + G+K+ + ++ A +++G +V+DNL EDV M L LG
Sbjct: 6 EKLVIIEGNNPLYGEVIINGAKNAAVAVIPAALMADGESVIDNPLIEDVFAMDDILLRLG 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ ++++ A L A+ G A +
Sbjct: 66 AKIEYDNHSLKIDARNLHSCVAPYESVKKIR-----ASYYLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRV-NGI-----GGLPGGKVKLSGSI 178
G RPI + G LGAD VR+ NG+ L G K+ L +
Sbjct: 118 GGCNFGSRPIDQHIKGFTALGAD-----VRIENGMKAYADRLVGTKIYLD-VV 165

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S L++AA A G I II+ P+V T + G K + + D I+G
Sbjct: 166 SVGATINLMLAAVKAKG---ITIIENAAKEPHVVDANFLNSMGAKIKGAGT-DIIRIEG 221

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
K K A + + +Y +A A T G V V+ L+ A+++E MGA+V
Sbjct: 222 VDKLYPTKYAIIIPDQIEAGTYMIAACA-TKGHVIVKNVIPKHLESLT--AKLIE-MGAEV 277

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
E S+ E R+ L+ + P D+ + V+ +G T+I
Sbjct: 278 ITYEDSI-----EVICRQRLRGSSIKTMPYPGFPTDLQPQMTVLLSLCNG-TSIVTEG 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
W E EL K+GA+++ ++ E L V A+D
Sbjct: 330 VW-----ENRYQYVDELKKMGANIKVEGRVAVVEGVESLQGAEVVAVD 372

>ref|YP_004024659.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor kronotskyensis 2002]
gb|ADQ46840.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor kronotskyensis 2002]
Length = 419

Score = 49.7 bits (117), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 99/408 (24%), Positives = 167/408 (40%), Gaps = 54/408 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++V++ + G V + G+K+ + ++ A +++G +V+DNL EDV M L LG
Sbjct: 6 EKLVIIEGNNPLDGEVIINGAKNAAVAVIPAALMADGESVIDNPLIEDVFAMDDILLRLG 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ ++++ A L A+ G A +
Sbjct: 66 AKIEYDNHSLKIDARNLHSCVAPYESVKKIR-----ASYYLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRV-NGI-----GGLPGGKVKLSGSI 178
G RPI + G LGAD VR+ NG+ L G K+ L +
Sbjct: 118 GGCNFGSRPIDQHIKGFTALGAD-----VRIENGMKAYADRLVGTKIYLD-VV 165

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S L++AA A G II+ P+V T + G K + + D I+G

Sbjct: 166 SVGATINMLAAVKAKGTT---IIENAAKEPHVVDVANFLNSMGAKIKGAGT-DVIRIEG 221

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
K K A + + +Y +A A T G V V+ L+ + A+++E MGA+V

Sbjct: 222 VDKLYPTKYAIIPDQIEAGTYMIAACA-TKGHVIVKNVIPKHLESLE--AKLIE-MGAEV 277

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
E S+ E R+ L+ + P D+ + V+ +G T+I

Sbjct: 278 ITYEDSI-----EVICRQRLRGSSIKTMPYPGFPTDLQPQMTVLLSLCNG-TSIVTEG 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
W E EL K+GA+++ ++ E L V A+D

Sbjct: 330 VW-----ENRYQYVDELKKMGANIKVEGRVAVVEGVESLQGAEVVAVD 372

>ref|ZP_08088814.1| hypothetical protein HMPREF9474_00563 [Clostridium symbiosum
WAL-14163]
ref|ZP_08105355.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14673]
gb|EGA95590.1| hypothetical protein HMPREF9474_00563 [Clostridium symbiosum
WAL-14163]
gb|EGB20655.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14673]
Length = 430

Score = 49.7 bits (117), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 100/434 (23%), Positives = 183/434 (42%), Gaps = 36/434 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + IL + +++ +++NL + D++ +L A+ +G
Sbjct: 2 EQYIMKGGNPLVGEVIISGAKNAALGILAAASIMTDEDVLIENLPDVRDINVLEAIEEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D+ + V + V E ++ A A+ +A L
Sbjct: 62 ADV--DRLDRHTVRINARNIKEVSVDEYIRKIR----ASYFIGALLGKYKSAEVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA ++ G V + I L G + L +S
Sbjct: 115 GGCNIGSRPIDQHLKGFRALGAKIEVEKGA----VVAHAI-DLVGSHIYLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ II+ P+V + G + + + D IKG K
Sbjct: 169 NIMMAATLAEGET---IIENPAKEPHVVDVANFLNSMGANIKGAGT-DVIRIKGVHKLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
+ + + D A F+ AAIT G + V+ L+ A+++E +G +V + +
Sbjct: 225 TEYSIIP-DQIEAGTFMCAAAITRGDIMVQNVIPKHLEA--ISAKLIE-LGCEVMEFDEA 280

Query: 305 VTVTGGPPREPFR-KHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
V V G P++ K L + P + +TLA A+G + + + + R K +
Sbjct: 281 VRVVGPRKQRHTDIKTLPPYPGFPTDMQPQMTVTLA----LAEGTSIVTESIFENRFKYVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
ELT++G SV+ II+ KL ++ D R A +A A TI
Sbjct: 337 -----ELTRMGGSVKVEGFSIIISGVRKLTGAQVNA-PDLRAGAALVIAGLAADGYTI 388

Query: 423 RDP-GCTRKTFFPDY 435
D G ++ + ++
Sbjct: 389 VDEIGYIQRGYENF 402

>ref|YP_003675988.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter mathranii subsp. mathranii str. A3]
gb|ADH59977.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter mathranii subsp. mathranii str. A3]
Length = 416

Score = 49.7 bits (117), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 67/260 (25%), Positives = 113/260 (43%), Gaps = 20/260 (7%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

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      + G+VK+ G+K+   I+  + LS G  V+D++  +DV+ M+  ++  G   E  +
Sbjct: 14  LKGSVKISGAKNSVLPPIAASLLSSGEIVLDDIPTLKDENVMIELIKHFGAICEFENEKL 73

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      +  +      + P E K+   FL   I  R   A  ++  GG A      +  RPI
Sbjct: 74  KIKIDIKDVEAPYELVKKMRASFLVMGPILARLGHAKISMPGGCA-----IGSRPI 124

Query: 135  GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      + G + LGAD+  +G      R      L G K+ L   S      ++MAA  A
Sbjct: 125  DLHLKGFQTLGADIT--IGHGYVEARAQ---KLTGKKIYLDFFP-SVGATENIMMAAVFAD 178

Query: 195  GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G   I II+   P +      + + G K + + + D   I+G ++ K  ++  +  D
Sbjct: 179  G---ITIIENAAEPEIVDLANFLNKGAKIKGAGT-DTIRIEGVKELKGVEHTVIP-DR 233

Query: 255  SSASYFLAGAAITGGTVTVE 274
      A  F+  AA+TGG V +E
Sbjct: 234  IEAGTFMVAAAMTGGNVLIE 253

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>ref|NP_661455.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
      tepidum TLS]
sp|Q8KEX7.1|MURA_CHLTE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|AAM71797.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
      tepidum TLS]
      Length = 424

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Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 101/409 (24%), Positives = 170/409 (41%), Gaps = 50/409 (12%)

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Query: 5   EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
      +++V++ K+I GT+  GSK+ +  I+   L+ +GT  +D  + +DV  +  L  L
Sbjct: 2   DKLVIRGGKQICGTIPASGSKNSALPIIAATLLTPDGTFAIDRTPDLKDVRTFIQLLNYL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      G   A+ + + ++   G+   +A E+      ++ + A++   G   G
Sbjct: 62  G----AETSFENLLKVSTGQLKSIEAPYEL-----VKKMRASIYVLGPLLARFG 107

Query: 118  NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      +   L G   RP+  ++ +++LGA V   G   RVNG   L G  +   S
Sbjct: 108  HTRVSLPGGCAPGPRPVDLHIMVMEKLGATVTIEKG--FINARVNG-SRLRGTHIDFPIS 164

Query: 178  ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      +AL MA+ +A G   I+D   P +E   + + G K +   +   I
Sbjct: 165  SVGATGNAL-MASVMAKGTT---ILDNAALEPEIECLCNFLVKMGAKIDGIGT-TTLVID 219

Query: 238  GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAK 297
      G  + K+ +   +  D   A   L  AAITGG+VTV   L   +   G
Sbjct: 220  GVDQLKAVEFENI-FDRIEAGTLLCAAATGGSVTVTSVAPEQL---ASVLDAFRQSGCT 275

Query: 298  VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVA--MTLAVVALF--ADGPTAIRDV 353
      VT   SVT+T P   L  +D+   P+   M   +AL  A G  +  I  D
Sbjct: 276  VITNGNSVTLTAP-----AELNPVDITARPYPEFPTDMQAQWMALMTQARGDSTIID- 327

Query: 354  ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYD 402
      R+   ER   I  EL +LGA +E   ++ ++  P++L  T  +  +  D
Sbjct: 328  ---RIY-LERFNHI-PELNRLGAHIEIRDNWALVHGPQELTGTKVMSTD 371

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>ref|YP_003733525.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
      sp. DR1]
gb|ADI92152.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
      sp. DR1]
      Length = 418

```

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 103/415 (24%), Positives = 173/415 (41%), Gaps = 52/415 (12%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAATILADSPITITNPNLKDVNTLVKLIGGLGVTIGYENDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V + G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGY----VHASVDGRLKGGEVVF-D-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AALADG---VTTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSIQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V L+ + KF E MGA+VT + + +
Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPALLESVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ P D+ L V + G I S + E M
Sbjct: 285 MMGKRP-----KAVSFRTLPHPEFPPTDMAQLMAVNVIGRGFATI---SETIFENRFM 334

Query: 365 VAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T E L + D + +FSL A V
Sbjct: 335 HV--PELSRMGANIQVEGHD-AVVTGVETLQAAPVMATD---LRASFSLVLAALV 383

>ref|ZP_06691517.1| conserved hypothetical protein [Acinetobacter sp. SH024]
gb|EFF88149.1| conserved hypothetical protein [Acinetobacter sp. SH024]
gb|ADY84120.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
calcoaceticus PHEA-2]
Length = 418

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 102/413 (24%), Positives = 173/413 (41%), Gaps = 48/413 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLDGEVRISGAKNAALPLLAATILADSPITITNPNLKDVNTLVKLIGGLGVTIGYENDT 70

Query: 74 KRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V + G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGYVHASVE----GRLKGGEVVF-D-MVTVGGTENILMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A
Sbjct: 174 AALADG---VTTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSIQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG V L+ + KF E MGA+VT + + +
Sbjct: 230 VADRIETGSY-LAAAAITGGRVKTTHTDPALLESVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA+ P+ M ++A+ A G R A+ E
Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPPTDMAQLMAVNAIG----RGFATISSETIFENRFM 334

Query: 367 IRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T E L + D + +FSL A V
Sbjct: 335 HVPPELSRMGANIQVEGHD-AVVTGVETLQAAPVMATD---LRASFSLVLAALV 383

>ref|ZP_06552740.1| hypothetical protein AWRIB429_0130 [Oenococcus oeni AWRIB429]
gb|EFD89283.1| hypothetical protein AWRIB429_0130 [Oenococcus oeni AWRIB429]
Length = 271

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 67/253 (26%), Positives = 118/253 (46%), Gaps = 19/253 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G++ LPG KS+S+R +++A++S G + + N NS D L A LG VE K +
Sbjct: 12 LNSLLLPKPGDKSISHRSIMVASISRGISRIKNFSNSTDCLSTLNAFLDLG--VEIKKYGR 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+V G G +D K+ + +GN+G R L + N V D + +RP+
Sbjct: 70 DLIVYSGGLD-AFKDPKKPLN--MGNSGTTTTRLLGLLAGQSFNTCLVGDA--SLSKRPM 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ + ++G + G P+ V G L L + S+Q SAL+ +A A
Sbjct: 125 YRVNTNPITEVGGEFS-LTGNGTLPITVIGHPSLKAFDYHLPIA-SAQVKSALIFSALQA- 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNAYVEGD 253
D I +K + ++E+ ++ FG + + I + K S + + GD
Sbjct: 182 -DEPSIIFEKEATRNLHLEI---MLNDFGADIK----TNGLCITVMPRPKLSGRTISIPGD 233

Query: 254 ASSASYFLAGAAI 266
SSA++F+ A++
Sbjct: 234 ISSA AFFMVAASL 246

>ref|ZP_06068840.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
lwoffii SH145]
gb|EEY90342.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acinetobacter
lwoffii SH145]
Length = 418

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 105/419 (25%), Positives = 179/419 (42%), Gaps = 44/419 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++ ++Q ++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG
Sbjct: 2 DKFLIQGGIKLEGEVRISGAKNAALPLLAAMILADTPITLRNVPNLKDVNTLVKLIAGLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+++ + A +F P E K L + R +A V+ GG A
Sbjct: 62 ITMTYEGDVTVAADTSTLDNQFAPYELVKTMRASILVLGPLLARYGSKAVSLPGGCA---- 117

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RP+ + L+ LGA+++ G V G L GG+V ++
Sbjct: 118 -----IGSRPVDQHLKALEALGAEIEVEAGY----VHAKVDGRLKGGEVVFV-DMTVGGT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+LMAA LA G + I P + +++ + G K E D+ D + G ++
Sbjct: 168 ENILMAAVLADG---VTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLIVTGVERLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOGDV-KFAEVLEMMGAKVT--- 299
+ A V + SY LA AAITGG + + ++ + KF E MGA+VT
Sbjct: 224 GCEYAVVADRIETGSY-LAAAAITGGRIKTTHTDPSLMEAVLDKFEE----MGAEVTRGD 278

Query: 300 -WTETSVTVTGPPREPFGKRHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRV 358
W E + P F +M A +AV A+ A G I S +
Sbjct: 279 DWIELDMLGKRPKAVSFQTLPHPEFPTDMQ-----AQIMAVNAI-AQGFATI----SETI 328

Query: 359 KETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
E M EL ++GA+++ EG D ++T EKL+ + D R + + LAA A
Sbjct: 329 FENRFMHV--PELARMGANIQVEGND-AVVTGVEKLSAAPV-MATDLRASFSVLALALA 383

>ref|ZP_04431559.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
coagulans 36D1]
gb|EEN92594.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
coagulans 36D1]
Length = 437

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 90/383 (23%), Positives = 153/383 (39%), Gaps = 40/383 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ + G V++ G+K+ ++ + L SEG +++ ++ DV + LR L
Sbjct: 2 EKIIIVRGGNRLQGAVQVEGAKNAVLPIAASLLASEGKSIIRDVPQLSDVFTISEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
V + + V + +E E V+ MR+ + + A G A
Sbjct: 62 NAEV---TFLENEITVDASRELSIETPFYVVR-----KMRASFLVLGPLLARTGKAR 110

Query: 121 YVLDGVPVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RPI + G + +GA VD G + + G L G K+ + S
Sbjct: 111 VALPGGCAIGSRPIDLHLKGFAMGAKVDVGNGF---IEASVSGRLHGAKIYMDFP-SV 165

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G +I+ P + + G + + + I+G +
Sbjct: 166 GATQINIMMAASLADGQT--VIENCAKEPEIVDLANFLNEMGANVKGAGTGT- IKIEGVE 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K + + + D A F+ AAIT G V V+G + LE MG +
Sbjct: 222 KLHAADHTIIP-DRIEAGTFMVAAAITKGNVLVKGA VPEHIS---SLIAKLEEMGVITIE 277

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VAS 355
E V V GP + LKA+D+ P D+ + + L A+G + I + V
Sbjct: 278 EENGVRVIGP-----ETLKAVDIKTMPPYGFPTMQSQMMALLLCAEGTSVITETVFE 330

Query: 356 WRVKETERMVAIRTELTKLGASV 378
R E + +L G SV
Sbjct: 331 NRFMHVEEFRMRNADLKIEGRSV 353

>ref|YP_002753299.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
capsulatum ATCC 51196]
sp|C1F8M5.1|MURA_ACIC5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACO33518.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
capsulatum ATCC 51196]
Length = 436

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 96/411 (23%), Positives = 169/411 (41%), Gaps = 53/411 (12%)

Query: 17 GTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-AKR 75
GTV++ G+K+ + + A L+E +++N+ D+ L ++G VE A+
Sbjct: 14 GTVRVSGAKNSALPCMAAAAILTEDEVILENIPQVRDIETERKLLTSMGA EVELGYGRAQH 73

Query: 76 AVVVGC-----GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ C K+ + L LG + R+ A V+ GG A +
Sbjct: 74 RTTISCRVLSDP TAKYEIVKTRMASALVLGP--LVARTGLARVSMPGGCA-----I 122

Query: 130 RERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + GL+Q+GA + G + R+ G + K+ ++G+ L+M
Sbjct: 123 GARPIDLHLIKGLEQMGATIVYEHGYIEARAERLKG-AQIHFDKITVTGT-----EDLMM 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ +++ P V L+ G + E + + + I+G +K ++
Sbjct: 176 AAVLAEGET---VLENAAREPEVTDLAALLTAMGAQIEGAGTSE-IRIQGVEKLHGARGH- 230

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV-TWTETSVTV 307
+ D A FL AITGG + V C L + LE G ++ + S+ V
Sbjct: 231 RINPDRIEAGTFLIAGAITGGDLCSHCNPAHLGAVIAK---LEEAGVRIDVLGKDSLRLV 287

Query: 308 TGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
HLK IDV+ + P D+ +A A+G T +++ + E
Sbjct: 288 R-----SEGLKPIDVSTEEYPGFPTMQAQYMALATQAEGTTLVKE----NIFENRF 336

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAA 414
M EL ++G+AAA + L+ A+ D R + + LAA
Sbjct: 337 MHV--QELVRMGANIKTAGRIASVRGKTPLSAAAV-MCSDLRASASLVLA 384

>ref|ZP_02871517.1| 3-phosphoshikimate 1-carboxyvinyltransferase [candidate division
TM7 single-cell isolate TM7a]
Length = 120

Score = 49.3 bits (116), Expect = 0.001, Method: Composition-based stats.
Identities = 37/126 (29%), Positives = 61/126 (48%), Gaps = 12/126 (9%)

Query: 228 SDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC---GTTSLQGD 284
++ + F IKG Q YKS + VEGD S ++++ I+ C SLQGD
Sbjct: 4 NNDYKSFEIKGNQSYKS-FDYTVEGDYSQVAFWIVAGIISANRDNEVKCLHVNKNSLQGD 62

Query: 285 VKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFA 344
+ E++ MGA + + V V P + K +++++ PD+A L V+A +
Sbjct: 63 REIIIEIVTRMGANLEIFDDYVIVK-PSKT-----KGTVIDISQCPDIAPILTVLAAQS 114

Query: 345 DGPTAI 350
+G T I
Sbjct: 115 EGETRI 120

>ref|ZP_06851848.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
parascrofulaceum ATCC BAA-614]
gb|EFG74849.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
parascrofulaceum ATCC BAA-614]
Length = 417

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 100/373 (26%), Positives = 147/373 (39%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
AE ++ +SG V + G+K+ +++ A L+EGT+ + N + DV M LR L
Sbjct: 2 AERFLVTGGNRLSGEVAVGGAKNSVLKMAAALLAEGTSTITNCPDILDVPLMAEVLRLGL 61

Query: 64 GLSVEADKAAKRAVVVGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVARIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLGDGVPVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--QCNIHGCVVAEAD---TLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA LA G + I P V ++ + G + E + S I
Sbjct: 163 -SVGATENILMAAVLAEG--VTTIHNAAREPDVVDLCTMLNQMGARVEGAGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G ++V G LQ L GA
Sbjct: 218 GVPRLY-PTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAHLQ---VVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S +T R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDNSFRITQYERP-----KAVNVATLPFPGFPTDLQPMAIALASIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+
Sbjct: 327 VFEARFRFVEEMI 339

>ref|ZP_04795951.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis W23144]
gb|EES37360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis W23144]
Length = 421

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 81/305 (26%), Positives = 126/305 (41%), Gaps = 20/305 (6%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G V + G+K+ +L + L SEG + + N+ DV + L TL
Sbjct: 2 DKIVINGGNRLTGEVNVEGAKNAVLPLVTASLLASEGQSKLVNVPESDVTETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+VE DK K AV V E E V + + M L A + G+A L
Sbjct: 62 NANVEYDKD-KNAVVDATKTLNEEAPYEYVSKMRASI-LVMGPLLRL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGAD+ G + N GL G + L S
Sbjct: 116 PGGCAIGTRPIEQHIKGFALGADIHLENGN----IYANAKDGLGAHIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ + P + + G K + + D I G +K
Sbjct: 171 QNIIMAASLASGK---SIIENVAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVEKLY 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++A + + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHAIIIPDRIEAGTLIIAG-AITRGDIFVRGAIKEHM---ASLIYKLEEMGIDLEYNEE 282

Query: 304 SVTVT 308
+ VT
Sbjct: 283 GIRVT 287

>ref|YP_001118249.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
vietnamiensis G4]
gb|ABO53414.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
vietnamiensis G4]
Length = 449

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 96/412 (23%), Positives = 166/412 (40%), Gaps = 58/412 (14%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRT 62
G +++V++ + +SG + + G+K+ + IL LS +DN+ N +DV L L
Sbjct: 29 GMDKLVIEGRRRLSGEIVVSGAKNAALPILCAGLLSAEPVELDNVPLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + +++++ A++ G
Sbjct: 89 MGVSQSETD-----GCRVRLDASVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAREPEVSDLAHLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMM 294
I+G ++ +++ + D A FL A GG V + G L + K E +
Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVMTGVRPHILDAVIDKLREAGVSI 302

Query: 295 GAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
+W + R P A+ + ++ P A + A F A+ VA
Sbjct: 303 DEGDSWLRVRM-----DRRP-----SAVTIRTSEYP--AFPTDMQAQF----MALNTVA 345

Query: 355 SWRVKETERMVAIR---TELTKLGASVEEGPDYCIITPPEKL---NVTAD 399
S + E + R EL +LGA++ + ++T +KL NV A D
Sbjct: 346 SGTAQVVETIFENRFMHVQELNRLGANITIDGNTALVTGVKLSGANVMATD 397

>ref|ZP_01075177.1| prephenate [Marinomonas sp. MED121]
gb|EAQ66937.1| prephenate [Marinomonas sp. MED121]
Length = 761

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 82/311 (26%), Positives = 138/311 (44%), Gaps = 35/311 (11%)

Query: 11 PIKEISGTVKLPKSKLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
P I G + L G K LS+ + +AAL EG + + NL + V L ALR +G+ VE D
Sbjct: 223 PASLIKGEINLRGDKFLSHIAITIAALCEGVSDLSNLDMGQGVKVTQLALRDMGVVVE-D 381

Query: 71 KAAKRAVVVGC---GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127


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      +R + G   G K P+      + + ++ +++ L   + A      T++ D
Sbjct: 382 FGGQRLRIHGVGLNGLKAPI-----APINVHDSALSLHVLFPVLAQKFAVTFIADDA- 434

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-KVKLSGSISSQYLSAL 186
      + +P DL+ +K +GA V      + C P +      L   KV + G S Q   A
Sbjct: 435 -LSAQPFVLDLLDIVKSMGASVTS-ESGCLPFAIATDNQLINQFKVDVKGH-SRQLKLAA 491

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVE-----MTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      LMA ++ D E+ ++D + S   VE      + ++ + VKA S      I   Q
Sbjct: 492 LMAGVMSQKDTLNLDAIES-DGVEGLLALFSCQITSKSCVKASSS-----IALAQA 543

Query: 242 YKSPKNAYVE--GDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
      K P+ A ++ D   A++ + A+++ G+   G   S Q + F +L GAK+
Sbjct: 544 QK-PRAQLDMPADMDKAAWLILLASLSPGSRLEVGNLALS-QINTHFLNLLIQGGAKI- 600

Query: 300 WTETSVTVTGP 310
      E+S ++ P
Sbjct: 601 --ESSHNLSEP 609

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>gb|ADP66777.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera aphidicola str. TLW03 (Acyrtosiphon pisum)]
Length = 416

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 94/427 (22%), Positives = 165/427 (38%), Gaps = 45/427 (10%)

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Query: 5   EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E++ ++ K ++G V + GSK+ + IL + L+EG + N+ N D++ L L LG
Sbjct: 2   EKLYVEGNKILNGHVIISGSKNAALPILFMTILTEGKIKIGNIPNLTDINIALKLLVYL 61

Query: 65   LSVEADKAA---KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
      + + +K      ++ + C   +   + + +      + A G A
Sbjct: 62   VKITGNKTLCIDASSINIFCPPYNLINKIRASIWIL-----GPLLARFGKAKI 109

Query: 122  VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
      L G ++ RPI + GL QLGA ++ L +C V   G   GK L IS
Sbjct: 110  FLPGGCKIGSRPIDLHLNGLTQLGATIN--LKNNCIDAYVK---GRLQGYILMEKISVG 164

Query: 182  YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      ++ AA LA G   IID   P +   + + G   + S ++ IKG K
Sbjct: 165  ATITIMSAAATLAKGST---IIDNAACEPEIVDIAKFLNTLGADIIGAGS-NKICIKGVLK 220

Query: 242  YKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
      + + D   FL AA + G +T   C T +      L   GAK+
Sbjct: 221  LTGGTHQVIP-DRIETGTFLVAAAASQGHIT---CHKTEPKHLTNVLMKLTEAGAKIKTG 276

Query: 302  ETSVTVTGPPREPFFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
      + + +   + P   K++++   P   D+   A++   + G   I +
Sbjct: 277  KDWIKLDMRGKRP-----KSLNICTAPYPGFPTDMQAQFALLNSISKGIGTITETI--- 327

Query: 358  VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
      E   +EL ++GA ++   + I   KL +++   D R +   LA C
Sbjct: 328  ---FENRFIYTSELIRMGAKIKIKNNTIICCGIPKL-ISSNVFSSDLRASATLILAGCIA 383

Query: 418  VPVTIRD 424
      +TI +
Sbjct: 384  AGITIVN 390

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>ref|YP_003478076.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter italicus Ab9]
gb|ADD03514.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter italicus Ab9]
Length = 417

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 96/396 (24%), Positives = 157/396 (39%), Gaps = 45/396 (11%)

```

Query: 5   EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E+ V++ K ++G+V++ G+K+ + IL A L++ +V+DNL + D+ + +R LG

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Sbjct: 2 EK FVIKGGKPLTGSVQISGAKNSAVAILPAALLADTPSVIDNLPDINDIKLLAQMIRHLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K G +P D +++ G + AV A G

Sbjct: 62 GKVEEKKHEIMIDPTGLNSFYPPRDLASKMRASYLVGALLSKFNEAVIAMPGGCNI--- 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RPI + G + LGA G +R+ L G + +S

Sbjct: 119 GV-----RPIDQHIKGFALGAKTTIEGGL----IRIKA-DKLVGNHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G + I++ P+V + G + + + D I G K

Sbjct: 168 NLMLAAVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDKLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTETS 304
+ + +Y +A AA T G V ++G L+ + A++ E MG V +

Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TKGDVYIKGVIPNHLEAII--AKLTE-MGVIVEEHDDV 279

Query: 305 VTVT--GPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAI-RDVASWR 357
V + GP LK +D+ P D+ AV+ A+G + I ++ R

Sbjct: 280 VRIKREGP-----LKHVDIRTLPPYPGFPTDMQQPFAVLLALAEGISVITENIYENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
K EL K+GA V I EKL

Sbjct: 331 FKYL-----NELEKMGAKVRIEGRNAIFEGVEKL 359

>ref|YP_003646229.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Tsukamurella
paurometabola DSM 20162]
gb|ADG77890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Tsukamurella
paurometabola DSM 20162]
Length = 417

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 108/445 (24%), Positives = 175/445 (39%), Gaps = 45/445 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ ++ ++G V + G+K+ +++ A L+EGT+V+ N DV M LR LG

Sbjct: 3 EKFLVHGGARLTGEVTVGGAKNSVLKMAAALLAEGTSVLTNCPEILDVPLMADVLRGLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAM-RSLTAAVTAAGGNATYVL 123
VE D R DA ++ + + G M R A V GG+A

Sbjct: 63 AEVELDGETARITTPAVLNHRADFDVAVKQFRASVCVLGPLMAREHRAVVALPGGDA---- 118

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RP+ GL+ LGA G C + + L G ++ L S

Sbjct: 119 -----IGSRPLDMHQSGLRALGATSSIEHG--CVVAQAD---SLVGAEITLEFP-SVGAT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+LMAA LA G + +I + P + ++ + G E + D ++G K

Sbjct: 168 ENILMAAVLAKG---LTVISNVAREPEIVDLCTMLVQMGADIEGVGT-DTLMVRGVDKLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
P V GD A+ + A +T G +TV G +L + L+ GA VT

Sbjct: 224 -PTEHRVIGDRIVAATWGFAAVMTRGDITVNGIAPETLG---VVLQKLQDAGATVTERAD 279

Query: 304 SVTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVAL----FADGPTAI-RDVASWRV 358
+ P R A++V P L +A+ ADG + I +V R

Sbjct: 280 GFRIASPERP-----HAVNVATLPFPGFPTDLQPMAGMACVADGTSMITENVFEARF 332

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAE 417
+ E MV +LGA + +I E+L+ + + D R + LA CA+

Sbjct: 333 RFVEEMV-----RLGADARTDGHHAIVIRGVEQLSSAPVWSTDI-RAGVGLVLAGLCAD 384

Query: 418 VPVTIRDPGCTRKTFPDYFDVLSTF 442
+ D + +P++ L+

Sbjct: 385 GVTEVHDVFIHIDRGYPNFVGTLTAL 409

>ref|YP_003476026.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter italicus Ab9]

gb|ADD01464.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter italicus Ab9]
Length = 416

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 67/260 (25%), Positives = 113/260 (43%), Gaps = 20/260 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+VK+ G+K+ I+ + LS G V+D++ +DV+ M+ ++ G E +
Sbjct: 14 LKGSVKISGAKNSVLPPIAASLLSSGEIVLDDIPTLKDVMVMIELIKHFGAICEFENERL 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ + + P E K+ FL I R A ++ GG A + RPI
Sbjct: 74 KIKIDIKDVEAPYELVKMRASFLVMPILARLGHAKISMPGGCA-----IGSRPI 124

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGAD+ +G R L G K+ L S ++MAA A
Sbjct: 125 DLHLKGFQTLGADIT--IGHGYVEARAQ---KLTGKKIYLDFFP-SVGATENIMMAAVFAD 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G I II+ P + + + G K + + + D I+G ++ K ++ + D
Sbjct: 179 G---ITIIENAAEPEIVDLANFLNKGAKIKGAGT-DTIRIEGVKELKGVEHTVIP-DR 233

Query: 255 SSASYFLAGAAITGGTVTVE 274
A F+ AA+TGG V +E
Sbjct: 234 IEAGTFMVAAAMTGGNVLIE 253

>ref|NP_227924.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
maritima MSB8]
sp|Q9WXW3.1|MURA_THEMEA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAD35202.1|AE001697_2 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
maritima MSB8]
Length = 421

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 105/448 (23%), Positives = 179/448 (39%), Gaps = 54/448 (12%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++V+Q + G V++ GSK+ + I+ A L + ++ N+ +DV M+ LR++G
Sbjct: 3 KLIVVQGGAVLEGEVEISGSKNAALPIMAAAILCDEEVILKNVPRQLQDVFMIDILRSIGF 62

Query: 66 SVEADK---AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE ++ KR D +EV L A ++ + G A
Sbjct: 63 RVEFEENELKIKRE-----NDISQEVYPYELVRKMRASFNVLGPIAVRTGRAKVA 111

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLG--TDCPPVRVNGIG-GLPGGKVKLSGSIS 179
L G + RP+ + GLK++G + G C R++ + LP V + +
Sbjct: 112 LPGGCSIGVPRVPDFHLEGLKMGFSIKVEHGFVEACFERRIDYVTITLPPPSVGATEHLM 171

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+ +ALL A + + + +E P + + R G E + + R I+G
Sbjct: 172 TT--AALLKGARVVIENAAME-----PEIVDLQNFINRMGGHIEGAGT-SRIVIEGV 220

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+K + + + + +Y +A AA + G V+ L F E LE GAK
Sbjct: 221 EKMQGVVEYSIIPDRIEAGTYLVAIAA-SRGKGLVKNVNPDLH---TNFFKELEETGAK-- 274

Query: 300 WTETSVITVTGPPREPFRGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAI-RDVA 354
+ V G E R+ KA+DV N P D+ + A G + I +V
Sbjct: 275 -----LKVLGNEVEIEMRERPKAVDVTNPPYGFPTDLQPQMAYLSTASGVSVITENVF 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
R + EL ++GA +E + I+ EKL+ ++ D R A +A
Sbjct: 330 KTRFLHVD-----ELKRMGADIEVSGNVAIVKGVEKLSGAPVEG-TDLRATAALLIAG 381

Query: 415 CAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
VT + F Y DV+ F

Sbjct: 382 IIADGVT--EISNVEHIFRGYEDVIDKF 407

>ref|ZP_01814316.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrionales
bacterium SWAT-3]
gb|EDK28244.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrionales
bacterium SWAT-3]
Length = 421

Score = 49.3 bits (116), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 98/422 (23%), Positives = 170/422 (40%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 11 KPLSGEVTISGAKNAALPILFASILAEEPVEVSNVPHLRDIDTTEMLLKRLGAKVSRN-- 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ + E+ F + ++++ A++ A G G L G
Sbjct: 69 -----GSVHVDGS--EINEFCAPYDL-VKTMRASIWALGPLVARFGEQVSLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ + G L G + + +S +
Sbjct: 116 CAIGARPVDLHIHGLEQLGATITLEDGY---VKASVDGRLKGAHIVMD-KVSVGATITI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G ++D P + T + + G K + + D I+G ++ +
Sbjct: 171 MCAATLAEGKT---VLDNSAREPEIVDTADFLNKLGAISGAGT-DTITIEGVERLGGGQ 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVT 306
++ V D FL AA++GG V L+ + LE GAKV E ++
Sbjct: 227 HSVV-ADRIETGTFLVAAAVSGGKVCRNTNAHLLEAALA---KLEEAGAKVETGEDWIS 282

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ RE LKA+ + P D+ ++ + A G I +
Sbjct: 283 LDMTGRE-----LKAVKIVTAPHPGFPPTDMQAQFTLLNMMAKGSGVITETIF-----EN 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
R + I EL ++GA E + I E+L+ + D R + + +A C TI
Sbjct: 332 RFMHI-PELQRMGAKAEIEGNTAICGETEQLSGAQV-MATDLRASASLVIAGCIAQGETI 389

Query: 423 RD 424
D
Sbjct: 390 VD 391

>ref|YP_003471188.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
lugdunensis HKU09-01]
ref|ZP_07913111.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
lugdunensis M23590]
gb|ADC87061.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
lugdunensis HKU09-01]
gb|EFU83023.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
lugdunensis M23590]
Length = 421

Score = 48.9 bits (115), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 94/371 (25%), Positives = 145/371 (39%), Gaps = 35/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
+ IV++ +SG V++ G+K+ +L + L +EGT+ + N+ DV + L TL
Sbjct: 2 DRIVIKGGHRLSGEVQVEGAKNAVLPLVTASLLATEGTSKLINVPKLSDVETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V D A AV V E E V + + M L A + G+A L
Sbjct: 62 NADVSYDIAGN-AVTVDATATLNEEAPYEYVSKMRASI-LVMGPLLARL-----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGAD+ G + N GL G + L S
Sbjct: 116 PGGCAIGSRPIEQHIKGFALGADIHLENGN----IYANAKNGLQGANIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

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      ++MAA LA G      +I+      P +      +      G +      + + D      I G K
Sbjct: 171 QNIIMAASLANGK---SVIENAAKEPEIVDLANYINEMGGRITGAGT-DTITIHGVNKLK 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      ++ +      + + +AG AIT G V V G      +      LE MG ++ + E
Sbjct: 227 GVVHSIIPDRIEAGTMIAG-AITRGDVYVRGAIKEHM---TSLVYKLEEMGVQLAFDEE 282

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
      V VT P      L+ +DV      P      D+      + + L A+G      I +
Sbjct: 283 GVRVTAPDT-----LQPVDVKTLPHPGFPTDMQSQMMALLLTAEGHKVITETVTFENRF 335

Query: 356 WRVKETERMVA 366
      V E      RM A
Sbjct: 336 MHVAEFRMNA 346

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>ref|YP_755129.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Syntrophomonas wolfei subsp. wolfei str. Goettingen]
gb|ABI69758.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Syntrophomonas wolfei subsp. wolfei str. Goettingen]
Length = 419

Score = 48.9 bits (115), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 82/371 (22%), Positives = 148/371 (39%), Gaps = 40/371 (10%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      ++G V++ G+K+      +L+ + L++G T++DN+      DV M+ L LG++ ++
Sbjct: 13 LNGRVVRVSGAKNAGLVLLVASTLADGETILDNMPRIIRDVEVMVQILNELGVNARWNEDGS 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      ++      G      V+ + E      L      A      L      A+      A      L G      + RP+
Sbjct: 73 LSICPPYPAGSMKVKTSYE-----LSKKLRASNLLLGALLGREREAVISLPGGCDIGSRPM 127

Query: 135 GDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
      + G++ LGA+VD      G      +      P G      S      ++M A
Sbjct: 128 DLHIKGIQALGAEVDDIEHGF-----IYARSKTPSGARVYLDFPSVGATENIMMMASRTP 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G      +I+      P +      +      G +      + + D      ++G + K+ + A + D
Sbjct: 182 GQ---SVIENAAKEPEIVDLANFLNSMGARIRGAGT-DLIKVEGVPELKACRYAIIP-DR 236

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
      A ++ GAAI+GG V VE      T L      L+ GA V T+ V V
Sbjct: 237 IEAGTYMVGAAISGGDVQVENVIPTLH---PIVAKLQETGAIVEETDQGVVV----- 286

Query: 315 FGRKHLKAIDVNMNKMP-----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
      R      + + V++ +P      D+      + +      A+G + I +      E      I
Sbjct: 287 --RAGRQVLPVDIKTLPPYGFPTDMQSQMMALLSLAEGSSVIVE-----NVFENRFQIV 338

Query: 369 TELTKLGASVE 379
      EL ++GAS++
Sbjct: 339 DELKRMGASIQ 349

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>ref|YP_003784095.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Corynebacterium pseudotuberculosis FRC41]
gb|ADK29488.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Corynebacterium pseudotuberculosis FRC41]
gb|ADL11148.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium pseudotuberculosis C231]
gb|ADL21562.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium pseudotuberculosis 1002]
gb|ADO26957.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Corynebacterium pseudotuberculosis I19]
Length = 418

Score = 48.9 bits (115), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 105/429 (24%), Positives = 166/429 (38%), Gaps = 39/429 (9%)

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Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G+V++ G+K+      +++      A L+EGTT + N      DV YM+ L LG SVE+D

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Sbjct: 13 LEGSVRVSGAKNSVLKLMMAALLAEGTTTLTNCPIQILDVPYMRVLEGLGCSVESDNGTV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
R + + + + V+ F + + + TA G A L G + RP+

Sbjct: 73 R---ISTPAEISSDADFDAVRQFRASV-----CVLGPLTARCGRAVVALPGDAIGSRPL 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
GL++LGA G L G K+ L S +L AA LA

Sbjct: 125 DMHQSGLEKLGAKTRIQHGAVVAEAE-----QLRGAKITLDFP-SVGATENILTA AVLAD 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G I+D P + +++ G + I G K P V GD

Sbjct: 179 GTT---ILDNAAREPEIFDLCTMLKEMGADIS-GEGTSTITITGVDKLY-PTHEVIGDR 233

Query: 255 SSASYFLAGAAITGGTIVTEGCGTTSIQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A + +A+T G +TV G +L + E L++ GA+V E V R P

Sbjct: 234 IVAGTWAYASAMTQGDITVGGIAPRNHLPL---EKLKVAGAEVETYE HGFVR-MNRRP 289

Query: 315 FGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR----TE 370
+A+D P L +A+ I VA TE + R E

Sbjct: 290 -----QAVDYQTLFPFGFPTDLQPMIAI-----GIATVAQTSVITENIFEARFRFVDE 337

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 430
L +LGA + ++ E+L+ T + + D A CAE + D +

Sbjct: 338 LMRGADATVDGHHVLRGVEQLSSTPVWSSDIRAGAGLVLAGLCAEGVTEVHDVFHIDR 397

Query: 431 TFPDYFDVL 439
+P++ + L

Sbjct: 398 GYPNFVEDL 406

>ref|YP_001312124.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
gb|ABR37168.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
Length = 421

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 91/403 (22%), Positives = 161/403 (39%), Gaps = 39/403 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E +V+ + GTV + G+K+ + IL A + S+G ++DN+ + EDVH + LR+L

Sbjct: 2 ERLVINGGNLLEGTVDINGAKNAAVAILPAAIMASDGKCIIDNIPDIEDVHCLERILRSL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G + K + + + ++V+ A A+ A A VL

Sbjct: 62 GCDII--KIDNNTLEIDSSNVNFDCTDDVRRMR-----ASYFFIGALLARFKKARVVL 114

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV F+ V+ + L G + +S

Sbjct: 115 PGGCSIGVRPIDQHIKFEALGADV--FIEHGAVNVKAD---KLVGANIFFD-VVSVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+++AA LA G + +++ + P+V + G + + D IKG + K

Sbjct: 169 INVMIAATLAEG--VTVLENAKEPHVVDVANFLNSMGADIRGAGT-DVIRIKGVESLK 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSIQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ A TGG V + L+ L MGA + +

Sbjct: 225 GCSYSVIP-DQIEAGTFMIAAVATGDDVYIRNVIPKHLE---SITAKLTEMGAVIEGDD 280

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ VT + P LK +++ P D+ ++ + G + I + + W +

Sbjct: 281 CIRVT--VKSP-----LKGVNIKTTPYPGFPTDIQQPMSTLLSIVPGRSLITE-SIWENR 332

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYD 402
EL K+GA+++ II +KL + D

Sbjct: 333 HKH-----IDELKKMGANIKVEGRVAIIDGAQKLTGAVVKATD 370

>ref|NP_765253.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis ATCC 12228]

ref|YP_189271.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus epidermidis RP62A]
ref|ZP_06612752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Staphylococcus epidermidis M23864:W2(grey)]
sp|Q8CRN6.1|MURAl_STAES RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1; AltName: Full=Enoylpyruvate transferase 1; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1; Short=EPT 1
sp|Q5HMC2.1|MURAl_STAEQ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1; AltName: Full=Enoylpyruvate transferase 1; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1; Short=EPT 1
gb|AA05297.1|AE016749_243 UDP-N-acetylglucosamine 1-carboxyvinyl transferase 1 [Staphylococcus epidermidis ATCC 12228]
gb|AAW55092.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Staphylococcus epidermidis RP62A]
gb|EFE60145.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Staphylococcus epidermidis M23864:W2(grey)]
Length = 421

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 81/305 (26%), Positives = 126/305 (41%), Gaps = 20/305 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G V + G+K+ +L + L SEG + + N+ DV + L TL
Sbjct: 2 DKIVINGGNRLTGEVNVGAKNAVLPLVTASLLASEGHSKLVNVPESDVTINNVLSTL 61
Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+VE DK K AV V E E V + + M L A + G+A L
Sbjct: 62 NANVEYDKD-KNAVKVDATKTLNEEAPYEYVSKMRASI-LVMGPLLRL----GHAIVAL 115
Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGAD+ G + N GL G + L S
Sbjct: 116 PGGCAIGTRPIEQHIKGFALGADIHLNGN----IYANAKDGLKGAHIHLDFP-SVGAT 170
Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ + P + + G K + + D I G +K
Sbjct: 171 QNIIMAASLASGK---SIIENVAKEPIVDLANYINEMGGKITGAGT-DTITIHGVEKLY 226
Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++A + + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHAIIPDRIEAGTLIAG-AITRGDIFVRGAIKEHM--ASLIYKLEEMGVLDLEYEE 282
Query: 304 SVTVT 308
+ VT
Sbjct: 283 GIRVT 287

>ref|ZP_06059231.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter calcoaceticus RUH2202]
gb|EEY75777.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Acinetobacter calcoaceticus RUH2202]
Length = 418

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 102/415 (24%), Positives = 173/415 (41%), Gaps = 52/415 (12%)

Query: 14 EISGTVKLPKSKLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V++ G+K+ + +L L++ + N+ N +DV+ ++ + LG+++ +
Sbjct: 11 KLEGEVRISGAKNAALPLLAATILADSPITITNPNLKDVTNLVKKLIGGLGVTIGYENDT 70
Query: 74 KRAVVVCGCGKF-PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLGDVPRM 129
+A +F P E K MR+ + + A GNA L G +
Sbjct: 71 VKADTSTLDNQFAPYELVK-----TMRASILVLGPLLARYGNAKVSPLPGGCAI 118
Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + L+ LGA ++ G V + G L GG+V ++ +LMA
Sbjct: 119 GSRPVDQHLKALEALGAHIEVENGY----VHASVDGRLKGGEVVFDMVTVGGTENILMA 173
Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I P + +++ + G K E D+ D + G + + A

Sbjct: 174 AALADG---VTIRNAAREPEITDLAQMLIKMGAKIEGLDT-DTLVVTGVESLHGCEYAV 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVT 308
V + SY LA AAITGG + L+ + KF E MGA+VT + + +

Sbjct: 230 VADRIETGSY-LAAAAITGGRIKTTHTDPALESVLDKFEE---MGAEVTRGDDWIELD 284

Query: 309 GPPREPFGKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ P D+ L V + G I S + E M

Sbjct: 285 MLGKRP-----KAVSFRTLPHPEFPTDMQAQLMAVNVIGRGFATI---SETIFENRFM 334

Query: 365 VAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
EL+++GA+++ EG D ++T E L + D + +FSL A V

Sbjct: 335 HV--PELSRMGANIQVEGHD-AVVTGVETLQAAPVMATD---LRASFSLVLAALV 383

>ref|YP_397892.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9312]
sp|Q319I9.1|MURA_PROM9 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABB50456.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9312]
Length = 456

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 92/385 (23%), Positives = 156/385 (40%), Gaps = 36/385 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++G VK+ G+K+ + +L + L+ +++N+ D+ M L+ LG+++ DK

Sbjct: 23 KLVGIVKINGAKNSALVLLASSLLTNEKIILENIPYLTIDIEKMGNILKNLGVNL-IDKND 81

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ + P + +E+ L N A A+ G A L G + RP

Sbjct: 82 QLEID-----PTNISIKELPYELVNLGRASFFCIGALLTKFGEAQVPLPGGCNIGSRP 134

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + + GL LGAD+ G +R N L G +KL S L+MAA LA

Sbjct: 135 IDEHINGLIALGADIIIEGIVKAKIRGNK-NKLHGTHIKLKCP-SVGATETLIMAASLA 192

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G IE + P ++ ++ + G K + + I G K + + D

Sbjct: 193 EGRTTIENAARE---PEIQDLCHMLNKMGAKEI-YDSGKETIIDGVNKLGGCTHKVIP-D 247

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVVTGPPRE 313
A FL AA T ++T+ L+ L+ G+K+T S+++

Sbjct: 248 RIEAGTFLIAAAATSSSITISPVIPHHLEA---VTNKLQESGSKITIKGNSISIKS---- 300

Query: 314 PFGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTE--- 370
K +K +D+ P L A F TA+ +A+ K TE + R

Sbjct: 301 ----KEIKGVDIETAPFPGFPTDLQ--APF----TALMTIANGESKITETIFENRMNHIH 350

Query: 371 -LTKLGASVEEGPDYCIITPPEKLN 394
L K+GA ++ + I + LN

Sbjct: 351 LLNKMGAIRIKLNENVAIYKGVKTLN 375

>ref|ZP_04446643.1| hypothetical protein COLINT_03386 [Collinsella intestinalis DSM
13280]
gb|EEP43887.1| hypothetical protein COLINT_03386 [Collinsella intestinalis DSM
13280]
Length = 427

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 89/380 (23%), Positives = 153/380 (40%), Gaps = 41/380 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
ISGTV + G+K+ + +++ L+ G T ++N+ N DVH M L+ +G ++ D +

Sbjct: 12 ISGTVAVSGAKNSALKLMAATLLAPGATTLENVNIISDVHVMGKVLKRMGATI--DVLDE 69

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYVLDGVPRMRE 131


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      + +      E   + V      MR+ TA      +   G A   + G   +
Sbjct: 70  HTLRIDTSAVSSWEAPYDLVA-----KMRASTAVMGPLLGRFGCAKIAMPGGCNLGA 121
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      R I   ++GL LG   D   TD   + +   GL G V L + S       L+MAA
Sbjct: 122 RKIDMHILGLGALGVQFD---TDHGYIHADAPEGLTGTAVTLEFA-SVGATENLIMAAV 176
Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      A G   +ID   P +   ++   G K   + +   I+G ++   P   V
Sbjct: 177 KAKGTT---VIDNAAREPEIVDLANMLNEMGAKITGAGT-PVVQIEGVEELH-PVTHRVV 231
Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
      GD   A F+ AA+   VE G   +   +   + LE+MG ++   E V
Sbjct: 232 GDRIEAGTFITAAALMADESGVEVTGFNPINLGMVIKK-LELMGVRIDRIENGVRAYRAD 290
Query: 312 REPFGRLKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
      R       ++ +D+   P   D+   + V++ ADG + I +   + E M A
Sbjct: 291 R-----IEPVDIQTLPFPGFPTDMQAQIMVLSALADGNSIITE----NIFENRFMFA- 338
Query: 368 RTELTKLGASVEEGPDYCII 387
      +EL ++GA +   + ++
Sbjct: 339 -SELVRMGADIRVESHAMV 357

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>ref|ZP_02536200.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase [Endoriftia persephone
'Hot96_1+Hot96_2']
Length = 225

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 44/150 (29%), Positives = 68/150 (45%), Gaps = 9/150 (6%)

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Query: 244 SPKNAYVEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      +P +   D SSA++F+ GA I G+ VT+E G   + V   +L +MGA +
Sbjct: 19  APAASMCPADISSATFFMVGACIAEGSDVTLEHVGINPTRDGV--INILRLMGADIEVLN 76
Query: 303 TSVTVTGPPREPFGGRK--HLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
      TV G P   +   LK I +   ++P D   L + A A+G T +   R
Sbjct: 77  PR-TVGGEPPVADIRVRASRLKGIHPEEQVPLAIDEFPALFIAACAEGETVLTGAEEELR 135
Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCII 387
      VKE++R+ +   L LG   + PD +I
Sbjct: 136 VKESDRIQVMADGLVTLGIDAQATPDGIVI 165

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>ref|ZP_01550531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stappia
aggregata IAM 12614]
gb|EAV40885.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stappia
aggregata IAM 12614]
Length = 429

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 74/307 (24%), Positives = 131/307 (42%), Gaps = 37/307 (12%)

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Query: 14  EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      E++G + + G+K+ +   +++ + L++ T + N+   DV ++ L G+   +
Sbjct: 11  ELNGVIPISGAKNAALPLMIASLLTDETLTSLNVPRLRDVAQLMQILSNHGVYDYSVN--G 68
Query: 74  KRAVVVGCGGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNAT 120
      KR+   G+   A+E V   F   + RS A V+ GG A
Sbjct: 69  KRSGQDDLAGQTLNLTAREIVDTTAPYELVSKMRASFVWIGPLVARSHARVSLPGGCA- 127
Query: 121 YVLDGVPRLMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
      + RP+   + GL LGA+++   D V V   GGL G +V+   +S
Sbjct: 128 -----IGTRPVDFIDGLAALGAIEI----DGGYVIVKAPGGLKGARVEFP-KVSV 174
Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G E EI++   V++ + ++ G K E +   I+G
Sbjct: 175 GATHTIMMAATLASG--ETEIVNAAREPEVVDLA-KCLKAMGAKIE-GEGTSTIRIQGVP 230
Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300

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+ +A V + +Y +A A+TGG V ++G + L+ + E L GA +T
Sbjct: 231 RLHGAHHAVVPDRIETGYAMA-VAMTGGDVLLQGARSDDLLETAL---ETLRQTGADITQ 286

Query: 301 TETSVTV 307
T + V

Sbjct: 287 TADGIKV 293

>ref|ZP_07547188.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter wiegelii Rt8.B1]
gb|EFN49500.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter wiegelii Rt8.B1]
Length = 416

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 75/319 (23%), Positives = 131/319 (41%), Gaps = 34/319 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+VK+ G+K+ I+ + LS G V+D++ EDV+ M+ ++ G + +
Sbjct: 14 LKGSVKISGAKNSVLPPIAASLLSSGEIVLDDIPTLEDVNVMIELIKHFGAICDFENEKL 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V + P + K+ FL I R A ++ GG A + RPI
Sbjct: 74 KVKVDIKDIEAPYDLVKMRASFLVMGPILARLGHAKISMPGGCA-----IGSRPI 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGAD+ +G R L G K+ L S ++MAA A
Sbjct: 125 DLHLKGFQTLGADIT--IGHGYVEARAK---KLTGKKIYLDFFP-SVGATENIMMAAVFAE 178

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + II+ P + + + G + + + D I+G ++ K ++ + D
Sbjct: 179 G---VTIENAAEEPEIVDLANFLNKMGANIKGAGT-DTIRIEGVKELKGAHTVIP-DR 233

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR-- 312
A F+ AA+TGG V +E ++ + TE + +T P+
Sbjct: 234 IEAGTFMVAAAMTGGNVLIENVIVDHYVRSII-----AKLTECGIKITEEPKGL 281

Query: 313 EPFGRKHLKAIDVNMNMKMP 331
G K+ KA+D+ P
Sbjct: 282 RVKGIKNYKAVIDIKTLPP 300

>ref|YP_003638954.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermincola sp.
JR]
gb|ADG81053.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermincola
potens JR]
Length = 417

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 97/431 (22%), Positives = 164/431 (38%), Gaps = 40/431 (9%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G VK+ G+K+ + I+ A L++ ++DN+ N DV+ ML ++ LG VEAD K
Sbjct: 14 GEVKIAGAKNAALAIIAAALLTDAPVIIDNVPNISDVNVMLDIVKNLG--VEADWCEKNT 71

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGD 136
+ + G + E V+ A L + A G L G + RP+
Sbjct: 72 IRIHVPGDIGYQTPYELVKKLR-----ASNLLLGPLLARQGRVEISLPGGCNIGSRPMDL 126

Query: 137 LVVGLKQLGADVDCFLGT---DCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
GL +GA+++ G C L G K+ L S ++MAA LA
Sbjct: 127 HFKGLAGMGAEIELEHGVIKGKCDR-----LEGAKIYLDFFP-SVGATENIMMAAVLA 177

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G IE + K P + + G K + + D I G + + + + + D
Sbjct: 178 KGQTVIENVAKE---PEIVDLANFLNSMGAKVRGAGT-DVIRIDGVERLRGGGRYSVIP-D 232

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
A F+ A T G + ++G TT ++ L GA++ + V V
Sbjct: 233 RIEAGTFMVAAVATDGDLLIDGVITTHIE---PLIAKLREAGAEIREEDEKVRVR----- 284

Query: 314 PFGRKHLKAIDVNMNMPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVAIRTEL 371
R L+ ID+ P M ++A+ T ++ + E + + E
Sbjct: 285 --RRSKLRPIDIKTLPPGFPDMQSQMMAML---TTVKGTSVIVENIFENRLQVADEF 338

Query: 372 TKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKT 431
++GA ++ II EKL + D A AE I + +
Sbjct: 339 KRMGAKIKVEGRTAI IQGVEKLQGA VKASDLRAGAALIIAGLMAEGETEICNTHYIERG 398

Query: 432 FPDYFDVLSTF 442
+ +D L+
Sbjct: 399 YEGIYDKLNAL 409

>ref|YP_002418285.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
splendidus LGP32]
sp|B7VKU1.1|MURA_VIBSL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAV20010.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
splendidus LGP32]
Length = 422

Score = 48.9 bits (115), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 99/422 (23%), Positives = 169/422 (40%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 12 KPLSGEVTISGAKNAALPILFASILAEFPVEVSNVPHLRDIDTTMELLKRLGAKVSRN-- 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ E+ F + +++ A++ A G G L G
Sbjct: 70 -----GSVHVDG--REINEFCAPYDL-VKTMRSI WALGPLVARFGEGQVSLPGG 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ + G L G + + +S +
Sbjct: 117 CAIGARPVDLHIHGLEQLGATIVLEDGY---VKASVDGRLKGAHIVMD-KVSVGATITI 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G ++D P + T + + G K + + D I+G ++ +
Sbjct: 172 MCAATLAEGTT---VLDNSAREPEI VDTADFLNKLGA KISGAGT-DTITIEGVERLGGGQ 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
++ V D FL AA++GG V L+ + LE GAKV E ++
Sbjct: 228 HSVV-ADRIETGTFLVAAAVSGGKVCRNTNAHLLEAALA---KLEEAGAKVETGEGWIS 283

Query: 307 VTGPPPEPFGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ RE LKA+ + P D+ ++ + A G I +
Sbjct: 284 LDMDTRE-----LKAVKIVTAPHPGFPDMQAQFTLLNMMAKGSGVITETIF-----EN 332

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
R + I EL ++GA E + I EKL+ + D R + + +A C TI
Sbjct: 333 RFMHI-PELQRMGAKAEIEGNTAICGETEKLSGAQV-MATDLRASASLVIAGCIAQGETI 390

Query: 423 RD 424
D
Sbjct: 391 VD 392

>ref|YP_001906282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
tasmaniensis Et1/99]
sp|B2VGU0.1|MURA_ERWT9 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAO95374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
tasmaniensis Et1/99]
Length = 420

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 98/420 (23%), Positives = 171/420 (40%), Gaps = 51/420 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG+ KA +
Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEEPVEIQNPVKLDIDTTMKLLSQLGV-----KAER 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V K + A E+ +++++ A++ A G G L G
Sbjct: 67 NGSVYLDASKVDIYCAPYEL-----VKTMRASIWALGPLVARFQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLGQLGAEIKLEEGY----VKASVDGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P + T + G K + S DR I+G ++
Sbjct: 172 AATLATGTT---VIENAAREPEIVDTANFLNLTGAKISGAGS-DRITIEGVERLGGGVYR 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ + ++ +AG AI+GG V +L D A++ E GA++ + V++
Sbjct: 228 VLPDRIETGTFLVAG-AISGGKVICRAAQPDTL--DAVLAKLRE-AGAEIEVGDDWVSLD 283

Query: 309 GPPREPFGFRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ + P D+ +++ L A+G I + + E M
Sbjct: 284 MHGKRP-----KAVSLRTAPHPGFPTDMQAQFSLNLVAEGTGVTET-----IFENRFM 333

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAACAEVPTVIRD 424
EL ++GA E I EKL+ + D R + + LA C VT+ D
Sbjct: 334 HV--PELARMGAHAIEIESTLICHGVEKLSSAQV-MATDLRASASVLGACIAEGVTVVD 390

>ref|ZP_07818998.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eremococcus
coleocola ACS-139-V-Col8]
gb|EFR31374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eremococcus
coleocola ACS-139-V-Col8]
Length = 435

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 88/371 (23%), Positives = 150/371 (40%), Gaps = 36/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSE-GTTTVVDNLLNSEDVHYMLGALRTL 63
EEI++Q + G VK+ G+K+ IL A L+E G + N+ DVH + L +
Sbjct: 2 EEIIVQGGNRLQGAVKVEGAKNAVLPILAGAILAETGQVHLSNVPVLSDVHTLNELNRI 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ + D+ + ++ G VE E + A + + + A G+A +
Sbjct: 62 GVVNQFDEVNQMILDASG---HVESVAEYDFVSKMRASVV---VMGPLLARFGHAKVAM 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA ++ G L G ++ L S
Sbjct: 116 PGGCAIGMRPIDLHLKGFEALGAKINSQAGYVEAQA-----DQLKGARIYLDFFP-SVGAT 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G+ I++ + P + + R G K + + + I+G +
Sbjct: 170 ENIMMAATLAEGET---ILENVAREPEIVDLANFLNRMGAKIVGAGT-ETIRIRGVKALH 225

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+++ + D A F+ AA+T G V VEG + + L MG +
Sbjct: 226 GTEHSVIP-DRIEAGTFMVAAAVTQGDVFVEGA---MREHNRPLISKLTGEMGVVFEHDE 281

Query: 304 SVTVTGPPEPFGFRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA----S 355
+ V GP + LKA DV P D+ + + L ADG + + +
Sbjct: 282 GIRVIGPAK-----LKATDVKTLPYPGFPTDMQAQMTIAQLLADGTSVMNETVFENRF 334

Query: 356 WRVKETERMVA 366
++E RM A
Sbjct: 335 MHLEELRRMSA 345

>ref|YP_002310095.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
piezotolerans WP3]
sp|B8CIN2.1|MURA_SHEPW RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;

AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACJ27508.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
piezotolerans WP3]
Length = 419

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 97/389 (24%), Positives = 156/389 (40%), Gaps = 46/389 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V + G+K+ + IL+ L+E V N+ + DV+ LR LG V K
Sbjct: 12 LAGDVVISGAKNAALPILMAGVLAETDFNVSNNVPSLRDVNTSCELLRCLGAETVTRSGDDK 71

Query: 75 RAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+ +F P E K MR+ + + A G A L G +
Sbjct: 72 VCISTTNLNEFCAPYELVK-----TMRASILILGPLLARYGKADVSLPGGCAI 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL+Q+GA ++ G ++ G L G + + IS LLMA
Sbjct: 120 GARPVNLHLQGLEQMGAKIEVKEGY----IKARVDGRLKGAHIFMD-MISVGATENLLMA 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G+ +I+ P V + G K E + + D I+G + + +
Sbjct: 175 AALADGET---VIENAAREPEVVDLANCLIAMGAKIEGAGT-DTVRIQGVESLQGC-DYQ 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V D FL AA+T G + SL+ LE GA +T + + +
Sbjct: 230 VMPDRIETGSFLVAAAVTRGKIRCADPKSLEA---VLAKLEDAGASITTGDDWIELDM 286

Query: 310 PPREFPGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ P KA+++ P D+ V+ A+G I + + E M
Sbjct: 287 QGQRP-----KAVNIKTVAYPGFPTDMQAQFCVLNALAEGTATITET----IFENRFMH 336

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN 394
EL+++GA++E + CII EKLN
Sbjct: 337 V--PELSRMGATMELEGNTCIIHGIEKLN 363

>ref|ZP_03343953.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Salmonella enterica
subsp. enterica serovar Typhi str. 404ty]
Length = 60

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 29/50 (58%), Positives = 37/50 (74%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVH 54
E + LQPI + G + LPGSKS+SNR LLLAAL+ G T + NLL+S+DV
Sbjct: 2 ESLTLQPIARVDGAINLPGSKSVSNRALLAALACGKTALTNNLSDDDVR 51

>emb|CAP05278.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. B01]
Length = 188

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 34/101 (33%), Positives = 52/101 (51%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCII---TPPEKL 393
LA+ A FA+G T + + RVKE++R+ A+ L GA EG + + L
Sbjct: 88 LAIAASFAEGETVMDGLDELVRKESDRLA AVARGLEANGADCTEGEMSLTVRGRPGGKGL 147

Query: 394 NVTADITYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFF 433
++T+ DHR+AM+F + A E PVT+ D +FP
Sbjct: 148 GGGTVETHLDHRIAMSFLVMGLASEKPVTVDDSTMIATSFP 188

>ref|YP_004151432.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermovibrio
ammonificans HB-1]
gb|ADU96791.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermovibrio
ammonificans HB-1]
Length = 434

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 109/430 (25%), Positives = 175/430 (40%), Gaps = 59/430 (13%)

```
Query: 1  MAGAEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
      M  E+ +++ +E+ GTVK+ GSK+ S  I+  + L+ G+  + N+   DV    L
Sbjct: 1  MESEEFPIIRGGRELRGTVKVS GSKNASLPPIIFASILT-GSLTLHNVPRLTDVFTACKLL 59

Query: 61  RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS--LT-AAVTAAG 117
      +G      + V   G   PV  A  E+      IAMR+  LT   + A  G
Sbjct: 60  EAMGFHTSFSGNTLK--VSFSGDLNPV--APYELV-----IAMRASILTLGPLLARYG 108

Query: 118  NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVVRVNGIGGLPGGKVKLSGS 177
      L  G   +  RP+   + GL +LGAD+  + G   V+   G  L  G  ++
Sbjct: 109  RGVFLPFGGCAIGVRPVDLHLKGLSRGLGADIKVYHGFIVGEVK----GRLKGAEIYDFDP 164

Query: 178  ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFY 235
      +LMAA LA  G   +I   P  +   R  ++R  G  ++ E +D  +  +
Sbjct: 165  TVGG-TENVLMAAVLAEGKT---VIRNAAKEPEIVDLARALKRAGAVIEGEGTDVIEVW- 219

Query: 236  IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAE---V 290
      G   SP   V  D   A  F++  A  GG  V  +E   + +L+  V  KF+E   V
Sbjct: 220  ---GVDELSPFYETVMPDRIEAGTFMSAVAAAGGDVIEDFPSYALKAVVDKFSEAGLVV 276

Query: 291  LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADG 346
      E+  G+KV  +      R+  L+  D+   P   D+      A+G
Sbjct: 277  EELPGSKVRVVK-----RERLRGTDIVTQPYPGFPTDMAQFMAAMCLAEG 322

Query: 347  PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRM 406
      +  IR+   + E  M   EL  +LGA+++  +  +   E+L  V  A  T  D  R
Sbjct: 323  DSVIRET----IFENRFMHV--PELQRLGANLKVDGNTVVFVRGVEEL-VGAKVTATDLRA 375

Query: 407  AMAFSLAACA 416
      +  +  +A  A
Sbjct: 376  SASLVIAGLA 385
```

```
>ref|YP_002127468.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alteromonas
      macleodii 'Deep ecotype']
sp|B4RWE6.1|MURA_ALTMD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enolpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ACG67474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alteromonas
      macleodii 'Deep ecotype']
      Length = 420
```

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 75/316 (23%), Positives = 133/316 (42%), Gaps = 32/316 (10%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      +++V++ ++GTV++ G+K+ +  +L+ + L++  N+   D++   LR  LG
Sbjct: 2  DKLVIKKSALNGTVRISGAKNAALPLLMTSLLTDSPCRYTNVPRLRDINTTTALLREL 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
      VE  A  +V+   V  +  + V      R++ A++  G   G
Sbjct: 62  --VEVALPAPNDIVIDASTLESVTASYDLV-----RTMRASILVLGPLLAKQ 108

Query: 119  ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVVRVNGIGGLPGGKVKLSGSI 178
      A  L  G  +  RP+   + GL+++GA ++  G   +R   G  L  G  ++  +  +
Sbjct: 109  ANVLPGGCAIGARPVNLHLTGLEKMGAKIEVDEGY----IRAKVDGRLKGARIFMD-MV 163

Query: 179  SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
      S   LLMAA LA  G   I++  P  +   +  + G  K  +  S  D+  I+G
Sbjct: 164  SVGATENLLMAALADGTT---ILENAAREPEIVDLANCLIQMGAKISGAGS-DKITIEG 219

Query: 239  GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      +   A  +  D   FL  AA+TGG  V      +L      + LE  GAK+
Sbjct: 220  VETLNGCDYAVLP-DRIETGTFLVAAAVTGGKVRCTNAAPDTLDA---VLDKLEQAGAKI 275

Query: 299  TWTETSVTVTGPPREP 314
```

T E + + R+P
Sbjct: 276 TTGEDWIELDMGRKP 291

>ref|ZP_04577736.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oxalobacter
formigenes H0xBLS]
gb|EE028698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oxalobacter
formigenes H0xBLS]
Length = 417

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 66/269 (24%), Positives = 116/269 (43%), Gaps = 19/269 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++++ + G + + G+K+ + IL + L+ + N+ + +DV ML L+ +G
Sbjct: 2 DKLIINGGNRLHGEIPISGAKNAALPILCASLLTADDIELTNVPHLKDVQTM LTLQMQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
++V+ D +V G +A E+ + A + + L A G A L
Sbjct: 62 VTVKKDGKNGK----IVMNGNTVHNFNAPYELVKTMRRAILVLCPLVARF----GEAKVSLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ + GL+ LGA+V+ G + L G ++ ++ I+
Sbjct: 114 GGCAIGSRPVEQHIKGLRALGAEEVEIKAGYIYAKAK-----KLKGTRI-VTDMITVTGTE 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAA LA G+ +I P V L+ + G K E DR I G ++
Sbjct: 168 NLLMAATLAEGET--VIKNAAREPEVTDLAHLLVKMGAKIE-GIGTDRLVIHGVERLHG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTV 273
++ + D FL A TGG VT+
Sbjct: 224 ARHDVIP-DRIETGTFLCAVAATGGDVTL 251

>ref|ZP_01899239.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Moritella sp.
PE36]
gb|EDM66304.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Moritella sp.
PE36]
Length = 420

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 98/388 (25%), Positives = 156/388 (40%), Gaps = 44/388 (11%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++G V + G+K+ + IL LS+ T + N+ D+ L LR LG +A++ A
Sbjct: 11 QLNGDVTISGAKNAALPILFATLLSDETTITLKNVPELRDIKTTLQLLRELQ--AQAERNA 68

Query: 74 KRAVVVGCG----GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
VV+ G K P E K L + + TA V+ GG A +
Sbjct: 69 DGDVVITAGTVNCQKAPYELVKTMRASILALGPLTAKFSTADVSLPGGCA-----I 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL+ + A+++ G RV+G L G ++ L +S LLMA
Sbjct: 120 GARPVNHLHIHGLEMMQANINVEEG--YIKARVDG--RLKGARI-LMDMVSVTGTENLLMA 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G + I+ P V + G K S D I+G +K
Sbjct: 175 AVLADG---VTTIENAAAREPEVVDLANFLNGLGAKISGMGS-DVLTIEGVEKLHG-GTYT 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVTEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V+ D FL AA+TGG + L + LE GAK+ + +++
Sbjct: 230 VQPDRIETGTFLVAAAVTGGGIKCHKTDPSLLDAVIL---KLEEAGAKIETGDDWISLDM 286

Query: 310 PPREFPGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
R+ LKA+++ P D+ V+ A G + I + + E M
Sbjct: 287 KGRD-----LKAVNIKTVPYPGFPDMDQAQFTVLNTVAKGTSTIVET----IFENRFMH 336

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKL 393
EL ++GA +E + I E L
Sbjct: 337 V--PELARMGADIELEGNTAICRDTESL 362

>ref|YP_002017759.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pelodictyon
 phaeoclathratiforme BU-1]
 sp|B4SEZ5.1|MURA_PELPB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
 gb|ACF43142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pelodictyon
 phaeoclathratiforme BU-1]
 Length = 424

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 105/416 (25%), Positives = 166/416 (39%), Gaps = 64/416 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
 +++V++ ISGT+ GSK+ S I+ L+ GT + ++ + +D+ L L
 Sbjct: 2 DKLVIKGGSRISGTITASGSKNTSLPIAATLLTGNGTFTLHHIPDLKDIVTFTQLLHHL 61

Query: 64 GLSVEAD----KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAG 116
 G + K + R V + P E K+ MR+ + + A
 Sbjct: 62 GAETTYEGNTLKVSSRN---QSLQAPYELVKK-----MRASIYVLGPMLARF 106

Query: 117 GNATYVLDGVPFRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVK 173
 G+A L G RPI ++ +++LGA + F+ P G L GG +
 Sbjct: 107 GHARVSLPGGCAFGPRPIDLHLMAMEKLGATITITETGFIDATIPG-----GKLQGGHIT 160

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
 S S LMAA LA G I + P +E + + G + + + +
 Sbjct: 161 FPIS-SVGATGNALMAAVLAEGTT---TISNAAAEPEIETLCKFLIAMGATIRGTGTTE- 215

Query: 234 FYIKGGQKYKSP--KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEV 290
 I+G K+ KN + D A LA AAITGG +TV G ++ + KF
 Sbjct: 216 LEIEGNTLKAIEFKNVF---DRIEAGTLLAAAIAITGGDITVNGVEPEQMKAVLKKFVHA 272

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADG 346
 G V T+ S+T+ P K L DV P D+ + A+G
 Sbjct: 273 ----GCLVETDNSITLKSP-----KKLIPTDVTAKPYPAFPTDMAQWIALMTQAEG 321

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
 + I D ER I EL +LGA +E + I+ P++L+ T + + D
 Sbjct: 322 SSHITDKVYH-----ERFNHI-PELNRLGAHIEIHKNAIVHGPQQLSGTVKMSTD 371

>ref|YP_003777449.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Herbaspirillum
 seropedicae SmR1]
 gb|ADJ65541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase protein
 [Herbaspirillum seropedicae SmR1]
 Length = 416

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 92/402 (22%), Positives = 168/402 (41%), Gaps = 57/402 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
 +++++ K +SG V + G+K+ + IL A L+ V+ N+ + +DV + G ++ +G
 Sbjct: 2 DKLLIRGGKRLSGDVTISGAKNAALPILCAALLTADDLVLNPHLQDQVVTITGLMKQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
 L V+ + +V G +A E+ +++++ A++ G G
 Sbjct: 62 LRVQENGQD---MVLNGNDITRPEAPYEL-----VKTMRASILVLGPLLARFGQ 107

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
 A L G + RP+ + GL+ +GA++ G + L G ++ ++ I
 Sbjct: 108 AKVSLPGGCATGSRPVDQHIKGLQAMGAIEIHGGYIYAKAKR-----LKGARI-VTDMI 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
 + LLMAA LA G+ +++ P V L+ + G K E + DR I+G
 Sbjct: 162 TVTGTEENLLMAAVLADGET---VLENAAREPEVGDLANLLVKMGAKIEGIGT-DRLVIQG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
 ++ + + D FL A TGG VT+ L + + L GA +
 Sbjct: 218 VEQLHGASHEVI-ADRIETGTFLCAVAATGGDVTLLRRTRAGLLDAAL---DKLRDAGAIL 273

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA 354
T E + + R P KA+ + P D+ + ADG +
Sbjct: 274 TSGEDWIRIQ-MARRP-----KAVSFRTTEYPGFPTDMQAQFMALNCIADGTS----- 320

Query: 355 SWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
V ET R + ++ EL +LG +++ + I+T EK
Sbjct: 321 --HVTETIFENRFMHVQ-ELNRLGTAIDVEGNTAIVTGVEKF 359

>ref|NP_933254.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
vulnificus YJ016]
sp|Q7MPA3.1|MURA_VIBVY RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
dbj|BAC93225.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Vibrio vulnificus
YJ016]
Length = 421

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 99/427 (23%), Positives = 170/427 (39%), Gaps = 51/427 (11%)

Query: 8 VLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V+ + + G V + G+K+ + IL + L+E V N+ + D+ + L+ LG V
Sbjct: 6 VIGSTQPLMGEVTISGAKNAALPILFASILAEPEVEANVPHLRDIDTTMELLKRLGAKV 65

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATY 121
E + G V+ + + + + + + A++ A G G
Sbjct: 66 ERN-----GSVHVDPS--IDEYCAPYDL-VKTMRASIWALGPLVARFGQGQV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 SLPGGCAIGARPVDLHITGLEQLGATITLEDGY---VKAHVDGRLQGAHIVMD-KVSVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G ++D P + T + + G K + + D I+G ++
Sbjct: 166 ATITIMCAATLAEGTT---VLDNAAREPEIVDTAKFLNTLGAKISGAGT-DTITIEGVER 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K+A V D FL AA++GG V C T LE GA V
Sbjct: 222 LGGGKHAVV-ADRIETGTFVLAAAVSGGKV---CHNTQAHLLAEVLAKLEAGALVETG 277

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWR 357
E ++V RE LKA+++ P D+ ++ + A G I +
Sbjct: 278 EDWISVDMTGRE-----LKAVNIRTAPHPGFPTDMQAQFTLLNMMAKGGGVITET---- 327

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + +A C
Sbjct: 328 IFENRFMHV--PELKRMGAKAEIEGNTVICGDVERLSAAQV-MATDLRASASLVIAGCIA 384

Query: 418 VPVTIRD 424
TI D
Sbjct: 385 KGETIVD 391

>ref|ZP_05855351.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Blautia hansenii
DSM 20583]
gb|EEX20752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Blautia hansenii
DSM 20583]
Length = 430

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 98/425 (23%), Positives = 172/425 (40%), Gaps = 41/425 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E+ +++ + G V++ G+K+ + IL A +++ T ++NL + D++ +L A++ +G
Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALAILAAAIMTDETVHIENLPDVRDINVLEAIKEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V+ + + G VE E ++ A L A+ NA L

Sbjct: 62 ATVDRIGPTEVKIAGATIGNITVE--YEYIKKIR-----ASYLLGALLGKYKNAEVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA VD G L G + + +S

Sbjct: 115 GGCNIGSRPIDQHLKGFRALGASVDIIHGAVVAKAE-----HLTGKHIFMD-MVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G+ IE P+V + G + + + D I+G K

Sbjct: 169 NVMAAAMAQGNNTTIE---NAAREPHVVDVANFLNSMGANIKGAGT-DVIRIQGVDKLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + D A F+ AA T G + V+ L+ LE +G +V + +

Sbjct: 225 TTYSIIP-DQIEAGTFMCAAAATMGDMVKNVIPKHLEATTA--KLEEIGCQVEEFDDA 280

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
V V K LK +V P D+ AV A+G + + + + R K

Sbjct: 281 VRVV-----ANKRLKRTNVKTMYPGYPTDMQPQFAVALTLAEGTSIVTESIFENRFK 333

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
+ ELT++GA+++ + II +KL + + D R A +A A

Sbjct: 334 YAD-----ELTRMGANIKVEGNTAIDGVQKLAGARV-SAPDLRAGAALVIAGLAAEG 385

Query: 420 VTIRD 424
+TI D

Sbjct: 386 ITIVD 390

>ref|ZP_03394652.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
amycolatum SK46]
gb|EEB62287.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
amycolatum SK46]
Length = 426

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 74/282 (26%), Positives = 119/282 (42%), Gaps = 23/282 (8%)

Query: 3 GAEIEVLQPIKEISGTVKLPKSGSKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G E +++ ++G V++ G+K+ +++ A L+EGTTV+ N +DV M L

Sbjct: 8 GNERFLVKGGATLNGQVQISGAKNSVLKLMGAALLAEGTTVLTNCP EIDDVPLMQKVLEG 67

Query: 63 LGLSV--EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
LG SV E D+ + + + V+ F + + +TA NA

Sbjct: 68 LGCSVTREGDR-----IEITVPEELSHHADFDVRQFRASV-----CVLGPLTARTRNAI 117

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ GL++LGA ++ C V G L G +KL S

Sbjct: 118 VALPGGDAIGSRPLDMHQAGLEKLGART--YIHHGCV---VAEAGRLKGANIKLDFP-SV 171

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+L AA LA G ++D P + ++ G K + S + ++G +

Sbjct: 172 GATENILTAAVLAEGTT---VLDNAAREPEIVDLCEMLVEMGAKISGAGS-NTITVEGVE 227

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQ 282
K P V GD A + AA+TGG +TV G L

Sbjct: 228 KLH-PTEHKVVGDRIIAGTWAYAAAMTGGDITVVGINPKYLH 268

>ref|YP_003993105.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor hydrothermalis 108]
gb|ADQ07736.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor hydrothermalis 108]
Length = 419

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 78/308 (25%), Positives = 132/308 (42%), Gaps = 22/308 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V++ + G V + G+K+ + ++ A +++G +V++NL EDV M L LG

Sbjct: 6 EKLVIIEGGYPLEGEVINGAKNAAVAVIPAALMADGESVIENLPLIEDVFAMDDILLKLG 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

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      +E D  + +      ++ ++++      A  L  A+      G A  +
Sbjct: 66 AKIEYDNHSLKIDARNLHSYIAPYESVKIR-----ASYYLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      G      RPI  + G + LGADV      G      ++      L G K+ L  +S
Sbjct: 118 GGCNFGSRPIDQHIGKFRALGADVRIENGM----IKAYA-DRLVGTKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
      L++AA  A G  I II+      P+V T  +      G K + + + D  I+G K
Sbjct: 172 NLMLAAVKAG---ITIIENAAKEPHVVDTANFLNSMGAKIKGAGT-DVIRIEGVDKLYP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      K A +      + +Y +A  A T G V V+      L+      A+++E MGA+V  E S
Sbjct: 228 TKYAIIPDQIEAGTYMIAACA-TKGHVIVKNVIPKHLES LT--AKLVE-MGAEVITYEDS 283

Query: 305 VTVTGPFR 312
      + V      R
Sbjct: 284 IEVICKSR 291

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>ref|YP_001166802.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides ATCC 17025]
sp|A4WQ33.1|MURA_RHOS5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABP69497.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides ATCC 17025]
Length = 422

```

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 99/425 (23%), Positives = 171/425 (40%), Gaps = 53/425 (12%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      + I+++ E+ G + + G+K+ ++ LS+ + N D+ M L++LG
Sbjct: 2 DSILVKNGGELRGQIPIAGAKNAACLALMPATLLSDEPLTLTNAPRLSDIRMTMTQLLSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
      V + + + +      + D + + +      +R + A++ G      G+
Sbjct: 62 AEVASLQGGQVLAL----SSHALTDHRADYDI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDC--FLGTDCCPPVRVNGIGGLPGGKVKLS 175
      A  L G  + RP+ + L+ +GAD+D ++ P      GGL G +V
Sbjct: 110 AVVSLPGGCAIGARPVDLHLKALEAMGADLDLRDGYIHAKAPA-----GGLRGARVAFP 163

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      +S      LMAA LA G      +++ P +      R + R G + E S
Sbjct: 164 -IVSVGATENALMAATLAKGTT---VLENAAREPEIVDLARCLRRMGAQIEGEGSAT-IT 218

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
      ++G +      + V      +Y LA AI GG V + G G L G F E L+ G
Sbjct: 219 VQGVDRLGGAHPVVTDRIELGTYMLA-PAICGGEVELLG-GRIELVG--AFCEKLDAAAG 274

Query: 296 AKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPFAIR 351
      V TE + V      GR +KA+DV P D+ + + A+G + +
Sbjct: 275 ISVEETERGLRVA---RRNGR--VKAVDVTTEPFPGFPTDLQAQMMALLCTAEGTSVLE 328

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
      + ++ E M A ELT++GA +E +T EKL + D R +++
Sbjct: 329 E---KIFENRFMHA---PELTRMGARIEVHGHTARVTGVEKLRGAPV-MATDLRASVSLI 381

Query: 412 LAACA 416
      LA A
Sbjct: 382 LAGLA 386

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>ref|ZP_05112851.1| hypothetical protein SADFL11_736 [Labrenzia alexandrii DFL-11]
gb|EEE43450.1| hypothetical protein SADFL11_736 [Labrenzia alexandrii DFL-11]
Length = 136

```

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.

Identities = 35/109 (32%), Positives = 52/109 (47%), Gaps = 2/109 (1%)

Query: 329 KMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT 388
M D LA+ A FA+G T + + RVKE++R+ A+ L G E D +T
Sbjct: 9 SMIDEYPVLAIAAAFAEGDTFMPGLEELRVKESDRLAAVARGLEANGIPCIETEDTLTVT 68

Query: 389 -PPEKLNVTATIDTYDDHRMAMAF-SLAACAEPVPTIRDPGCTRKTFPDY 435
+ + T+ DHR+AM+F L A PVT+ D +FP +
Sbjct: 69 GSASDIGGGTVVTHLDHRIAMSFLILGIAAHKPVTVDGAVIATSFPTF 117

>ref|ZP_02862694.1| hypothetical protein ANASTE_01915 [Anaerofustis stercorihominis DSM
17244]
gb|EDS72205.1| hypothetical protein ANASTE_01915 [Anaerofustis stercorihominis DSM
17244]
Length = 423

Score = 48.5 bits (114), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 89/410 (21%), Positives = 164/410 (40%), Gaps = 44/410 (10%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E+I++ + ++G V + G+K+ + IL L+ +++NL + +D+ + +
Sbjct: 1 MKNMEKIIINGRRLTGEVTTITGAKNAALGILPATVLASDKFLIENLPDIQDIRNYISIM 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
+ LG + E A E ++ A L A+ G
Sbjct: 61 KKLGAIRKTSKGLSIDTTAIADCTSDEIADESTKMR-----ASYLLGALLGRNGFVE 114

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
G + RPI + G + LGA VD +++ GL G + + +S
Sbjct: 115 LPPPGGCDIGARPIDQHIKGFALGAKVDV-----KGSIKIESPNGLNGTNIYMD-VVSV 168

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+++AA A G + +I+ P+V + G + + + D I G +
Sbjct: 169 GATINIMLAAVKAKG--LTVIENAAKEPHVVDIANFLNLMGASVKGAGT-DVIRIMGVE 224

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + V ++ +Y +A AA T G V ++ L D A+++E MGA V+
Sbjct: 225 ELHGCEYSVVPDQITAGTYMIAAAA-TKGDVLIKNVIPPHL--DSITAKLIE-MGADVSV 280

Query: 301 TETSVTVTGPPREPFRGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASW 356
E GR+++K +V P D+ + ++ A+G ++I
Sbjct: 281 DEDDNI-----RVVGREYIKPCNVKTLPPYGFPTDLQQPMGLIMCLANGVSSI----- 328

Query: 357 RVKETERMVAIR----TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
TE + R TEL K+GA+V + + T P +L T I D
Sbjct: 329 ----TESIFENFRFYVTELQKMGANVRVNGNTAVFTGPSELYGTKIQATD 374

>ref|ZP_03729812.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dethiobacter
alkaliphilus AHT 1]
gb|EEG77544.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dethiobacter
alkaliphilus AHT 1]
Length = 421

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 76/276 (27%), Positives = 112/276 (40%), Gaps = 33/276 (11%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I L+ E+SG V++ G+K+ I+ + L E ++ ++ +DVH M L LG
Sbjct: 5 ITLEGGVELSGRVRIEGAKNACLPIIAASLLCEDRVILHDIPPLDDVHTMCQVLNALGAE 64

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+ K+ +V P + K E L A + + A G A L G
Sbjct: 65 TDYFPEEKKLIV-----DPQDLGKAEAPYDLVRKMRAFLVIGPLLARYGRARVSLPGG 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL--- 183
+ RPI + GLK +GA+V V G G + KL G YL
Sbjct: 119 CAIGIRPIDLHLKGLKAMGAEV-----VIGHGFIE TLADKLCG--ERVYLDFFP 164

Query: 184 -----SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238

```

      ++MAA LA G   + +I+      P V   R +   G K   + + D   I G
Sbjct: 165 SVGATENIMMAASLAEG---VTVIENAAEEPEVVDLARFINAMGGKVTGAGT-DTIRITG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
      K   +   + D   A F+  AAITGG+VTVE
Sbjct: 221 VSKLSGTEYTVIP-DRIEAGTFMLAAAITGGSVTVE 255

```

```

>ref|ZP_04629099.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
      bercovieri ATCC 43970]
gb|EEQ06013.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
      bercovieri ATCC 43970]
Length = 421

```

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 174/431 (40%), Gaps = 59/431 (13%)

```

Query: 9   LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      +Q   +SG V + G+K+ +   IL A L+E   + N+   +D+   + L LG +E
Sbjct: 6   VQGRTRLSGEVTISGAKNAALPILFAALLAEEPVELQNVPKLKDIDTTIKLLGQLGKIE 65

```

```

Query: 69  ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
      D +   V           DA+ +V F   + +++++ A++ A G   G
Sbjct: 66  RDSSGSVFV-----DAR-DVNEFCAPYDL-VKTMRASIWALGPLVARFGKGQVS 112

```

```

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      L G   + RP+   + GL+QLGA++   G   V+ +   G L G   +   +S
Sbjct: 113 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGA 167

```

```

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
      ++ AA LA G   +I+      P + T   +   G K   + S DR I+
Sbjct: 168 TVTIMSAATLAEGST---VIENAAPEIIVDTANFLNTLGAKISGAGS-DRITIEGVARL 223

```

```

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      GG Y+   V D   FL AAI+GG V   +L D   A++ E GA
Sbjct: 224 GGGVYR-----VLPDRIETGTFLVAAAISGGKVVCRQTRPDTL--DAVLAKLRE-AGAD 274

```

```

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
      +   + +++   + P   KA+ +   P   D+   +++ L A+G   I +
Sbjct: 275 IEVGDDWISLDMHGQRP-----KAVTIRTAPHPGFPTDMAQFSLNLVAEGTGIVITET 328

```

```

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
      + E M   EL ++GA E   + I   E+L+   +   D R + + LA
Sbjct: 329 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVEQLSGAQV-MATDLRASASLVLA 381

```

```

Query: 414 ACAEVPVTIRD 424
      C   VTI D
Sbjct: 382 GCIADGVTIVD 392

```

```

>ref|NP_759664.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
      vulnificus CMCP6]
sp|Q8DEB6.1|MURA_VIBVU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|AAO09191.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
      vulnificus]
Length = 421

```

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 99/427 (23%), Positives = 170/427 (39%), Gaps = 51/427 (11%)

```

Query: 8   VLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
      V+   + + G V + G+K+ +   IL + L+E   V N+ +   D+   + L+ LG V
Sbjct: 6   VIGSTQPLVGEVTISGAKNAALPILFASILAEPPVEVANVPHLRDIDTTMELLKRLGAKV 65

```

```

Query: 68  EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATY 121
      E +   G   V+ +   +   +   + +++++ A++ A G   G
Sbjct: 66  ERN-----GSVHVPDSS--IDEYCAPYDL-VKTMRASIWALGPLVARFGQGQV 110

```

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 SLPGGCAIGARPVDLHITGLEQLGATITLEDGY----VKAHVDGRLQGAHIVMD-KVSVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G ++D P + T + + G K + + D I+G ++
Sbjct: 166 ATITIMCAATLAEGTT---VLDNAAREPEIVDTAKFLNTLGAKISGAGT-DTITIEGVER 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K+A V D FL AA++GG V C T LE GA V
Sbjct: 222 LGGGKHAVV-ADRIETGTFLVAAVSGGKV---CHNTQAHLLLEAVLAKLEEAGALVETG 277

Query: 302 ETSVTVTGPPREFFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E ++V RE LKA+++ P D+ ++ + A G I +
Sbjct: 278 EDWISVDMTGRE-----LKAVNIRTAPHPGFPTDMQAQFTLLNMMAKGGGVITET---- 327

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + +A C
Sbjct: 328 IFENRFMHV--PELKRMGAKAEIEGNTVICGDVERLSAAQV-MATDLRASASLVIAGCIA 384

Query: 418 VPVTIRD 424
TI D
Sbjct: 385 KGETIVD 391

>ref|ZP_04714868.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alteromonas
macleodii ATCC 27126]
Length = 399

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 74/308 (24%), Positives = 129/308 (41%), Gaps = 36/308 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ ++GTV++ G+K+ + +L+ + L++ N+ D++ LR LG
Sbjct: 2 DKLVIKKGPAALNGTVRISGAKNAALPLMLTSLTDSPCRYTNVPRLDINTTTALLREL 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE A +V+ V + E V R++ A++ G G
Sbjct: 62 --VEVALPAPNDIVIDASTLQSVTASYELV-----RTMRASILVLGPLLAKQKG 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + GL+++GA ++ G +R G L G ++ + +
Sbjct: 109 ANVSLPGGCAIGARPVNLHLTGLEKMGAKIEVDEGY---IRAEDVDGRLKGARIFMD-MV 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S LLMAA LA G I++ P + + + G K + S D+ I+G
Sbjct: 164 SVGATENLLMAAALADGTT---ILENAAREPEIVDLANCLIQMGAKISGAGS-DKITIEG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ A + D FL AA+TGG + +L + LE GAK+
Sbjct: 220 VETLNGCDYAVLP-DRIETGTFLVAAAVTGGKIRCTHAAPDTLDA---VLDKLEQAGAKI 275

Query: 299 T----WTE 302
T W E
Sbjct: 276 TTGDDWIE 283

>gb|EGD01795.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
TJI49]
Length = 420

Score = 48.1 bits (113), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 68/278 (24%), Positives = 117/278 (42%), Gaps = 33/278 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ +SG + + G+K+ + IL LS +DN+ N +DV L L +G
Sbjct: 2 DKLVIEGGHRLSGEIVVSGAKNAALPILCAGLLSAEPVELDNVNLKDVRTTLKVLNQM 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ + D GC + V + + + + A++ G G
Sbjct: 62 VKSDTD-----GCRVRLDASRVNVLVAPYE-----LVKTMRASILVLGPLLARFGE 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 108 AKVSLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIEARAKR-----LKGARI-VTDM 160

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
I+ LLMAA LA G+ II+ P V L+ G K + + DR I+
Sbjct: 161 ITVTGTENLLMAATLADGET---IIENAAREPEVSDLAHLLVAMGAKIDGIGT-DRLVIQ 216

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
G + ++A + D A FL A GG VT+ G
Sbjct: 217 GVDRLHGARHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 253

>ref|YP_001490753.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Arcobacter
butzleri RM4018]
sp|A8EYW0.1|MURA_ARCB4 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABV68083.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Arcobacter
butzleri RM4018]
Length = 422

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 87/382 (22%), Positives = 156/382 (40%), Gaps = 58/382 (15%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K+ISG+V++ G+K+ + ++ L + + NL N D++ L
Sbjct: 10 KDISGSVEISGAKNAALPLIACITILGKNEITIGNLPNVVDINTFL----- 54

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GNATYV 122
+++ GG F E+ K ++ N A +++ A++ G G+
Sbjct: 55 ---KLILKLGGSFVKEENKVKINTSTINNTTATYDIVKTMRASILVLGPLLARFGHCEVS 111

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + +RP+ + L+Q+GA ++ G ++ GL G K+ ++
Sbjct: 112 LPGGCAIGQRPVDLHLKALEQMGAKIEILQGY----IKATAPNGLKGAKIVFD-KVTVGG 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQK 241
++MAA LA G + I P + ++ GVK E + I+G GQK
Sbjct: 167 TENIVMAAALAHG--VTTIINAAKEPEIVQLCEVLANSGVKIE-GIGTSKIVIEGTGQK 222

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K V D A ++ AAIT + + L+ + LE M +V
Sbjct: 223 LIDIKPFDVIPDRIEAGTYMCAAIAITNKKLKINKVIPLHLEAVI---SKLEEMNFEVLQD 279

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWR 357
E SVT+ P E +K +++ + P D+ +A A+G + I + R
Sbjct: 280 ENSVTIL-PTNE-----IKPVNIITTEYPGFPTDMQAQFMALATQANGTSTIDE----R 328

Query: 358 VKETERMVAIRTELTKLGASVE 379
+ E M +EL +LGA +
Sbjct: 329 LFENRFMHV--SELLRLGADIH 348

>ref|NP_940224.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
diphtheriae NCTC 13129]
sp|Q6NFK1.1|MURA_CORDI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAE50416.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
diphtheriae]
Length = 418

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 112/441 (25%), Positives = 168/441 (38%), Gaps = 61/441 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV + G+K+ +++ A L+EGTT + N DV YM+ L LG S

Sbjct: 13 LEGTVHVS GAKNSVLKLM AALLAEGTTTTLTNC PKILDVPY MVRVLEGLGCS----- 64

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAG-----GNATYVLDGVP 127
VV G + E NA A+R A+V G G A L G

Sbjct: 65 ---VVHSGSTVEITTPAE----ISSNADFDAVRQFRASVCVLGPLTSRCGKAVVALPGGD 117

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ GL++LGA G V L G + L S +L

Sbjct: 118 AIGSRPLDMHQSGLEKLGAKTHIEHGA-----VVAQADQLRGANIHLDFP-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G ++D P + +++ G E + I+G +K P

Sbjct: 172 TAAVLAEGTT---VLDNAAREPEILDLCVMLKEMGADIE-GEGTSTITIRGVEKLH-PTQ 226

Query: 248 AYVEGDASSASYFLAGAAITGGT VTVVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD A + AA+T G +TV G +L + E L++ GA+VT + V

Sbjct: 227 HEVIGDRIVAGTWAYAAAMTQGDITVGGIAPRNLHLAL---EKLKVAGAEVTYDHGFRV 283

Query: 308 TGPPREPFGRKHLKAIDVNMNKM PDMVAMTLAVVAL----FADGPTAIRDVASWRVKETER 363
R P A+D P L +A+ ADG + I TE

Sbjct: 284 R-MDRRPM-----AVDYQTLFPFGFPTDLQPMAGISTVADGVSVI-----TEN 326

Query: 364 MVAIR---TELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVP 419
+ R EL +LGA + ++ EKL+ T + + D A CA+

Sbjct: 327 IFEARFRFVDELVR LGADATVDGHVVMRGVEKLSSTPVWSSDIRAGAGLVLAALCADGV 386

Query: 420 VTIRDPGCTRKTFPDYFDVLS 440
+ D + +P++ + L

Sbjct: 387 TEVNDVFHIDRGYPNFVEDLQ 407

>ref|NP_213879.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aquifex aeolicus VF5]
sp|O67315.1|MURA_AQUAE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
pdb|2YVW|A Chain A, Crystal Structure Of Udp-N-Acetylglucosamine 1-Carboxyvinyltransferase From Aquifex Aeolicus Vf5
gb|AAC07268.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aquifex aeolicus VF5]
Length = 425

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 88/385 (22%), Positives = 159/385 (41%), Gaps = 59/385 (15%)

Query: 7 IVLQPIKEISGTVKLP GSKSLSNRILL LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
V++ K ++G VK+ G+K+ + I+ L+E + N+ + DV L LR LG

Sbjct: 13 FVIRGGKPLTGKVKISGAKNAALPIMFATILTEEPCTITNVPDLLDVRNTLLLLRELGA 72

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNAT 120
+E V + + F+ N I +R + A+V + G G A

Sbjct: 73 LE---FLNNTVFI-----NPSINSFITNQEI-IRRMASVLSLGPLLGRFGRAV 117

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RPI + K+ GADV+ G ++ V ++G+

Sbjct: 118 VGLPGGCSIGARPIDQHLKFFKEAGADVEVREGYVYNLKEKRRVHFKFDLVTVTGT--- 174

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKG 238
+ALL A + E I++ + P V + ++++ G VK E + Y+KG

Sbjct: 175 --ENALLYLASVP---EESILENIALEPEVMDLIEVLKMGGAHVKVEGRSA----YVKG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGT VTVVEGCGTTS LQGDVKFAEVLEMMGAKV 298
+ K ++ + D A F+ GA +T G + +E L+ V E L+++G +V

Sbjct: 225 SENLKGTFHVSVIP-DRIEAGTFMVGAVLTDGEILLENARINHLRAVV---EKLKLIGGEV 280

Query: 299 TWTETSVTVTGPPREPFGRKHLKAIDVNMNKM P----DVAMTLAVVALFADGPTAIR-DV 353
++ V F ++ L+A D+ P D+ + A G + I+ ++

Sbjct: 281 VEENGNLRV-----FRKESLRACDIETQVYPGFPTDMQAQFMALLSVAKGKSRIKENI 333

Query: 354 ASWRVKETERMVAIRTELTKLGASV 378

R + EL +LGA++
Sbjct: 334 FEHRFHHAQ-----ELNRLGANI 351

>ref|ZP_02364356.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
oklahomensis C6786]
Length = 449

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 98/412 (23%), Positives = 172/412 (41%), Gaps = 62/412 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ + ++G + + G+K+ + IL L+ +DN+ N +DV L L +G
Sbjct: 31 DKLVIIEGRRRLAGEIAVSGAKNAALPILCAGLLTAEPVHLDNVPNLKDVRTTLKLLDQMG 90

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ E D A R V+ PV A E+ +++++ A++ G G
Sbjct: 91 MREETDGA--RVVLDASRVDPNPV--APYEL-----VKTMRASILVLGPLLARFGY 136

Query: 119 ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 137 AKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LKGARI-VTDM 189

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
++ LLMAA LA G+ +I+ P V L+ G K + S DR I+
Sbjct: 190 VTVTGTENLLMAATLADGET---VIENAAAREPEVSDLAHLLVAMGAKID-GISTDRLVIQ 245

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + +A + D A FL A GG VT+ G A++L+ + K
Sbjct: 246 GVDRLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTGM-----RAQILDVIDK 294

Query: 298 VTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
+ ++ G + A+ + ++ P D+ + ADG
Sbjct: 295 LREAGVTIEEGDRLRVKMDRRPGAVAIARTSEYPAFPTDMQAQFMALNAVADG----- 347

Query: 354 ASWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTAD 399
S +V ET R + ++ EL +LGAS+ + ++T KL NV A D
Sbjct: 348 -SAQVIETIFENRFMHVQ-ELNRLGASIAVDGNTALVTGVPKLSGANVMATD 397

>ref|ZP_06895435.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseomonas
cervicalis ATCC 49957]
gb|EFH12860.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseomonas
cervicalis ATCC 49957]
Length = 419

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 69/267 (25%), Positives = 113/267 (42%), Gaps = 29/267 (10%)

Query: 15 ISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + + G+K+ + ++ A L++ V+ N DV M + GL+VE DKA++
Sbjct: 12 LEGRIAIGGAKNAALPLMATAALLTQEAVVLTNAPALADVATMGHLIAQHGLTVEHDKASR 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 128
R ++ G +F +A ++ +R + A++ G G A L G
Sbjct: 72 RILLDGAATQF---EAPYDL-----VRKMRASILVLGPLLARFGQARVSLPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+Q+GA +D D + G L G ++ L +S LLM
Sbjct: 119 IGTRPVDLHLKGLEQMGAVIDL---DSGYINAKVDGRLKGARI-LFPQVSVGATENLLM 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + + P + + G + E S DR I G +A
Sbjct: 174 AATLAEGTTQ---LINAAREPEITDLANCLISMGARIEGVGS-DRLTIHGVDSLHGTTHA 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEG 275
+ D A F AITGG + +EG
Sbjct: 230 ILP-DRIEAGTFACAGAITGGELLLEG 255

>ref|YP_004189900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio

vulnificus M06-24/O]
gb|ADV87697.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
vulnificus M06-24/O]
Length = 421

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 99/427 (23%), Positives = 170/427 (39%), Gaps = 51/427 (11%)

Query: 8 VLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V+ + + G V + G+K+ + IL + L+E V N+ + D+ + L+ LG V
Sbjct: 6 VIGSTQPLLGEVTISGAKNAALPILFASILAEEPVEVANVPHLRDIDTTMELLKRLGAKV 65

Query: 68 EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATY 121
E + G V+ + + + + + + A++ A G G
Sbjct: 66 ERN-----GSVHVPSS--IDEYCAPYDL-VKTMRASIWALGPLVARFGQGQV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 SLPGGCAIGARPVDLHITGLEQLGATITLEDGY----VKAHVDGRLQGAHIVMD-KVSVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G ++D P + T + + G K + + D I+G ++
Sbjct: 166 ATITIMCAATLAEGTT---VLDNAAREPEIVDTAKFLNTLGAKISGAGT-DTITIEGVER 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K+A V D FL AA++GG V C T LE GA V
Sbjct: 222 LGGGKHAVV-ADRIETGTFLVAAVSGGKV---CHNTQAHLLAEVLAKLEEAGALVETG 277

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWR 357
E ++V RE LKA+++ P D+ ++ + A G I +
Sbjct: 278 EDWISVDMTGRE-----LKAVNIRTAPHPGFPTDMQAQFTLLNMMAKGGGVITET---- 327

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + +A C
Sbjct: 328 IFENRFMHV--PELKRMGAKAEIEGNTVICGDVERLSAAQV-MATDLRASASLVIAGCIA 384

Query: 418 VPVTIRD 424
TI D
Sbjct: 385 KGETIVD 391

>ref|YP_297317.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
eutropha JMP134]
sp|Q46WL0.1|MURA_RALEJ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAZ62473.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
eutropha JMP134]
Length = 416

Score = 48.1 bits (113), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 92/399 (23%), Positives = 150/399 (37%), Gaps = 85/399 (21%)

Query: 15 ISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD---- 70
+ G +++ G+K+ + IL L+ T +DN+ N +D ML LR +G+ E
Sbjct: 12 LKGEIRVSGAKNAALPILCAGLLTADTVTIDNVPNLQDTRTMLKLLRQMGMAEMTGSTA 71

Query: 71 -----KAAKRAVV-----GCG-GKFPVEDAKEEVQ 95
K + +++V GCG G PV+ + +Q
Sbjct: 72 TLKGTDINSPEAPYELVKTMRASILVGLPLVARFGEARVSLPGGCGIGARPVDQHIKGLQ 131

Query: 96 LFLGNAGI-----AMRSLTAAVTAAGGN----ATYVLDGVPRM----RERPI 134
I R +T +T G A + DG + RE +
Sbjct: 132 AMGAEISIEHGFHARASRLKGARVVTDMITVTGTENLLMAATLADGETVLENAAREPEV 191

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA--LLMAAPL 192
DL L ++GA +D +GTD + V G+ L G + S+ + + A L AA
Sbjct: 192 TDLANLLVKMGAKIDG-IGTD--RLIVQGVDKLHGA----THSVVADRIEAGTFLCAAAA 244

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI-KGGQKYKSPKNAYVE 251

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      +LGD+ + I LI  ++ L + G E D W R + + Q      + Y
Sbjct: 245 SLGDLVLRDIPPLI----LDAVLIKLREAGANIETGDDWIRLSMSQRAQAVSFRTSEYPA 300

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
      + F+A A+ GT + T + + L +GA +T + VTG P
Sbjct: 301 FPTDMAQAFMALNAVAEGTARIT---ETIFENRFMHVQELNRLGANITAEGNTAVVTGVP 357

Query: 312 REPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAI 350
      R      + A D+      + +L + L ADG T I
Sbjct: 358 R--LSGASVMATDLR-----ASASLVIAGLVADGDTVI 388

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>ref|YP_391256.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thiomicrospira
      crunogena XCL-2]
sp|Q31GZ1.1|MURA_THICR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ABB41582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thiomicrospira
      crunogena XCL-2]
      Length = 418

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Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 97/413 (23%), Positives = 166/413 (40%), Gaps = 77/413 (18%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      +++V++ ++ G+V++ G+K+ + IL+ LSE V+ N+ + +DV + L T+G
Sbjct: 2 DKLVIEGPCQLEGSVQISGAKNAALPILMGCLLSETPVVLSNVPHLKDVTITIQLLATMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
      + V D+ + ++A E+ + + + M L A G A L
Sbjct: 62 VEVMFDEELNIEI---DASNITTKEAPYELVKTMRASILTMGPPLLARF----GEAKVSLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADV-----DCFLGTDC--PPVRVNGIGGLPGGK 171
      G + RP+ + G++++GA++ D +G D PV V G
Sbjct: 115 GGCAIGSRPVNIHIEGMQKMGAEIKVEQGYIIATADRLVGADITMEPVTVTGT----- 167

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
      LLMAA LA G + K P V + + G K D+
Sbjct: 168 -----ENLLMAAVLAEGRTTLRNAAKE---PEVSDLAHFLNKMGAKITGIDT- 211

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEV 290
      D I+G +K + D A +LA AA+T VTV+ L + KF E
Sbjct: 212 DTLVIEGVEKLTGVSRYRVIP-DRIEAGTYLAAAALTKSCVTVKDVVPEHLTAVLDKFT 270

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADG 346
      GA VT T+ ++T+ + LK +++ + P D+ V+ A+G
Sbjct: 271 ----GALVTTTNDNTITL-----DMRNRSLKPVNIIVDPYPAPFTDMAQFVVMNCLAEG 320

Query: 347 PTAIRDVASWRVKET--ERMVAIRTELTKLGASVE-----EGPDYCIITP 389
      V+ET E +EL ++GA + +G D+ I P
Sbjct: 321 -----EANVEETIFENRFMHVSELVRMGADIVHEGNVAHTKGV DHLIGAP 365

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>ref|NP_391557.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis subsp. subtilis str. 168]
ref|ZP_03593483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis subsp. subtilis str. 168]
ref|ZP_03597769.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis subsp. subtilis str. NCIB 3610]
ref|ZP_03602169.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis subsp. subtilis str. JH642]
ref|ZP_03606454.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis subsp. subtilis str. SMY]
ref|YP_004205513.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
      subtilis BSn5]
sp|P70965.1|MURA1_BACSU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
      AltName: Full=Enoylpyruvate transferase 1; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
      Short=EPT 1
emb|CAB03688.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus

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subtilis subsp. subtilis str. 168]
emb|CAB15693.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. subtilis str. 168]
dbj|BAI87334.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. natto BEST195]
gb|ADV94486.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis BSn5]
Length = 436

Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 91/359 (25%), Positives = 146/359 (40%), Gaps = 45/359 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L SE +V+ ++ DV+ + LR L
Sbjct: 2 EKIIIVRGQKLNKGTVEGAKNAVLPIAASLLASEEKSVIDCVPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V + V V E E V R + A+V G G
Sbjct: 62 GADVHFEN---NEVTNASYALQTEAPFEYV-----RKMRAVSLVMGPLLARTG 107

Query: 118 NATYVLGDVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + +GA++ G V+ G L G K+ L
Sbjct: 108 HARVALPGGCAIGSRPIDQHLKGFEAMGAIEKVGNGFIEAEVK---GRLQAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +E + K P + + G K + + I+
Sbjct: 164 -SVGATENLIMAAALAEGTTTLENVAKE---PEIVDLANYINGMGGKIRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K K+ ++ D A F+ AAIT G V V+G L +E MG
Sbjct: 219 GVEKLHGKVKH-HIIPDRIEAGTFMVAIAITEGNVLVKAVPEHL---TSLIAKMEEMGVT 274

Query: 298 VTWTETSVTVTGPPREPFRGKHLKVIDNMNKMPP---DVAMTLAVVALFADGPTAIRD 352
+ + V GP K LK ID+ P D+ + + L A G + I +
Sbjct: 275 IKDEGEGLRVIGP-----KELKPIDIKTMPHPGFPTDMQSQMMALLLRASGTSMTIE 326

>ref|ZP_04639705.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia mollaretii ATCC 43969]
gb|EEQ11694.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia mollaretii ATCC 43969]
Length = 421

Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 174/431 (40%), Gaps = 59/431 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E
Sbjct: 6 VQGRTRLSGEVTISGAKNAALPILFAALLAEPEVLQNVPKLKDIDTTIKLLGQLGTKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D + V DA+ +V F + +++ A++ A G G
Sbjct: 66 RDSSGSVVFV-----DAR-DVNEFCAPYDL-VKTMRAIWLGLPLVARFGKGQVS 112

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 113 LPGGCAIGARPVDLHITGLEQLGAIEKLEEGY---VKASVNGRLKGAHIVMD-KVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + S DR I+
Sbjct: 168 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKISGAGS-DRITIEGVARL 223

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 224 GGGVYR-----VLPDRIETGTFVLVAAAISGGKVVCRQTRPDTL--DAVLAKLRE-AGAD 274

Query: 298 VTWTETSVTVTGPPREPFRGKHLKVIDNMNKMPP---DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA+ + P D+ +++ L A+G I +
Sbjct: 275 IEVGDDWISLDMHGQRP-----KAVTIRTAPHPGFPTDMQAQFSLNLAEGTGVITET 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413

+ E M EL ++GA E + I E+L+ + D R + + LA
Sbjct: 329 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVQELSGAQV-MATDLRASASLVLA 381

Query: 414 ACAEVPVTIRD 424
 C VTI D

Sbjct: 382 GCIADGVITVD 392

>ref|ZP_06873785.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii ATCC 6633]
ref|YP_003867971.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii str. W23]
gb|EFG92305.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii ATCC 6633]
gb|ADM39662.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii str. W23]
Length = 436

Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 91/359 (25%), Positives = 146/359 (40%), Gaps = 45/359 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L SE +V+ ++ DV+ + LR L
Sbjct: 2 EKLIIVRGQKLNQTVKVEGAKNAVLPIVIAASLLASEEKSVIDCVPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCCKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V + V V E E V R + A+V G G
Sbjct: 62 GADVHFEN---NEVTVNASYALQTEAPFEYV-----RKMRASVLVMGPPLLARTG 107

Query: 118 NATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + +GA++ G V+ G L G K+ L
Sbjct: 108 HARVALPGGCAIGSRPIDQHLKGFEMGAIEKVGNGFIEAEVK----GRLQGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIK 237
S L+MAA LA G +E + K P + + G K + + I+
Sbjct: 164 -SVGATENLIMAAALAEGETTTLENVAKE---PEIVDLANYINGMGKIRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVVKFAEVLEMMGAK 297
G +K K+ ++ D A F+ AAIT G V V+G L +E MG
Sbjct: 219 GVEKLHGKVKH-HIIPDRIEAGTFMVAIAITEGNVLVKGAVPEHL---TSLIAKMEEMGVT 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD 352
+ + V GP K LK ID+ P D+ + + L A G + I +
Sbjct: 275 IKDEGEGLRVIGP-----KELKPIDIKTMPHPGFPTDMQSQMALLLRASGTSMITE 326

>ref|YP_199929.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
ref|YP_450219.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae MAFF 311018]
ref|YP_001915036.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae PXO99A]
sp|Q5H3C7.1|MURA_XANOR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
sp|Q2P682.1|MURA_XANOM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
sp|B2SJY7.1|MURA_XANOP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
gb|AAW74544.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
dbj|BAE67945.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae MAFF 311018]
gb|ACD60504.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzae PXO99A]
Length = 424

Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 96/385 (24%), Positives = 156/385 (40%), Gaps = 45/385 (11%)

```
Query: 6  EIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      +IV+  + + G V + G+K+  IL  L++  + N+ +  DV M+  L  LG
Sbjct: 3  KIVVTGGQALQGEVNIISGAKNAVLPILCATLLADAPVQISNVPHLHDVITMVKLLSELGA 62

Query: 66  SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
      V D+  A R+++V      P E K  L  + R TA V+  GG
Sbjct: 63  EVTIDEGTLAKGRSILVDPKSVTHQIAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119  ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      A      + RP+  + GL+ LGA++  G  ++  G L GG+  +
Sbjct: 123  A-----IGSRPVDQHIKGLQALGAEISVENGY----IKATSHGRLKGGRYVFD-MV 168

Query: 179  SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
      S      +LMAA LA G  +++  P V  M  G + E + + R ++G
Sbjct: 169  SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCMIALGAQIEGAGT-PRIVVQG 224

Query: 239  GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      Q+  +A + D  FL AA+TGG+VTV  +L D  ++ E GA +
Sbjct: 225  VQRLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETL--DAMLDKLTE-AGATI 280

Query: 299  TWTETSVTVTGPPEPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
      T T S+T+  + P  +A+ +  P  D+  +  ADG I +
Sbjct: 281  TTTADSITLDMQGKRP-----RAVSLTTAPYPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355  SWRVKETERMVAIRTELTKLGASVE 379
      + E M  EL +LGA ++
Sbjct: 334  ---IFENRFMHV--NELLRLGADIQ 353
```

```
>ref|YP_002910234.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
glumae BGR1]
gb|ACR27530.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
glumae BGR1]
Length = 448
```

Score = 47.8 bits (112), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 79/311 (25%), Positives = 134/311 (43%), Gaps = 36/311 (11%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
      E +V+  + +SG +++ G+K+ + IL  LS  +DN+ + +DV ML L +G
Sbjct: 30  ERLVITGGRRLSGEIRVSGAKNAALPILCAGLLSAEPLRLDNVPLQDVRTMLALLGGMG 89

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
      +  D A R  +  PV A E+  +++++ A++  G  G
Sbjct: 90  VKSAVDGA--RVTLDAASVTDPV--APYEL-----VKTMRASILVLGPLLARFGY 135

Query: 119  ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
      A L G  + RP+  + GL+ +GA++  G  +  R+ G L  + ++G+
Sbjct: 136  AKVSLPGGCAIGARPVDQHIKGLQAMGAEITIEHGYIEARATRLKG-ARLVTDMITVTGT 194

Query: 178  ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      LLMAA LA G+  +I+  P V  L+  G + +  DR I+
Sbjct: 195  -----ENLLMAATLADGET---VIENAAAREPEVTDLANLLVAMGARID-GIGTDRLVIQ 244

Query: 238  GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G ++  +A V D  A FL AA GG +T+ G  L D  ++ E GAK
Sbjct: 245  GVERLHGASHAVVP-DRIEAGTFLCAAAAAGGELTLRGMANLL--DAVLGKLRE-TGAK 300

Query: 298  VTWTETSVTVT 308
      +  + ++ VT
Sbjct: 301  LDERDDALRVT 311
```

```
>ref|YP_002468681.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. Tuc7 (Acyrtosiphon pisum)]
sp|B8D7S1.1|MURA_BUCAT RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
```

```

Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACL30186.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. Tuc7 (Acyrtosiphon pisum)]
gb|ADP66205.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. LL01 (Acyrtosiphon pisum)]
gb|ADP67361.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. JF99 (Acyrtosiphon pisum)]
Length = 416

Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 93/427 (21%), Positives = 165/427 (38%), Gaps = 45/427 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E++ ++ K ++G V + GSK+ + IL + L+EG + N+ N D++ L L LG
Sbjct: 2 EKLYVEGNKILNGHVIIISGSKNAALPILFMTILTEGKIKIGNIPNLTDINIALKLLVYLG 61

Query: 65 LSVEADKAA---KRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ + ++ ++ + C + + + + + A G A
Sbjct: 62 VKITGNETLCIDASSINIFCPPYNLINKIRASIWIL-----GPLLARFGKAKI 109

Query: 122 VLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
L G ++ RPI + GL QLGA ++ L +C V G GK L IS
Sbjct: 110 FLPGGCKIGSRPIDLHLNGLTQLGATIN--LKNNCIDAYVK---GRLQGKYILMEKISVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G IID P + + + G + S ++ IKG K
Sbjct: 165 ATITIMSAAATLAKGST---IIDNAACEPEIVDIAKFLNTLGADIIGAGS-NKICIKGVLK 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + D FL AA + G +T C T + L GAK+
Sbjct: 221 LTGGTHQVIP-DRIETGTFLVAAAASQGHIT---CHKTEPKHLTNVLMKLTEAGAKIKTG 276

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWR 357
+ + + + P K++++ P D+ A++ + G I +
Sbjct: 277 KDWIKLDMRGKRP-----KSLNICTAPYPGFPTDMQAQFALLNSISKIGITITETI--- 327

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
E +EL ++GA ++ + I KL +++ D R + LA C
Sbjct: 328 ---FENRFIYTSSELIRMGAKIKIKNNTIICCGIPKL-ISSNVFSSDLRASATLILAGCIA 383

Query: 418 VPVTIRD 424
+TI +
Sbjct: 384 AGITIVN 390

>gb|AAB32919.1| enolpyruvylshikimate-3-phosphate synthase type A [Pneumocystis
carinii]
gb|AAA97399.1| encodes EPSP synthase domain [Pneumocystis carinii f. sp. mustelae]
prf||2210353D AROM protein
Length = 108

Score = 47.8 bits (112), Expect = 0.004, Method: Composition-based stats.
Identities = 28/89 (31%), Positives = 47/89 (52%), Gaps = 5/89 (5%)

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN-----TAIDTYDD 403
T I +++ ++KE R+ A+ EL K G E P+ + + ++ ++ Y+D
Sbjct: 20 TEITGISNQKIKECNIRINAMIYELKKFGIEAGELPNGIYVKSLSKISDLLSPTNGVNCYND 79

Query: 404 HRMAMAFSLAAC-AEVPVTIRDPGCTRKT 431
HR+AM+FS+ AC + P I D C KT
Sbjct: 80 HRIAMSFVSLACVSPKPTIILDKTCINKT 108

>ref|YP_003922109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
amyloliquefaciens DSM 7]
emb|CBI44639.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
amyloliquefaciens DSM 7]
Length = 436

Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.

```

Identities = 90/359 (25%), Positives = 146/359 (40%), Gaps = 45/359 (12%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      E+I+++  +++GTVK+ G+K+  ++  + L SE  +V+ ++  DV+ +  LR L
Sbjct: 2  EKIIIVRGQKLNGLTVKVEGAKNAVLPIAASLLASEEKSVIDVPTLSDVYTINEVLRHL 61

Query: 64  GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      G V +  V V  E E V  R + A+V  G  G
Sbjct: 62  GADVHFEN---NEVTVNASYALETEAPFEYV-----RKMRAVSLVMGPLLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      ++  L G  +  RPI  + G + +GA +  G  V  G L G K+ L
Sbjct: 108 HSRVALPGGCAIGSRPIDQHLKGFEAMGAKIKVGNGFIEAEVE---GRLQAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      S  L+MAA LA G  +E + K  P +  +  G K  + +  I+
Sbjct: 164 -SVGATENLIMAAALAEGTTTLENVAKE--PEIVDLANYINAMGGKIRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G +K + ++  +  D  A  F+  AAIT G V V+G  L  +E MG K
Sbjct: 219 GVEKLRGVRHNIIP-DRIEAGTFMVAAAITEGNVLKGAPEHL---TSLIAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
      +T  + V GP +  LK ID+  P  D+  +  + L A G + I +
Sbjct: 275 ITDEGEGLRVIGPAQ-----LKPIDIKTMPHPGFPTDMQSQMMALLLRASGTSMITE 326
```

```
>ref|ZP_05089357.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ruegeria sp.
      R11]
gb|EEB71049.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ruegeria sp.
      R11]
      Length = 422
```

Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 95/409 (23%), Positives = 165/409 (40%), Gaps = 42/409 (10%)

```
Query: 15  ISGTVKLPKSGKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G + + G+K+  ++  LSE  + N  D+  M  L++LG  V + +  +
Sbjct: 12  LKGQIPIAGAKNACLTLMPTLLSEEPLTLTNAPRLSDIKTMTLLQLSGLAEVSSLQDGQ 71

Query: 75  RAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      V+  A ++  + + + +  + A +  G A  L G  + RP+
Sbjct: 72  --VLALSSHNLTSHVADYDIVRKMRAVSLVLPMLARL---QAVVSLPGGCAIGARPM 125

Query: 135 GDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      + GL+ LG++  D +L  P  GL G  V+LS + S  ++MAA
Sbjct: 126 DLHIHGLEALGAIEELKDGYLHAKAP-----NGLKGAVVELSFA-SVGATENIMMAAT 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      LA G  +I  P +  + + G + E  S D  I+G +  + V
Sbjct: 178 LAKGTT---VIKNAAREPEIVDLADCLRKMGQAIEGDGSPD-ITIQGVDRHLHGATHQVVT 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVTGPP 311
      +Y LA  AI GG V + G  + L+  F  LE  G ++  + S+TV
Sbjct: 234 DRIELGTYMLA-PAICGGEVELLGGRSLLE---SFCAKLEAAGVEIENDNSLTVR--- 286

Query: 312 REPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
      G  +KA+DV  P  D+  +  +  A+G + + +  ++ E  M A
Sbjct: 287 ---RGDNRVKAVDVVTEFPFGFPTDLQAQMMALMCTAEGTSVLEE---KIFENRFMHA- 338

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACA 416
      EL ++GA +E  +  +T  EKL  +  D R +++  LA  A
Sbjct: 339 -PELVRMGAQIEVHGGHATVTGVEKLGAPV-MATDLRASVSLILAGLA 385
```

```
>ref|ZP_02886904.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      graminis C4D1M]
gb|EDT07553.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      graminis C4D1M]
      Length = 420
```


Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 70/281 (24%), Positives = 125/281 (44%), Gaps = 27/281 (9%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      +++V++ +SG V + G+K+ + IL + LS +DN+ + +DV ML L +G
Sbjct: 2  DKLVIIEGGYPLSGEVVVGAKNAALPILCASLLSAEPVQLDNVPDLQDVRTMLKLLGQMG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
      + +E+ + G+ ++ +K + + MR+ + + A G+A
Sbjct: 62  VRIESAE-----GRVSLDASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110

Query: 122  VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
      L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+
Sbjct: 111  SLPGGCAIGARPVDQHIKGLQAMGAETIDHGFIEARAER-----LKGARI-ITDMITV 163

Query: 181  QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      LLMAA LA G+ +I+ P V L+ + G K E + DR I+G
Sbjct: 164  TGTENLLMAAVLAEGET---VIENAAREPEVGDLAHLVLVQMGAKIEGIGT-DRLVIQGV 219

Query: 241  KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
      K K+ + D A FL A GG VT++ +L
Sbjct: 220  KLHGAKHTVIP-DRIEAGTFLCAVAAAGGDVTLKNVRPQTL 259
```

```
>ref|NP_240203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. APS (Acyrtosiphon pisum)]
sp|P57466.1|MURA_BUCAI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
pir||A84975 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
[imported] - Buchnera sp. (strain APS)
dbj|BAB13089.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. APS (Acyrtosiphon pisum)]
Length = 416
```

Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 97/427 (22%), Positives = 169/427 (39%), Gaps = 45/427 (10%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E++ ++ K ++G V + GSK+ + IL + L+EG + N+ N D++ L L LG
Sbjct: 2  EKLYVEGNKILNGHVIIISGSKNAALPILFMTILTEGKIKIGNIPNLTDINIALKLLVYL 61

Query: 65  LSVEADKAA---KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
      + + ++ ++ + C P + +++ A I M + A G A
Sbjct: 62  VKITGNETLCIDASSINIFC----PPYNLINKIR-----ASIWM---LGPLLARFGKAKI 109

Query: 122  VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQ 181
      L G ++ RPI + GL QLGA ++ L +C V G GK L IS
Sbjct: 110  FLPGGCKIGSRPIDLHLNGLTQLGATIN--LKNNCIDAYVK---GRLQGYILMEKISVG 164

Query: 182  YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      ++ AA LA G IID P + + + G + S ++ IKG K
Sbjct: 165  ATITIMSAAATLAKGST---IIDNAACEPEIVDIAKFLNTLGADIIGAGS-NKICIKGV 220

Query: 242  YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
      + + D FL AA + G +T C T + L GAK+
Sbjct: 221  LTGGTHQVIP-DRIETGTLVAAAASQGHIT---CHKTEPKHLTNVLMKLTEAGAKIKTG 276

Query: 302  ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
      + + + + P K++++ P D+ A++ + G I +
Sbjct: 277  KDWIKLDMRGKRP-----KSLNICTAPYPGFPTDMQAQFALLNSISKGIGTITETI--- 327

Query: 358  VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
      E +EL ++GA ++ + I KL +++ D R + LA C
Sbjct: 328  ---FENRFIYTSSELIRMGAKIKIKNNNTIICYGIPKL-ISSNVFSSDLRASATLILAGCIA 383

Query: 418  VPVITIRD 424
      +TI +
Sbjct: 384  AGITIVN 390
```

>ref|ZP_07965738.1| aroA protein [Segniliparus rugosus ATCC BAA-974]
gb|EFV13032.1| aroA protein [Segniliparus rugosus ATCC BAA-974]
Length = 94

Score = 47.8 bits (112), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 28/87 (32%), Positives = 42/87 (48%), Gaps = 1/87 (1%)

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACA 416
R ET+R+ A+ +++ LG E D ITP + L + DHRMA A ++
Sbjct: 2 RGHETDRLAALASQINGLGHCVELDDGLSITP-KPLRGGLWKAFADHRMATAGAIIGLK 60
Query: 417 EVPVTIIRDPGCTRKTFPDYFDVLSTFV 443
V + D CT KT P + D+ +T
Sbjct: 61 TPGVQVDDVDCTSKTLPGFADLWATMC 87

>ref|YP_459350.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erythrobacter
litoralis HTCC2594]
gb|ABC64553.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Erythrobacter
litoralis HTCC2594]
Length = 447

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 105/441 (23%), Positives = 175/441 (39%), Gaps = 77/441 (17%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++V++ +SGT+ + G+K+ + ++ A L++ + NL D+ +
Sbjct: 20 GMDKLVIRGGNRLSGTIPISGAKNSALTLPICALLTDEPLTLRNLRLADIDGFQHLMNQ 79
Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAK----EEVQLFLGNAGIAM-RSLTAAVTAAG- 116
G V+ GK P + + E ++ A + R + A++ G
Sbjct: 80 FG-----VMTAVQGRPEDFGRVMTMEATRITSSVAPYDLVRKMRASILVLGP 127
Query: 117 -----GNATYVLGDVPRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVVRVNGI---GGLP 168
G AT L G + RPI + L+ LGA+++ G V + GGLP
Sbjct: 128 MLARMGEATVSLPGGCAIGNRPIDLHLKALEALGAEIEMAQGY-----VKAVAPDGGLP 181
Query: 169 GGVKLSGSISSQYLSALLMAAPLALGDVEI-----EIIDKLISIPYVEMTLRLMERF 221
GGK +S +MAA LA G + EI+D +L+
Sbjct: 182 GGFDFP-VVSVGATENAVMAAVLAKGTSHLFNAAREPEIVD-----LCKLLAAM 230
Query: 222 GVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
G + E S D + G K V GD A + AAITGG V +EG +
Sbjct: 231 GAEIEGIGSSD--LVIHGKRLHGYATYRVMGDRIEAGSYACAAAITGGDVMLEGANAEEM 288
Query: 282 QGDVKFAEVLEMMGAKVTWTETSVTVT--GPPREPFGKHLKAIDVNMNKMPPDVA--MTL 337
Q + L +G V T++ V + GP LKA ++ P +A M
Sbjct: 289 QATI---HALRNIGVTVEETKSGVHIIADGP-----LKATNLTTAPYPGLATDMQA 336
Query: 338 AVVALF--ADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 395
+++L A+G + +++ + E M EL ++GA +E I+ E L
Sbjct: 337 QLMSLLCKAEGTSVLKET---IFENRFMHV--PELNRMGADIETEGRTAIVKGVETLTG 390
Query: 396 TAIDTYDDHRMAMAFSLAACA 416
+ D R +M+ +A A
Sbjct: 391 AEV-MATDLRASMSLIIAGLA 410

>ref|ZP_06756496.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Scardovia
inopinata F0304]
gb|EFG26164.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Scardovia
inopinata F0304]
Length = 443

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 91/376 (24%), Positives = 158/376 (42%), Gaps = 42/376 (11%)

Query: 13 KEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+L ++ ++ A L+ G +V+ N+ DV + LR G+ V+ + +
Sbjct: 17 KPLNGTIKVRGAKNLVSKAMVAALLAPGNSVLKNVPEIRDVQVVSLLRLHGVDDVDVNGS 76

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRER 132
+ + P A +V+ G + I + + + G A G R+ +R
Sbjct: 77 TGIIVTIDAHHVEMP---AVSDVETLSGASRIPIL-FSGPLLHRLGEAFIPTLGGCRIGDR 132

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS----GSISSQYLSALLM 188
PI + L++LGA+VD + + GL G K+ L G+ L+A+L
Sbjct: 133 PIDFHLETLRKLGANVD---KEHEDGIHITAPDGLTGAKIHLPPYPSVGATEQTILAAVLA 189

Query: 189 AAPLALGD--VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSP 245
L VE EI+D LI+I +++ G A S DR I+G ++ K
Sbjct: 190 DGKTELSGAAVEPEIMD-LIAI-----LQKMG--AVISVDVDRITIRIEGVKELKGY 237

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSV 305
+ + AS+ A A T G V ++G + + F V +G+ T+ +
Sbjct: 238 THTALTDRIEVASASAALA-TRGDVFIKATQPEM---MTFLNVYRKVGGEFEVTDEGI 293

Query: 306 TVTGPPPREPFGRKHLKAI--DVMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P G H AI DV+ M D L V A G + + + E
Sbjct: 294 HFW---HPGGDLHAVALETVDVHPGFMTDWQQPLVVALTQAKGLSIVHETVY-----EN 343

Query: 364 MVAIRTELTKLGASVE 379
L ++GA+++
Sbjct: 344 RFGFTKPLVQMGATIQ 359

>ref|YP_003677894.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter mathranii subsp. mathranii str. A3]
gb|ADH61883.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter mathranii subsp. mathranii str. A3]
Length = 417

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 94/396 (23%), Positives = 157/396 (39%), Gaps = 45/396 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ K ++G+V++ G+K+ + IL A L++ +V+DNL + D+ + +R LG
Sbjct: 2 EKFFVIKGGKPLTGSVQISGAKNSAVAILPAALLADTPSVIDNLPDINDIKLLTQMIRHLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE K G +P D +++ G + AV A G
Sbjct: 62 GKVEEKKHEIMIDPTGLNSFYPPRDLASKMRASYLVGALLSKFNEAVIAMPGGCNI--- 118

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
GV RPI + G + LGA G +R+ L G + +S
Sbjct: 119 GV-----RPIDQHIKGFALGAKTTIEGGL----IRIKA-DKLVGNHIYFD-VVSVGATI 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++A+ A G + I++ P+V + G + + + D I G +
Sbjct: 168 NLMLASVKAEG---VTILENCAKEPHVVDVANFLNMGANIKGAGT-DTIKITGVDRHLG 223

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETS 304
+ + +Y +A AA T G V ++G L+ + A++ E MG V +
Sbjct: 224 CHYTIIPDQIEAGTYMVAAAA-TKGDVYIKGVIPNHLEAII--AKLTE-MGVIVEEHDDV 279

Query: 305 VTVT--GPPPREPFGRKHLKAIDVMNMKMP----DVAMTLAVVALFADGPTAI-RDVASWR 357
V + GP LK +D+ P D+ AV+ A+G + I ++ R
Sbjct: 280 VRIKREGP-----LKHVDIRTLPPYGFPTDMQQPFVALLALAEISVITENIYENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
K EL K+GA V I EKL
Sbjct: 331 FKYL-----NELEKMGAKVRIEGRNAIFEGVEKL 359

>ref|ZP_07891665.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Arcobacter
butzleri JV22]
gb|EFU69976.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Arcobacter
butzleri JV22]
Length = 429

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.

Identities = 87/382 (22%), Positives = 156/382 (40%), Gaps = 58/382 (15%)

Query: 13 KEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K+ISG+V++ G+K+ + ++ L + + NL N D++ L
Sbjct: 17 KDISGSVEISGAKNAALPLIACITILGKNEITIGNLPNVVDINTFL----- 61

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GNATYV 122
+++ GG F E+ K ++ N A ++++ A++ G G+
Sbjct: 62 ---KLILKLGGSFVKEENKVKINTSTINNTTATYDIVKTMRASILVLGPLLARFGHCEVS 118

Query: 123 LDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + +RP+ + L+Q+GA ++ G ++ GL G K+ ++
Sbjct: 119 LPGGCAIGQRPVDLHLKALEQMGAKIEILQGY---IKATAPNGLKGAKIVFD-KVTVGG 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG-GQK 241
++MAA LA G + I P + ++ GVK E + I+G GQK
Sbjct: 174 TENIVMAAALAHG--VTTIINAAKEPEIVQLCEVLANSVGKIE-GIGTSKIVIEGTGQK 229

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K V D A ++ AAIT + + L+ + LE M +V
Sbjct: 230 LIDIKPFDPVDPRIEAGTYMCAAAITNKKLKINKVIPLHLEAVI---SKLEEMNFEVLQD 286

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E SVT+ P E +K +++ + P D+ +A A+G + I + R
Sbjct: 287 ENSVTIL-PTTE-----IKPVNIITTEYPGFPTDMQAQFMALATQANGTSTIDE----R 335

Query: 358 VKETERMVAIRTELTKLGASVE 379
+ E M +EL +LGA +
Sbjct: 336 LFENRFMHV--SELLRLGADIH 355

>ref|ZP_05132794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
7_2_43FAA]
gb|EEH99688.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
7_2_43FAA]
Length = 419

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 97/386 (25%), Positives = 157/386 (40%), Gaps = 51/386 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E++V+ K + G+V + G+K+ + IL A + SEG ++DN+ + EDVH + L +L
Sbjct: 2 EKLIVINGGKVLKGSVDINGAKNSAVAILPAAIMASEGKCIIDNVPDIEDVHCLERILTS 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGG 117
G SV +K + + VE ++V+ F+G + R A V GG
Sbjct: 62 GCSV--NKLNNNTLEIDATDVRSVEACTDDVRRMRASYFIG--ALLSRFKKARVELPGG 117

Query: 118 NATYVLGDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
V RPI + G + LGA V G L G +
Sbjct: 118 CPIGV-----RPIDQHIKGFELGAKVTIEHGAVIVEAE-----NLHGANIFFDVV 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
++ +++AA LA G +E + K P+V + G + + + D +K
Sbjct: 164 TVGATIN-VMIAATLAEGTTVLENVAKE---PHVVDVANFLNSMGADIKGAGT-DVIRVK 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K S N V D A F+ AA T G VT++ L+ A L MGA
Sbjct: 219 GVEKL-SGCNYSVIPDQIEAGTFMIAAAATKGDVTIKNVIPKHLE---SIAAKLIEMGAI 274

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
V + SV V + LK ++V P DV ++ + G + I +
Sbjct: 275 VEEGDDSVRV-----YVEGDLKGVNVKTAPYPGFPTDVQQPMSALLSIVPGKSLISE- 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVE 379
+ W + EL K+GA+++
Sbjct: 327 SIWESRHKH-----IDELKKMGATIK 347

>ref|YP_001439629.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cronobacter
sakazakii ATCC BAA-894]

sp|A7MNS2.1|MURA_ENTS8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABU78793.1| hypothetical protein ESA_03582 [Cronobacter sakazakii ATCC BAA-894]
Length = 419

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 99/421 (23%), Positives = 170/421 (40%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKIDITTMKLLSQLGKTVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVWIDAS--QVNIFCAPYEL-VKTMRSI WALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLEQLGAEIKLEEGY---VKASVQRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P + T + G K + D+ I+G ++
Sbjct: 172 AATLAEGTT---VIENAAREPEIVDTANFLNTLGAKITGQGT-DKITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG V +L D A++ E GA + E +++
Sbjct: 226 YRVLDPRIETGTFLVAAISGGKVMCRNRPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA++V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET---IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|ZP_06599658.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oribacterium sp.
oral taxon 078 str. F0262]
gb|EFE90934.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oribacterium sp.
oral taxon 078 str. F0262]
Length = 534

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 88/432 (20%), Positives = 173/432 (40%), Gaps = 31/432 (7%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDEVHYMLGALRTL 64
++ +++ + G V + G+K+ + ++ A L++ T V++NL + DV+ ML LR LG
Sbjct: 105 QQFIMRGGHPLRGEVVGAKNAALGLIAAAILTDDTVVIENTLPDVRDVNVMLDVLREL 164

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+VE + V + G + E ++ A A+ +A L
Sbjct: 165 AAVE--RTGSHTVSICAAGIRELSINDEFIRIR-----ASYFIGALLGKYHSAVPLP 217

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LG D+ G + GL G + L +S
Sbjct: 218 GGCAIGSRPIDQHLKGFALGTDIRIQNGCVVAEAK----DGLKGTHIYLD-VVSVGATI 272

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+++AA L+ IE + K P++ + G + + D I+G ++
Sbjct: 273 NIMLA AVLSEKRTTIENVAKE---PHIVDVANFLNSMGANIRGAGT-DTIRIRGVKRLHG 328

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
A + D A F+ AA + G + ++ L+ A+++EM V + E+
Sbjct: 329 TSYAVIP-DQIEAGTFMCAAAAASRGDILIKNVIPKHLESIS--AKLVEMGNTVVEYDESI 385

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRD-VASWRVKETER 363
+ + P K L + P +++TL + A G + + + + R K +
Sbjct: 386 RVIGSAVQRPTDVKTLPPYGPFTDMQPQISVTLGL----ARGISVVTESIFESRFKYVD- 440

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
EL ++G +++ + II +++ D A CAE T+R
Sbjct: 441 -----ELARMGGAIVVEGNVSIIDGIRSYTGASVNALDLRAGAALVIAGLCAEGITTVR 494

Query: 424 DPGCTRKTFFPDY 435
+ G ++ + +
Sbjct: 495 EIGYIQRGYEHF 506

>ref|YP_001763704.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
cenocepacia MC0-3]
gb|ACA89582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
cenocepacia MC0-3]
Length = 449

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 66/280 (23%), Positives = 118/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEIEVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ K +SG + + G+K+ + IL L+ +DN+ N +DV L L
Sbjct: 29 GMDKLAIEGGKRLSGEIVVSGAKNAALPILCAGLLTADPVDLDNVPNLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + ++++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVNNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVSDLAHLLVAMGAKIDGIGT-DRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +++ + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVMLTG 282

>ref|ZP_06114897.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
hathewayi DSM 13479]
gb|EFC98648.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
hathewayi DSM 13479]
Length = 430

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 100/427 (23%), Positives = 183/427 (42%), Gaps = 49/427 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ ++G V + G+K+ + IL + +++ V++NL + D++ +L A+ +G
Sbjct: 2 EQYIMKGGNPLAGEVTIGGAKNAALGILAAASIMTDEDVVIENLPDVRDINVLEAIEEIG 61

Query: 65 LSVE-ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 117
VE D+ R GK+ E + ++ + R + A+ G
Sbjct: 62 ADVERIDRHTVR-----INGKYIHEVSVDEYI-----RKIRASYFFIGAMLGKYK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + LGA+V G V + I L + L
Sbjct: 108 SAQVPLPGGCNIGSRPIDQHLKGFRALGAEVKIERGA---VIAHAI-DLVASHIYLD-V 161

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S ++MAA LA G I++ + P+V + G + + + D IK
Sbjct: 162 VSVGATINIMMAATLAEGQT---ILENVAKEPHVVDVANFLNSMGANIKGAGT-DTIRIK 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K + + + D A F+ AAIT G VTV+ L+ A++LE MG +

Sbjct: 218 GVRKLHGTEYSIIP-DQIEAGTFMCAAAITRGDVTVKNVIPKHLEA--ISAKLLE-MGCE 273

Query: 298 VTWTETSVTVTGPPREPFGFR-KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRD-VAS 355
 V + +V V G + K L + P + +TLA A+G + + + +

Sbjct: 274 VVEFDDAVRVVGKTLQRHTDIKTLPPYPGFPTDMQPMQMTVTLA----LAEGASVVTESIFE 329

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC 415
 R + + EL+++G +V+ + +I +KL +++ D R A +A

Sbjct: 330 NRFRYVD-----ELSRMGGNVKGVEGNVAIDGVKKLTGASVNA-PDLRAGAALVIAGL 381

Query: 416 AEVPVTI 422

A TI

Sbjct: 382 AAEGYTI 388

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>ref|NP_819777.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 493]
ref|ZP_01947182.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii 'MSU Goat Q177']
ref|YP_001424158.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii Dugway 5J108-111]
ref|YP_001596938.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 331]
ref|ZP_02219823.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 334]
ref|YP_002303720.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii CbuG_Q212]
ref|YP_002305812.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii CbuK_Q154]
sp|Q83DI0.1|MURA_COXBU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|A9KDT8.1|MURA_COXBN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|A9NDE8.1|MURA_COXBR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B6J8R8.1|MURA_COXB1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B6J0U7.1|MURA_COXB2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAO90291.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 493]
gb|EAX32200.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii 'MSU Goat Q177']
gb|ABS77531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii Dugway 5J108-111]
gb|ABX78184.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 331]
gb|EDR35181.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii RSA 334]
gb|ACJ18575.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii CbuG_Q212]
gb|ACJ20667.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Coxiella
burnetii CbuK_Q154]
Length = 434
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Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 92/389 (23%), Positives = 155/389 (39%), Gaps = 48/389 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 ++G++++ G+K+ IL L E ++ N+ + DV M+ L +G + D+ +

Sbjct: 12 LNSGIRISGAKNAVLPIAATLLIEEPVILSNIPHLNDVTTMIELLGRMGAQITIDE--R 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
 ++ V C V + E V +++ A++ G G A L G
 Sbjct: 70 MSIEVDCSQIQNVHASYELV-----KTMRASILVLGPLLRSFGKAEVSLPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 + RP+ + G++ LGAD++ G V G L G ++ L G I+ L+M
 Sbjct: 119 IGSRPVDVHIDGMRALGADIELVDGFIHATVE----GRLKGAELNL-GKITVTGTENLIM 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
 AA LA G II P V+ + + G + + + D I G + S +
 Sbjct: 174 AATLAEGQT---IIHNAACEPEVQDLANFLNKMGARISGAGT-DTIVIDGVDR-L-SGGSY 228

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
 + D A +L AA+T G V + +L E L GA+V E V +
 Sbjct: 229 SILPDRIEAGTYLVAAAMTRGHVIRIDVFPKTLGA---VLEKLHEAGARVKIGENWVDLD 285

Query: 309 GPPREPFGFRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
 R KA+D+ P D+ + + A+G I + V E M
 Sbjct: 286 MQGRR-----KAVIDVTAPYPEMPTDMQAQFMALNVVAEGQAVITET-----VFENRFM 335

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKL 393
 EL ++GA ++ +I EKL
 Sbjct: 336 HV--HELQRMGADIKLQGSKALIRGKEKL 362

>ref|ZP_03992331.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oribacterium
 sinus F0268]
 gb|EEJ50461.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oribacterium
 sinus F0268]
 Length = 430

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 95/435 (21%), Positives = 170/435 (39%), Gaps = 55/435 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTL----- 64
 + G V + G+K+ + I+ A L++ +++NL + D++ ML AL+ +G
 Sbjct: 13 LRGDVVISGAKNAALGIVAGALLTDEEVIIENLPDVRDINVMLEALKAIGAKVHRIESHV 72

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 +S++AD+ + ++V +DA ++ A A+ A L
 Sbjct: 73 VSIQADQLSMKSV-----DDDAIRIR-----ASYFIGALLGKYHQAKVALP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
 G + ERPI + G LGA+V+ G L G + L +S
 Sbjct: 116 GGCAIGERPIDQHIGFTALGAEEISDGYFVAKAE-----ELVGQHIYLD-VVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
 L++AA LA G II+ + P++ + G + + D I+G ++
 Sbjct: 170 NLMLAAVLADGQT---IENVAKEPHIVDVANFLNSMGANIRGAGT-DTIRIRGVERLHG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTET 304
 + D A F+ AA+T G + ++ ++ A L MG V +
 Sbjct: 226 TTYGVIP-DQIEAGTFMCAAATRGNLIKNIIPKHME---SIAAKLRDMGNTVYEGDEE 281

Query: 305 VTVTGPPEPFGFR-KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
 + V G ++ + K L + P +A+TLA A+G + + + + R E
 Sbjct: 282 IQVIGGEKQRGTKIKTLPYPGFPTDMQPQIAVTLA----LAEGKSTVTESIFENRFLYVE 337

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
 EL K+GA + I EKL + D A AE +
 Sbjct: 338 -----ELKKMGADITVEDRVATILGQEKLGATLHALDLRAGAALVLAGLAAEGVTVL 390

Query: 423 RDPGCTRKTFPDYFD 437
 D G R+ + ++F+
 Sbjct: 391 EDIGYIRRGY-EFFE 404

>ref|ZP_06412234.1| 5-enolpyruvylshikimate-3-phosphate synthase-like protein [Frankia
 sp. EUN1f]
 gb|EFC84880.1| 5-enolpyruvylshikimate-3-phosphate synthase-like protein [Frankia


```

    sp. EUN1f]
    Length = 90

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 25/53 (47%), Positives = 33/53 (62%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
      + TV +PGSKS +NR L+LAAL++G + + L S D M ALR LG V
Sbjct: 24 VRATVAVPGSKSGTNRALVLAALADGVSRLRGPLRSRD TLLMAAALRN LGAQV 76

>ref|YP_001011775.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
      marinus str. MIT 9515]
sp|A2BY07.1|MURA_PROM5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ABM72668.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Prochlorococcus
      marinus str. MIT 9515]
      Length = 458

Score = 47.4 bits (111), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 90/387 (23%), Positives = 161/387 (41%), Gaps = 44/387 (11%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G VK+ G+K+ + +L + L++ ++DN+ D+ M L+ LG+ + +K +
Sbjct: 24 LRGNVKISGAKNSALVLLAASLLTDEKIIILDNVPLLT DIEKMGNILKNLGVKLH-NKDHQ 82

Query: 75 RAVVVGCGGKFPVEDAK----EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      + D+K +E+ L N A A+ G A+ L G +
Sbjct: 83 LII-----DSKNISIQELPYELVNGLRASFFCIGALLTRFGKASLPLPGGCNIG 131

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      ERPI + + GL+ LGA++ + L G ++L+ S L+MAA
Sbjct: 132 ERPINEHINGLRALGAEI-IEKEVVKAKLIKKS LFGANIRLNCP-SVGATETLIMAA 189

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      LA G II+ P ++ +++ + G K + ++ I G QK + +
Sbjct: 190 SLAEGRT---IIENAAREPEIQDLCQMLNKMGAKEI-YGAGKEKIIDGVQKLHGCSHKVI 245

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
      D A FL AA T ++T+ L+ LE G+K+ S++++G
Sbjct: 246 P-DRIEAGTFLIAAATSSSITISPVPINHLEA---VLNKLSESGSKIEKKNSISISG- 300

Query: 311 PREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
      K +KA+ + P D+ + A G + I S R+ E RM
Sbjct: 301 -----KSIKAVKIKTAPFGFPTDLQAPFMALMTIAKGTSMI----SERIFEN-RMHH 348

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKL 393
      + L ++GA++ + II +KL
Sbjct: 349 VNL-LNQMGAAITVDDNTAIINGVKKL 374

>ref|ZP_07403093.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
      matruchotii ATCC 14266]
gb|EFM49315.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
      matruchotii ATCC 14266]
      Length = 425

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 102/432 (23%), Positives = 162/432 (37%), Gaps = 39/432 (9%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G+VK+ G+K+ +++ A L+EGTT + N DV M LR LG V D
Sbjct: 13 LEGSVKVSAGKNSVLKLMMAALLAEGTTTLTNCPEILDVPLMAEVLRLGLGCEVSVVDHETV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
      R DA + + A + +T+ G A L G + RP+
Sbjct: 73 RITTPATVSSDADFDAVRQFR-----ASVCVLGLTSRTGRAVVALPGGDAIGSRPL 124

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

```

GL++LGA G V L G +++L S +L AA LA
Sbjct: 125 DMHQSGLEKLGATTYIRHGA-----VVAEATKLVGAIEIDFP-SVGATENILTA AVLAE 178
Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G +E + I + + LR M A+ + + G P V GD
Sbjct: 179 GRTVLENAAREPEIVDLVCMRLRQM-----GAQLTGECSPTIVIDGVDKLYPTQHEVIGDR 233
Query: 255 SSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
A + AA+T G +TV G L + E+L+ GA+++ E V P R
Sbjct: 234 IVAGTWAYAAAMTRGDI TVSGIAPRHLHLPL---EMLKFAGAQISSYENGFRVNMHPHRP- 289
Query: 315 FGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR-----TE 370
KA+D P L +A+ I +A TE + R E
Sbjct: 290 -----KAVDYQTLPPFGFPTDLQPMAL-----GISAIAEGTSVITENIFEARFRFVDE 337
Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRDPGCTRK 430
+ +LGA + ++ E+L+ T + + D A CA+ + D +
Sbjct: 338 MMRLGADATVDGHVVLRGVEQLSSTPVWSSDIRAGAGLVLAGLCADGETEVHDVYHIDR 397
Query: 431 TFPDYFDVLSTF 442
+P++ + L
Sbjct: 398 GYPNFVENLQQL 409

>ref|ZP_07053752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria grayi
DSM 20601]
gb|EF184765.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria grayi
DSM 20601]
Length = 443

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 91/402 (22%), Positives = 166/402 (41%), Gaps = 54/402 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ K+++GTVK+ G+K+ I+ L S+G + +DN+ + DV+ + L+ L
Sbjct: 14 EKIIIVRGGKQLNGTVKVEGAKNAVLPIIAATLLASKGKSKLDNVP SLSDVYTINEVLKYL 73
Query: 64 GLSVEADKAAKRAVVVGC GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V+ + V V G + E V R + A+V G G
Sbjct: 74 NADVQFEDG---QVTVDASGAITS DAPFEYV-----RKMRA SVVVMGP LLARTG 119
Query: 118 NATYVL DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RP+ + G + +GA V+ G L G K+ L
Sbjct: 120 SAKVALPGGCAIGSRPVDLHLKGFEAMGAVVNIENGYIEATAE-----KLTGAKIYLD FP 174
Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +I+ + P + + + G + + + + I+
Sbjct: 175 -SVGATQNMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIE 229
Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAK 297
G ++ + ++ + D F+ AAI GG V +E + + LE MG +
Sbjct: 230 GVKELVATEHNIIP-DRIEVGTFMIAAAIAGGNVLIEDAVPEHISSVIA---KLEEMGVQ 285
Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD- 352
+ + + V P + LKA+DV P D+ + ++ + ++G + + +
Sbjct: 286 IIEEDKGIRVIAPEK-----LKAVDVKTMPHPGFPTDMQAQMTIIQMLSEGTS LMTET 338
Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V R E M + ++ G SV II+ P KL
Sbjct: 339 VFENRFMHVEEMRRMNADMKIEGHSV-----IISGPAKLQ 373

>ref|ZP_07229751.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. tomato Max13]
ref|ZP_07251782.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. tomato K40]
Length = 538

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.

Identities = 59/235 (25%), Positives = 94/235 (40%), Gaps = 45/235 (19%)

Query: 225 AEHSDSWDRFYIKGGQ----KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 280
A+H ++ D ++ + + K P D +SA F+ +I+ EGC
Sbjct: 310 ADHHEAPDDVVRSAEGVSHRIKGPT-----DVTSAVLFMVATSIS-----EGCDL-- 355

Query: 281 LQGDVKFA-----EVLEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMPDV 333
L DV+ ++L +MG V V E H+++ + +P+
Sbjct: 356 LLEDVRVGSMECAIDILRLMGDDVVLQ----NVRELADERLADLHVR SARLKGADIPEA 411

Query: 334 AMTLAV-----VALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYC 385
+TLA+ A A+G T +R + + E+E + + LT LG E PD
Sbjct: 412 LVTLAIGTFPALIAAACAEGRTILRGAETLQAGESECVRLMADGLTVLGIEAEPVDPGI 471

Query: 386 II---TPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTTPDYF 436
II TP ID D R+ MAF +A+ A P+ I D FP +
Sbjct: 472 IIEGGTP----GGGEIDARGDQRIVMAFRVASLRASAPIRIHDCADAATLPHFL 522

>ref|YP_003785769.1| UDP-N-acetylglucosamine 1 carboxyvinyltransferase [Brachyspira
pilosicoli 95/1000]
gb|ADK31268.1| UDP-N-acetylglucosamine 1 carboxyvinyltransferase [Brachyspira
pilosicoli 95/1000]
Length = 425

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 94/377 (24%), Positives = 155/377 (41%), Gaps = 46/377 (12%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K I+GTVK+ GSK+ S +L+ + L++ + N+ + DV ++ L LG V D
Sbjct: 10 KNINGTVKISGSKNASLPLLVASILTDEPVTLHNVPDLVDVQVLINILEPLGKKV--DFK 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTA-----AVTAAGGNATYVLDGVP 127
V++ GK ++A ++ + + I + L A V+ GG A
Sbjct: 68 NNTTVIISQNGK--SDEAPYKLVKKMRGSIIVLGPLLAKRKHCKVSYPGGCA----- 117

Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA-- 185
RPI + G++ LGA +D G V+ N L G + LSG L
Sbjct: 118 -FGPRPIDLHLKGMEALGAKIDITAGYIDATVKDN----LIGADINLSGKNGPTVLGTDN 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G II P L++ G K E + I+G + K
Sbjct: 173 VMMAATLAKGTT---IIRNAAREPECTNLAEELLKAMGAKIEGIGT-STLTIEGVENLKG 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSV 305
+ + D FLA AA G + +E L ++L +G + T++++
Sbjct: 229 EFEVIP-DRIETGTFLAMAAAGRGKLENTNPEHL---TYVLDLLSIGCDIKTTKSTI 284

Query: 306 TVTGPPREPFGKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKET---E 362
+ +E LK ++ P L A+F I+ S ++KET +
Sbjct: 285 EIDASNKE-----LKPFEIETLPYPGFPTDLQ--AIFTTLACTIK--GSSKIKETIYPD 334

Query: 363 RMVAIRTELTKLGASVE 379
R + EL ++GA +E
Sbjct: 335 RFSNV-PELIRMGADIE 350

>ref|YP_003208752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cronobacter
turicensis z3032]
emb|CBA27360.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Cronobacter
turicensis z3032]
Length = 419

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 99/421 (23%), Positives = 170/421 (40%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLSLGQTKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128

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          G  ++ +  +V +F      + +++++ A++ A G      G      L G
Sbjct: 68  -----GSVIDAS--QVNIFCAPYEL-VKTMRSIALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
          + RP+  + GL+QLGA++  G      V+ +  G L G  + +  +S      ++
Sbjct: 117 IGARPVLDLHITGLEQLGAEIKLEEGY---VKASVQGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
          AA LA G      +I+      P +  T +  G K      + D+  I+G ++
Sbjct: 172 AATLAEGTT---VIENAAREPEIVDTANFLNTLGAKITGQGT-DKITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
          Y V D      FL AAI+GG V      +L D  A++ E  GA +  E  +++
Sbjct: 226 YRVLDPRIETGTFLVAAAISGGKVMCHNTRPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFGGRKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
          + P      KA++V      P      D+      ++ L A+G  I +      + E
Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACAEVPTIR 423
          M      EL ++GA  E  +  I      EKL+  +  D R + +  LA C      T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
          D
Sbjct: 390 D 390

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>ref|ZP_03396860.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. tomato T1]
gb|EEB60204.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. tomato T1]
Length = 535

```

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 59/235 (25%), Positives = 94/235 (40%), Gaps = 45/235 (19%)

```

Query: 225 AEHSDSWDRFYIKGGQ---KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 280
          A+H ++ D  ++ +  + K P      D +SA  F+  +I+      EGC
Sbjct: 307 ADHHEAPDDVVRSAEGVSHRIKGPT-----DVTSVLFMVATSIS-----EGCDL-- 352

Query: 281 LQGDVKFA-----EVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKVIDNMNMKMPDV 333
          L DV+      ++L +MG V      V      E      H+++ +  +P+
Sbjct: 353 LLEDVVRGSMCEGAIDILRLMGDDVVLQ---NVRELADERLADLHVR SARLKGADIPEA 408

Query: 334 AMTLAV-----VALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYC 385
          +TLA+      A A+G T +R  + +  E+E +  +  LT LG  E  PD
Sbjct: 409 LVTLAIGTFPALLIAAACAEGRTILRGAETLQAGESECVRLMADGLTVLGIEAEPVPGDI 468

Query: 386 II---TPPEKLNVTIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFFPDYF 436
          II  TP      ID  D R+  MAF +A+  A  P+  I  D      FP +
Sbjct: 469 IIEGGTP---GGGEIDARGDQRIVMAFRVASLRASAPIRIHDCADAATLFPHFL 519

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>ref|ZP_03708546.1| hypothetical protein CLOSTMETH_03307 [Clostridium methylpentosum
DSM 5476]
gb|EEG29194.1| hypothetical protein CLOSTMETH_03307 [Clostridium methylpentosum
DSM 5476]
Length = 416

```

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 85/304 (27%), Positives = 126/304 (41%), Gaps = 33/304 (10%)

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Query: 15 ISGTVKLPGSKSLSNRIALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
          +SG + +  G+K+ S  +L      +S G +V+ N      DV      L  LG SV  E  D
Sbjct: 12  LSGEISVHGAKNSSLPLLAATLISAGRSVLHNCPQLSDVDTACRILEHLGCSVQREGDTV 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQ---LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
          +  + C  + P E      E++  +FLG  IA R  TA V  GG      +

```

Sbjct: 72 TVDSSEMSC-SEIP-ESLMSEMRSSIVFLG--AIAARLG TARVCFPGGC-----EL 118

Query: 130 RERPIGDLVVLGKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + L+QLG ++ G DC G L G K+ LS S +L+

Sbjct: 119 GPRPIDLHLSALQQLGLEIQDDHGYLDC-----TVHGRLKGAKISLSFP-SVGATENILL 172

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G+ +I+ S P + + G + I+G + S ++

Sbjct: 173 AACTAEGEGET---VINNAASEPEIVDLANFLNSCGADIRGAGEQS-ILIRGVDELHSAEH- 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+V D A+ +L+ AA TGG + V C L D F VLE MG K+ S+ +

Sbjct: 228 WVIPDRIVAATYLSAAATGGELFVRNCCPEHL--DSVFP-VLEEMGCKLIVGRDSIYIR 284

Query: 309 GPPR 312
R

Sbjct: 285 AKSR 288

>ref|NP_621855.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacter tengcongensis MB4]
sp|Q8RD88.1|MURAI_THETN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAM23459.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Thermoanaerobacter
tengcongensis MB4]
Length = 415

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 74/312 (23%), Positives = 132/312 (42%), Gaps = 32/312 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTVK+ G+K+ I+ + LS +++++ + EDV+ M+ ++ G E D

Sbjct: 13 LKGTVKISGAKNSVLPPIAASLLSSDEVILEDIPSLEDVNVMIELIKNFGALCELDNGKL 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V + P E K+ FL + + A G+A + G + RPI

Sbjct: 73 KIKVDIKDVEAPYELVKKMRASFL-----VMGPILAKLGHAKISMPGGCAIGARPI 123

Query: 135 GDLVVLGKQLGADVDCFLGTDGTPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGAD+ +G R L G K+ L S ++MAA A

Sbjct: 124 DLHLKGQSLGADIT--IGHGYVEARAK---KLTGKKIYLDLP-SVGATENIMMAAVFAD 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + +I+ P + + + G + + + D I+G ++ K ++ + D

Sbjct: 178 G---VTVIENAAEPEIVDLANFLNKGANIKGAGT-DTIRIEGVKELKGAHTVIP-DR 232

Query: 255 SSASYFLAGAAITGGTVTVTEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGPPRE 313
A F+ AA+TGG V +E ++ + K E G K+T + + V G

Sbjct: 233 IEAGTFMVAAAMTGGNVLINIVDHSVIAKLTEC----GVKITEEKGLRVKGV--- 285

Query: 314 PFGRKHLKAIDV 325
K+ KA+D+

Sbjct: 286 ----KNYKAVDI 293

>ref|ZP_02464987.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
thailandensis MSMB43]
Length = 449

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 71/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ + + ++G + + G+K+ + IL + LS +DN+ N +DV L L

Sbjct: 29 GTDKLAIDGGRRLAGEIAVSGAKNAALPILCASLLSAEPVRLDNVPLKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ +++++ A++ G

Sbjct: 89 MGMREETDGA--RVVLDA SRVDNPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYARVSLPGGCAIGARPVDQHIKGLQAMGAEIHIEHGYIEARAKR-----LAGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLMAATLADGET--VIENAREPEVTDLAHLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAGGDVTLTG 282

>ref|YP_001466853.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
concisus 13826]
gb|EAT98623.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
concisus 13826]
Length = 422

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 96/422 (22%), Positives = 165/422 (39%), Gaps = 70/422 (16%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG VK+ G+K+ + I+ L L++ + N+ N D+ + L LG E
Sbjct: 12 KLSGEVKISGAKNAALPIIALTLLAKNKINLTNIPNVADIKTLCQLLVNLGAKCE----- 66

Query: 74 KRAVVVCGCGKFPVEDA----KEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVL 123
F E++ V N I +R + A++ G G+ L
Sbjct: 67 -----FKDENSLCIDTSSVNSTTANYDI-VRKMRASILTLGPLLARFGHCEVSL 114

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + +RPI + L+++GA+++ G V GL G K+ I+
Sbjct: 115 PGGCAIGQRPIDLHLSALEKMGANIEIKQGY---VVATAPNGLKGAKIVFD-KITVTGS 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G E L ++ P V ++ + GVK E + + GQ
Sbjct: 170 ENIIMAAALAHGTTE-----LFNVALEPEVVQICEILAKSGVKIEGIGTSELKITGSGQ 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEV---LEMMGA 296
K + V D A +L AIT ++V + + KF E+ +E+ G
Sbjct: 224 KLEICDIEVIPDRIEAGTYLCAGAITNSKISVTKANAAMTAILNKFEEMGFGIEVDGD 283

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRD 352
K+T T+ +K +++ + P D+ + L A+G + I +
Sbjct: 284 KITILPTN-----EIKPVEIRTTEYPGFPTDMQAQFMALCLAANGVSTIDE 329

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSL 412
R+ E M +EL ++GA + + P LN + D R + A L
Sbjct: 330 ----RLFENRFMHV--SELARMGADIRLNGHIASVYAPANLNAADV-MATDLRASSALIL 382

Query: 413 AA 414
AA
Sbjct: 383 AA 384

>ref|ZP_07256020.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. tomato NCPPB 1108]
Length = 538

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 59/235 (25%), Positives = 94/235 (40%), Gaps = 45/235 (19%)

Query: 225 AEHSDSWDRFYIKGGQ---KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 280
A+H ++ D ++ + + K P D +SA F+ +I+ EGC
Sbjct: 310 ADHHEAPDDVVRSAEGVSHRIKGPT-----DVTSAVLFMVATSIS-----EGCDL-- 355

Query: 281 LQGDVKFA-----EVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDV 333
L DV+ ++L +MG V V E H+++ + +P+
Sbjct: 356 LLEDVVRVSMCEGAIDILRLMGGDVVLQ----NVRELADERLADLHVRSARLKGADIPEA 411

Query: 334 AMTLAV-----VALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYC 385
+TLA+ A A+G T +R + + E+E + + LT LG E PD
Sbjct: 412 LVTLAIGTFPALLIAAACAEGRTILRGAETLQAGESECVRLMADGLTVLGIEAEPVPDGI 471

Query: 386 II---TPPEKLNVTATIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYF 436
II TP ID D R+ MAF +A+ A P+ I D FP +
Sbjct: 472 IIEGGTP----GGGEIDARGDQRIVMAFRVASLRASAPIRIHDCADAATLFPHFL 522

>ref|ZP_06638530.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
odorifera DSM 4582]
gb|EFE96437.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
odorifera DSM 4582]
Length = 432

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 104/427 (24%), Positives = 172/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E
Sbjct: 19 VQGRTRLRSGEVAISGAKNAALPILFAALLAEEPVELQNVPKLKDIDTTIKLNLQLGTKIE 78

Query: 69 ADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ +V V G V F + +++ A++ A G G
Sbjct: 79 RNG----SVFVDASG-----VHEFCAPYDL-VKTMRASIWALGPLVARFGRGQVS 123

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 124 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 178

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + S D+ I+G ++
Sbjct: 179 TVTIMSAATLATGTT---IIENAAREPEIVDTANFLNTLGAKISGAGS-DKIIIEGVERL 234

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVGCGTTSLSQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+GG V +L D A++ E GA +
Sbjct: 235 GG--GVYRVLPDRIETGTFVLVAAAISGGKVLCRDTRPDTL--DAVLAKLRE-AGADIEVG 289

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA+ V P D+ +++ L A+G I +
Sbjct: 290 EDWISLDMHGQRP-----KAVTVRTAPHPGFPTDMQAQFSLNLVAEGTGVITET---- 339

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + LA C
Sbjct: 340 IFENRFMHV--PELIRMGAAHAEIESNTVICHGVEQLSGAQV-MATDLRASASLVLAGCIA 396

Query: 418 VPVTIRD 424
VTI D
Sbjct: 397 DGVTIID 403

>ref|ZP_02430755.1| hypothetical protein CLOSCI_00968 [Clostridium scindens ATCC 35704]
gb|EDS07954.1| hypothetical protein CLOSCI_00968 [Clostridium scindens ATCC 35704]
Length = 430

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 97/423 (22%), Positives = 175/423 (41%), Gaps = 37/423 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E+ +++ + G V++ G+K+ + IL A +++ T +VDNL + D++ +L A+ +G
Sbjct: 2 EQYIIKGGHPLVGEVEIGGAKNAALAILAAAIMTDETVLVDNLPDVNDINVLLDAISGIG 61

Query: 65 LSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V + + V+ G V + ++ A L A+ A L
Sbjct: 62 ANVH--RVDRHTVKINGKGINDVNIEYDIKKIR-----ASYLLGALLGKYKRAEVALP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGADV G ++ GK +S
Sbjct: 115 GGCNIGSRPIDQHIKGFRLGADV DIEYG-----KIMAEADRLVGKHIYFDVVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
 ++MAA +A G + I++ + P+V + G + + D I+G Q+ S
 Sbjct: 169 NVMMATMADG---LTIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVQRLHS 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
 + + + D A F+ AA T G VTV L+ + A+++E +G +V + +
 Sbjct: 225 TEYSVIP-DQIEAGTFMFAAAATKGDVTVLNVIPKHLEATI--AKLVE-IGCEVEEFDDA 280

Query: 305 VTVTGPPEPFRGRKHLKAI---DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET 361
 V V + H+K + + P + +TL AL T + R K
 Sbjct: 281 VRVV--SKGDLTSTHVKTLPYPGFPTDMQPQIGVTL---ALCQGTSTITESIFENRFKYL 335

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVT 421
 + EL ++GA+V+ + I +K + + D R A +A A +T
 Sbjct: 336 D-----ELARMGANVKIEGNSATIEGVKKFTGARV-SAPDLRAGAALCIAGLATDGIT 387

Query: 422 IRD 424
 I D
 Sbjct: 388 IVD 390

>ref|YP_443499.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
 thailandensis E264]
 ref|ZP_02375416.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
 thailandensis TXDOH]
 ref|ZP_02389288.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
 thailandensis Bt4]
 ref|ZP_05585978.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
 thailandensis E264]
 gb|ABC37019.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
 thailandensis E264]
 Length = 449

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 71/280 (25%), Positives = 122/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDEVHYMLGALRT 62
 G +++V++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
 Sbjct: 29 GTDKLVIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLAQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
 +G+ E D A R V+ PV A E+ +++++ A++ G
 Sbjct: 89 MGMREETDGA--RVVLDASRVDPNPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLGDGVRPMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
 G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
 Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEIRIEHGYIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
 I+ LLMAA LA G+ +I+ P V L+ G K + DR
 Sbjct: 188 DMITVTGTENLLMAATLADGET--VIENAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
 I+G ++ +A + D A FL A GG VT+ G
 Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|NP_791573.1| prephenate dehydrogenase/3-phosphoshikimate
 1-carboxyvinyltransferase family protein [Pseudomonas
 syringae pv. tomato str. DC3000]
 gb|AAO55268.1| prephenate dehydrogenase/3-phosphoshikimate
 1-carboxyvinyltransferase family protein [Pseudomonas
 syringae pv. tomato str. DC3000]
 Length = 535

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 59/235 (25%), Positives = 94/235 (40%), Gaps = 45/235 (19%)

Query: 225 AEHSDSWDRFYIKGGQ---KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 280
 A+H ++ D ++ + + K P D +SA F+ +I+ EGC
 Sbjct: 307 ADHHEAPDDVVRSAEGVSHRIKGPT-----DVTSVLFMVATSIS-----EGCDL-- 352

Query: 281 LQGDVKFA-----EVLEMMGAKVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDV 333
L DV+ ++L +MG V V E H+++ + +P+
Sbjct: 353 LLEDVRVSGMCEGAIDILRLMGDDVVLQ---NVRELADERLADLHVR SARLKGADIP EA 408

Query: 334 AMTLAV-----VALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYC 385
+TLA+ A A+G T +R + + E+E + + LT LG E PD
Sbjct: 409 LVTLAIGTFPTLLIAACAEGRTILRGAETLQAGESECVRLMADGLTVLGIEAEPVDPGI 468

Query: 386 II---TPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTIRDPGCTRKTFPDYF 436
II TP ID D R+ MAF +A+ A P+ I D FP +
Sbjct: 469 IIEGGTP----GGGEIDARGDQRIVMAFRVASLRASAPIRIHDCADAATLFPHFL 519

>ref|YP_002468128.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. 5A (Acyrtosiphon pisum)]
ref|ZP_05635442.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. LSR1 (Acyrtosiphon pisum)]
sp|B8D9G9.1|MURA_BUCA5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACL30740.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. 5A (Acyrtosiphon pisum)]
Length = 416

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 93/427 (21%), Positives = 165/427 (38%), Gaps = 45/427 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ ++ K ++G V + GSK+ + IL + L+EG + N+ N D++ L L LG
Sbjct: 2 EKLYVEGNKILNGHVIIISGSKNAALPILFMTILTEGKIKIGNIPNLTDINIALKLLVYL 61

Query: 65 LSVEADKAA---KRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ + ++ ++ + C + + + + + A G A
Sbjct: 62 VKITGNETLCIDASSINIFCPYPNLIKIRASIWIL-----GPLLARFGKAKI 109

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G ++ RPI + GL QLGA ++ L +C V G GK L IS
Sbjct: 110 FLPGGCKIGSRPIDLHLNGLTQLGATIN--LKNNCIDAYVK---GRLQGKYILMEKISVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G IID P + + + G + S ++ IKG K
Sbjct: 165 ATITIMSAAATLAKGST---IIDNAACEPEIVDIAKFLNLTGADIIGAGS-NKICIKGV 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWT 301
+ + D FL AA + G +T C T + L GAK+
Sbjct: 221 LTGGTHQVIP-DRIETGTFLVAAAASQGHIT---CHKTEPKHLTNVLMKLTEAGAKIKTG 276

Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ + + + P K++++ P D+ A++ + G I +
Sbjct: 277 KDWIKLDMRGKRP-----KSLNICTAPYPGFPTDMQAQFALLNSISKIGITITETI--- 327

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAE 417
E +EL ++GA ++ + I KL +++ D R + LA C
Sbjct: 328 ---FENRFIYTSELIRMGAKIKIKNNTIICYGIPKL-ISSNVFSSDLRASATLILAGCIA 383

Query: 418 VPVTIRD 424
+TI +
Sbjct: 384 AGITIVN 390

>ref|ZP_05092716.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
gb|EEB75413.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
Length = 415

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 74/312 (23%), Positives = 132/312 (42%), Gaps = 32/312 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTVK+ G+K+ I+ + LS +++++ + EDV+ M+ ++ G E D
Sbjct: 13 LKGTVKISGAKNSVLPPIAASLLSSDEVILEDIPSLEDVNVMIELIKNFGALCELDNGKL 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
+ V + P E K+ FL + + A G+A + G + RPI
Sbjct: 73 KIRVDIKDVEAPYELVKKMRASFL-----VMGPILAKLGHAKISMPGGCAIGARPI 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGAD+ +G R L G K+ L S ++MAA A
Sbjct: 124 DLHLKGFQSLGADIT--IGHGYVEARAK---KLTGKKIYLDFFP-SVGATENIMMAAVFAD 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G + +I+ P + + + G + + + D I+G ++ K ++ + D
Sbjct: 178 G---VTVIENAAEPEIVDLANFLNKGANIKGAGT-DTIRIEGVKELKGAHTVIP-DR 232

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGPPRE 313
A F+ AA+TGG V +E ++ + K E G K+T + + V G
Sbjct: 233 IEAGTFMVAAAMTGGNVLIENIVDVHRSVIAKLTEC----GVKITEEGGLRVKGV--- 285

Query: 314 PFGRKHLKAIDV 325
K+ KA+D+
Sbjct: 286 ----KNYKAVIDI 293

>ref|ZP_06285360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis SK135]
gb|EFA87274.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
epidermidis SK135]
Length = 421

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 80/305 (26%), Positives = 125/305 (40%), Gaps = 20/305 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G V + G+K+ +L + L SEG + + N+ DV + L TL
Sbjct: 2 DKIVINGGNRLTGEVNVEGAKNAVLPLVTASLLASEGHSKLVNVPESDVTINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+VE DK K V V E E V + + M L A + G+A L
Sbjct: 62 NANVEYDKD-KNTVKVDATKTLNEEAPYEVSKMRASI-LVMGPLLRL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGAD+ G + N GL G + L S
Sbjct: 116 PGGCAIGTRPIEQHIKGFALGADIHLENGN----IYANAKDGLKGAGHIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ + P + + G K + + D I G +K
Sbjct: 171 QNIIMASLASGK---SIIENVAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVEKLY 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
++A + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHAIPDRIEAGTLLIAG-AITRGDIFVRGAIKEHM---ASLIYKLEEMGVDLEYEE 282

Query: 304 SVTVT 308
+ VT
Sbjct: 283 GIRVT 287

>ref|NP_563522.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens str. 13]
ref|YP_697297.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens ATCC 13124]
ref|YP_699863.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens SM101]
ref|ZP_02633702.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens E str. JGS1987]
ref|ZP_02635475.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens B str. ATCC 3626]
ref|ZP_02643001.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens NCTC 8239]

ref|ZP_02863341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens C str. JGS1495]
sp|Q8XH79.1|MURA2_CLOPE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2
dbj|BAB82312.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens str. 13]
gb|ABG82237.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens ATCC 13124]
gb|ABG85439.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens SM101]
gb|EDS81700.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens C str. JGS1495]
gb|EDT13649.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens E str. JGS1987]
gb|EDT24263.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens B str. ATCC 3626]
gb|EDT78102.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens NCTC 8239]
Length = 417

Score = 47.4 bits (111), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 81/303 (26%), Positives = 126/303 (41%), Gaps = 36/303 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVE--- 68
K + G++++ G+K+ + IL A L S+G ++DN+ + DVH + +R+LG +VE
Sbjct: 10 KALKGSIEINGAKNAAVAILPAAILASKGECIIDNVPDIADVHCLEIRIIRSLGCNVEKLD 69
Query: 69 ----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
A + V CG D ++ + + R A V GG V
Sbjct: 70 NNTLKNIAEEIKTVEACG-----NDVRKMRASYFYFIGALLARFKEAKVELPGGCPIGV-- 122
Query: 125 GVPRMRERPIGDLVVLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISSQYLS 184
RPI + G + LGA V G VN + G +S
Sbjct: 123 -----RPIDQHIKGFALGAKVSIHGA-----VNIMAEKLIGTNIFFDVVSVGATI 169
Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA LA G +++ P+V + G + + + D IKG ++ K
Sbjct: 170 NLMIAATLAEGTT--VLENAAREPHVVDVANFLNANGANVKGAGT-DVIRIKGVKELKG 225
Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N V D A F+ AA T G VT++ L+ A++LE MGAKV + S
Sbjct: 226 C-NYSVVPDQIEAGTFMIAAAATRGDVTIQNVIPKHLES--ISAKLLE-MGAKVEEGDDS 281
Query: 305 VTV 307
V V
Sbjct: 282 VRV 284

>ref|ZP_05390962.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
ref|ZP_06855260.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
gb|EET88565.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
gb|EFG88006.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
carboxidivorans P7]
Length = 420

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 94/408 (23%), Positives = 167/408 (40%), Gaps = 50/408 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
+++V+ K + G++++ G+K+ + IL A L S+ +DN+ N EDVH + + +L
Sbjct: 2 DKLIVINGGKPLFGSIEINGAKNAAVAILPAAILASKNVNIDNIPNIEDVHCLEIRIESL 61
Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
G +E K +VV+ V E+V+ MR+ L A+ A
Sbjct: 62 GCKIE---VGKNSVVIDSTTINNVDNATEDVR-----KMRASYYLIGALLGRFKKAR 110

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RPI + G + LGA VD G C V + L G + +S
Sbjct: 111 VELPGGCFIGVRPIDQHIKGFALGAKVDITHG--CVVVEAD---RLIGTNIFFD-VVSV 164

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+++AA LA G +E + K P++ + G + + + D + G +
Sbjct: 165 GATINVMLAATLAEGVTTLENVAKE---PHIVDVANFLNSMGANIKGAGT-DVIRVGVK 220

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + + + +Y +A AA GG V +E + LE + AK+
Sbjct: 221 ELQGCSYSVIPDQIEAGTYMIA-AASCGGEVRLNI-----IPKHLESISAKLIE 269

Query: 301 TETSVTVTGPPREPFGKRHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASW 356
+ T + G LK +++ P DV ++ + A G + I + + W
Sbjct: 270 SGTEIIEDGDCITVKSNGKLKGVNIKTQPYPGFPTDVQQPMSTLLTVAKGRSIISE-SIW 328

Query: 357 --RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
R K + EL K+GA+++ II +KL + D
Sbjct: 329 ESRFKHVD-----ELKKMGANIKVEGRTAIDGVDKLTGAVVKATD 369

>ref|ZP_05121187.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus 16]
gb|EED24989.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus 16]
Length = 419

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 104/418 (24%), Positives = 165/418 (39%), Gaps = 51/418 (12%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V + G+K+ + IL + L+E V N+ + D+ + L+ LG VE + +
Sbjct: 15 GEVTISGAKNAALPILFASILAEEPVEVANVPHLRDIDTTMELLKRLGAKVERNGS---- 70

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMR 130
V V G + + L +++++ A++ A G G L G +
Sbjct: 71 VHVDAG---SINEYCAPYDL-----VKTMRASIWALGPLVARFGQGQVSLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+QLGA + G V+ N G L G + + +S ++ AA
Sbjct: 120 ARPVDLHIHGLEQLGATITLEDGY---VKANVDGRLKGAHIVMD-KVSVGATITIMCAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G +D P + T + + G K + + D I+G +K K+A V
Sbjct: 175 TLAEGKT---TLDNAAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVEKLGKGKHAVV 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D FL AA++GG V C TS LE GA V E ++V
Sbjct: 231 -ADRIETGTFLVAAVSGGKV---CRNTSAHLLAALAKLEEAGALVETGEDWISVDMT 286

Query: 311 PREPFGKRHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
RE LKA+ + P D+ ++ + A G I S + E M
Sbjct: 287 GRE-----LKAVTIRTAPHPGFPTMQAQFTLLNMMAKGGGVI----SETIFENRFMHV 336

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++GA E + I E+L+ + D R + + +A C TI D
Sbjct: 337 --PELMRMGAKAEIEGNTVICGDVEELSGAQV-MATDLRASASLVIAGCIASGETIVD 391

>ref|YP_002229476.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
cenocepacia J2315]
emb|CAR50620.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
cenocepacia J2315]
Length = 449

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 66/280 (23%), Positives = 118/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEIEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + +SG + + G+K+ + IL L+ +DN+ N +DV L L
Sbjct: 29 GMDKLAIEGGRRLSGEIVVSGAKNAALPILCAGLLTADPVDLDNVPNLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + +++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAREPEVSDLAHLLVAMGAKIDGIGT-DRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ ++A + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARGHAVIP-DRIEAGTFLCAVAAAGGDVMLTG 282

>ref|YP_772235.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria AMMD]
gb|ABI85901.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria AMMD]
Length = 449

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 67/280 (23%), Positives = 118/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++V++ + +SG + + G+K+ + IL LS +DN+ N +DV L L
Sbjct: 29 GMDKLVVEGGRRLSGEIVVSGAKNAALPILCAGLLSAEPVELDNVPLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + +++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAREPEVSDLAHLLVAMGAKISGIGT-DRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +++ + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARGHSVIP-DRIEAGTFLCAVAAAGGDVLLTG 282

>ref|YP_003589699.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bacillus tusciae
DSM 2912]
gb|ADG06555.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bacillus tusciae
DSM 2912]
Length = 422

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 72/277 (25%), Positives = 116/277 (41%), Gaps = 25/277 (9%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M + I ++ + G V++ G+K+ + IL L+EG VV+++ + +D+ M+ L
Sbjct: 1 MKALDRIAVEGGTPLEGAVRVHGAKNAALPILAAATLLAEGVCVVEDVPDLQDIRVMVDIL 60

Query: 61 RTLGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGN 118
R LG SV+ R E+ +++ +FL +A R A V+ GG
Sbjct: 61 RALGASVDYSPPVVRVDARRISRTEVPEELMRQMRSSIFLMGPLLA-RYCHARVSRPGGC 119

Query: 119 ATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
+ RPI + GL LGA +D G DC R++ G + L +
Sbjct: 120 T-----IGSRPIDLHLKGLAALGASIDEMHGYIDCRTRLH-----GAAIYLD-T 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +I P + + R G + E + D I

Sbjct: 164 PSVGATENLMMAAVLAEGTT---VIGNAAREPEIVDLANFLNRLGARVEGA-GEDTLVIS 219

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274

G Q ++A + D A ++TGG VT+E

Sbjct: 220 GVQGLIGGQHAIIP-DRIVAGTLAIAVSMTGGDVTLE 255

>emb|CAC20647.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Mycobacterium chelonae]
Length = 417

Score = 47.0 bits (110), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 103/410 (25%), Positives = 159/410 (38%), Gaps = 53/410 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63

+E ++ ++G V + G+K+ +++ A L+EGT+ + N + DV M LR L

Sbjct: 2 SEHFLTGTGGARLTGNVAVTGAKNSVLKMAAALLAEGTSTITNCPDILDVPLMADVLRGL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117

G +VE + R ++ K E A+R A+V G

Sbjct: 62 GATVELEGDVVRIT-----SPDEPKYEADF-----AAVRQFRASVCVLGPLVGRCR 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGS 177

A L G +R RP+ GL+QLGA +C + C V L G ++L

Sbjct: 108 RAKVALPGGDAIRSRLDMHQAGLRQLGA--ECTIEHGCV--VAEAKALHGADIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237

S +LMAA LA G + I P V ++ + G + E + + I

Sbjct: 163 -SVGATENILMAAVLADG--VTTIHNAAREPDVVDLCTMLVQMGAEIAGTSTLTVI- 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297

G P V GD A+ + AA+T G VTV G LQ L GA

Sbjct: 218 -GVPKLHPTEHRVIGDRIVAATWGLAAAMTRGDVTVTGVDPEHLQ---LVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNMKMPDVAMTLAVVAL----FADGPTAI-RD 352

VT + V R KAI+V P L +A+ ADG + I +

Sbjct: 274 VTQNDNGFRVVQYERP-----KAINVATLPFGFPTDLQPMAGLAAIADGTSMITEN 326

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402

V R + E+M+ +LGA + ++ +L+ + + D

Sbjct: 327 VFEARFRFVEKMM-----RLGADARTDGHHAVVRGIRQLSSAPVWSSD 369

>ref|ZP_08116402.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium xylanolyticum LX-11]
gb|EGB25525.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium xylanolyticum LX-11]
Length = 417

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 67/268 (25%), Positives = 117/268 (43%), Gaps = 20/268 (7%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66

IV++ + GTVK+ G+K+ I+ + LS+G ++D++ +DV+ M+ +R LG

Sbjct: 6 IVVESPALKGTGTVKVSAGAKNSVLPPIAASLLSQGEVIIDDVPELKDVMNMIELIRFLGAK 65

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126

+ V + P E K+ FL I R A ++ GG A

Sbjct: 66 CTLQDGKCLKINVDIKDVEAPYELVKMRASFLVMGPILARLGHAKISLPGGCA----- 118

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

+ RPI + G + LGA++D G + L G KV L S +

Sbjct: 119 --IGTRPIDLHLKGFQTLGAEIDIGHGYVEAKAK-----KLVGKKVYLDFFP-SVGATENI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246

+MAA A G + I+ P V + + G + + + D I+G ++ K+ +

Sbjct: 171 MMAAVFADG---LTTIENAAEEPEVVDLANFLNKMGANIKGAGT-DTIRIEGVKELKATE 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVE 274

+ + + +Y +A +A+TGG V +E

Sbjct: 227 HTVIPDRIEAGTYMVA-SAMTGGDVLIE 253

>ref|ZP_01065877.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp.
MED222]
gb|EAQ52754.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp.
MED222]
Length = 421

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 98/422 (23%), Positives = 170/422 (40%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 11 KPLSGEVTISGAKNAALPILFASILAEPEVFSNVPHLRDIDTTMELLKRLGAKVSRN-- 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ + E+ F + +++++ A++ A G G L G
Sbjct: 69 -----GSVHVDGS--EINEFCAPYDL-VKTMRASIWALGPLVARFGEGQVSLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ + G L G + + +S +
Sbjct: 116 CAIGARPVDLHIHGLEQLGATIVLEDGY----VKASVDGRLKGAHIVMD-KVSVGATITI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G ++D P + T + + G K + + D I+G ++ +
Sbjct: 171 MCAATLAEGTT---VLDNSAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVERLGGGQ 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
++ V D FL AA++GG V L+ + LE GAKV E ++
Sbjct: 227 HSVV-ADRIETGTFVLVAAAVSGGKVCRNTNAHLLEAALA---KLEEAGAKVETGEGWIS 282

Query: 307 VTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ RE LKA+ + P D+ ++ + A G I +
Sbjct: 283 LDMTVRE-----LKAVKIVTAPHPGFPTDMQAQFTLLNMMAKGSGVITETIF-----EN 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEPVVTI 422
R + I EL ++GA E + I +KL+ + D R + + +A C TI
Sbjct: 332 RFMHI-PELQRMGAKAEIEGNTAICGETKKLSGAQV-MATDLRASASLVIAGCIAQGETI 389

Query: 423 RD 424
D
Sbjct: 390 VD 391

>ref|ZP_07147705.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
resistens DSM 45100]
Length = 418

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 78/286 (27%), Positives = 119/286 (41%), Gaps = 30/286 (10%)

Query: 17 GTVKLPKSGKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V++ G+K+ +++ A L+EGTT + N DV YM LR LG VE + + +
Sbjct: 15 GAVRVSGAKNSVLKLSAALLAEGTTTLTNCPEIADVPYMAEVLRLGLGAEVELEGSKVQI 74

Query: 77 VV--VGCGGKFPVEDAKEEVQLFLGNAG-IAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
V V F DA + + + G + R L A V GG+A + R
Sbjct: 75 TVPDQVEHNADF---DAVRQFRASVAVLGPLTARCLKARVALPGGDA-----IGSR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ GL++LGA G + L G ++KL S +L AA L
Sbjct: 123 PLDMHQSGLEKLGAATTRIEHGCVVAEQ-----RLRGAEIKLDFP-SVGATENILTAAVL 176

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G ++D P + ++ G K S + ++G +K +P V G
Sbjct: 177 AEGTT---VLDNAAREPEIVDLNMLNMTMGAKISGGGS-NTITVEGVEKL-NPTTFEVVG 231

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
D A + AA+T G +TV G L E L++ GA+V
Sbjct: 232 DRIVAGTWAYAAAMTQGDITVGGIDPQHLH---LVLEKLLLAGAQV 274

>ref|ZP_07093610.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
sp. oral taxon 836 str. F0141]
gb|EFK39776.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
sp. oral taxon 836 str. F0141]
Length = 409

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 83/321 (25%), Positives = 130/321 (40%), Gaps = 31/321 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+IV++P + G +++ G+K+ + IL L V++++ +DV M+ LR LG
Sbjct: 2 EKIVVRPSGPLKGIKIRIGGAKNAALPILAAACLLGTEDIVLEDVPKLKDVEIMIEVLR 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V+ D ++V E+ + + M L A + G A L
Sbjct: 62 VKVKYDG---DLIVINSKNLTSYQTNIELMSKMRASFLVMGPELLARM---GKAVNSLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGT---DCPPVRVNGIG-LPGGKVKLSGSISS 180
G + RPI + G K LGA V+ G ++ N I P S
Sbjct: 114 GGCAIGSRPIDLHLKGFALGAKVEMTHGNISAKADKLQANNIYLDLP-----SV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++M A LA G+ IE K P + + + G K + + IKG Q
Sbjct: 164 GATENIIMTATLAEGETLIENCAKE---PEIVDLASFLNKGAKITGAGT-STIKIKGVQ 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K K + + D A F+ AITGG V +E T ++ LE GA+V
Sbjct: 220 KLKGCYHQIIP-DRIVAGTFMIAPAITGGDVLENVITNHMK---PILAKLEEAGAEVIV 275

Query: 301 TETSVTVTGPPR-EPFGRKHL 320
+ V V G + PF K L
Sbjct: 276 DDDKVRVIGKEKIYPFEIKTL 296

>emb|CBX27296.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [uncultured
Desulfobacterium sp.]
Length = 417

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 92/394 (23%), Positives = 163/394 (41%), Gaps = 41/394 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I+++ +SG VK+ G+K+ + IL+ + L +G+ N+ + D+ L LG
Sbjct: 2 DKIIIVEGGYPLSGEVKISGAKNAALPILISSLLVDGCTYSNVPDLMDIESTKNLLINLG 61

Query: 65 LSVEADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E D + G + P E ++ L + R A V+ GG +
Sbjct: 62 VCMETDGDIVKMDAAGLNNYEAPYELVRKMRASILVLGPLVARLKKARVSLPGGCS---- 117

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RPI + GL LGA+VD G L G ++ +++
Sbjct: 118 -----IGARPINLHLKGLAALGANVDLVHGYVEASADT-----LKGAEIYFD-TVTVTGT 166

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
L+MAA LA G I+ P V ++ + G K E + I G + K
Sbjct: 167 ENLMMAAVLAEGT---SILRNAAREPEVVALADVLNKGAKIEGIGT-SVLKITGVESLK 222

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + + D A F+ AA+TG + + C L+ + L++ G+ +T +
Sbjct: 223 -PVSVSIIIPDRIEAGTFMVSAALTGSDIKIINCEPAHLESVILK---LKLSGSDITIGDN 278

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVK 359
S+ V G + + +ID+ P D+ V+ A G + I S +
Sbjct: 279 SIRVKGGDK-----ISSIDIKTMPYPGFPTDMQAQFMVLMMSVAKGFSVI-----SETIF 327

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
E R + + +EL ++GA ++ D +IT KL
Sbjct: 328 EN-RFIHV-SELKRMGADIKISGDTAMITGVPKL 359


```
>ref|NP_638143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. ATCC 33913]
ref|YP_242407.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. 8004]
sp|Q8P719.1|MURA_XANCP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|Q4UX36.1|MURA_XANC8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAM42067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. ATCC 33913]
gb|AAY48387.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. 8004]
Length = 424
```

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 97/400 (24%), Positives = 160/400 (40%), Gaps = 45/400 (11%)

```
Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVHISGAKNAVLPLCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSILVDPKSVTHQIAPYELVKMTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L GG+ +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY----IKATSNGLKGGRYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRITVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFVLVAAAMTGGSVTVRRARPDTLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNMKP---DVAMTLAVVALFADGPTAIRDVA 354
T T SVT+ + P +A+++ P D+ + ADG I +
Sbjct: 281 TTTADSVTLDMHGKRP-----RAVNLTTPAPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368
```

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>ref|YP_003319676.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sphaerobacter
thermophilus DSM 20745]
gb|ACZ38854.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sphaerobacter
thermophilus DSM 20745]
Length = 424
```

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 101/412 (24%), Positives = 160/412 (38%), Gaps = 54/412 (13%)

```
Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
A+ I ++ + G V + G+K+ + + A L++ ++DN+ ED M+ LR L
Sbjct: 7 AKTIRVRGGTRLYGRVAIGGAKNAALPAMAAALLTDEECLLDNVPVLEDTLVMVELLRWL 66

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G VE D+ +R + C DA E+ + + A+ +G G
Sbjct: 67 GADVEFDQENRRVRI--CAANINRFDAPPEL-----VERMRASFLVSGPLLSRFG 114

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A+ G R+ RP+ + G +++GA+V G R L G ++ +
Sbjct: 115 EASSPPGGCRLGTRPVDVLDLGRFRRMGAEVTHTDGGYVMRARR-----LYGAELYMDYP 169
```

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM--ERFGVKAEHSDSWDRFY 235
S LLM AA LA G I I ++ LR M GV H
Sbjct: 170 -SHTGTENLLMAATLARGTTTIVNASSEPEISFLGSILRDMGARITGVGTPH-----IR 222

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+ G + + + A + D A F AAIT G V ++ + + L G
Sbjct: 223 VHGVDRLRGYRAAILP-DRIEAGTFAIAAAITDGEVILDNVSEPDMM--LPLTYKLEAG 278

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR 351
A+V W +TS+ V GR L + ++ P D+ AV+ A G + I
Sbjct: 279 AEVWVNQTSMLVR-----GRGELHSTEIQALPFPGFPTDLQAAFAVLMTQAKGQSRIF 331

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEE-GPDYCIITPPEKLNVT AIDTYD 402
+ RV A EL KLGA + II P +L ++ D
Sbjct: 332 E---RVFNDRLRYA--AELAKLGADITVIDKQQAIIINGPTRLRGADVEALD 377

>ref|ZP_05860438.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Jonquetella
anthropi E3_33 E1]
gb|EEX48459.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Jonquetella
anthropi E3_33 E1]
Length = 451

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 101/397 (25%), Positives = 168/397 (42%), Gaps = 46/397 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEG--TTVDNLLNSEDVHYMLGALRTLGLSV---EA 69
++GTV + G+K+ + +L A L G T V N+ D ++ L+++GLSV +
Sbjct: 37 LNGTVAVQGAKNALPVLASAILLGGGQTLTVHNVPRMLDTETLVTLQSMGLSVTFSDG 96

Query: 70 DKAARAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
AKR CG D +E+ + L A + + A G A L G +
Sbjct: 97 TVVAKR-----CG-----DLGQELPVTLVQKMRASSVLGPELLAREGRAVMPLPGGCAI 145

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL ++GA V+ G + L GG++ L S LLMA
Sbjct: 146 GTRPMDLHLKGLAKMGASVELRHGAHVAESK-----LRGGRIYLDFF-SVGATENLLMA 199

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G+ IE + I + +L+ M G K + +I G + S +
Sbjct: 200 ATLAQGETIIEAAREPEIVNLAASLQAM---GAKITGVGTGI-IHIGCSELHSGEVTI 255

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+ ++ +Y LAG IT G VTV+ D A++ E A V++ VT
Sbjct: 256 IPDRIAAGTYLLAG-VITDGHVTVD--NVVPQHFDSSLAKLEE---AHVSYERAETKVTV 309

Query: 310 PPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P RK +++ V+ P D+ + A G + +++ + E+ R +
Sbjct: 310 FPS----RKSFRSVSVSTLPYPGFPTDIQPMVAALSLASGTSIVKE----SIFES-RFL 360

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD 402
+ EL ++GA +E + II+ LN +A+ D
Sbjct: 361 HV-PELKRMGADIEVQNSAIIISGVACLNLSAVKATD 396

>ref|ZP_02905697.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria MEX-5]
gb|EDT43119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria MEX-5]
Length = 449

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 67/280 (23%), Positives = 117/280 (41%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRT 62
G +++V++ + +SG + + G+K+ + IL LS +DN+ N +DV L L
Sbjct: 29 GMDKLVVEGGRRLSGEIVVSGAKNAALPILCAGLLSAEPVELDNVPLNKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + +++++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVNDLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVSDLAHLLVAMGAKIT-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +++ + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAGGDVLLTG 282

>ref|YP_001807067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria MC40-6]
gb|ACB62851.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
ambifaria MC40-6]
Length = 449

Score = 47.0 bits (110), Expect = 0.006, Method: Compositional matrix adjust.
Identities = 67/280 (23%), Positives = 117/280 (41%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++V++ + +SG + + G+K+ + IL LS +DN+ N +DV L L
Sbjct: 29 GMDKLVVEGGRRLSGEIVVSGAKNAALPILCAGLLSAEPVELDNVPLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D GC + V + ++++ A++ G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVSDLAHLLVAMGAKIT-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +++ + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAGGDVLLTG 282

>ref|ZP_08092037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14163]
ref|ZP_08106388.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14673]
gb|EGA92474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14163]
gb|EGB19538.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
symbiosum WAL-14673]
Length = 418

Score = 47.0 bits (110), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 97/403 (24%), Positives = 154/403 (38%), Gaps = 50/403 (12%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
L PIK G + + GSK+ ++ A L+ G TV++N+ +DV M+G L +LG S
Sbjct: 9 LCPK---GEITVQGSKNAVLPMAGAVLNNGITVINNVPRIQDVFCMMGILDSLGCSCV 65

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDG 125
D + G +F + A+ E MRS L A+ A G
Sbjct: 66 LDGHSLTIDAAGL-SRFSIPKAEME-----KMRSSIMLLGALLGRCKEAEVYYPG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----S 179
+ +RPI ++ L+++GA + G + P+R + +P +L G++ S
Sbjct: 115 GCMIGKRPIDLHLMALEKMGARIREQGDE--PLRAS----VP----RLRGTVVDFPFPS 164

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+ AA A G +++ P + R M G D I+GG

Sbjct: 165 VGATENAIFAAVAASGKT---VLNGCAKEPEIVELCRFMNMGASV-RGVGGDVLVIEGG 220

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+ V GD + +L AA GG + + G G+ QG VL+ MGA V

Sbjct: 221 LPLHDSEFT-VGGDRIAGGTYLLAAAGAGGEILLTGTGS---QGLKTVTSVLKQMGAAVF 276

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVK 359
E + + R L A + P L V + + R +++ K

Sbjct: 277 EEEELIYLKAAGR-----LSAASIKTGPYPGFPTDLQSVMMAV--MSRARGISTIEEK 327

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
E EL KLGA + D I L ++ +D

Sbjct: 328 IFESRFKTANELQKLGAIEIVIEDIAKIQGRPLLKGCEVNAWD 370

>ref|YP_001422952.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
amyloliquefaciens FZB42]
gb|ABS75721.1| MurAA [Bacillus amyloliquefaciens FZB42]
Length = 436

Score = 47.0 bits (110), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 90/359 (25%), Positives = 145/359 (40%), Gaps = 45/359 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L SE +V+ ++ DV+ + LR L

Sbjct: 2 EKLIIVRGQKLNKGTVEGAKNAVLPIAASLLASEKSVICDVPVTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V + V V E E V R + A+V G G

Sbjct: 62 GADVHFEN---NEVTNASYALETEAPFEYV-----RKMRAVSLVMGPLLARTG 107

Query: 118 NATYVLVDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
++ L G + RPI + G + +GA + G V G L G K+ L

Sbjct: 108 HSRVALPGGCAIGSRPIDQHLKGFEAMGAKIKVGNGFIEAEVE---GRLQAKIYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +E + K P + + G K + + I+

Sbjct: 164 -SVGATENLIMAAALAEGTTTLENVAKE---PEIVDLANYINAMGGKIRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K ++ + D A F+ AAIT G V V+G L +E MG K

Sbjct: 219 GVEKLHGVRHNIIP-DRIEAGTFMVAAAITEGNVLKGA VPEHL---TSLIAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD 352
+T + V GP + LK ID+ P D+ + + L A G + I +

Sbjct: 275 ITDEGEGLRVIGPAQ-----LKPIDIKTMPHPGFPTDMQSQMMALLLRASGTSMTIE 326

>ref|YP_003180311.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Atopobium
parvulum DSM 20469]
gb|ACV51720.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Atopobium
parvulum DSM 20469]
Length = 427

Score = 47.0 bits (110), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 96/386 (24%), Positives = 155/386 (40%), Gaps = 51/386 (13%)

Query: 13 KEISGTVKLPKSKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++G V + G+K+ + +++ ++ G T + N+ N DVH M L+TLG +E

Sbjct: 10 NSVTGEVTVGAKNSALKLMAATIMAPGVTTLTNPNIADVHVMGKVLKTLGARIE---- 65

Query: 73 AKRAVVVCGCG-KFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLVDGVPRMR 130
VVG K D E L A ++ + + G A + G +

Sbjct: 66 -----VVLHELKIDTTDITSWETPYSLVAQMRASTAVLGPLISRFGKAVVAMPGGCNIG 120

Query: 131 ERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
R I ++GL+ LG + G + + G+ G V L+ + S L+MA+

Sbjct: 121 ARKIDMHILGLEALGVEFKVEHGN---IHASAPHGVTGETVSLAFA-SVGATENLMMA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G + +ID P + ++ + G + + S I G + P V

Sbjct: 176 VFAKG---VTVIDNAAREPEIVDLANMLNKMGANIQGAGS-PVIEIHGVTELH-PVEHEV 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT----WTETSVT 306
GD A FLA A+TG +TV G L +K E MG V W S

Sbjct: 231 VGDRIEAGTFLAIGALTGEPITVHGFEPNHLGLVLK---KYEQMGITVETGDRWARASR- 286

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMMPDV-----AMTLAVVALFADGPTAIRDVASWRVKET 361
++ LKAID+ P A T+ ++AL A G I + V E

Sbjct: 287 -----QQDLKAIDIQTLFPFGFPTDMQAQTMTLLAL-AKGTCIITE---NVFEN 331

Query: 362 ERMVAIRTELTKLGASVEEGPDYCI 387

M+A +EL+++GA + + I+

Sbjct: 332 RFMLA--SELSRMGADITIEGHHAIV 355

>ref|ZP_01113773.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Reinekea sp.
MED297]

gb|EAR10152.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Reinekea sp.
MED297]

Length = 420

Score = 47.0 bits (110), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 88/365 (24%), Positives = 148/365 (40%), Gaps = 48/365 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V++ G+K+ + IL L++ T + NL + D+ M+G L ++G+SV ++

Sbjct: 12 LNGEVRVSGAKNAALPILTATLLTKETVTLHNLPHLNDITTMIGLLGSMGVSVVLNEDMS 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V C G A E+ +++++ A++T G G A L G

Sbjct: 72 VEV---CAGTIREYTAPYEM-----VKTMRASITVLGPLLGHFGEANVSLPGGCA 118

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + G++ LGA +D D + G L G + + +LM

Sbjct: 119 IGARPVDLHLRGMEALGATIDV---DSGYITARSNGRLKGARYFFDKNTVGGT-ENVLM 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +E + K P V +R+++ G K E + + D I+G +

Sbjct: 174 AAVLAEGTTVLENAKE---PEVVDLIRMLQAMGAKIEGAGT-DTLVIEGVESLHGCDYT 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD-VKFAEVLEMMGAKVTWTETSVTV 307
+ + +Y +AG A+ G V V+ L VK E GAK+T + V V

Sbjct: 230 IMPDRIEAGTYLVAG-ALAGDRVVKVNVVPQDLDPVLVKLQEA----GAKLTVGDDWVEV 284

Query: 308 TGPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVA----SWRVK 359
RE L A+D+ P D+ + A G + + +

Sbjct: 285 DMVGRE-----LTAVDIRTAPHPAFPTDMQAQFTTLNAVAKGTGTVEETVFENRFMHIS 338

Query: 360 ETERM 364

E ERM

Sbjct: 339 ELERM 343

>ref|YP_004182161.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Terriglobus
saanensis SP1PR4]

gb|ADV82167.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Terriglobus
saanensis SP1PR4]

Length = 426

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 85/369 (23%), Positives = 155/369 (42%), Gaps = 41/369 (11%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-AKR 75
GT+K+ G+K+ + + A L+E V++N+ D+ L +G VE A+

Sbjct: 14 GTIKVSGAKNSALPCMAAAILTEEEVLENIPQVRDIETERKLLLEAMGAQVELGYGRAQH 73

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ C +AK E+ + + + L A V G A + G + +RPI

Sbjct: 74 RTTIRC-AVLSDEPAKYEIVKTMRASSLVLGPLVARV----GMARVAVPGGCSIGDRPID 128

Query: 136 DLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

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      + GL+ +GA +      G +      R+ G +      K+ ++G+      LLMAA LA
Sbjct: 129 LHLKGLELMGAKITQDHGYIEARADRLKG-AHILFDKITVTGT-----EDLLMAATLAD 181

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
      G+      I++      P V      ++      G K E + + + ++G K      ++ + D
Sbjct: 182 GET---IMENCAQEPEVTDLANMLISMGAKIEGAGT-SKITVQGVSKLHGTRH-RINPDR 236

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREP 314
      A F+      AI+GG + V+ C      L +      LE G ++      + ++ V
Sbjct: 237 IEAGTFIIAGAISGGDLNVDCNPGHLAAVIAK---LEECGVRLDVGKENIRVR----- 287

Query: 315 FGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADG-PTAIRDVASWRVKETERMVAIRT 369
      HLKA DV+ + P      D+      +A ++G T I ++      R      +
Sbjct: 288 -SEGHLKAADVSTVEYPGFPTDMQAQYMALATQSEGTSTVIENIFENRFMHV-----S 339

Query: 370 ELTKLGASV 378
      EL ++GA++
Sbjct: 340 ELVRMGANI 348

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>emb|CBL05022.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gordonibacter
pamelaeae 7-10-1-b]
Length = 429

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 119/445 (26%), Positives = 173/445 (38%), Gaps = 53/445 (11%)

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Query: 4      AEEIVL-QPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
      AEEI++ Q      ++G V + G+K+ + +++ + L GTT + N+      D+ M      LR
Sbjct: 2      AEEIIIVQGTGVLAGEVPVSGAKNSALKLMAASLLGGGTTAIHNVPLISDIAIMSEVLRC 61

Query: 63      LGLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
      L VE +      +VV G      E E V      A IA + +      G A
Sbjct: 62      L NARVERE---GHTLVVDTGSVDKWETPYELVSKM--RASIA---VLGPLIGRFGQARVA 113

Query: 123      LDGVPVRMRERPIGDLVVLKQLGAD--VDC-FLGTD CPPVRVNGIGLPGGKVKLSGSIS 179
      + G ++ R I      +VGL+ LG + VD FL      P      GL G V L S
Sbjct: 114      MPGGCQIGARKIDMHLVGLEALGVEFVVDHGFLEATTTPH-----GLAGAHVVLDFFP-S 165

Query: 180      SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
      LLMAA A G +E + I + L M      A S      F G
Sbjct: 166      VGATENLLMAAVAAEGTTTVENAAREPEIVDLANMLNAM-----GARVSGGSSFIEVEG 220

Query: 240      QKYKS--PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      +S P      GD A FL G A+ GG VTV G + L+ +      LE MG
Sbjct: 221      VPVESLHPCEHTTVGDRIEAGTFLTGGALMGFPVTVRGIDPSYLRMALM---KLEAMGCD 277

Query: 298      VWTETSVTV--TGPPREPFRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIR 351
      V      +TV GP      L ID+ P      D+      ++A A+G + I
Sbjct: 278      VQAGADCITVRREGP-----LAPIDLQTLPHPGFPTDLQAQFMLLAARAEGTSVIT 328

Query: 352      DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFS 411
      +      V E M A +EL ++GA +      + ++ + L      + + D R A
Sbjct: 329      E----NVFENRFMFA--SELMRMGADIVIEDHHALVRGVDGLQGADVSST-DLRAGAALV 381

Query: 412      LAAC-AEVPVTIRDPGCTRKTFPDY 435
      LA AE + D + + DY
Sbjct: 382      LAGVSAEGETRVHDIRHIDRGYEDY 406

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>ref|YP_001020026.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylibium
petroleiphilum PM1]
gb|ABM93791.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylibium
petroleiphilum PM1]
Length = 434

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 93/408 (22%), Positives = 160/408 (39%), Gaps = 58/408 (14%)

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Query: 5      EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      ++++++ + + G V + G+K+ + L A L+      N+ +DV L LR +G

```

Sbjct: 11 DKLIIRGRRRLHGEVAISGAKNAALPELCAALLTAEPVRFNSNPRLQDVSTTLKLLRNMG 70

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
E ++ V + G PV + L +++++ A++ G G

Sbjct: 71 AVAERSESRPDEVTIDAG--PVSSPEAPYDL-----VKTMRASILVLGPLLARFGE 119

Query: 119 ATYVLDGVPRMRERPIGDLVVGKQLGADVDC--FLGTDCCPPVRVNGIGGLPGGKVKLS 175
AT L G + RP+ + GL+ +GA + ++ P GGL G ++ +

Sbjct: 120 ATVSLPGGCAIGSRPVDQHIKGLQAMGAQISVEHGYIIAKAP----KASGGLRGARIT-T 174

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRF 234
++ LLMAA LA G+ +E + IP EM + + G K E S +

Sbjct: 175 DMVTVTGTENLLMAATLADGETVLENAQEPEIPDLAEMLISM---GAKIEGHGS-SKI 229

Query: 235 YIKGGQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLE 292
I+G + +P+ + V D A FL A GG V ++ L + K E

Sbjct: 230 RIQGVQLHAPRGGHRVVPDRIEAGTFLCAVAAAGGEVLLKHARADHLDAVIDKLREAGV 289

Query: 293 MMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPT 348
+ A W + LKA+ ++ P D+ + A+G

Sbjct: 290 RIEAGSDWIRVA-----SDGKLKAVGFRTSEYPAPFTDMQAQFMALDCIAEG-- 336

Query: 349 AIRDVASWRVKET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ RV ET E EL +LGA +E I+T +L+

Sbjct: 337 -----TARVTETIFENRFMHVDELVRLGAKIEVDGHTAIVTGVPQLS 378

>ref|YP_003743403.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
billingsiae Eb661]
emb|CAX61556.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
billingsiae Eb661]
Length = 420

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 98/421 (23%), Positives = 169/421 (40%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG+ E + +

Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKIDIDTTMKLLSQLGVKAERNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V +V ++ + +++++ A++ A G G L G

Sbjct: 70 -----VHLDASDVNIYCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++

Sbjct: 117 IGARPVDLHITGLEQLGAEIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P + T + G K + S DR I+G ++

Sbjct: 172 AATLATGTT---VIENAAAREPEIVDTANFLNTLGAKITGAGS-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG V +L D A++ E GA++ +++

Sbjct: 226 YRVLPDRIETGTFLIAAAISGGKVLCHATQPDTL--DAVLAKLRE-AGAEIQTGPDWISL 282

Query: 308 TGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA++ P D+ +++ L A+G I + R

Sbjct: 283 DMHGKRP-----KAVNFRTAPHPGFPTDMQAQFSLNLVAEGTGIVTETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ I EL ++GA E + I EKL+ + D R + + LA C TI

Sbjct: 332 FMHI-PELIRMGAAHAEIESNTAICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
D

Sbjct: 390 D 390

>ref|YP_003650793.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermobispora
bispora DSM 43833]

gb|ADG86900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermobispora
bispora DSM 43833]
Length = 425

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 68/232 (29%), Positives = 102/232 (43%), Gaps = 26/232 (11%)

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+MAA LA G +I+ P V + ++ R G K + ++G + K+
Sbjct: 172 LVMAATLAKGTT--VIENAALEPEVLVDVIAMLTRMGAKIRGGGTGF-ITVEGVENLKAV 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
++ V D A F AAITGG VT+ G L G V++ LE MG + ET+
Sbjct: 228 EHT-VMPDRDLGAGVFAMAAITGGEVTLVGAEQLHL-GVVRWK--LEQMGVEF---ETNG 280

Query: 306 TVTGPPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V RE K L+ I+V + P D+ + VA ADG + I + +
Sbjct: 281 AVLHVRE---KPLRPINVTDTYPGFATDLQSPIMAVACLADGTSYIHE-----RIF 330

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLA 413
+ A+ EL K+GA +E ++ P L T + T D R +A LA
Sbjct: 331 DGRFALAGELNKMGAKEIEVQGSRAVHGPPTPLRGTQV-TAHDLRSGIALVLA 381

>ref|YP_001356424.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Nitratiruptor
sp. SB155-2]
sp|A6Q3K8.1|MURA_NITSB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
dbj|BAF70067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Nitratiruptor
sp. SB155-2]
Length = 420

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 98/420 (23%), Positives = 176/420 (41%), Gaps = 61/420 (14%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G+V + G+K+ + ++ LS+ + +DNL + +D+ +L L+ LG S
Sbjct: 10 KTLNGSVPIGAKNAALPLIASTILSKQSVQIDNLPDVQDIKTLRLQLNLGAS----- 63

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA---MRSLTAAVTAAG-----GNATYV 122
+ ED + + +A +R++ A++ G G
Sbjct: 64 -----YQYEDGLATIDASKLTSTVATYDIVRTMRASILVLGPILAKYGRCEVS 111

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + +RPI + L+Q+GA + G V GL G + + I+
Sbjct: 112 LPGGCAIGQRPIDLHLQALEQMGAKITIKAGY---VVAEAPNGLKGSTI-IFDKITVTG 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA LA G I K P V +++ GV+ + S D I+G +
Sbjct: 167 TENIVMAAALAKGTTTIIINAKE---PEVVQLCEVLKDAGVQIDGIGS-DELIIEGTBRE 222

Query: 243 KSPKNA-YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
A +V D A +L AIT T+++E L D + L+ MG +
Sbjct: 223 PIEMRAIHVIPDRIEAGTYLCAGAITNSTLSIENVIPHLL--DSVLVK-LKQMGFPLDVN 279

Query: 302 ETSVTVTGPPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E+++T+ P R ++ +++ ++ P D+ +AL A+G + I + R
Sbjct: 280 ESNITIH-PART-----IEPVEIVTSEYPGFPTDMQAQFMALALLANGASIIIE---R 328

Query: 358 VKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
+ E M +EL + GA+++ +G +I P E + T D R + A LA A
Sbjct: 329 LFENRFMHV--SELKRFGANIQLKGNATVIGPTELWGADVMT--DLRASSALVLAGLA 384

>ref|ZP_00958670.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseovarius
nubinihibens ISM]
gb|EAP77132.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseovarius
nubinihibens ISM]
Length = 422

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 89/378 (23%), Positives = 149/378 (39%), Gaps = 53/378 (14%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG + + G+K+ ++ LSE + N D+ M L++LG V + + +
Sbjct: 12 LSGEIPIAGAKNACLTLMPATLLSEEPLTLTNAPRLSDIKTMTQLLQSLGAEVTSMDGQ 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V + + E + +R + A+ G G A L G
Sbjct: 72 ----VQAMSSHDINNHYAEYDI-----VRKMRASNVLVGPMLARLGQAVVSLPGGCA 119

Query: 129 MRERPIGDLVVLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL++LGA++ D +L P GGL G ++ G S
Sbjct: 120 IGSRPMDLHIFGLEKLGAEIELKDGYLHAKVP-----GGLKGAVIEF-GFASVGATEN 171

Query: 186 LLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
+LMAA LA G ++ P + + + G + E D I+G +
Sbjct: 172 VLMAATLAKGTT---VLRNAAREPEIVDLANCLRMGAQIE-GDGTSEIIVIQGVDRHLGA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V +Y LA AI GG V G L+ F + LE G +VT TE +
Sbjct: 228 THPVVTDRIELGTMYLA-PAICGGEVECLGRRDLLEA---FCQKLEAAGVEVTETERGL 283

Query: 306 TVTGGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V+ GR ++A+DV P D+ + A+G + + + ++ E
Sbjct: 284 KVS----RKNGR--VQAVDVTTEPFPGFPTDLQAQFMALMCTAEGDSVLEE---KIFEN 333

Query: 362 ERMVAIRTELTKLGASVE 379
M A EL ++GA +E
Sbjct: 334 RFMHA--PELQRMGARIE 349

>ref|YP_003346247.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
naphthophila RKU-10]
gb|ADA66833.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
naphthophila RKU-10]
Length = 421

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 105/447 (23%), Positives = 178/447 (39%), Gaps = 48/447 (10%)

Query: 6 EIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
++V+Q + G V++ GSK+ + I+ A L + ++ N+ +DV M+ LR++G
Sbjct: 3 KLVVQGGTVLEGEVEISGSKNAALPIMAAAILCDEEILKNVPRLQDVFVMDILRSIGF 62

Query: 66 SVEADK---AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE D+ KR + + P E ++ F IA+R+ A V GG + V
Sbjct: 63 RVEFDENELKIKRENDISQ--EVPYELVRKMRASFNVLGPIAVRTGRAKVALPGGCSIGV 120

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
RP+ + GLK++G + G V +V ++ S
Sbjct: 121 -----RPVDFHLEGLKKMGFSIKVEHGF-----VEATFERRTDQVTITLPPFSVG 165

Query: 183 LSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+ LM L + +I+ P + + R G + E + + R I+G +K
Sbjct: 166 ATEHLMTTAALLEGTRV-VIENAAMEPEIVDLQNFINRMGGRIEGAGT-SRIVIEGVEKM 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ + + + +Y +A AA + G V+ L F E LE GAK
Sbjct: 224 QGVEYSIIPDRIEAGTYLVAIAA-SRGKGLVKNVNPDL---TNFFEKLEETGAK----- 274

Query: 303 TSVTVTGGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V G E R+ +A+DV N P D+ + A G + I +V R
Sbjct: 275 --LKVLGNEVEIEMRERPEAVDVTNPNPGFPTDLQPMMAYLSTAGSVSVITENVFKTR 332

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
+ EL ++GA +E + I+ EKL+ ++ D R A +A
Sbjct: 333 FLHVD-----ELKRMGADIEVSGNVAIVKGVEKLSGAPVEG-TDLRATAALLIAGIIA 384

Query: 418 VPVTIRDPGCTRKTFFPDYFDVLSTFVK 444

VT + F Y DV+ F K
Sbjct: 385 DGV--EISNVEHIFRGYEDVIDKFSK 409

>ref|NP_350124.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium acetobutylicum ATCC 824]
sp|Q97DD9.1|MURA2_CLOAB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2; AltName: Full=Enoylpyruvate transferase 2; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2; Short=EPT 2
gb|AAK81464.1|AE007850_5 UDP-N-acetylglucosamine enolpyruvyl transferase [Clostridium acetobutylicum ATCC 824]
gb|ADZ22582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium acetobutylicum EA 2018]
Length = 418

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 96/402 (23%), Positives = 164/402 (40%), Gaps = 65/402 (16%)

Query: 17 GTVKLPGSKSLSNRILLAL--SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
G+V++ G+K+ + IL A + SEG +V+DN+ + +D+ + + +LG V K +
Sbjct: 14 GSVEIGGAKNAVAAILPAAIMASEGISVIDNIPDIQDIQRLERIITSLGCKV---KRVQN 70

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMRER 132
V + V E+ G MR+ L A+ G A L G + R
Sbjct: 71 TVEIDSTNLTSTVNADTED-----GSKMRASYLLIGALLGRFGKAKVELPGGCPGV 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS-----ISSQYLSAL 186
PI + G + LGA V GT + KL G+ +S L
Sbjct: 123 PIDQHKGFEALGATVKISHGT-----VEAQADKLIGTNIYFDVSVGATINL 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
++A+ A G +E K P++ + G + + + D I G +K K
Sbjct: 171 MLASVFAEGTTVLENAAKE---PHIVDVANFLNSMGANIKGAGT-DVIRIAGVEKLGKCN 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ + +A+Y +A AA GG VT++ L+ + L MGA + + VT
Sbjct: 227 YSVIPDQIEAATYMIATAA-CGGCVTIKNVIPKHLE---SISAKLIEMGADIKGDDYVT 282

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASW--RVKE 360
+ K+LK +++ P D ++ + + G + + + + W R+K
Sbjct: 283 IE-----SHKNLKGVNITLTPYPGFPTDAQQPMSTLLSISQGRSIVNE-SIWESRLKH 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTAD 399
+ EL K+GA+++ II EKL NV A D
Sbjct: 335 VD-----ELKKMGANIKVEGTVAIIDGVEKLTGANVKATD 369

>ref|YP_004001889.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase [Caldicellulosiruptor owensensis OL]
gb|ADQ04089.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Caldicellulosiruptor owensensis OL]
Length = 419

Score = 46.6 bits (109), Expect = 0.007, Method: Compositional matrix adjust.
Identities = 98/402 (24%), Positives = 161/402 (40%), Gaps = 42/402 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+IV++ + G V + G+K+ + ++ A + EG +V++NL EDV M L LG
Sbjct: 6 EKIVIEGGYPLEGEVIINGAKNAAVAVIPAALMVEGESVIENTPLIEDVFAMDDILLKL 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E + + + +++ A L A+ G A +
Sbjct: 66 AKIEYYNHSCLKIDAKNLHSYIAPYETVRKIR-----ASYLLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RPI + G K LGADV G ++ L G K+ L +S
Sbjct: 118 GGCNFGSRPIDQHIKGFALGADVRIENGM----IKAYA-DRLVGAKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G II+ P+V T + G K + + + D I+G K

Sbjct: 172 NLMLAAVKAKGTT---IIENAAKEPHVVDNANFLNSMGAKIKGAGT-DVIRIEGVDKLTP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K A + + +Y +A A T G V V+ L+ A+++E MGA++ E S

Sbjct: 228 AKYAIIPDQIEAGTYMIAACA-TRGHVIVKNVIPKHLEALT--AKLIE-MGAEIITYEDS 283

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ E R+ LK+ + P D+ + V+ G T+I W

Sbjct: 284 I-----EVICRQKLKSSSIKTMYPYPGFPTDLQPQMTVLLSLCSG-TSIVTEGVW---- 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
E EL K+GA+++ ++ E L V A+D

Sbjct: 332 -ENRYQYIDELKKMGANIKVEGRVAVVEGVESLQGAEEVAVD 372

>ref|YP_985078.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax sp.
JS42]
gb|ABM41002.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax sp.
JS42]
Length = 450

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 73/284 (25%), Positives = 124/284 (43%), Gaps = 43/284 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ + + G V + G+K+ + L A L+ + N+ +DV ML +R +G

Sbjct: 12 DKLLIRGGRPLVGEVPISGAKNAALPELCAALLTADPVTLHNVPRLQDVATMLRLIRNMG 71

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG-- 116
+ V+ R C V DA V+L G +++++ A+V A G

Sbjct: 72 VQVD-----RIANPDC---SVADAAGIVRLDAGGLSTPEAPYDLVKTMRASVLALGPL 121

Query: 117 ----GNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV 172
G AT L G + RP+ + GL+ +GA + G I LP G

Sbjct: 122 LARFGEATVSLPGGCAIGSRPVDQHIKGLQAMGAQIVVEHGYM-----IARLPQGW 173

Query: 173 KLSGS-ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
+L G+ I++ ++ LLMAA LA G+ +++ P V ++ + G + E

Sbjct: 174 RLKGARITDMVTVTGTENLLMAATLAEGET---VLENAQEPEVADLAEMLIKMGARIE 230

Query: 227 -HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGG 269
H S R I+G ++ ++A V D A FL A TGG

Sbjct: 231 GHGTS--RIRIQGVERLHGCEHAVV-ADRIEAGTFLCAVAATGG 271

>ref|ZP_01453229.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mariprofundus
ferrooxydans PV-1]
gb|EAU53902.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mariprofundus
ferrooxydans PV-1]
Length = 431

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 105/424 (24%), Positives = 163/424 (38%), Gaps = 41/424 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I++Q ++GTVK G+K+ + +L A L +G + + D+ M+ L G

Sbjct: 2 DKIIIIQGGNALTGTVKASGAKNAALPLAAAILVDGRVITYHRIPHLHDISTMMTLLAWQG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V D C E K E L A + + A G AT L

Sbjct: 62 ADVAYDDQY-----CLHVDTREANKPEAPYELVKTMRASSLVGLPLLARFGEATVSLP 114

Query: 125 GVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + GL+ +GA +D G V G L G + ++

Sbjct: 115 GGCAIGARPIDMHLRGLAMGATIDVAQGNIIARVD---GRLRGAHIVFD-QVTVTGTE 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L+MAA LA G+ ++D P + + G + S +R I+G +

Sbjct: 170 NLMMAAVLAEGET---VLDNAAREPEIVNLAESLRGLGAVIQEGGS-NRIVIQGVDRHLHG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

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      +   +   +A+Y AG ITGG VTV G           A +LE AKV T
Sbjct: 226 GEMTTIADRIETATYLAAG-LITGGDVTVTGTD-----ASMLEAFLAKVRDTGAL 274

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      V           R LKA+D+   P   D+   +   ADG + IR+   + E
Sbjct: 275 VETGDDYIRCKARGRLKAVDIQTQPHPGFPTDLQAQFMAMMTLADGVSVIRET----IFE 330

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLAACAE 417
      M   EL ++G +   + I+   ++L+ V A D   + +A LAA E
Sbjct: 331 NRFMHV--QELARMGVDIRLDGNTAIVHGRKQLSGAPVMATDLRASASLVLA-GLAAKGE 387

Query: 418 VPVT 421
      V+
Sbjct: 388 TTVS 391

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>ref|ZP_03717239.1| hypothetical protein EUBHAL_02316 [Eubacterium hallii DSM 3353]
gb|EEG35856.1| hypothetical protein EUBHAL_02316 [Eubacterium hallii DSM 3353]
Length = 437

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 104/441 (23%), Positives = 185/441 (41%), Gaps = 43/441 (9%)

```

Query: 5   EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E+ +++   + G V + G+K+ + IL A +++G ++DN+ N D + +L A+ +G
Sbjct: 2   EQYIIKGGNPLVGEVVGAKNAALGILAAAIMTDGECLIDNMPNVRDNTNVLQAMEGIG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRSLTAAVTAAGGNAT 120
      ++ D+   VV+   GK   +   L + N I   A   L A+   A
Sbjct: 62  ATI--DRKGDNEVVI--SGK----NIDSTGDLIVDNEYIRKIRASYYLIGALLGKYRKAQ 113

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGLPGGKVKLSGSISS 180
      VL G   + RPI   + G + LGA+V   G           L G ++ L   +S
Sbjct: 114 VVLPGGCDIGSRPIDQHIKGFALGAEVKIEHGMIIAQAE-----QLVGNRIYLD-VVSV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G+   +I+   P++   +   G   + + D IKG +
Sbjct: 168 GATININMAASLAQGNT---VIENAAKEPHIVDVANFLNSMGANIRGAGT-DVIRIKGVE 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      K+   + + + D   A F+ AA T G V ++   L+   A+++E +GA++
Sbjct: 224 KPHDTEYSVIP-DQIEAGTFMMAAAATRGDVLIKNVIPKHLE--TISAKLIE-IGAEIEE 279

Query: 301 TETSVTVTGPPREPFGGR-KHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
      ++ +V V   R   + K L   +   P +A+TL   L   T   +   R +
Sbjct: 280 SDDAVRVVAAQRLRHTQIKTLPPYPGFPPTMQPQMAITL---GLSTGTSTITESIFENRFR 336

Query: 360 ETERMVAIRTELTKLGASVE--EGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CA 416
      E           EL ++GA+++ EG + II EK   ++   D R A   +A A
Sbjct: 337 YVE-----ELRRMGANIKMVEG-NTAIHGVEKYTGASV-AAPDLRAGAALVIAGLAA 387

Query: 417 EVPVTIRDPGCTRKTFFPDYFD 437
      E   T+   G   ++ + + FD
Sbjct: 388 EGYTTVTQIGYIQRGY-ERFD 407

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>ref|YP_003975118.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
atrophaeus 1942]
gb|ADP34187.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
atrophaeus 1942]
Length = 436

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 90/359 (25%), Positives = 145/359 (40%), Gaps = 45/359 (12%)

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Query: 5   EEIVLQPIKEISGTVKLPKSKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      E+I+++   ++++GTVK+ G+K+   ++ + L SE +V+ ++   DV+ +   LR L
Sbjct: 2   EKIIIVRGQKLNGLTVKVEGAKNAVLPIAASLLASEEKSVIDCVPTLSDVYTINEVLRHL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      G V +   V V           E   E V           R + A+V   G   G

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Sbjct: 62 GADVHFEN---NEVTVNASYALQTEAPFEYV-----RKMRAVLVLMGPLLARTG 107

Query: 118 NATYVLGDGVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
++ L G + RPI + G + +GA + G V G L G K+ L

Sbjct: 108 HSRVALPGGCAIGSRPIDQHLKGFEAMGAKIKVGNGFIEAEVE---GRLQGAKIYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +E + K P + + G K + + I+

Sbjct: 164 -SVGATENLIMAAALAKGTTTLENVAKE---PEIVDLANYINAMGGKIRGAGTGT-IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K K+ ++ D A F+ AAIT G V V+G L +E MG K

Sbjct: 219 GVDKLHGKVKH-HIIPDRIEAGTFMVAATAITEGNVLKGVAVPEHL---TSLIAKMEEMGVK 274

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
+ + V GP + LK ID+ P D+ + + L A+G + I +

Sbjct: 275 IQDEGEGLRVIGPAK-----LKPIDIKTMPHPGFPTDMQSQMMALLLRANGTSMITE 326

>ref|ZP_02948415.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
butyricum 5521]

ref|ZP_04529594.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
butyricum E4 str. BoNT E BL5262]

gb|EDT76636.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
butyricum 5521]

gb|EEP52412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
butyricum E4 str. BoNT E BL5262]

Length = 421

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 89/380 (23%), Positives = 155/380 (40%), Gaps = 39/380 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E +V+ + G+V + G+K+ + IL A + S+G ++DN+ + EDVH + LR+L

Sbjct: 2 ERLVINGGYLLKGSVDINGAKNAAVAILPAAIMASKGKCIIDNIPDIEDVHCLERILRSL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G ++ +K + + + E+V+ A A+ + A VL

Sbjct: 62 GCNI--NKIDNNTLEIDSANVDNFDCTEDVRRMR-----ASYFFIGALLSRFKRARVVL 114

Query: 124 DGVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV G VN G +S

Sbjct: 115 PGGCSIGVRPIDQHIKGFALGADVITIEHGA-----VNVKADRLIGANIFFDVVSVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+++AA LA G +E + K P+V + G + + D IKG + +

Sbjct: 169 INVMIAATLAEGITTLENVAKE---PHVVDVANFLNSMGADIRGAGT-DVIRIKGVESLQ 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AA TGG V + L+ A+++E MG V +

Sbjct: 225 GCAYSVIP-DQIEAGTFMIAAATGDDVYIRNVIPKHLES--ISAKLIE-MGVTVEEND 280

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
S+ VT K LK +++ P D+ ++ + G + I + + W +

Sbjct: 281 SIRVTVD-----KPLKGVNIKTTTPYPGFPTDIQQPMSTLLSIVPGRSLITE-SIWENR 332

Query: 360 ETERMVAIRTELTKLGASVE 379
EL K+GA+++

Sbjct: 333 HKH-----IDELKKMGANIK 347

>ref|ZP_01861862.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
SG-1]

gb|EDL63091.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus sp.
SG-1]

Length = 438

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 107/445 (24%), Positives = 172/445 (38%), Gaps = 61/445 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63

Sbjct: 2 E+I+++ + ++GTVK G+K+ ++ L SEG +V+ ++ DV+ + LR L
EKIIVRGQQLNGTVKAEGAKNAVLPIAATLLASEGKSVIKDVPPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V + V V + VE E V R + A+V G G

Sbjct: 62 NTDV---TFSNNEVTVDASRELFVEAPFEYV-----RKMRAVSLVMGSLLGRTG 107

Query: 118 NATYVLGDVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RPI + G + +GA V +G V+G L G KV L

Sbjct: 108 RARVALPGGCAIGSRPIDQHLKGFEAMGAKVK--VGNGFIEAEVDG--RLKGAKVYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G +E + K P + + + G + + + I+

Sbjct: 164 -SVGATENIMMAAVLAEGTTVLENAKE---PEIVDLANFLNKMGANVKAGTGT-IRIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
G ++ ++ + D A F+ AAIT G V V+G + +E MG

Sbjct: 219 GVERLYGVEHNIIP-DRIEAGTFMVAIAITQGNVLVKGAIAEHMS---SLVAKMEEMGVT 274

Query: 298 VTWTETSVTVTGPPREPFGRLKHLKIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD- 352
+ + V GP + LK ID+ P D+ + + L A+G + I +

Sbjct: 275 IIEEAELRVIGPEK-----LKPIDIKTMPHPGFPTDMQSQMALLLRAEGTSVISET 327

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSL 412
V R E E ++ A ++ II P L + D R A A ++

Sbjct: 328 VFENRFMHVE-----EFRRMNADIKIEGRSVIINGPVTLLQGAEVGA-TDLRAAAALTI 379

Query: 413 AACAEVPTVIRDPGCTRKTFPDYFD 437
A G TR T + D

Sbjct: 380 AGLVA-----EGYTRVTELHHL 397

>gb|ADP67872.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Buchnera
aphidicola str. JF98 (Acyrtosiphon pisum)]
Length = 343

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 62/267 (23%), Positives = 109/267 (40%), Gaps = 24/267 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ ++ K ++G V + GSK+ + IL + L+EG + N+ N D++ L L LG

Sbjct: 2 EKLYVEGNKILNGHVIISGSKNAALPILFMTILTEGKIKIGNIPNLTDINIALKLLVYL 61

Query: 65 LSVEADKAA---KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ + ++ ++ + C + + + + + A G A

Sbjct: 62 VKITGNETLCIDASSINIFCPPYNLINKIRASIWIL-----GPLLARFGKAKI 109

Query: 122 VLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G ++ RPI + GL QLGA ++ L +C V G GK L IS

Sbjct: 110 FLPGGCKIGSRPIDLHLNGLTQLGATIN--LKNNCIDAYVK---GRLQGYILMEKISVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ AA LA G IID P + + + G + S ++ IKG K

Sbjct: 165 ATITIMSAATLAKGST---IIDNAACEPEIVDIKFLNTLGADIIGAGS-NKICIKGV 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITG 268
+ + + ++ +A AA G

Sbjct: 221 LTGGTHQVIPDRIETGTFLVAAAASQG 247

>emb|CBX30742.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [uncultured
Desulfobacterium sp.]
Length = 417

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 92/394 (23%), Positives = 163/394 (41%), Gaps = 41/394 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I+++ +SG VK+ G+K+ + IL+ + L +G+ N+ + D+ L LG

Sbjct: 2 DKIIVEGGYPLSGEVKISGAKNAALPILISSLLVDGCTYSNVPDLMDIESTKNLLINLG 61

Query: 65 LSVEADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+ +E D + G + P E ++ L + R A V+ GG +
Sbjct: 62 VCMETDGDIVKMDAAGLNNYEAPYELVRKMRASILVLGPLVARLKKARVSLPGGCS---- 117

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RPI + GL LGA+VD G L G ++ +++
Sbjct: 118 -----IGARPINLHLKGLAALGANVDLVHGYVEASADT-----LKGAEIYFD-TVTVTGT 166

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
L+MAA LA G I+ P V ++ + G K E + I G + K
Sbjct: 167 ENLMAAVLAEGT---SILRNAAREPEVVALADVLNKMGAKEGIGT-SVLKITGVESLK 222

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
P + + D A F+ AA+TG + + C L+ + L++ G+ +T +
Sbjct: 223 -PVSVSIIIPDRIEAGTFMVSAALTGSDIKIINCEPAHLESVILK---LKLSGSDITIGDN 278

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
S+ V G + + +ID+ P D+ V+ A G + I S +
Sbjct: 279 SIRVKGDK-----ISSIDIKTMPYPGFPDMQAQFMVLSVAKGFSVI---SETIF 327

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
E R + + +EL +LGA ++ + +IT KL
Sbjct: 328 E-NRFIHV-SELKRLGADIKISGNTAMITGVSKL 359

>ref|YP_003652039.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Thermobispora
bispora DSM 43833]
gb|ADG88146.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Thermobispora
bispora DSM 43833]
Length = 452

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 94/379 (24%), Positives = 148/379 (39%), Gaps = 47/379 (12%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++P + G V + GSK+ ++ ++ A L G + + N +V L+ LG+ VE
Sbjct: 26 IEPGGLRGDVHVRGSKNAVSKHMVAAMLGIGPSTLHNAPEVGEVGLTAAMLQALGVHVE 85

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKE----EVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
G+ +E E + + G I + L + AG +
Sbjct: 86 ISP-----GEITIERGAIEIRPYVPEEYTGLENRIPILMLGPLLHLAGEAFVPFVG 134

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG----LPGGKVKLSGSISS 180
G P R RP+ V L+ +GA+V+ V NGI L G +++L S
Sbjct: 135 GDPIGR-RPVNYHVDALRAMGAEE-----VGENGISAKATRLHGARIQLPYP-SV 183

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+L+ A LA G I+ + VE+ L ++R G E + DR + G
Sbjct: 184 GATETILLTAVLAEGKTVIK--GAAMEPEVVELAL-FLQRMGALIELNP--DRRIVIEGV 238

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + GD A +L +TGG V V GC L V L MGA+ T
Sbjct: 239 DRLHGASTRLAGDRIEAFSYLVAGLVGTGGEVRVHGCHQDRL---VTAITTLARMGAQFTI 295

Query: 301 TETSVTVTGPPREPFGFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
T+ +T T P R D + M D L V+ ADG + + +
Sbjct: 296 TDEWLTATAPDGL---RPAVQTDTHPGFMTDWQTPLVVLFTQADGMSVLHETVF----- 347

Query: 361 TERMVAIRTELTKLGASVE 379
R+V + L K+G +E
Sbjct: 348 ENRLVYV-PALQKMGCEIE 365

>emb|CBJ36651.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum CMR15]
Length = 451

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 63/264 (23%), Positives = 113/264 (42%), Gaps = 21/264 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK--- 71

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+SG +++ G+K+ + I+ A L+ + N+ N +DV ML LR +G++ D
Sbjct: 42 LSGEIRVSGAKNAALPIMCAALLTPEPLTLHNVPNLQDVRTMLKLLRQMGVAGTQDGHVD 101
Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
      A + + + L LG + A G+A L G +
Sbjct: 102 TLDAAIDAPEAPYDLVKTMRASILVLG-----PLLARFGHARVSLPGGCGIGA 150
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
      RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLMAA
Sbjct: 151 RPYDQHIKGLQMGAEIVIEHGY-IEAKLADGAKRLHGARI-VTDMVTVTGTENLLMAAV 208
Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
      LA G+ +++ P V L+ + G + + + DR ++G + K ++ +
Sbjct: 209 LADGET---VLENAAREPEVTDLANLLVKMGARIDGIGT-DRLVVQGV EALKGAEHTVI- 263
Query: 252 GDASSASYFLAGAAITGGTVTVVEG 275
      D A FL A GG VT+ G
Sbjct: 264 ADRIEAGTFLCAVAAAGGDVTLRG 287

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>ref|ZP_07843301.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
      hominis subsp. hominis C80]
gb|EFS19699.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
      hominis subsp. hominis C80]
Length = 421

```

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 94/371 (25%), Positives = 146/371 (39%), Gaps = 35/371 (9%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      ++I++ ++G V++ G+K+ IL + L SEG + + N+ + DV + L TL
Sbjct: 2 DKIIINGGNRLTGEVQVEGAKNAVLPILTASLLASEGKSKLTNPVPLSDVVTINNVLSTL 61
Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
      V+ DK +V V E E V + + M L A + G+A L
Sbjct: 62 NAKVDYDKE-NGSVTVDASATLNEEAPYEYVSKMRASV-LVMGPPLLARL----GHAIVAL 115
Query: 124 DGVPMMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      G + RPI + G + LGAA+ G + GL G + L S
Sbjct: 116 PGCAIGARPIEQHIKGF EALGAEIHLNGNIYASTK----EGLKGANIHLDFP-SVGAT 170
Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      ++M A LA G IE + K I + + M + A D I G +K
Sbjct: 171 QNIIMGASLAQGKTVIENVAKEPEIVDLANYINEMGNGVIGA---GTDITIHGVEKLT 226
Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      K+A + D A F+ AAIT G V V+G + LE MG + + E
Sbjct: 227 GVKHAIIP-DRIEAGTFIIAAAITRGDVFVKGA VKEHM---TSLIYKLEEMGVNLDNFEE 282
Query: 304 SVTVTGPPREPFRGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA----S 355
      V VT L+ +D+ P D+ + V+ L A+G + +
Sbjct: 283 GVHVT-----TNGELQPVDIKTLPHPGFPPTMQSQMMVLLLLTAEGHKVVTETVTFENRF 335
Query: 356 WRVKETERMVA 366
      V E RM A
Sbjct: 336 MHVAEFRRMNA 346

```

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>ref|ZP_06291770.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
      lacrimalis 315-B]
gb|EFA89480.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
      lacrimalis 315-B]
Length = 418

```

Score = 46.6 bits (109), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 82/321 (25%), Positives = 130/321 (40%), Gaps = 31/321 (9%)

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Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E+I+++P + G +++ G+K+ + IL L V++++ +DV M+ LR LG
Sbjct: 2 EKIIVRPSGPLKGIKIRIGGAKNAALPILAAACLLGTEDIVLEDVPKLKDVEIMIEVLRRLG 61

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Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V+ D ++V E+ + + M L A + G A L
Sbjct: 62 VKVKYDG---DLIVINSKNLTSYQNTYELMSKMRASFLVMGPELLARM---GKAVNSLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGT---DCPPVRVNGIG-GLPGGKVKLSGSISS 180
G + RPI + G K LGA V+ G ++ N I P S
Sbjct: 114 GGCAIGSRPIDLHLKGFKALGAKVEMTHGNISAKADKLQANNIYLDFFP-----SV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++M A LA G+ IE K P + + + G K + + IKG Q
Sbjct: 164 GATENIIMTATLAEGETLIENCAKE---PEIVDLASFLNKMGAKITGAGT-STIKIKGVQ 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K K + + D A F+ AITGG V +E T ++ LE GA+V
Sbjct: 220 KLKGCYHQIIP-DRIVAGTFMIAPAITGGDVLENVITNHMK---PILAKLEEAGAEVIV 275

Query: 301 TETSVTVTGPPR-EPFGRKHL 320
+ V V G + PF K L
Sbjct: 276 DDDKVRVIGKKKIYPFEIKTL 296

>ref|ZP_07204034.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [delta
proteobacterium NaphS2]
gb|EFK06674.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [delta
proteobacterium NaphS2]
Length = 421

Score = 46.6 bits (109), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 44/155 (28%), Positives = 65/155 (41%), Gaps = 12/155 (7%)

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
G + P + D A F+ AAIT G V VEGC L E L+ GA +
Sbjct: 217 GVDHLEPCEHTIIPDRIEAGTFMIAAAITRGNVLVEGCRPEHLTA---LTEKLKQAGAVI 273

Query: 299 TWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
T +T++ V GP ++++DV P A L A F T + + +R
Sbjct: 274 TKEKTAIRVQGP-----DAIESVDVKTMPFPGFATDLQ--AQFMALMTVAKGWSMFRE 324

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
E +EL +LGA +E + ++ EKL
Sbjct: 325 TVFENRFIHSVSELRRRLGADIEINGNQALVKGREKL 359

>ref|YP_004229675.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1001]
gb|ADX56615.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1001]
Length = 420

Score = 46.6 bits (109), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 69/273 (25%), Positives = 121/273 (44%), Gaps = 27/273 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++V++ +SG V + G+K+ + IL + LS +DN+ + +DV ML L +G
Sbjct: 2 DKLVIIEGGYPLSGEVVVGAKNAALPILCASLLSAEPVHLDNVPDLQDVRTMLKLLGQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+ +E+ G+ ++ +K + + MR+ + + A G+A
Sbjct: 62 VRIESGD-----GRVSLDASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGT---TDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-ITDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ +I+ P V L+ + G K E + DR I+G
Sbjct: 164 TGTENLLMAAVLAEGET---VIENAAREPEVGDLAHLLVQMGAKIEGIGT-DRLVIQGV 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
K K+ + D A FL A GG VT+
Sbjct: 220 KLHGAKHTVIP-DRIEAGTFLCAVAAGGDVTL 251

>ref|YP_002526349.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides KD131]
sp|B9KL51.1|MURA_RHOSK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACM01848.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides KD131]
Length = 422

Score = 46.6 bits (109), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 99/425 (23%), Positives = 170/425 (40%), Gaps = 53/425 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I+++ E+ G + + G+K+ ++ LS+ + N D+ M L++LG
Sbjct: 2 DSILVKGNGELRGQIPIAGAKNACLALMPATLLSDEPLTLTNAPRLSDIRTMTQLLQSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V + + + + + D + + + +R + A++ G G+
Sbjct: 62 AEVASLQGGQVLAL----SSHALTDHRADYDI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDGPPVRVNGIGGLPGGKVKLS 175
A L G + RP+ + L+ +GA++D ++ P GGL G +V
Sbjct: 110 AVVSLPGGCAIGARPVDLHLKALEAMGAELDLRDGYIHAKAPA-----GGLKGARVVFP 163

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFY 235
+S LMAA LA G +++ P + R + R G + E S
Sbjct: 164 -LVSVGATENALMAATLAKGTT---VLENAAREPEIVDLARCLRRMGAQIEGEGSST-IT 218

Query: 236 IKGQKQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + + V +Y LA AI GG V + G G L G F E L+ G
Sbjct: 219 IEGVDRLGGATHPVVTDRIELGTYMLA-PAICGGEVELLG-GRIELVG--AFCEKLDAA 274

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIR 351
V TE + V GR +KA+DV P D+ + + A+G + +
Sbjct: 275 ISVEETERGLRVA---RKNGR--VKAVDVMTPEFPFGFTDLQAQMMALLCTAEGTSVLE 328

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFS 411
+ R+ E M A EL ++GA +E +T EKL + D R +++
Sbjct: 329 E---RIFENRFMHA--PELIRMGARIEVHGTTATVTGVEKLRGAPV-MATDLRASVSLI 381

Query: 412 LAACA 416
LA A
Sbjct: 382 LAGLA 386

>ref|YP_001998201.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobaculum
parvum NCIB 8327]
sp|B3QM48.1|MURA_CHLP8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACF11001.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobaculum
parvum NCIB 8327]
Length = 424

Score = 46.6 bits (109), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 101/407 (24%), Positives = 175/407 (42%), Gaps = 48/407 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 64
++V++ K++SGTV GSK+ + ++ L+ +GT ++ + + +DV + L LG
Sbjct: 3 KLIVIRGGKKLSGTVAASGSKNSALPVIAATLLTPDGTGFINRIPDLKDVRTFIQLLEYLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+V + + V +E E V+ MR+ + + A G+
Sbjct: 63 AAVSFEN---NRLEVSSDLKSIAPYELVK-----KMRASIYVLGPLLARFGHTRV 111

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G RP+ ++ +++LGA V G +VNG L G ++ S

Sbjct: 112 SLPGGCAFGPRPVDLHIMAMEKLGATVTIEQG--FIDAKVNG-SRLRGAEIFDPISVGA 168

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+AL MAA A G ++ P +E R +++ G + I+G +

Sbjct: 169 TGNAL-MAAVTAEGKT---VLQNAALEPEIECLCRFLQKMGANISGIGT-TTLVIEGVDQ 223

Query: 242 YKSPK--NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
K+ + N + D A L AAITGG+VTV G L G V + G VT

Sbjct: 224 LKAVEFDNIF---DRIEAGTLLGAAAITGGSVTVTGTVP EHL-GSV--LDAFRQAGCIVT 277

Query: 300 WTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVA--MTLAVVALF--ADGPTAIRDVAS 355
+ ++T+T P + L+ +D+ P+ M +AL A G + I D

Sbjct: 278 VKDDAITLTAP-----EELQPVDITARPYEFPPTDMQAQWMALMTQAAGDSTIID--- 327

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD 402
R+ ER + EL +LGA +E ++ ++ P++L T + + D

Sbjct: 328 -RIY-LERFNHL-PELNRLGAHIEIRDNWALVHGPQELTGTKVMSTD 371

>ref|YP_828618.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Solibacter usitatus Ellin6076]
sp|Q01PT7.1|MURA_SOLUE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABJ88333.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Solibacter usitatus Ellin6076]
Length = 418

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 76/289 (26%), Positives = 117/289 (40%), Gaps = 33/289 (11%)

Query: 112 VTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGK 171
+ A G A L G + RPI + GL+QLGA ++ G + GL G

Sbjct: 101 LVARSGRARVSLPGGCAIGARPINLHIFGLEQLGAKINQTHGY----IEAVAPDGLRGAV 156

Query: 172 VKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW 231
V I+ L+MAA LA G+ ++ P V L+ + G K E + +

Sbjct: 157 VHFD-RITVTGTEDLMAAVLAKGET---LLRNAAREPEVVDLAELLIKMGAKIEGAGTS 212

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVL 291
I+G + +A + D A FL AITGG +TV C + L

Sbjct: 213 T-IRIQVESLGGAVHAI-ADRIEAGTFLVAGAITGGDLTVDCIPEHVGA---LVSKL 267

Query: 292 EMMGAKVTW-TETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAV--VALF--ADG 346
+ G VT +ET+V V G R L+++D+ + P A L +AL A+G

Sbjct: 268 QQAGVDVTQPSETTVRVRGTGR-----LRSVDMTTEEYPGFATDLQAQYMALMTQAEG 320

Query: 347 -PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
I ++ R + EL ++GA++ I+ P +L

Sbjct: 321 IAVVIENIFENRFMHAQ-----ELARMGANIRIDGRQAIVAGPRELT 362

>ref|ZP_02357249.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
oklahomensis E0147]
Length = 449

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 97/412 (23%), Positives = 171/412 (41%), Gaps = 62/412 (15%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ + ++G + + G+K+ + IL L+ +DN+ N +DV L L +G

Sbjct: 31 DKLVEIEGRRRLAGEIAVSGAKNAALPILCAGLLTAEPVHLDNVPNLKDVRTTLKLLDQMG 90

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ E D A R V+ PV A E+ ++++ A++ G G

Sbjct: 91 MREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARFGY 136

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ + GL+ +GA++ G + R L G ++ ++

Sbjct: 137 AKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LKGARI-VTDM 189

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
++ LLMAA LA G+ +I+ P V L+ G K + DR I+
Sbjct: 190 VTVTGTENLLMAATLADGET---VIENAAAREPEVSDLAHLLVAMGAKID-GIGTDRLVIQ 245

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + +A + D A FL A GG VT+ G A++L+ + K
Sbjct: 246 GVDRLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTGM-----RAQILDAVIDK 294

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPPTAIRDV 353
+ ++ G + A+ + ++ P D+ + ADG
Sbjct: 295 LREAGVTIEEGDRLRVKMDRRPGAVAIPTSEYPAFPTDMQAQFMALNAVADG----- 347

Query: 354 ASWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVT AID 399
S +V ET R + ++ EL +LGAS+ + ++T KL NV A D
Sbjct: 348 -SAQVIETIFENRFMHVQ-ELNRLGASIAVDGNTALVTGVPKLSGANVMATD 397

>emb|CBK73555.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Butyrivibrio
fibrisolvens 16/4]
Length = 431

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 42/149 (28%), Positives = 72/149 (48%), Gaps = 7/149 (4%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+ V++ +SG V++ G+K+ + IL A +++ T ++NL N +D++ ++GAL +G
Sbjct: 2 EQYVIKGGTPLSGEVEISGAKNAALGILAGAIMTDETVTIENLPNVKDINVLIGALEDIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
S+ ++ V + + E ++ A L A+ NA L
Sbjct: 62 ASI--NRVDDHTVKINGSSISRLSVDYEYIKIR-----ASYLIMGALLGKYKNAEVALP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLG 153
G + RPI V GLK LGA+VD G
Sbjct: 115 GGCLIGARPIDLHVKGLKALGANVDVSYG 143

>ref|ZP_04587482.1| prephenate dehydrogenase/3-phosphoshikimate
1-carboxyvinyltransferase family protein [Pseudomonas
syringae pv. oryzae str. 1_6]
Length = 534

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 51/194 (26%), Positives = 85/194 (43%), Gaps = 17/194 (8%)

Query: 253 DASSASYFLAGAAITGGT-VTVEGCGTT-SLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D +S+ F+ +I+ G + +E G + + +G + +VL +MG + T G
Sbjct: 332 DVTSSVLFMVATSISEGCDDLLEDVGVSPACEGAI---DVLRLMGGDIALQNV RATAGGT 388

Query: 311 PREPFGRK-HLKAIDVNMNKMP---DVAMTLAVVALFADGPPTAIRDVASWRVKETERMVA 366
+ R LK +DV +P D L V A A+G T +R + + ++ ER+
Sbjct: 389 LADLHVR SARLKGVDVPEALVPLAIDTFPVLLVAAACAEGRTILRGAQALQAEQAERVRL 448

Query: 367 IRTELTKLGASVEEGPDYCI---TPPEKLNVT AIDTYDDHRMAMAFSLAAC-AEVPVTI 422
+ L LG E D II TP + +D D R+ MAF +A+ A P+ I
Sbjct: 449 MADGLLT LGIEAEPVLDGIIIEGGTP---DGGEVDARGDQRIVMAFRVASLRASAPIRI 504

Query: 423 RDPGCTRKTFPDYF 436
++ FP +
Sbjct: 505 QNCADAATVFPFHL 518

>ref|ZP_04625219.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
kristensenii ATCC 33638]
gb|EEP90313.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
kristensenii ATCC 33638]
Length = 421

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 172/431 (39%), Gaps = 59/431 (13%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + I+ A L+E + N+ +D+ + L LG +E
Sbjct: 6 VQGRTRLSGEVTISGAKNAALPIMFAALLAEDPVELQNVPKLKDIDTTIKLLSQLGTKE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D A +V V G V F + +++++ A++ A G G
Sbjct: 66 RD--ASGSVFDASG-----VDEFCAPYDL-VKTMRASIWALGPLVARFGKGQVS 112

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 113 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY----VKASVNGRLKGAHIVMD-KVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+
Sbjct: 168 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNLTGAKITGAGT-DRITIEGVARL 223

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 224 GGGVYR-----VLPDRIETGTFLVAAAISGGKVVCVRQTRPDTL--DAVLAKLRE-AGAD 274

Query: 298 VTWTETSVTVTGPPREPFRGKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA+ P D+ +++ L A+G I +
Sbjct: 275 IEIGEDWISLDMQGKRP-----KAVTFRTAPHPGFPTDMQAQFSLNLAEGTGVTET 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLA 413
+ E M EL ++GA E + I E+L+ + D R + + LA
Sbjct: 329 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVQEQLSGAQV-MATDLRASASLVLA 381

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 382 GCIADGVTIIVD 392

>ref|ZP_03932203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49725]
gb|EEI15101.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49725]
Length = 422

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 107/438 (24%), Positives = 167/438 (38%), Gaps = 55/438 (12%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDDVHYMLGALRTLGLSVEADKAAK 74
++GTVK+ G+K+ +++ A L+EGTT + N DV M L LG V D +
Sbjct: 13 LAGTVKVDGAKNSVLKLMMAALLAEGTTTLTNCPEILDVPLMKKVLLEGLGCEVTIDGSTV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAG-----GNATYVLDGVP 127
R AK + NA A+R A+V G G+A L G
Sbjct: 73 RITT-----PAKPQ-----SNADFAVRQFRASVCVLGPLTSRCGHAKVALPGGD 117

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ GL++LGA G V L G ++L S +L
Sbjct: 118 AIGSRPLDMHQTGLEKLGATTTRIEHG-----AVVAEASELRGSTIRLDFF-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G ++ P + +++ G E + I G ++ +P
Sbjct: 172 TAAVLAEGTT---VLHNAAREPEIVDLCEMLKSMGANIE-GEGETSEVTIHGVERL-NPTE 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD A + AA+T G +TV G L + E L+ GA + E V
Sbjct: 227 HEVIGDRIVAGTWAYAAAMTQGDITVGGIAPRHLHLPL---EKLKSAGADIETYENGFRV 283

Query: 308 TGPPREPFRGKHLKAIDVNMNMKMPDVAMTLAVVAL----FADGPTAI-RDVASWRVKETE 362
R A+D P L +A+ A+G T I +V R + +
Sbjct: 284 RMEKRP-----TAVDYQTLFPFPGFPTDLQPMAGISAIAGTTTITENVFESRFRFVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPVTI 422
M+ +LGA + + ++ E L+ T + + D A A CA+ T+
Sbjct: 337 EML-----RLGADAQVDGHHVVVRGKEHLSSTHVWSSDIRAGAGLVLSALCADEATTV 389

Query: 423 RDPGCTRKTFPDYFDVLS 440
D + +P + + LS
Sbjct: 390 HDVVFHIDRGYPHFVENLS 407

>gb|ABC00785.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 30

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 24/30 (80%), Positives = 26/30 (86%), Gaps = 1/30 (3%)

Query: 86 PVE-DAKEEVQLFLGNAGIAMRSLTAAVTA 114
P+E DAKEEV+LFLGNAG AMR LTA AV A
Sbjct: 1 PIEKDAKEEVKLFLGNAGTAMRPLTAAVVA 30

>ref|YP_149237.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
kaustophilus HTA426]
sp|Q5KUG7.1|MURA2_GEOKA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2
dbj|BAD77669.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
kaustophilus HTA426]
Length = 428

Score = 46.2 bits (108), Expect = 0.009, Method: Compositional matrix adjust.
Identities = 93/397 (23%), Positives = 158/397 (39%), Gaps = 49/397 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+ G+K+ + ++ A L++ ++ L + DVH + + +G S D
Sbjct: 12 LRGTIKVSGAKNSAVALIPAAILADSPVTIEGLPDISDVHILGSLIEEIGGSFSD---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVLDGVP---RMR 130
GK V D V + L N + +R+ + A G + G+P +
Sbjct: 68 -----GKEAVIDPTNMVSMPLPNGKVKKL RASYL MGAMLGRFKRAVVG L PGGCHLG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + G + LGA V G +R L G ++ L +S +++AA
Sbjct: 120 PRPIDQHIKGFALGATVTNEQG--AIYLRAE---ELRGARIFLD-VVSVGATINIMLAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G II+ P + L+ G K + + + D I G +K ++A +
Sbjct: 174 VRAKGR---IENAAKEPEIIDVATLLSNMGAKIKGAGT-DVIRIDGVEKLSGCRHAI 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ +Y +A AA T G V V+ ++ L MG +V E + V G
Sbjct: 230 PDRIEAGTYMIAAAA-TNGEVVDNVIPQHVE---SLTAKLREMGVRVETGEDQILVCGT 285

Query: 311 PREPFGKRHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
LKA+DV P D+ + A+G + + D + S R K +
Sbjct: 286 -----DVLKAVDVKTLVYPGFPTDLQQPFTALLTKANGTSVVTDTIYSARFKHVD--- 335

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD 402
EL ++ A+V+ I+T P KL + D
Sbjct: 336 ----ELRRMNANVKVEGRSAIVTGPVKLQGAKVKASD 368

>ref|YP_003633629.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brachyspira
murdochii DSM 12563]
gb|ADG71430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brachyspira
murdochii DSM 12563]
Length = 425

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 83/317 (26%), Positives = 128/317 (40%), Gaps = 34/317 (10%)

Query: 8 VLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
V++ K I G +K+ GSK+ S +L+ + L++ ++ N+ + DVH ++ L LG V
Sbjct: 5 VIEGSKNIGGVLKVSGSKNASLPLLVASILTDEPVILHNVPDLADVHVLIDILEPLGKKV 64

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA-----VTAAGGNATYV 122
D V++ GK E+A ++ + + I + L A V+ GG A
Sbjct: 65 --DFKNNTTVIISHNGK--SEAPYKLVKKMRGSIIVLGPLLAKRKHCRVSYPGGCA--- 117

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
RPI + G++ LGA +D G V N L G + LSG
Sbjct: 118 -----FGPRPIDLHLKGMEALGAKIDITAGYIDAKVEDN----LIGADMDLSGKFGPTV 167

Query: 183 LSA--LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
L ++MAA LA G II P + L+ G K D I+ G
Sbjct: 168 LGTDNVMMASLAKGTT---IIRNAAKEPECVNLVDLLNAMGAKIT-GGGTDTITIE-GV 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
Y V D FLA AA G + +E L ++L +G +
Sbjct: 223 DYLGHAFTVIPDRIETGTFLAIAAAGRGKLENAEPKHL---FVLDLLSDIGCDIKT 279

Query: 301 TETSVTVTGPPRE--PF 315
T+T++ + RE PF
Sbjct: 280 TDTTIEIDASNRELKPF 296

>ref|ZP_01551380.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylophilales
bacterium HTCC2181]
gb|EAV46438.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylophilales
bacterium HTCC2181]
Length = 421

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 86/378 (22%), Positives = 158/378 (41%), Gaps = 46/378 (12%)

Query: 5 EEIVLQPIKEISGTVKVLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++Q +SG V++ G+K+ + IL+ + LS + NL + D+ L+ +G
Sbjct: 2 DKLLIQGPTTSLSGDVEISGAKNAALPILMCSLLSSDVLELSNLPDLHDIKTTKKLLQAMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ + K V++ E E V +++ A++ G G
Sbjct: 62 VEI---TDGKNTVLLRAKSITSYEAPYEMV-----KTMRASILVLGPLLRSRFG 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
A + G + RP+ + GL+ +GA + G D + G L G K+ +
Sbjct: 108 ARVSMPPGGCAIGSRPVDIHIKLEAMGALIKISHGYIDASCAHLPG-KRLQGAKIFMD-Q 165

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
++ L+MAA LA G I +D P + +++ G K E S DR ++
Sbjct: 166 VTVTGTENLMAAVLADG---ITTLDNSAREPEIVDLGMCLKKMGAKIEGLGS-DRIVVE 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + S N + D A +L AA+TGG V T ++ ++ ++LE G
Sbjct: 222 GVRNLHSA-NHTIMFDRIEAGTYLVAAAMTGGKVVCRNVDPTKMEAIQ--KLLE-CGVH 277

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADG----PTA 349
+ T+ S+T+ K +KA+++ P D+ + ADG +
Sbjct: 278 IESTKESITIKSD-----KKIKAVNITTAPYPGFPTDMAQFMALNTVADGVGEITES 330

Query: 350 IRDVASWRVKETERMVAI 367
I + V+E +RM A+
Sbjct: 331 IFENRFMHVQELQRMGAV 348

>ref|YP_003529687.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
amylovora CFBP1430]
ref|YP_003540154.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
amylovora ATCC 49946]
emb|CBJ47765.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
amylovora ATCC 49946]
emb|CBA19271.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
amylovora CFBP1430]
emb|CBX79144.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
amylovora ATCC BAA-2158]
Length = 420

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 101/434 (23%), Positives = 170/434 (39%), Gaps = 67/434 (15%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      +Q  ++G V + G+K+ + IL A L+E + N+ +D+ + L LG+ E
Sbjct: 6  VQGPTRLNGEVTISGAKNAALPILFAALLAEPEVIQNVPKLKDIDTTMKLLGQLGVKAE 65

Query: 69 ADKAAK---RAVVVGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNA 119
      + + V + C P E + + + + A + + A G G
Sbjct: 66 RNSVHLSDASNVDIYCA---PYE-----LVKTMRASIWALGPLVARFGQG 107

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCTPPVRVNGIGGLPGGKVKLSGSIS 179
      L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 108 QVSLPGGCAIGARPVDLHITGLEQLGAIEIKLEEGY----VKASVAGRLKGAHIVMD-KVS 162

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-- 237
      ++ AA LA G +I+ P + T + G K + S DR I+
Sbjct: 163 VGATVTIMSAATLATGTT---VIENAAREPEIVDTANFLNLTGAKITGAGS-DRITIEGV 218

Query: 238 ---GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLLEMM 294
      GG Y+ V D FL AI+GG VT +L D A++ E
Sbjct: 219 DRLGGGVYR-----VLPDRIETGTFLVAGAISGGKVTCAAQPDTL--DAVLAKLRE-A 269

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAI 350
      GA + E +++ + P KA+++ P D+ +++ L A+G I
Sbjct: 270 GADIEMGEDWISLDMHGKRP-----KAVNLRITAPHPGFPTDMAQFSLNLLVAEGTGV 323

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
      + + E M EL ++GA E I EKL+ + D R + +
Sbjct: 324 TET----IFENRFMHV--PELVRMGAAHAEIESHTLICHGVEKLSSAQV-MATDLRASASL 376

Query: 411 SLAACAEVPTIRD 424
      LA C T+ D
Sbjct: 377 VLAGCIAEGTTLVD 390
```

```
>sp|Q39K93.1|MURA_BURS3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ABB07123.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
      383]
      Length = 449
```

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 66/280 (23%), Positives = 117/280 (41%), Gaps = 33/280 (11%)

```
Query: 3  GAEIEVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
      G +++V++ +SG + + G+K+ + IL L+ +DN+ N +DV L L
Sbjct: 29  GMDKLVIEGGHRLSGEIVVSGAKNAALPILCAGLLTGDPVDLDNVPNLKDVRTTLKVLNQ 88

Query: 63 LGLSVEADKAAKRAVVVGCCKGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
      +G+ E D GC + V + + + + A + + G
Sbjct: 89 MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCTPPVRVNGIGGLPGGKVKLS 175
      G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEISIEHGFIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVSDLAHLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEG 275
      I+G ++ +++ + D A FL A GG V + G
Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVRLTG 282
```

```
>ref|ZP_01011608.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Maritimibacter
      alkaliphilus HTCC2654]
gb|EAQ14915.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacterales
```


bacterium HTCC2654]
Length = 421

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 98/409 (23%), Positives = 160/409 (39%), Gaps = 42/409 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG + + G+K+ ++ LSE + N D+ M L++LG EA
Sbjct: 12 LSGEIPIAGAKNACLALMPATLLSEDPLTLTNAPRLSDIKTMTLLQSLG--AEATGLQD 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ A ++ + + + L A G+A L G + RP+
Sbjct: 70 GQVLAMSSHDLTSSRADYDIVRKMNASNLVLGPLIARF----GHAEVSLPGGCAIGARPM 125

Query: 135 GDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
GL++LGA++D +L P GL G ++ L + S ++MAA
Sbjct: 126 DLHTFGLKGLGAEIDLRDGYLFAKAP-----NGLKGAEIPLKFA-SVGATENIVMAAT 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G ++ P + ++ + G + E + R I+G + + V
Sbjct: 178 LAKGTT---VLTNAAREPEIVDLVKCLRAMGAQIE-GEGETSRIEIQVDRHLGHATHQVVA 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVWTETSVTVTGPP 311
+Y LA AI GG V C L F E L+ G V TE + V+
Sbjct: 234 DRIELGTMYLA-PAIAGGEVE---CLGGKLDLVAFAVEKLDEAGVAVEETERGLKVS--- 286

Query: 312 REPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GR LKA+DV P D+ + ADG + + + + E M A
Sbjct: 287 -RKNGR--LKAVDVTTEFPFGFPTDLQAQFMAMLCCTADGTSELNET---IFENRFMHA- 338

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACA 416
ELT++GA +E +T +KL + D R +++ LA A
Sbjct: 339 -PELTRMGAEIEVHGGRRARVTGVDKLRGAPV-MATDLRASVSLILAGLA 385

>ref|ZP_00945241.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum UW551]
ref|YP_002260902.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate
transferase) (udp-n-acetylglucosamine enolpyruvyl
transferase) (ept) protein [Ralstonia solanacearum
IPO1609]
gb|EAP72333.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum UW551]
emb|CAQ62843.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate
transferase) (udp-n-acetylglucosamine enolpyruvyl
transferase) (ept) protein [Ralstonia solanacearum
IPO1609]
Length = 453

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 64/267 (23%), Positives = 117/267 (43%), Gaps = 27/267 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ V+ N+ N +DV ML LR +G VE +
Sbjct: 44 LSGEIRVSGAKNAALPIMCAALLTAELPLVLRNVPNLQDVRTMLKLLRQMG--VEGTQNGH 101

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+ P +A ++ +++++ A++ G G+A L G
Sbjct: 102 DVTLDAAADIHAP--EAPYDL-----VKTMRASILVLGPLLARFGHARVSLPGGCG 149

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLM
Sbjct: 150 IGARVPDQHIKGLQMGAEIVIEHGY-IEAKLADGAKRLRGARI-VTDMVTVTGTENLLM 207

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ +++ P V L+ + G + E + DR ++G ++
Sbjct: 208 AAVLADGET---VLENAAREPEVTDLANLLVKMGARIEGIGT-DRLVVQGVDAALNGAEHT 263

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEG 275
+ D A FL A GG VT+ G
Sbjct: 264 VI-ADRIEAGTFLCAVAAAGGDVTLRG 289

>ref|YP_002989223.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dickeya dadantii Ech703]
gb|ACS87401.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dickeya dadantii Ech703]
Length = 420

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 103/430 (23%), Positives = 169/430 (39%), Gaps = 59/430 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++G V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 6 VQGPTRLTG EVTISGAKNAALPILFAALLAEPEVEIQNVPKLRDIDTTMKLLSQLGAHVE 65

Query: 69 ADKAAK---RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNA 119
+ + AV V C P E + + + + A + + A G G
Sbjct: 66 RNGSVHVDASAVNVFCA---PYE-----LVKTMRASIWALGPLVARFQGQ 107

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSIS 179
L G + RP+ + GL+QLGA + G V+ G L G + + +S
Sbjct: 108 QVSLPGGCAIGARPVDLHINGLEQLGAQITILEEGY----VKATVDGRLKGAHIVMD-KVS 162

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
++ AA LA+G II+ P + T + G K + S D+ I G
Sbjct: 163 VGATVTIMSAAVLAVGRT---I IENAREPEIVDTANFLNLTGAKISGAGS-DKIVIDGV 218

Query: 240 QKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ Y V D FL AA++GG V +L D A++ E GA +
Sbjct: 219 ERLGG--GVYRVLPDRIETGTFLVAAVSGGKVVCNTRPETL--DAVLAKLRE-AGADI 273

Query: 299 TWTETSVTVTGPPREPFGKRHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
E +++ + P KA++V P D+ +++ L A+G I +
Sbjct: 274 DVGEDWISLDMHGQRP-----KAVNVRTAPHPGFPTDMQAQFSLNLVAEGTGVTETI 327

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAA 414
R + I EL ++GA E + I E L+ + D R + + LA
Sbjct: 328 F-----ENRFMH I-PELIRMGQAQAEIESNTVICHGVEHLSGAQV-MATDLRASASLVLG 380

Query: 415 CAEVPVTIRD 424
C VT+ D
Sbjct: 381 CIADGVTLVD 390

>ref|ZP_02002319.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beggiatoa sp. PS]
gb|EDN67683.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Beggiatoa sp. PS]
Length = 163

Score = 46.2 bits (108), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 35/123 (28%), Positives = 61/123 (49%), Gaps = 5/123 (4%)

Query: 320 LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWVRKETERMVAIRTELTKLGA 376
L I++ N++P D L + A A+G T + RVKE++R+ + L +G
Sbjct: 28 LHGIEIPKNQVPLAIDEFPILFIAASCAEGKTVLTGAELRVKESDRIKVMADGLQTVGI 87

Query: 377 SVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFSLAA-CAEVPVTIRDPGCTRKTFPDY 435
D +I ++ I+++ DHR+AMAF++AA A + I D +FP++
Sbjct: 88 DATPTSDG-MIIQGGQIQGGVINSHGDHRIAMAFTIAALSARNQIIIEDCANVATSFNPF 146

Query: 436 FDV 438
D+
Sbjct: 147 VDL 149

>ref|ZP_05099909.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp. GAI101]
gb|EEB84211.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp. GAI101]
Length = 423

Score = 46.2 bits (108), Expect = 0.011, Method: Compositional matrix adjust.

Identities = 102/418 (24%), Positives = 163/418 (38%), Gaps = 39/418 (9%)

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Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ IV++ +SG + + G+K+ ++ LSE + N D+ M LR+LG
Sbjct: 2  DSIVVKGKGGALSGQIPIAGAKNACLTLPATLLSEEPLTLTNAPRLSDIRMTTELLRSLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V + K + + C G + V+ A + + A G+A L
Sbjct: 62  AEVSTMQEGK-VLALSCHGAINTRAEDIVRKMR-----ASNVLGPLLAREGHAQVSLP 115

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ L +GA++D G + GG G V S
Sbjct: 116  GGCAIGARPMDIHTDSLALMGAEIDLDRGY----LHAKAQGGSGLKGAVIDFPFASVGATE 171

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G I + I + LR M G + + D R I+G +
Sbjct: 172  NIMMAATLAKGTTVINNAAREPEIVDLADCLRAM---GAQID-GDGTSRIEIQGVDRLLGG 227

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V +Y LA AI GG V + G LQ F E L+ G VT TE
Sbjct: 228  ATRHVVTDRIELGTYMLA-PAICGGEVELLGGRLNLLQA---FCEKLDAAGIDVTETENG 283

Query: 305  VTVTGPPEPPFGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ V R++ + A+DV P D+ + + ADG + + + ++
Sbjct: 284  LKVA-----RRNGVISAVDVTTEFPFGFPTDLQAQMMALLCTADGTSVLEE---KI 331

Query: 359  KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
E M A EL ++GA +E +T +KL + D R +++ LAA A
Sbjct: 332  FENRFMHA--PELIRMGADIEVHGGTATVTGVKKLKGAPV-MATDLRASVSLILAAMA 386

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>ref|ZP_02328243.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
larvae subsp. larvae BRL-230010]
ref|ZP_08056912.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
gb|EFX45373.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
Length = 440

```

Score = 46.2 bits (108), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 89/372 (23%), Positives = 156/372 (41%), Gaps = 33/372 (8%)

```

Query: 6  EIVLQPIKEISGTVKLPKSGKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 64
+I+++ ++SG VK+ G+K+ I+ + L SEG +V+ + +DV + L +LG
Sbjct: 3  KIIVRGGRKLSGKVKVNGAKNAVLPIIAASLLASEGESVIQDAPPLDDVLVINKVLES LG 62

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E A R C +A E+ + + + M L A + G A L
Sbjct: 63  AKLEYTNNAIRI----CANSIQTCEASYELVRKMRASFLVMGPPLARL----GEARISLP 114

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + +GA+++ LG RV G L G K+ L + S
Sbjct: 115  GGCAIGTRPIDQHLKGFEAMGAIE--LGQGYIEARVK--GRLKGTKIYLDVA-SVGATE 169

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G I++ P + + G + + I+G +K +
Sbjct: 170  NIIMAAVLAEGTT---ILENAAKEPEIVDLANYLNAMGAVVRGAGTG-MIRIEGVEKLRG 225

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + +Y +A AAIT + VEG L+ L+ MG + E
Sbjct: 226  AVHTVTPDRIEAGTYMIA-AAITKSDLYVEGAIGDHLR---PVISKLQEMGVTL EEDENG 281

Query: 305  VTVTGPPEPPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD-VASWRVK 359
+ V G K LKA+DV P D+ + + + ADG + + + V R
Sbjct: 282  IRVIGTD-----KPLKAVDVKTLPYPGFPTMQSQMMALLMVADGTSVSETVFENRFM 335

Query: 360  ETERMVAIRTEL 371
+ + + E+
Sbjct: 336  HVDEFINMNAEI 347

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>ref|YP_364841.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas campestris pv. vesicatoria str. 85-10]
sp|Q3BQX2.1|MURA_XANC5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
emb|CAJ24841.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas campestris pv. vesicatoria str. 85-10]
Length = 424

Score = 46.2 bits (108), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 97/400 (24%), Positives = 161/400 (40%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNISSAKNAVLPLCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGLTAKGRSILVDPKSVTHQVAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L GG+ +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY----IKATSHGRLLKGGRYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L D ++ E GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETL--DAVLDKLTE-AGATI 280

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 281 TTTADSITLDMQGKRP-----RAVSLTTAPYPAFPPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|YP_001044160.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter sphaeroides ATCC 17029]
sp|A3PM22.1|MURA_RHOS1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
gb|ABN77388.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter sphaeroides ATCC 17029]
Length = 422

Score = 46.2 bits (108), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 99/425 (23%), Positives = 170/425 (40%), Gaps = 53/425 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+ I+++ E+ G + + G+K+ ++ LS+ + N D+ M L++LG
Sbjct: 2 DSILVKGNGELRGQIPIAGAKNACLALMPATLLSDEPLTLTNAPRLSDIRMTQQLQSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V + + + + + D + + + +R + A++ G G+
Sbjct: 62 AEVASLQGGQVLAL----SSHALTDHRADYDI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLS 175
A L G + RP+ + L+ +GA++D ++ P GGL G +V
Sbjct: 110 AVVSLPGGCAIGARPVDLHLKALEAMGAELDLRDGYIHAKAPA-----GGLKGARVVFP 163

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
+S LMAA LA G +++ P + R + R G + E S
Sbjct: 164 -LVSVGATENALMAATLAKGTT---VLENAAREPEIVDLARCLRRMGAQIEGEGSST-IT 218

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + + V +Y LA AI GG V + G G L G F E L+ G
Sbjct: 219 IEGVDRLGGAHPVVTDRIELGTYMLA-PAICGGEVELLG-GRIELVG--AFCEKLDAAAG 274

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIR 351
V TE + V GR +KA+DV P D+ + + A+G + +
Sbjct: 275 ISVEETERGLRVA----RRNGR--VKAVDVMTEPFPGFPTDLQAQMMALLCTAEGTSVLE 328

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTDAIDTYDDHRMAMAFS 411
+ R+ E M A EL ++GA +E +T EKL + D R +++
Sbjct: 329 E----RIFENRFMHA--PELIRMGARIEVHGATATVTGVEKLRGAPV-MATDLRASVSLI 381

Query: 412 LAACA 416
LA A
Sbjct: 382 LAGLA 386

>ref|ZP_04059651.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
hominis SK119]
gb|EEK12534.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
hominis SK119]
Length = 421

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 81/305 (26%), Positives = 124/305 (40%), Gaps = 20/305 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVDNLLNSEDVHYMLGALRTL 63
++I++ ++G V++ G+K+ IL + L SEG + + N+ + DV + L TL
Sbjct: 2 DKIIINGGNRLTGEVQVEGAKNAVLPILTASLLASEGKSKLTNPDLSDVVTINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ DK +V V E E V + + M L A + G+A L
Sbjct: 62 NAKVDYDKE-NGSVTVDASATLNEEAPYEYVSKMRASV-LVMGPELLARL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA++ G + GL G + L S
Sbjct: 116 PGGCAIGARPIEQHIKGFALGAEIHLNGNIYASTK----EGLKGANIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++M A LA G IE + K I + + M + A D I G +K
Sbjct: 171 QNIIMGASLAQKGTVIENVAKEPEIVDLANYINEMGGNVIGA----GTDITITIHGVEKLT 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
K+A + D A F+ AAIT G V V+G + LE MG + + E
Sbjct: 227 GVKHAIIP-DRIEAGTFIIAAAITRGDVVFKGAVKEHM---TSLIYKLEEMGVNLDNFNEE 282

Query: 304 SVTVT 308
V VT
Sbjct: 283 GVHVT 287

>ref|YP_002552204.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
ebreus TPSY]
sp|B9MDV0.1|MURA_DIAST RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACM32204.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
ebreus TPSY]
Length = 440

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 73/284 (25%), Positives = 124/284 (43%), Gaps = 43/284 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ + + G V + G+K+ + L A L+ + N+ +DV ML +R +G
Sbjct: 2 DKLLIRGGRPLVGEVPISGAKNAALPELCAALLTADPVTLHNVPRLQDVATMLRLIRNMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG-- 116
+ V+ R C V DA V+L G +++++ A+V A G
Sbjct: 62 VQVD-----RIANPCDS----VADAAGIVRLDAGALSTPEAPYDLVKTMRASVLALGPL 111

Query: 117 ----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV 172
G AT L G + RP+ + GL+ +GA + G I LP G
Sbjct: 112 LARFGEATVSLPGGCAIGSRPVDQHIKGLQAMGAQIVVEHG-----YMIARLPQGCT 163

Query: 173 KLSGS-ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAE 226
+L G+ I++ ++ LLMAA LA G+ +++ P V ++ + G + E
Sbjct: 164 RLRGARITTDMTVTGTENLLMAATLAEGE---VLENAAQEPEVADLAEMLIKMGARIE 220

Query: 227 -HSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGG 269
H S R I+G ++ ++A V D A FL A TGG
Sbjct: 221 GHGTS--RIRIQGVERLHGCEHAVV-ADRIEAGTFLCAVAATGG 261

>ref|YP_641033.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. MCS]
ref|YP_939928.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. KMS]
ref|YP_001072125.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. JLS]
gb|ABG09977.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. MCS]
gb|ABL93138.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. KMS]
gb|ABN99634.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
sp. JLS]
Length = 417

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 100/402 (24%), Positives = 150/402 (37%), Gaps = 67/402 (16%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLNLNSEDVHYMLGALRTL 63
+E V+ +SG V + G+K+ +++ + L+EGT+ + N + DV M LR L
Sbjct: 2 SERFVVTGGNRLSGEVAVGGAKNVSLKMAASLLAEGTSTITNCPDILDVPLMAEVLRL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R P DA A+R A+V G
Sbjct: 62 GATVELDGDVVRIT----SPDEPKYDADF-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L
Sbjct: 108 RARVALPGGDAIGSRPLDMHQAGLRQLGA--RCNIEHGCVVAEAD---ELHGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW----- 231
S +LMAA LA G + I P V ++ + G + + S
Sbjct: 163 -SVGATENILMAAVLAKG--VTTIHNAAREPDVVDLCAMLNQMGAVVVGAGSSTLTITG 218

Query: 232 -DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
DR Y P V GD A+ + AA+T G ++V G LQ
Sbjct: 219 VDRLY-----PTEHRVIGDRIVAATWGIAAAMTQGDISVTGVDPQHLQ---LVLHK 266

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMPDVAMTLAVVAL----FADG 346
L GA VT + V R KA++V P L +A+ ADG
Sbjct: 267 LHDAGATVTQDDNGFRVVQYERP-----KAVNVATLPFGFPPTDLQPMAGLASIADG 319

Query: 347 PTAI-RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 387
+ I +V R + E M+ +LGA + ++
Sbjct: 320 TSMITENVFEARFRFVEEMI-----RLGADARTDGHHAVV 354

>ref|ZP_06191504.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
odorifera 4Rx13]
gb|EFA16016.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
odorifera 4Rx13]
Length = 419

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 172/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVNDLNLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E

Sbjct: 6 VQGRTRLSGEVSISGAKNAALPILFAALLAEFPVELQNVPKLKDIDTTIKLLSQLGTKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ +V V G V F + + + + A + + A G G

Sbjct: 66 RNG----SVYVDASG-----VNEFCAPYDL-VKTMRASIWALGPLVARFGRGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S

Sbjct: 111 LPGGCAIGARPVDLHISGLEQLGAEIKLEEGY---VKASVEGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+ + AA LA G +I+ P + T + G K + S DR I+G + +

Sbjct: 166 TVTIMSAATLATGTT---VIENAAREPEIVDTANFLNTLGAKISGAGS-DRITIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AA++GG V +L D A++ E GA +

Sbjct: 222 GG--GVYRVLPDRIETGTFLIAAAVSGGKVMCRDTRPNTL--DAVLAKLRE-AGADIEVG 276

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E + + + + P KA+ V P D+ + + + L A+G I +

Sbjct: 277 EDWISLDMHGKRP-----KAVTVRTAPHPGFPTDMQAQFSLNLVAEGTGVITET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + LA C

Sbjct: 327 IFENRFMHV--PELIRMGAAHAEIESNTLICHGVEQLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
VT+ D

Sbjct: 384 DGVTIVD 390

>ref|ZP_04619481.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia aldovae
ATCC 35236]
gb|EEP95965.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia aldovae
ATCC 35236]
Length = 421

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 102/425 (24%), Positives = 171/425 (40%), Gaps = 59/425 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E D A

Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEFPVELQNVPKLKDIDTTIKLLSQLGTKIERD--AS 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+V V G V F + + + + A + + A G G L G

Sbjct: 70 GSVFVDASG-----VDEFCAPIYDL-VKTMRASIWALGPLVARFGKQVSLPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++

Sbjct: 119 IGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYK 243
AA LA G +I+ P + T + G K + + DR ++ GG Y+

Sbjct: 174 AATLAEGTT---VIENAAREPEIVDTANFLNTLGAKISGAGT-DRITVEGVARLGGGVYR 229

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V D FL AAI+GG V +L D A++ E GA + +

Sbjct: 230 -----VLPDRIETGTFLVAAAISSGKVVCHQTRPDTL--DAVLAKLRE-AGADIEVGDD 280

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + + + P KA+ + P D+ + + + L A+G I + +

Sbjct: 281 WISLDMHGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGTGVITET----IF 330

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP 419
E M EL ++GA E + I E+L+ + D R + + LA C

Sbjct: 331 ENRFMHV--PELIRMGAAHAEIESNTVICYGVQLSGAQV-MATDLRASASLVLAGCIAEG 387

Query: 420 VTIRD 424
VTI D

Sbjct: 388 VTIVD 392

>ref|ZP_07837024.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermaerobacter
subterraneus DSM 13965]
gb|EFR61711.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermaerobacter
subterraneus DSM 13965]
Length = 431

Score = 45.8 bits (107), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 110/421 (26%), Positives = 163/421 (38%), Gaps = 54/421 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E IV++ + + G V++ G+K+ + IL L+E T ++ ++ + +DV M L LG
Sbjct: 2 ERIVVRGGRPLQGQVRISGAKNAALPILAAATLLAEDTCLLYDIPSLDDVVTMRMLTQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
++VE+ AV P + + L +R + A++ G G
Sbjct: 62 VTVESTGEGALAV-----HPAAELQYAAPYDL-----VRRMRASILVLGPLLARLGR 108

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + +RPI + G LGADV+ G V V GL G + L
Sbjct: 109 ARAALPGGCAIGQRPIDLHLKGFAALGADVEVSGGE----VEVRAPRGLRGTSIYLDVP- 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++MAA LA G IE P + + G A+ + R
Sbjct: 164 SVGATENIMMAAVLAEGTTTIE--NAAEEPEIVDLANFLNTLG--ADVAGAGTRVIQIH 218

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
G + D A FL + GG VTV G L+ A+V E MGA V
Sbjct: 219 GVPVLGGGTYYTIIPDRIEAGTFLLAPLVAGGQVTVTVGVVPEHLKS--LLAKVRE-MGADV 275

Query: 299 TWTETSVTVTGPPREPFRGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA 354
VTV R KA+D+ P D+ + + A+G
Sbjct: 276 VVDGDEVTVAVSSRP-----KAVDIKTLPPGFPDQLQAPMMAALVTAEG----- 320

Query: 355 SWRVKET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSL 412
+ V ET E A EL ++GA ++ IIT E+L + T D R A L
Sbjct: 321 TATVTETLTFENRFAHVPELRRMGARIQIGQTAIITGVERLQGAPV-TATDLRSGAALVL 379

Query: 413 A 413
A
Sbjct: 380 A 380

>ref|YP_004218083.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
sp. MP5ACTX9]
gb|ADW69303.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
sp. MP5ACTX9]
Length = 426

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 87/376 (23%), Positives = 153/376 (40%), Gaps = 55/376 (14%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-AKR 75
GT+K+ G+K+ + + A L+E +++N+ +D+ L ++G V+ A+
Sbjct: 14 GTIKVSGAKNSALPCMAAAIILTEDELILENIPQVQDIETERKLLVSMGAEVQLGYGRAQH 73

Query: 76 AVVVGCG-----GKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+ C K+ + L LG + R+ A V GG A +
Sbjct: 74 RTHIKCAVLSDPVAKYEIVKTMRASSLVLGP--LIARTGIARVAMPGGCA-----I 122

Query: 130 RERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGG--LPGGKVKLSGSISSQYLSALL 187
RPI + L+Q+GA + G R N + G + K+ ++G+ +L
Sbjct: 123 GGRPIDMHLAALQMGATITQDHGY--LEARTNRLKAHIVFDKITVTGT-----EDIL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G+ I++ P V L+ G K E + + I+G + ++
Sbjct: 175 MAATLAEGET---ILENCAREPEVTDLAALLAMGAKIEGAGTST-MKIQGVTRLHGARRH 230

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A FL AITGG + V+ C + L LE MG ++ + S+ V

Sbjct: 231 K-INPDRIEAGTFLMAGAITGGDLNVDCCDP SHLGA---LIAKLEQMGVRIDVGKDSIRV 286
Query: 308 TGPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI-RDVASWRVKETE 362
LKA D++ + P D+ +A A+G T + ++ R +
Sbjct: 287 RSG-----GELKAADISTEYYPGFPTDMQAQFMALATQAEGTTNVTENIFENRFMHVQ 339
Query: 363 RMVAIRTELTKLGASV 378
EL ++GA++
Sbjct: 340 -----ELNRMGANI 348

>ref|ZP_06393255.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dethiosulfovibrio
peptidovorans DSM 11002]
gb|EFC92196.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dethiosulfovibrio
peptidovorans DSM 11002]
Length = 424

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 105/410 (25%), Positives = 168/410 (40%), Gaps = 46/410 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTV-VDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ GT+K G+K+ + ++ + L + T+ ++N+ +D+ M+ L+ LG +
Sbjct: 13 LKGTIKTQGAKNALPVMAASLLLNATLTLENVPKLDITTMVDLLKVLGADISFHD-- 70
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130
V + E VQ MR+ + + A G A L G +
Sbjct: 71 -HKVISISVPDSISWETPAPLVQ-----KMRASSLVLGPLLAREGRAVMPLPGGCSIG 121
Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + GL ++GA ++ G + GL G ++ L S LLMAA
Sbjct: 122 SRPIDLHLKGLAKMGASIELQHGAHVHASTK----GLKGCRIYLDFF-SVGATENLLMAA 175
Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G+ +E + + I + +LR M G K E + I+G + +
Sbjct: 176 ILAEGEVTLENVAREPEIVNLADSLRTM---GAKIE-GEGETVLRIQGSPLQGGNVRII 231
Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
++ +Y LAG I+ G VTV D A+ LE V++ SV+V GP
Sbjct: 232 PDRIAACYIILAG-VISDGEVTVSDVIPQHF--DSLAK-LEEASVDVSFDGNSVSV-GP 286
Query: 311 PREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
RK LKAI + P DV L V A G + I++ + E+ R +
Sbjct: 287 -----SRKKLKAISLKTLPYPGFPTDVQPQLMAVMSLAQGTSVIKE----SIFES-RFLH 336
Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
+ +EL K+GA VE + I+ N + + D R A LA A
Sbjct: 337 V-SELKKMGADVQLQNTAIVKGVNHFNCSEV-MATDLRAGAALILAGLA 384

>ref|YP_001027765.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
mallei NCTC 10229]
ref|YP_001082288.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
mallei NCTC 10247]
gb|ABN03429.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
mallei NCTC 10229]
gb|ABO06461.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
mallei NCTC 10247]
Length = 449

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEIEVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPDLKDVRTTLALLGQ 88
Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ +++++ A++ G
Sbjct: 89 MGMREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVGLPLLARF 134
Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175

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      G A  L G  +  RP+  + GL+ +GA++  G  +  R      L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      I+      LLMAA LA G+  +I+      P V      L+  G K +      DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
      I+G ++      +A +  D  A  FL  A  GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAGGDVTLTG 282

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>ref|YP_003949133.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase 1 [Paenibacillus
      polymyxa SC2]
gb|ADO58892.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Paenibacillus
      polymyxa SC2]
      Length = 453

```

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 93/351 (26%), Positives = 145/351 (41%), Gaps = 45/351 (12%)

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Query: 13  KEISGTVKLPKSGKSLNRIILLAAALS---EGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      ++G+VK+ G+K  N +L + A S      EG +V+ +  +DV +  L +LG V
Sbjct: 10  NRLTGSIVKSGAK---NSVLPPIIAASLLGEEGESVIMDAPPLDDVMTINKVLES LGAGVT 66

Query: 69  ADKAAKRA---VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      R      ++ C  + P E ++      FL  +  R      ++ GG A
Sbjct: 67  YQDEVIRVDARKIISC--EAPYEWVRKMRASFLVMGPLLTRLGRTRISLPGGCA----- 118

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      +  RPI  + G + LGA++  LG      + NG  L G KV L  + S
Sbjct: 119 ---IGTRPIDQHLKGFEALGAEIS--LGQGFIEAKSNG--RLRGAKVYLDVA-SVGATEN 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      ++MAA LA G  IE  K  P +      +  G K  + +  I+G +K
Sbjct: 171 IMMAATLAEGVTTIENAAKE---PEIVDLANFLNGMGAKVRGAGTG-VIRIEGVEKLGHV 226

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      K+  +      + +Y +A AAITGG V VEG  +  L G V      +E MG  +  E  +
Sbjct: 227 KHTVIPDRVEAGTYMVA-AAITGGNVYVEGAISDHL-GPV--ISKMEEMGVTIQPDENGI 282

Query: 306 TVTGPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPATAIRD 352
      V      K LKA+DV      P      D+  +  + L A+G + I  +
Sbjct: 283 RV-----IADKPLKAVDVKTLPPYGFPTDMQSQMMALQLAAEGTSIITE 326

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>ref|ZP_02890556.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      ambifaria IOP40-10]
gb|EDT03887.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      ambifaria IOP40-10]
      Length = 449

```

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 66/280 (23%), Positives = 117/280 (41%), Gaps = 33/280 (11%)

```

Query: 3  GAEEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
      G +++V++  + ++G + + G+K+ +  IL  LS      +DN+ N +DV  L  L
Sbjct: 29  GMDKLVVEGGRRRLAGEIVVSGAKNAALPILCAGLLSAEPVELDNVPLKDVRTTLKVLNQ 88

Query: 63  LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
      +G+  E D      GC  +      V  +      +++++ A++  G
Sbjct: 89  MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
      G A  L G  +  RP+  + GL+ +GA++  G  +  R      L G ++ ++
Sbjct: 135 GEAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LKGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      I+      LLMAA LA G+  +I+      P V      L+  G K      DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVSDLAHLLVAMGAKIT-GIGTDRLV 243

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Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
 I+G ++ +++ + D A FL A GG V + G
 Sbjct: 244 IQGVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVLLTG 282

>ref|YP_104237.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei ATCC 23344]
 ref|ZP_00440372.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei GB8 horse 4]
 ref|YP_994520.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei SAVPl]
 ref|ZP_02267386.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei PRL-20]
 ref|ZP_04881318.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei ATCC 10399]
 ref|ZP_04907675.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei FMH]
 ref|ZP_04913004.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei JHU]
 ref|ZP_04973552.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei 2002721280]
 sp|Q62GD7.1|MURA_BURMA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 gb|AAU48284.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei ATCC 23344]
 gb|ABM51113.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei SAVPl]
 gb|EDK54281.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei FMH]
 gb|EDK59261.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei JHU]
 gb|EDK84427.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei 2002721280]
 gb|EDP85672.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei ATCC 10399]
 gb|EEP85993.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei GB8 horse 4]
 gb|EES44787.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia mallei PRL-20]
 Length = 449

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKLSNRILLALSEGTTVDNLLNSEDVHYMLGALRT 62
 G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
 Sbjct: 29 GTDKLAIEGRRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPDLKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
 +G+ E D A R V+ PV A E+ ++++ A++ G
 Sbjct: 89 MGMREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGLPGGKVKLS 175
 G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
 Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAEIHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
 I+ LLMAA LA G+ +I+ P V L+ G K + DR
 Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
 I+G ++ +A + D A FL A GG VT+ G
 Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|ZP_02483554.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia pseudomallei 7894]
 ref|ZP_02507849.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia pseudomallei BCC215]

Length = 449

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPDLKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ +++++ A++ G
Sbjct: 89 MGMREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|ZP_02149399.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Phaeobacter
gallaeciensis 2.10]
gb|EDQ09111.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Phaeobacter
gallaeciensis 2.10]
Length = 423

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 92/415 (22%), Positives = 164/415 (39%), Gaps = 53/415 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + + G+K+ ++ LSE + N D+ M L++LG V + +
Sbjct: 12 LKGQIPIAGAKNACLTLMPTMLSEEPLTLTNAPRLSDIRMTTLLQSLGAEVSTLQDGQ 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 128
+ ++ + I +R + A++ G G+A L G
Sbjct: 72 VLAM-----SSHINNHTADYDI-VRKMRASILVLGPMLARDGHAVVSLPGGCA 119

Query: 129 MRERPIGDLVVGLKQLGADVDC--FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + L+ LG +D ++ P +GGL GG + +S
Sbjct: 120 IGARPVDLHLKALEALGAQLDLKDGYPVHAKAP-----LGGLKGGVIDFP-LVSVGATEN 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LMAA LA G II+ P + + + + G + E + I+G +
Sbjct: 173 ALMAATLAKGTT--IINNAAREPEIVDLAQCLRKMQAIE-GEGTSTITIQGVDRHLGA 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V +Y LA AI GG V + G + ++ F LE G ++T E S+
Sbjct: 229 THPVVTDRIELGTYMLA-PAICGGEVELLGGKRSLEA---FCNKLEAAGVEITENENSL 284

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKET 361
TV G +KA+DV P D+ + + A+G + + + ++ E
Sbjct: 285 TVR-----RGDNRVKAVDVVTEPFPGFPTDLQAQMMALMCTAEGTSVLEE---KIFEN 334

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
M A EL ++GA ++ + +T E L + D R +++ LA A
Sbjct: 335 RFMHA--PELIRMGAQIDVQGGHATVTGVEGLKGAPV-MATDLRASVSLILAGLA 386

>ref|YP_003751221.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum PSI07]
emb|CBJ49912.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum PSI07]
Length = 451

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.

Identities = 64/264 (24%), Positives = 116/264 (43%), Gaps = 21/264 (7%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSESDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ + N+ N +DV ML LR +G+ A
Sbjct: 42 LSGEIRVSGAKNAALPIMCAALLTPEPLTLHNVPNLQDVRTMLKLLRQMGV---AGTQNG 98

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMRE 131
V + E + + V+ MR+ + + A G+A L G +
Sbjct: 99 HDVTLDAAADIHTPEASYDLVK-----TMRASILVLGPLLARFGHARVSLPGGCGIGA 150

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLMAA
Sbjct: 151 RPVDQHIKGLQQMGAEIVIEHGY-IEAKLDAGAKRLRGARI-VTDMVTVTGTENLLMAAV 208

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G+ +++ P V L+ + G + + + DR ++G + K ++ +
Sbjct: 209 LADGET---VLENAAREPEVTDLANLLVKMGARIDGIGT-DRLVVQGV EALKGAHTVI- 263

Query: 252 GDASSASYFLAGAAITGGTVTVEG 275
D A FL A GG VT+ G
Sbjct: 264 ADRIEAGTFLCAVAAAGGDVTLRG 287

>ref|ZP_05920903.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pasteurella
dagmatis ATCC 43325]
gb|EEX49717.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pasteurella
dagmatis ATCC 43325]
Length = 424

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 95/416 (22%), Positives = 163/416 (39%), Gaps = 41/416 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSESDVHYMLGALRTLGLSVEADKAAK 74
+ GTV + G+K+ + IL L+E + N+ +D+ LR LG+SVE D
Sbjct: 12 LKGTVNISGAKNAALPILFATILAEKPVKLTNPVELKDIDTTFKILRKLGVSVVERDAEGA 71

Query: 75 RAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VHIDASKIDHFIAPYELVKTMRASIWALAPLVARFNQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL++LGA + G V+ L G ++ + IS +++MAA L
Sbjct: 123 PVDLHISGLERLGARIALEDGY---VKAYVDHRLVGTRIVVE-KISVGATLSIMMAATL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G IE P + T + + G K + + D ++G +++ V
Sbjct: 178 AKGTTTIE---NAAREPEITDTAIFLNKLGAKITGAGT-DTIIVEGVDHLGGCEHSIVP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPR 312
D FL AAI+GG + + +L + + L GA+V E ++T+
Sbjct: 233 DRIETGTFLVAAAIISGGRIQCKNTKADTLDAVI---DKLREAGA QVDVAENTITLDM LGN 289

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR 368
P +A+++ P D+ ++ + A+G + I + R + I
Sbjct: 290 RP-----RAVNIRTAPYPGFPTDMQAQFTLLNMVANGTSIITETIF-----ENRFMHI- 337

Query: 369 TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
EL ++G E + I E L+ + D R +++ LA C TI D
Sbjct: 338 PELIRMGGAIEGNTAICHGVEHLSGAEV-MATDLRASISLVLAGCIATGETIVD 392

>ref|ZP_04612843.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia rohdei
ATCC 43380]
gb|EEQ02633.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia rohdei
ATCC 43380]
Length = 421

Score = 45.8 bits (107), Expect = 0.013, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 172/431 (39%), Gaps = 59/431 (13%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSESDVHYMLGALRTLGLSVE 68

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      +Q      +SG V + G+K+ + IL A L+E      + N+      +D+      + L LG +E
Sbjct: 6      VQGRTRLSGEVTISGAKNAALPILFAALLAEDPVELQNVPKLKDIDTTIKLLNQLGKTIE 65

Query: 69      ADKAAKRAVVVGCCKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
      D A +V V G      V F      + +++ A++ A G      G
Sbjct: 66      RD--ASGSVFDASG-----VDEFCAPYDL-VKTMRASIWALGPLVARFGKGQVS 112

Query: 123      LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      L G      + RP+      + GL+QLGA++      G      V+ + G L      + + +S
Sbjct: 113      LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY----VKASVNGRLKAAHIVMD-KVSVGA 167

Query: 183      LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
      ++ AA LA G      +I+      P + T      + G K      + S DR I+
Sbjct: 168      TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKITGAGS-DRITIEGVARL 223

Query: 238      GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      GG Y+      V D      FL AA++GG V      +L D A++ E GA
Sbjct: 224      GGGVYR-----VLPDRIETGTFLVAAAVSGGKVVCRTQTRPDTL--DAVLAKLRE-AGAD 274

Query: 298      VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
      + E +++      + P      KA+ +      P      D+      +++ L A+G I +
Sbjct: 275      IEIGEDWISLDMHGQRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGTGVITET 328

Query: 354      ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
      + E M      EL ++GA E      + I      E+L+      + D R + + LA
Sbjct: 329      ----IFENRFMHV--PELIRMGAAHEIESNTVICYGVQELSGAQV-MATDLRASASLVLA 381

Query: 414      ACAEVPVTIRD 424
      C      VTI D
Sbjct: 382      GCIADGVITVD 392

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>ref|YP_001244411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
      petrophila RKU-1]
ref|YP_001738874.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga sp.
      RQ2]
sp|A5IKW2.1|MURA_THEP1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
sp|B1LA43.1|MURA_THESQ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ABQ46835.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga
      petrophila RKU-1]
gb|ACB09191.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermotoga sp.
      RQ2]
      Length = 421

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Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 102/447 (22%), Positives = 173/447 (38%), Gaps = 48/447 (10%)

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Query: 6      EIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      ++V+Q      + G V++ GSK+ + I+ A L +      ++ N+      +DV M+ LR++G
Sbjct: 3      KLVVQGGTVLEGEVEISGSKNAALPIMAAAILCDEEIIILKNVPRLQDVFVIMIDILRSIGF 62

Query: 66      SVEADK---AAKRAVVVGCCKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
      VE D+      KR      D +EV L      A ++      + G A
Sbjct: 63      RVEFDENELKIKRE-----NDISQEVPELVVRKMRASFNLGPIAVRTGRAKVA 111

Query: 123      LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      L G      + RP+      + GLK++G +      G      V      +V ++      S
Sbjct: 112      LPGGCSIGVRPVDHLEGLKKMGFSIKVEHGF-----VEATFERRTDQVTITLPPFSVG 165

Query: 183      LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
      + LM      L      + +I+      P +      + R G + E + + R I+G +K
Sbjct: 166      ATEHLMTTAALLEGTRV-VIENAAMEPEIVDLQNFINRMGGRIEGAGT-SRIVIEGVEKM 223

Query: 243      KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
      + + + +      + +Y +A AA + G      V+      L      F E LE G K

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Sbjct: 224 QGVEYSIIPDRIEAGTYLVAIAA-SRKGGLVKNVNPDL---TNFFEKLEETGVK----- 274

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAI-RDVASWR 357
+ V G E R+ +A+DV N P D+ + A G + I +V R

Sbjct: 275 --LKVFGNEVEIEMRERPEAVDVTTPYPGFPDLPQMMAYLSIASGVSVITENVFKTR 332

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
+ EL ++GA +E + I+ EKL+ ++ D R A +A

Sbjct: 333 FLHVD-----ELKRMGADIEVSGNVAIVKGVEKLSGAPVEG-TDLRATAALLIAGIIA 384

Query: 418 VPVTIRDPGCTRKTTFPDYFDVLSTFVK 444
VT + F Y DV+ F K

Sbjct: 385 DGVT--EISNVEHIFRGYEDVIDKFSK 409

>ref|YP_001179992.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor saccharolyticus DSM 8903]
gb|ABP66801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor saccharolyticus DSM 8903]
Length = 419

Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 93/402 (23%), Positives = 161/402 (40%), Gaps = 42/402 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++++ + G V + G+K+ + ++ A + EG ++++NL EDV M L LG

Sbjct: 6 EKLIIEGGNPLFGEVPIGAKNAAVAVIPAALMVEGESIIENLPLIEDVVFAMDDILLRLG 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ +++ A L A+ G A +

Sbjct: 66 AKIEYDNHSLKIDASNLSYIAPYESVRKIR-----ASYYLIGALLTRFGKAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RPI + G + LGADV G L G K+ L +S

Sbjct: 118 GGCNFGARPIDQHIKGFALGADVKIENGMKAYAE-----ELVGTKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA A G II+ P+V + G K + + + D I+G ++

Sbjct: 172 NLMLAAVKAKGTT--IIENAAKEPHVVDVANFLNAMGAKIKGAGT-DVIRIEGVKELHP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ A + + +Y +A A T G V V+ L+ A++LE MGA+V E S

Sbjct: 228 TRYAIIPDQIEAGTYMIAACA-TKGHVRVKSIIPKHLESLT--AKLLE-MGAEVNVYEDS 283

Query: 305 VTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V R L+A + P D+ + V+ G + + + W

Sbjct: 284 IEVRCKER-----LRASSIKTMPYPGFPDLPQMTVLLSLCSGTSVVTE-GVW---- 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
E EL K+GA+++ I+ E L V+A+D

Sbjct: 332 -ENRYQYVDELKMGANIKVEGRVAIVEGVESLQGAEVSAVD 372

>ref|ZP_07821337.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
harei ACS-146-V-Sch2b]
gb|EFR33643.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
harei ACS-146-V-Sch2b]
Length = 415

Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 76/308 (24%), Positives = 132/308 (42%), Gaps = 28/308 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I+++ + G V++ G+K+ + IL L V++++ +DV + LR LG

Sbjct: 2 DKILVKSGLKGVKVRISGAKNAALPILAAATILGTEEIVLEDVPELKDVEIITEVLRGLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
L +E D + V+ G + E+ + + + M L A + A + L

Sbjct: 62 LKIEKD--GNKLVIDPSG--LNSYETDYELMSKMRASFLVMGPPLAKLNKAYNS----LP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLG---TDCPPVRVNGIGGLPGGKVKLSGSISSQ 181

```

      G   + RPI   + G K LGA+++   G   +C           L G ++ L   S
Sbjct: 114 GGCNIGSRPIDLHLKGFKALGANIEMTHGEIKAEDK-----LVGTRIYLDFFP-SVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      ++ AA LA G+   I++   P +   + + G K   + +   IKG +K
Sbjct: 165 ATENIMTAAVLAEGET---IMENCAMEPEIVDLANFLNKMGAQVMGAGT-STIKIKGVEK 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVWTW 301
      +   + + D A F+ AAITGG +T+E   T+ L+ +   LE GAKV
Sbjct: 221 LRGCTHQIIP-DRIEAGTFMVAAAITGGDITIENIITSHLKPVIA---KLEETGAKVIEN 276

Query: 302 ETSVTVTG 309
      +V V G
Sbjct: 277 GDTVVRVVG 284

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>ref|ZP_01742541.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Rhodobacterales
      bacterium HTCC2150]
gb|EBA03123.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Rhodobacterales
      bacterium HTCC2150]
Length = 422

```

Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 97/422 (22%), Positives = 171/422 (40%), Gaps = 48/422 (11%)

```

Query: 5   EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      + I+++   E++G + + G+K+   ++   LSE   + N   D+ M   L++LG
Sbjct: 2   DSILVKGGGELNGEIPAGAKNACLTLMPTLLSEEPLTLTNAPRLSDIKTMTALLQSLG 61

Query: 65   LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
      V + + K   V   + + K + ++   +R + A++ G   G+
Sbjct: 62   AEVTSLQGGK----VLAMSSHDINNKHADYEI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      A L G + RP+   + GL+ +GA++D G   V   GGL GG V   +
Sbjct: 110 AEVSLPGGCAIGARPVDLHLKGLEAMGAELDRLDGY----VHAKATGGLKGVVDFP-FV 164

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
      S   +LMAA LA G   +I+   P +   + R G A   ++G
Sbjct: 165 SVGATENILMAATLAKGTT---VINNAAREPEIVDLAECLIRMGA-AISGHGTSTITVEG 220

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      +   + V   +Y L AITGG++ + G G SL   FAE L G ++
Sbjct: 221 KDRNLNGATHPVVTDRIELGTYYMLV-PAITGGSIELIG-GRMSLV--TAFAEKLAETGVEI 276

Query: 299 TWTETSVTVTGPPREPFRGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVA 354
      T+ + V+   GR + A+DV   P   D+ + + A+G + + +
Sbjct: 277 EETQRGLRVS----RKNGR--VSAVDVKTEPFPFGFPTDLQAQMMALLCTANGTSVLEET- 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIADTYDDHRMAMAFSLAA 414
      + E M A EL ++GA ++   +T E+L +   D R +++ LA
Sbjct: 330 ---IFENRFMHA--PELIRMGAIQIDVQGGGLAKVTGVERLKGAPV-MATDLRASVSLILAG 383

Query: 415 CA 416
      A
Sbjct: 384 LA 385

```

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>ref|ZP_05942724.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
      orientalis CIP 102891]
gb|EEX95250.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
      orientalis CIP 102891]
Length = 419

```

Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 100/418 (23%), Positives = 164/418 (39%), Gaps = 51/418 (12%)

```

Query: 17   GTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
      G V + G+K+ + IL + L+E   V N+   D+ + L LG VE +
Sbjct: 15   GEVTISGAKNAALPILFASILAEEPVEVTNVPRLRDIDTTMELLERLGAKVERN----- 68

```


Query: 77 VVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMR 130
G V+ + + + + + + + + A++ A G G L G +
Sbjct: 69 -----GSVHVPSS--INEYCAPYDL-VKTMRAIWLGLPLVARFGQGQVSLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+QLGA + G V+ N G L G + + +S ++ AA
Sbjct: 120 ARPVDLHIHGLEQLGATITLEDGY----VKANVDGRLKGAHIVMD-KVSVGATITIMCAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G ++D P + T + + G K + + D I+G ++ +A V
Sbjct: 175 TLAEGTT---VLDNSAREPEIVDTADFLNKLGAHISGAGT-DTITIEGVERLSGGTHAVV 230

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AA++GG VT C T LE GAKV E +++
Sbjct: 231 -ADRIETGTFLVAAVSGGKVT---CRNTKAHLLEAVLAKLEEAGAKVETGEDWISLDMT 286

Query: 311 PREPFGKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
RE LKA+ V P D+ ++ L A G I + + E M
Sbjct: 287 GRE-----LKAVTVRTAPHPGFPTDMAQFTLLNLMAKGGGVITET---IFENRFMHV 336

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTTIRD 424
EL ++GA E + I ++L+ + D R + + +A C TI D
Sbjct: 337 --PELMRMGAKEIEGNTVICGDVDELGAQV-MATDLRASASLVIAGCIAQGETIVD 391

>ref|YP_001067956.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106a]
ref|ZP_02457541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 9]
ref|ZP_02473084.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei B7210]
ref|ZP_02499890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 112]
ref|ZP_03793824.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pakistan 9]
ref|YP_002898519.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
ref|ZP_04814340.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
ref|ZP_04896885.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
ref|ZP_04968095.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|ABN91295.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106a]
gb|EDO87804.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|EDO93723.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
gb|EEH25789.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pakistan 9]
gb|ACQ95698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
gb|EES24965.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
Length = 449

Score = 45.8 bits (107), Expect = 0.014, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEIEVLQPIKEISGTVKLPKSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGRRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPDLKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ + + + + A++ G
Sbjct: 89 MGMREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAEPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|NP_875765.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
sp|Q7VAT0.1|MURAL_PROMA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAQ00418.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
Length = 457

Score = 45.8 bits (107), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 94/409 (22%), Positives = 170/409 (41%), Gaps = 40/409 (9%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++SG +K+ G+K+ + ++ A L+E ++N+ N D+ M L +G +V ++
Sbjct: 22 NDLGSGQIKISGAKNSALVLMAGALLTEENVHLNNVPLNTDIDVMTDLLLHIGANV--NRN 79

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ ++ +K E+ L +A A + A G L G R+ R
Sbjct: 80 TNQVLLQANQSDL----SKNELPYELVHALRASFCIGPLLARLGEVKTPLPGGCRIGCR 135

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI + + GLK LGA V T + VN L G K+K + S +LMAA L
Sbjct: 136 PIDEHIQGLKALGASVRIDNDTVIAKI-VNSRKRLIGTKIKFNCK-SVGATETVLMAATL 193

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
A G+ I++ P ++ ++ + G + + + + I+G K + +
Sbjct: 194 AEGET---ILENAAQEPEIQDLANMLNKMGANVQGAGT-SQIKIEGVSHLKGCVHDVIP- 248

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA---KVTWTETSVTVTG 309
D A FL +AIT +T+ + E +GA K+ S+ G
Sbjct: 249 DRIEAGTFLIASAITRCPLTISPV-----IPEHIGAVIKKLKQCGCSIEKAG 295

Query: 310 PPREPFGGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
+ F + + ++D++ + P D+ + A G + I + R RM
Sbjct: 296 KGLKIFPGKEISSVDMSTSPFPGFPTDLQAPFMALMSIATGTSKIETVFER-----RMQ 350

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA 414
+ EL ++GA + + I+ +L T+I T D R + A LA+
Sbjct: 351 HV-GELQRMGAQISLSENTAFISGVNELIATSI-TGGDLRSSAAMVLAS 397

>ref|ZP_02640560.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens CPE str. F4969]
gb|EDT25811.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens CPE str. F4969]
Length = 417

Score = 45.8 bits (107), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 81/303 (26%), Positives = 126/303 (41%), Gaps = 36/303 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVE--- 68
K + G++++ G+K+ + IL A L S+G ++DN+ + DVH + +R+LG +VE
Sbjct: 10 KALKGSIEINGAKNAAVAILPAAILASKGECIIDNVDPDIADVHCLERIIRSLGCNVEKLD 69

Query: 69 ----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
A + V CG D ++ + + R A V GG V
Sbjct: 70 NNTLKINAEIKTVEACG----NDVRKMRASYFFIGALLARFKEAKVELPGGCPIGV-- 122

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RPI + G + LGA V G VN + G +S

Sbjct: 123 -----RPIDQHIKGFELGAKVLIEHGA-----VNIMAEKLIGTNIFDVVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA LA G +++ P+V + G + + + D IKG ++ K

Sbjct: 170 NLMIAATLAEGTT--VLENAAREPHVVDVANFLNMGANVKGAGT-DVIRIKGVKELKG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N V D A F+ AA T G VT++ L+ A++LE MGAKV + S

Sbjct: 226 C-NYSVVPDQIEAGTFMIAAAATRGDVTIQNVIPKHLES--ISAKLLE-MGAKVEEGDDS 281

Query: 305 VTV 307

V V

Sbjct: 282 VRV 284

>ref|YP_109734.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei K96243]
ref|YP_335059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1710b]
ref|ZP_02449352.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 91]
ref|ZP_04952307.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1710a]
sp|Q63Q84.1|MURA_BURPS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|Q3JMZ4.1|MURA_BURP1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAH37151.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei K96243]
gb|ABA48016.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1710b]
gb|EET09326.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1710a]
Length = 449

Score = 45.8 bits (107), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRT 62

G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L

Sbjct: 29 GTDKLAIEGRRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116

+G+ E D A R V+ PV A E+ +++++ A++ G

Sbjct: 89 MGMREETDGA--RVVLDASRVDPNP--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGLPGGKVKLS 175

G A L G + RP+ + GL+ +GA++ G + R L G ++ ++

Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235

I+ LLMAA LA G+ +I+ P V L+ G K + DR

Sbjct: 188 DMITVTGTENLLMAATLADGET--VIENAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVEG 275

I+G ++ +A + D A FL A GG VT+ G

Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>emb|CAM89150.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
Length = 188

Score = 45.4 bits (106), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCII---TPPEKL 393

LA+ A FA+G T + + RVKE++R+ A+ L G EG + + L

Sbjct: 88 LAIAASFAEGETVMDGLDELRVKESDRLLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGL 147

Query: 394 NVTADITYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFF 433
+ T+ DHR+AM+F + A E PVT+ D +FP

Sbjct: 148 GGGTVATHLDHRIAMSFLVMGLASEKPVTVDDSTMIATSFP 188

>ref|YP_003382854.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Kribbella flavida
DSM 17836]
gb|ADB34055.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Kribbella flavida
DSM 17836]
Length = 428

Score = 45.4 bits (106), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 97/391 (24%), Positives = 158/391 (40%), Gaps = 49/391 (12%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ +++ A L+EGTT + + DV +M L TLG SV+ D A
Sbjct: 12 LDGSVEVAGAKNSVLKLMMAALLAEGTTTLRQVPGILDVTFMAQLLDTLGCSVKVDGEAG 71

Query: 75 RAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
A + P E + + +L +R L A+++ G G A L G
Sbjct: 72 TATIA-----VPGEIGHQC DYEL-----VRKLRASISVLGPLLGRGCGQAEVALPGGD 118

Query: 128 RMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ R + V GL+ +GA V F+ + P GL G +V L S
Sbjct: 119 NIGSRGLNMHVAGLEAMGAKVHIEHGFVMAEAPQ-----GLHGAEVWLDFF-SVGATE 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G +I+ P ++ ++ G + E + S R + G +
Sbjct: 171 TIMMAAVLAKGTT--VIENAREPEIQDIAAMLVAMGAQIEGAGS-PRIEVTGVEGLLK 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
P + V D + + AAIT G VT+ L+ + + L GA +T +
Sbjct: 227 PVDHTVVPDRIVSGSWAFAAAITKGDVTITNGHAEHLELPL---DKLSKAGADITVLDQG 283

Query: 305 VTVTGPPEPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKET-ER 363
V R K++DV P L F A+ D A+ + E
Sbjct: 284 FRVRMAERP-----KSVDVVTLPYPGFPTDLQA---FVIAMNAVSDGAAMVTENLFEG 333

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLN 394
ELT+LGA V+ + +I +L+
Sbjct: 334 RFTFAQELTRLGAHVQTDGHHAVIRGVPRLS 364

>ref|ZP_04809089.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Helicobacter
pullorum MIT 98-5489]
gb|EEQ63097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Helicobacter
pullorum MIT 98-5489]
Length = 422

Score = 45.4 bits (106), Expect = 0.015, Method: Compositional matrix adjust.
Identities = 91/418 (21%), Positives = 173/418 (41%), Gaps = 61/418 (14%)

Query: 14 EISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G++ + G+K+ + ++ L+ L++ ++NL D+ L L LG ++
Sbjct: 11 KLQGSIGISGAKNSALPLIALSTLAKNEITLENLPEVVDIKTFLSLLSMLGCGIQEIDNH 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
+ ++ + + K + +R + A++ G G L G
Sbjct: 71 TKTIITST-----LNNTKANYDI-----VRKMRASILVLGPLLGRFGYCEVSLPGGC 117

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG--LPGGKVKLSGSISSQYLSA 185
+ RP+ + LK++GA + G + NG+ G + K+ ++G+
Sbjct: 118 AIGARPVDLHIKALKKMGAKIQIQGGYIIAEAK-NGLKGNVINFDKITVTGT-----EN 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG--QKYK 243
+LMAA +A G +I K P V +++ G+ + S D I G Q
Sbjct: 171 ILMAAAMAKGKTKIINAAKE---PEVVQLCEVLKESGIDIQIGIGS-DEIEIYGTDMQPLI 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303

PK V D A +L AIT +T+ T L+ + LE +G K+ +++
Sbjct: 227 FPKPICVIPDRIEAGTYLCAGAITNSQITLNNINPTHLEAII---SKLEEIGFKLQFSQD 283

Query: 304 SVTVTGPPREPFGKRLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVK 359
S+T+ P + P +A +++ + P D+ +A +G + I++ R+
Sbjct: 284 SITIIY-PTQNP-----QAFELSTTEYPGFPTDMQAQFMALATQCEGSSIIQE----RLF 332

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTADITYDDHRMAMAFSLAA 414
E M +EL ++GA++ + I KL +V A D R + A LAA
Sbjct: 333 ENRFMHV--SELQRMGANITLKGNTATIQGKSKLYGADVMTDL----RASSALVLAA 384

>ref|ZP_03456331.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
ref|ZP_04887012.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
gb|EDU07996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1655]
gb|EEC32315.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]
Length = 449

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEIIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVDPDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ +++++ A++ G
Sbjct: 89 MGMREETDGA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAGGDVTLTG 282

>ref|NP_301844.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
leprae TN]
ref|YP_002503474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
leprae Br4923]
sp|P45821.1|MURA_MYCLE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAA63098.1| murZ [Mycobacterium leprae]
emb|CAC31531.1| UDP-N-acetylglucosamine-1-carboxyvinyltransferase [Mycobacterium
leprae]
emb|CAR71245.1| UDP-N-acetylglucosamine-1-carboxyvinyltransferase [Mycobacterium
leprae Br4923]
Length = 418

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 98/373 (26%), Positives = 144/373 (38%), Gaps = 46/373 (12%)

Query: 4 AEEIIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 63
AE V+ +SG V + G+K+ +++ L+EGT+ + N + DV M LR L
Sbjct: 2 AERFVVTGGNRLSGEVTVGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVLRLG 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE + G + D + F A+R A+V G
Sbjct: 62 GATVE-----LYGDVARITSPDEPKYDADF-----AAVRQFRASVCVLGVLGRCK 107

Query: 118 NATYVLVDGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C V L G +++L
Sbjct: 108 QARVALPGGDAIGSRPLDMHQAGLRQLGA--RCNIEHGC---VVASAETLRGAELQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA +A G + I P V ++ + G + E S I
Sbjct: 163 -SVGATENILMAAVVAEG---VTTIHNAAREPDVVDLCTMLNQMGAEVGVGS-PTMTIT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
G + P V GD A+ + AA+T G + V G LQ L GA
Sbjct: 218 GVPRLY-PTEHRVIGDRIVAATWGIAAAMTRGDIATGVDPAPHLQ---LVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVAL----FADGPTAI-RD 352
VT T+ S V R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQTDSDSFRVAQYERP-----KAVNVATLPFGFPTDLQPMIALTSIADGTSMITEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+
Sbjct: 327 VFEARFRFVEEMI 339

>ref|ZP_02404725.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei DM98]
Length = 449

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 121/280 (43%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D A R V+ PV A E+ ++++ A++ G
Sbjct: 89 MGMREETFDA--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLVDGVPRMRERPIGDLVVGKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAEIHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>sp|P33986.1|MURA_ACIGB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAA21618.1| UDP-N-acetylglucosamine 1-carboxyvinyl transferase [Acinetobacter
calcoaceticus]
Length = 419

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 105/425 (24%), Positives = 178/425 (41%), Gaps = 40/425 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ V+Q ++ G V++ G+K+ + +L L++ + N+ + +DV ++ + LG
Sbjct: 2 DKFVIQGGVKLEGEVRISGAKNAALPLLAAMILADTPITLKNVPLDKDVRTLVKLIGGLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+++ + A +F P E K L + R +A V+ GG A
Sbjct: 62 ITMSYEGETVIANTSTLDNQFAPYELVKTMRASILVLGPLLARYGSAKVSLPGGCA---- 117

Query: 124 DGVPRMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RP+ + L+ LGA ++ G V G L GG+V + ++

Sbjct: 118 -----IGSRPVDQHLKALEALGAQIEVEAGY----VHAKVDGRLKGGEV-IFDMVTVGGT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+L AA LA G + I P + ++ + G K E D+ D + G +

Sbjct: 168 ENILTAAVLAEG--VTIRNAAREPEITDLALMLIKMGAKIEGLDT-DTLVVTVGVESLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTE 302
+ + V + SY LA AAITGG V L+ + KF E MGA+VT E

Sbjct: 224 GCEYSVADRIETGSY-LAAAAITGGKVKTHTDPNLLSVLDKFEE----MGAEVTARGE 278

Query: 303 TSVTVTGPPREPFGKHLKAIDVNMNKMMPDVA--MTLAVVALFADGPTAIRDVASWRVKE 360
+ + + P KA+ P+ M ++A+ A G R A+

Sbjct: 279 DWIELDMLGKRP-----KAVSFRTLPHPEFTMDMQAQIMAVNAIG---RGFATISETI 328

Query: 361 TERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
E EL ++GA+++ EG D ++T EKL+ + D R + + LAA A

Sbjct: 329 FENRFMHVPELARMGANIQVEGND-AVVTGVEKLSAAPV-MATDLRASFSVLAAALAAEG 386

Query: 420 VTIRD 424
TI D

Sbjct: 387 ETIID 391

>ref|YP_353708.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides 2.4.1]
sp|Q3J077.1|MURA_RHOS4 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABA79807.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
sphaeroides 2.4.1]
Length = 422

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 99/425 (23%), Positives = 170/425 (40%), Gaps = 53/425 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEVDHYMLGALRTL 64
+ I+++ E+ G + + G+K+ ++ LS+ + N D+ M L++LG

Sbjct: 2 DSILVKNGELRGQIPIAGAKNACLALMPATLLSDEPLTLTNAPRLSDIRTMTQLLQSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V + + + + + D + + + +R + A++ G G+

Sbjct: 62 AEVASLQGGQVLAL----SSHALTDHRADYDI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDC---FLGTDCCPVRVNGIGGLPGGKVKLS 175
A L G + RP+ + L+ +GA++D ++ P GGL G +V

Sbjct: 110 AVVSLPGGCAIGARPVDLHLKALEAMGAELDLRDGYIHAKAPA-----GGLKGARVVFP 163

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
+S LMAA LA G +++ P + R + R G + E S

Sbjct: 164 -LVSVGATENALMAATLAKGTT--VLENAAREPEIVDLARCLRRMGAQIEGEGS-SIMT 218

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + + V +Y LA AI GG V + G G L G F E L+ G

Sbjct: 219 IQGVDRLGGAHPVVTDRIELGTYMLA-PAICGGEVELLG-GRIELVG--AFCEKLDAAG 274

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIR 351
V TE + V GR +KA+DV P D+ + + A+G + +

Sbjct: 275 ISVEETERGLRVA---RRNGR--VKAVDVMTPEFPFGFPTDLQAQMMALLCTAEGTSVLE 328

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFS 411
+ R+ E M A EL ++GA +E +T EKL + D R +++

Sbjct: 329 E----RIFENRFMHA--PELIRMGARIEVHGATATVTGVEKLRGAPV-MATDLRASVSLI 381

Query: 412 LAACA 416
LA A

Sbjct: 382 LAGLA 386

>ref|ZP_02954248.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens D str. JGS1721]

gb|EDT70748.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
perfringens D str. JGS1721]
Length = 417

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 80/303 (26%), Positives = 126/303 (41%), Gaps = 36/303 (11%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVE--- 68
K + G++++ G+K+ + IL A L S+G ++DN+ + DVH + +R+LG +VE
Sbjct: 10 KALKGSIENGAKNAAVAILPAAILASKGECIIDNVPDIADVHCLERIIRSLGCNVEKLD 69

Query: 69 ----ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
A + V CG D ++ + + R A V GG V
Sbjct: 70 NNTLKINAEEIKTVEACG-----NDVRKMRASYFFIGALLARFKEAKVELPGGCPIGV-- 122

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
RPI + G + LGA V G VN + G +S
Sbjct: 123 -----RPIDQHIKGFALGAKVSIIEHGA-----VNIMAEKLIGTNIFFDVVSVGATI 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L++AA LA G +++ P+V + G + + + D IKG ++ K
Sbjct: 170 NLMIAATLAEGTT---VLENAAREPHVVDVANFLNMGANVKGAGT-DVIRIKGVKELKG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N V D A F+ AA T G VT++ L+ A++LE +GAKV + S
Sbjct: 226 C-NYSVVPDQIEAGTFMIAAAATRGDVTIQNVIPKHLES--ISAKLE-IGAKVEEGDSDS 281

Query: 305 VTV 307
V V
Sbjct: 282 VRV 284

>ref|NP_245117.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pasteurella
multocida subsp. multocida str. Pm70]
sp|P57821.1|MURA_PASMU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAK02264.1| MurZ [Pasteurella multocida subsp. multocida str. Pm70]
Length = 425

Score = 45.4 bits (106), Expect = 0.016, Method: Compositional matrix adjust.
Identities = 95/428 (22%), Positives = 167/428 (39%), Gaps = 65/428 (15%)

Query: 15 ISGTVKLPKSGKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V + G+K+ + IL A L++ + N+ +D+ L LR LG+ VE D
Sbjct: 12 LRGSVNISGAKNAALPILFAAILAQEPVKLTNPVELKDIETTLKILRKLGVVVERDAEGA 71

Query: 75 RAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VHLDAKIDHVFAPYELVKTMRASIWALAPLVARFHRGQVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVGLKQLGADV-----DCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
P+ + GL++LGA + C +GT + KV + ++S
Sbjct: 123 PVDLHISGLERLGASIILEDGYVKAYVDHCLVGTR-----IVMEKVSVGATLS- 170

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G II+ P + T + + G K + + D ++G +
Sbjct: 171 -----IMMAATLAKGKT---IIENAAREPEITDTALFLNKMGAIVGAGT-DTITVEGVE 221

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ +++ V D FL AAI+GG + + +L + + L GA+V
Sbjct: 222 RLGCGCEHSIVP-DRIETGTFLVAAISGGRIECKNTKADTLDAVI---DKLREAGAQVDV 277

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPATAIRDVASW 356
TE S+T+ P +A+++ P D+ ++ + A G + I +
Sbjct: 278 TENSITLDMLGNRP-----RAVNIRTAPYPGFPTMQAQFTLLNMVACGTSIITETIF- 330

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
R + I EL ++G E + I + L+ + D R +++ LA C
Sbjct: 331 ----ENRFMHI-PELIRMGGKAEIEGNTAICHGVDHLSGAEV-MATDLRASISLVLAGCI 384

Query: 417 EVPVTIRD 424
TI D
Sbjct: 385 ATGETIVD 392

>ref|YP_003872749.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate transferase) [Paenibacillus polymyxa E681]
gb|ADM72211.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate transferase) [Paenibacillus polymyxa E681]
Length = 451

Score = 45.4 bits (106), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 93/349 (26%), Positives = 145/349 (41%), Gaps = 45/349 (12%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALS----EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
++G+VK+ G+K N +L + A S EG +V+ + +DV + L +LG V
Sbjct: 12 LTGSVKVSGAK---NSVLPIIAASLLGEEGESVIIIDAPPLDDVMTINKVLESLGAGVTYQ 68

Query: 71 KAAKRA---VVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ C + P E ++ FL + R ++ GG A
Sbjct: 69 DEVIRVDARKIISC--EAPYEWVRKMRASFLVMGPPLLTRLGRTRISLPGGCA----- 118

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + G + LGA++ LG + NG L G KV L + S ++
Sbjct: 119 -IGTRPIDQHLLKGFEALGAEIS--LGQGFIEAKSNG--RLRGAKVYLDVA-SVGATENIM 172

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G IE K P + + G K + + I+G +K K+
Sbjct: 173 MAATLAEGVTTIENAAKE---PEIVDLANFLNGMGAKVRGAGTG-VIRIEGVEKLHGVBKH 228

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ + +Y +A AAITGG V VEG + L G V +E MG + E + V
Sbjct: 229 TVIPDRVEAGTYMVA-AAITGNNVYVEGAISDHL-GPV--ISKMEEMGVTIQPDENGIRV 284

Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD 352
K LKA+DV P D+ + + L A+G + I +
Sbjct: 285 -----IADKPLKAVDVKTLPPPGFPTDMQSQMMLQLAAEGTSIITE 326

>gb|ABC00782.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 30

Score = 45.4 bits (106), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 22/27 (81%), Positives = 24/27 (88%)

Query: 88 EDAKEEVQLFLGNAGIAMRSLTAAVTA 114
+DAKEEV+LFLGNAG AMR LTAAV A
Sbjct: 4 KDAKEEVKLFLGNAGTAMRPLTAAVVA 30

>ref|YP_002262034.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aliivibrio salmonicida LF11238]
sp|B6EMB5.1|MURA_ALISL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAQ78196.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aliivibrio salmonicida LF11238]
Length = 422

Score = 45.4 bits (106), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 100/422 (23%), Positives = 164/422 (38%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG V + G+K+ + IL A L+E V N+ DV + L+ LG V + +
Sbjct: 11 KPLSGEVTISGAKNAALPILFAALLAEEPVEVANVPKLRDVTIIEQLRLGAKVSRNGS 70

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
V EV F + +++ A++ A G G L G
Sbjct: 71 -----VHIDASEVNNFCAPYDL-VKTMRASIWALGPLVARFGKGQVSLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ G L G + + +S +
Sbjct: 116 CAIGARPVDLHIHGLEQLGATIKLEDGY----VKAEDVGRKGAHIVMD-KVSVGATITV 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G I++ P + T + G K + D I+G ++
Sbjct: 171 MCAATLAEGTT---ILENAAREPEIVDTAHLNAIGAKVSGMGT-DTITIEGVERLGGGY 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ V D FL AA++GG V + + L+ LE GAKV E ++
Sbjct: 227 HEVV-ADRIETGTFLVAAAVSGGKVCKNTKASLLE---SVLAKLEEAGAKVESGEDWIS 282

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ RE LKA+++ P D+ ++ + A GP I +
Sbjct: 283 LDMTGRE-----LKAVNIRTAPHPAFPTDMAQFLLNMMAKGPGIITETIF-----EN 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
R + I EL ++GA E + I + L+ + D R + + +A C TI
Sbjct: 332 RFMHI-PELQRMGAHAIEGNTAICGTDGLSGAQV-MATDLRASASLVIAGCIAKGETI 389

Query: 423 RD 424
D
Sbjct: 390 VD 391

>emb|CAM88970.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM88979.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM88988.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM88997.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89006.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89015.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89024.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89033.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89042.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89051.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89060.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89069.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89078.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89087.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89096.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89105.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89114.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89123.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89132.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
emb|CAM89141.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella abortus]
Length = 188

Score = 45.4 bits (106), Expect = 0.017, Method: Compositional matrix adjust.
Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKL 393
LA+ A FA+G T + + RVKE++R+ A+ L G EG + + L
Sbjct: 88 LAIAASFAEGETVMDGLDELRVKESDRLA AVARGLEANGVDCTEGEMSLTVRGRPGGKGL 147

Query: 394 NVTADTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
+ T+ DHR+AM+F + A E PVT+ D +FP
Sbjct: 148 GGGTVATHLDHRIAMSFLVMGLASEKPVTVDSTMIATSFP 188

>ref|YP_004114357.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pantoea sp.
At-9b]
gb|ADU67801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pantoea sp.
At-9b]
Length = 419

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 103/427 (24%), Positives = 171/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ D+ + L LG VE

Sbjct: 6 VQGPTRLSGEVTISGAKNAALPILFAALLAEFPVEIQNVPKLRDIDTTMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G V DA+ EV +F + +++++ A++ A G G

Sbjct: 66 RN-----GSVHV-DAR-EVNVFCAPYDL-VKTMRASIWALGPLVARFGGQVVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S

Sbjct: 111 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVDGRLLKAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + + D+ I+G ++

Sbjct: 166 TVTIMSAATLATGTT---IENAAREPEIVDTANFLNTLGAKISGAGT-DKITIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G V +L D A+ L GA++

Sbjct: 222 GG--GVYRVLDPRIETGTFVAAAISRGKVLCRNTQPDTL--DAVLAK-LRDAGAEIETG 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +

Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPGFPTDMQAQFTLLNLVAEGTGVITETIF-- 328

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAE 417
R + I EL ++GA E + I E L+ + D R + + LA C

Sbjct: 329 ---ENRFMHV-PELIRMGAAHAEIESNTAICHGVETLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
T+ D

Sbjct: 384 EGTTLVD 390

>ref|YP_988537.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bartonella
bacilliformis KC583]
gb|ABM45225.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bartonella
bacilliformis KC583]
Length = 431

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 88/388 (22%), Positives = 155/388 (39%), Gaps = 66/388 (17%)

Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRT--LGLSVEADKA 72
++G + + G+K+ + +++ A L++ T +VDN+ + DV ++ L +G +VE +

Sbjct: 12 LNGVIPISGAKNAALPLMIAALLTDETLIVDNVPHLADVECLIRILNNHGIGYAVEGRQC 71

Query: 73 -----AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
AK + + P E ++ F + R A V+ GG A

Sbjct: 72 HTVCS DARTIYFTAKNITTI---RAPHYELVRKMRAFWVIGPLLRQCQEACVSLPGGCA 127

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-----KVKL 174
+ RP+ ++ GLK LGAD+ G V + GL G KV +

Sbjct: 128 -----IGTRPVDFILEGLKALGADIAIENG---VHAKALKGLKGASYHFPKVTV 174

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
G+ LLMAA LA G ++ P V ++ ++ G + D

Sbjct: 175 GGT-----HVLLMAAVLAEGKT---VLHNAACEPEVTNLVQALKAMGADIS-GEGETDVL 224

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
I G +K + + + +Y +A A+TGG V ++ L + VLE

Sbjct: 225 TIHGKVLHGARGVCPDRIEAGTYAMA-VAMTGGDVLLQDAVPEHL---TEVLTVLEKA 280

Query: 295 GAKVTWTETSVTGTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAI 350
G + + V R+P K +K++D+ P D+ + A+G T I

Sbjct: 281 GLSIEIKAEGIRVF---RDP--HKKMKSVDITAPFPAPFTDLQAQFMALMTLAEGNTHI 335

Query: 351 RDVASWRVKETERMVAIRTELTKLGASV 378
+ R + ++ EL +LGA +

Sbjct: 336 TETIF-----ENRFMHVQ-ELVRLGARI 357

>emb|CAM89195.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]
emb|CAM89204.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]

[illegible]

emb|CAM90086.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK4/01]
emb|CAM90095.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK10/01]
emb|CAM90104.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK15/02]
emb|CAM90113.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F23/97]
emb|CAM90122.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F96/2]
emb|CAM90131.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
VLA04.67]
emb|CAM90140.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
VLA04.72]
emb|CAM90149.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
VLA04/105]
emb|CAM90158.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
VLA04/06]
emb|CAM90167.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK31/04]
emb|CAM90176.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 39/94]
emb|CAM90185.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 44/94]
emb|CAM90194.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK24/00
(M192)]
emb|CAM90203.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 55/94]
emb|CAM90212.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 4/96]
emb|CAM90221.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 61/94]
emb|CAM90230.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK13/99]
emb|CAM90239.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK40/99]
emb|CAM90248.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK5/01]
emb|CAM90257.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F6/99]
emb|CAM90266.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F8/99]
emb|CAM90275.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F9/99]
emb|CAM90284.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F10/99]
emb|CAM90293.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F7/99]
emb|CAM90302.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
UK28/03-13840]
emb|CAM90311.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 59/94]
emb|CAM90320.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 5/95]
emb|CAM90329.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK43/99]
emb|CAM90338.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
UK1/2000]
emb|CAM90347.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp.
UK2/2000]
emb|CAM90356.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. 14/94]
emb|CAM90365.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. UK3/05]
emb|CAM90374.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. VLA05/4]
emb|CAM90383.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. VLA05/8]
emb|CAM90392.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F5/99]
emb|CAM90401.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella sp. F5/02]
emb|CAO99131.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella microti CCM
4915]
emb|CAO99132.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella microti]
Length = 188

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKL 393
LA+ A FA+G T + + RVKE++R+ A+ L G EG + + L
Sbjct: 88 LAIAASFAEGETVMDGLDELRVKESDRLA AVARGLEANGVDCTEGEMSLTVRGRPGKGGL 147

Query: 394 NVTADITYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFP 433
+ T+ DHR+AM+F + A E PVT+ D +FP
Sbjct: 148 GGGTVATHLDHRIAMSFLVMGLASEKPVTVDDSTMIATSFP 188

>ref|YP_003714284.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xenorhabdus
nematophila ATCC 19061]
emb|CBJ92208.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xenorhabdus
nematophila ATCC 19061]
Length = 420

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 99/420 (23%), Positives = 168/420 (40%), Gaps = 51/420 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+SG V + G+K+ + I+ A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LSGEVTISGAKNAALPIMFAALLAEEPVELQNPVELKDIDTTIKLLNRLGTVKVERNG--- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+V V G V + +L +++++ A++ A G G L G
Sbjct: 69 -SVFVDASG---VNEYCAPYEL-----VKTMRASIWALGPLVARFGQGVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA + G V+ G L G + + +S ++
Sbjct: 117 IGARPVDLHISGLEQLGAKIVLNIEGY---VKATVDGRLKGASIVMD-KVSVGATVTIMT 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P +E T + G K + + DR I+G ++ +
Sbjct: 172 AATLAEGTT---IIENAAPEIEDTANFLNLTGAKISGAGT-DRIVIEGVKRLGGGVHR 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D FL AAI+ G VT +L D A++ E GA + E +++
Sbjct: 228 VLP-DRIETGTFLVAAISRKVTCTHAKPDTL--DAVLAKLRE-AGADINVGEDWISLD 283

Query: 309 GPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ P D+ +++ + ADG I + R
Sbjct: 284 MHGQRP-----KAVTFRTAPHPGFPTDMAQFSLNLMVADGAGMITETIF-----ENRF 332

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTVIRD 424
+ I EL ++GA E + + EKL+ + D R + + LA C T+ D
Sbjct: 333 MHI-PELIRMGARAEIESNTVLCHGVKEKLSSAQV-MATDLRASASVLGACIAEGTTVVD 390

>ref|ZP_04851607.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
sp. oral taxon 786 str. D14]
gb|EES74748.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
sp. oral taxon 786 str. D14]
Length = 448

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 90/349 (25%), Positives = 143/349 (40%), Gaps = 45/349 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALS----EGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
++G VK+ G+K N+L + A S EG +V+ + +DV + L +LG +V D
Sbjct: 13 LAGNVKVSAGAK---NSVLPPIAASLLGEEGVSVIRDAPPLDDVMTINKVLES LGAAVTYD 69

Query: 71 K---AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 127
+ + C + P E ++ FL + R ++ GG A
Sbjct: 70 REVITVDARQIASC--EAPYEWVRKMRASFLVMGPLLTRMGFTRISLPGGCA----- 119

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + G + +GA++ LG + NG L G K+ L + S ++
Sbjct: 120 -IGTRPIDQHLLKGFEAMGAET--LHGGFIEAKTNG--RLRGAKIYLDVA-SVGATENIM 173

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G II+ P + + G + + I+G ++ + ++
Sbjct: 174 MAATLAEGTT---IIENAAKEPEIVDLANYLNSMGAVVRGAGT-GMIRIEGVERLRGCEH 229

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A F+ AAITGG V VEG L G V LE MG V E V V
Sbjct: 230 TVIP-DRIEAGTFMVAAAITGGNVFVEGAIADHL-GPV--ISKLEEMGVTVEVQENGVRV 285

Query: 308 TGPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD 352
K LKA+DV P D+ + + L ++G + I +
Sbjct: 286 -----IADKPLKAVDVKTLPYPGFPTDMAQMMALLLVSEGASVITE 327

>ref|YP_002287734.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oligotropha
carboxidovorans OM5]
sp|B6JDF7.1|MURA_OLICO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACI91869.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oligotropha
carboxidovorans OM5]
Length = 429

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 97/428 (22%), Positives = 180/428 (42%), Gaps = 68/428 (15%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++GT+ + G+K+ + +++ A L++ T +++N+ DV + R LG
Sbjct: 10 NKLNGTIPISGAKNAALPLMIAALLTDETLILENVPRADVALL---QRILG----- 58

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRS---LTAAVTAAGGN 118
V + GK P + + L + A I MR+ + + A
Sbjct: 59 -NHGVDIMSAGKRPGDREHQGQTLHISAANIIDTTAPYDLVSKMRASFWVIGPLLARMKE 117

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGAD--VDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
A L G + RP+ L++ L++LGA+ +D P GL G +++
Sbjct: 118 ANVSLPGGCAIGTRPVDLLIMALEKLGAIEVIDGGYAVARAP-----QGLHGAEIEFPK 171

Query: 177 -SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
++S +++ LMAA LA G +I P + + + G K + + R
Sbjct: 172 VTVSGTHVA--LMAATLAKGTT---VITNAACEPEIADVADCLNKMGAKITGAGT-SRIV 225

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G +K ++A + + +Y +A A+TGG V ++G +Q + +VL G
Sbjct: 226 IEGVEKLHGARGHAVLPDRIEAGTYAMA-VAMTGGDVQLQGARPELMQAAL---DVLIEAG 281

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIR 351
A +T T + V R G ++ +DV+ + P D+ L + A+G
Sbjct: 282 ATITQTNEGIRVQ---RNGSG---IRPVDVSTSPFPGFPTDLQAQLMALMTRAEG----- 330

Query: 352 DVASWRVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAM 408
S R+ ET R + ++ EL + GA + + I KL + D R ++
Sbjct: 331 ---SSRITETIFENRFMHVQ-ELARFGARIALDGETATIEGRPKLRGAPV-MATDLRASV 385

Query: 409 AFSLAACA 416
+ +AA A
Sbjct: 386 SLVIAALA 393

>ref|ZP_04637320.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
intermedia ATCC 29909]
gb|EEQ18471.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
intermedia ATCC 29909]
Length = 421

Score = 45.4 bits (106), Expect = 0.018, Method: Compositional matrix adjust.
Identities = 102/431 (23%), Positives = 173/431 (40%), Gaps = 59/431 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + I+ A L+E + N+ +D+ + L LG +E
Sbjct: 6 VQGRTRLSGEVTISGAKNAALPIMFAALLAEDPVELQNVPKLKDIDTTIKLLSQLGTKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D + +V V G V F + ++++ A++ A G G
Sbjct: 66 RDNSG--SVFVDASG-----VNEFCAPYDL-VKTMRASIWALGPLVARFGKGQVS 112

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 113 LPGGCAIGARPVDLHISGLEQLGAIEIKLEEGY---VKASVDGRLLGAHIVMD-KVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+
Sbjct: 168 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKISGAGT-DRITIEGVARL 223

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 224 GGGVYR-----VLPDRIETGTFLVAAAIISGGKVVCVRQTRPDTL--DAVLAKLRE-AGAD 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA+ + P D+ +++ L A+G I +
Sbjct: 275 IEIGDDWISLDMHGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGTGIVITET 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413

+ E M EL ++GA E + I E+L+ + D R + + LA
Sbjct: 329 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVQELSGAQV-MATDLRASASLVLA 381

Query: 414 ACAEVPVTIRD 424
 C VTI D

Sbjct: 382 GCIADGVITVD 392

>ref|YP_003829891.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Butyrivibrio proteoclasticus B316]
gb|ADL33309.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Butyrivibrio proteoclasticus B316]
Length = 429

Score = 45.4 bits (106), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 101/439 (23%), Positives = 181/439 (41%), Gaps = 47/439 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLQ 64
E+ V++ + G V++ G+K+ + IL A +++ T +DN+ + D + ML A+ + G
Sbjct: 2 EKYVIKGGNPLVGEVEIGGAKNAALAILAAATMTDETVEYIDNMPDESDTNAMLQAIATG 61

Query: 65 LSVEADKAAKRAVVVGGCGG--KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
V D+ + +V + F +ED +++++ A L A A V
Sbjct: 62 AHV--DRVDRHSVKINASAVRNFTIEDYIKKIR-----ASYLLGAFLLGKYKQAGVV 111

Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L + RPI + G LGA V+ G D L G + L +S
Sbjct: 112 LPSGCNIGLRPIDQHIGFTALGATVNIHGIIDAHA-----DALVGSHIYLD-VVSVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA +A G II+ P+V + G + + + D IKG ++
Sbjct: 165 ATINIMMAATMAEGKT---IIEAAKEPHVVDVFANFLNSMGANIKGAGT-DVIRIKGVER 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + + ++ LA AA T G +TV+ L+ A+++E MG +V +
Sbjct: 221 LHGTEYTIIPDQIEAGTFMLAAAA-TKGDITVKNVIPKHLES--ISAKLIE-MGCQVHES 276

Query: 302 ETSVTVTGPPREPFGFRKHLKAI---DVNMNKMPPDVAMTLAVVALFADGPTAIRD-VASWR 357
+ +V V R H+K + + P + + L A G + + + + R
Sbjct: 277 DDAVRVVATRR--LQNTHVKTLPYPGYPTDMQPQITVALG----LASGISIVTESIFENR 330

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CA 416
K + ELT++GA ++ II +K A+ + D R A +AA A
Sbjct: 331 FKYVD-----ELTRMGACIKVEGSTAIEGVDKYT-GAVVSAPDLRAGAAALVIAALTA 382

Query: 417 EVPVTIRDPGCTRKTFPDY 435
E T+ D + + D+
Sbjct: 383 EGYSTVEDIKYIERGYEDF 401

>emb|CAM89447.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis 1330]
emb|CAM89456.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89465.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89474.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89483.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89492.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89501.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89510.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89519.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89528.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89537.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89816.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89825.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89834.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89843.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89852.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89861.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89870.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89879.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella suis]
emb|CAM89897.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89906.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]

emb|CAM89915.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89924.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89933.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89942.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89951.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
emb|CAM89960.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella canis]
Length = 188

Score = 45.4 bits (106), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI---TPPEKL 393
LA+ A FA+G T + + RVKE++R+ A+ L G EG + + L
Sbjct: 88 LAIAASFAEGETVMDGLDELRVKESDRLLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGL 147

Query: 394 NVTADITYDDHRMAMAFSLAACA-EVPVTIRDPGCTRKTFP 433
+ T+ DHR+AM+F + A E PVT+ D +FP
Sbjct: 148 GGGTVATHLDHRIAMSFLVMGLASEKPVTVDDSTMIATSFP 188

>ref|ZP_08096916.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
brasiliensis LMG 20546]
gb|EGA67082.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
brasiliensis LMG 20546]
Length = 419

Score = 45.4 bits (106), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 100/422 (23%), Positives = 166/422 (39%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPKSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G V + G+K+ + IL + L+E V N+ D+ + L LG VE +
Sbjct: 11 KPLVGEVTISGAKNAALPILFASILAEPEVEVANVPRLRDIDTTMELLERLGAKVERN-- 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ + + + + +++++ A++ A G G L G
Sbjct: 69 -----GSVHVDPS--INEYCAPYDL-VKTMRASIWALGPLVARFGQGVSLPGG 115

Query: 127 PRMRERPIGDLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ N G L G + + +S +
Sbjct: 116 CAIGARPVDLHIHGLEQLGATITLEDGY----VKANVDGRLKGAHIVMD-KVSVGATITI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G ++D P + T + + G K + + D I+G ++ K
Sbjct: 171 MCAATLADGTT---VLDNAAREPEIVDTADFLNKLGAISGAGT-DTITIEGVERLGGGK 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
++ V D FL AA++GG VT C T LE GA V E ++
Sbjct: 227 HSVV-ADRIETGTFLVAAAVSGGKVT---CRNTKAHLLEAVLAKLEEAGAAVETGEDWIS 282

Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
V RE LKA+ + P D+ ++ L A G I + + E
Sbjct: 283 VDMTDRE-----LKAVTIRTAPHPGFPTDMQAQFTLLNLMAKGGGVITE----NIFENR 332

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA-EVPVTI 422
M EL ++GA E + I ++L+ + D R + + +A C TI
Sbjct: 333 FMHV--PELMRMGAKAEIEGNTVICGDVDELSGAQV-MATDLRASASLVIAGCIANGETI 389

Query: 423 RD 424
D
Sbjct: 390 VD 391

>ref|ZP_07036313.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
sp. oral taxon 386 str. F0131]
gb|EFI41457.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
sp. oral taxon 386 str. F0131]
Length = 427

Score = 45.4 bits (106), Expect = 0.019, Method: Compositional matrix adjust.
Identities = 90/390 (23%), Positives = 155/390 (39%), Gaps = 62/390 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+IV++ ++SG V++ G+K+ + IL + L +++++ +DV M+ L++LG
Sbjct: 11 EKIVVKSPKLSGVVVRVSGAKNAALPILAASILGTEDIILEDVPLKDVIMIEVLKSLG 70

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V +KA K +V+ + E M + A+ G G
Sbjct: 71 CVV--NKAGKNKLVINSKNLSSYVTSYE-----LMSKMRAFLVMGPLLGRMGK 117

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + RPI + G + LGA+++ N +G + KL G
Sbjct: 118 TVNSLPGGCNIGSRPIDLHLKGFEALGAEIE-----NNVGDITASAEKLG-- 163

Query: 179 SSQYL-----SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
YL ++ AA LA G+ +I+ P + + + G A
Sbjct: 164 CRVYLDFPSVGATENIITAAVLAEGEET--VIENAAMEPEIVDLANFLRKMGA-AVMGAG 219

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEV 290
IKG ++ K + + D A F+ AAITGG V V+ ++ ++
Sbjct: 220 TSTIRIKGVKELKGCCHQIIP-DRIEAGTFMVAIAITGGDIVDNVSSHMK--PVIK 275

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAI 350
LE GAK+ + + V G I +N+ +P + A F T +
Sbjct: 276 LEECGAKIIEEDDIRVIGED-----AIIPINIKTLPPGFPDMDQAQFLALMTKL 326

Query: 351 R--DVASWRVKETERMVAIRTELTKLGASV 378
+ ++A V E M A EL K+GA +
Sbjct: 327 KGNNAIETVFENRFMHA--DELVKMGADI 354

>ref|ZP_07889067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
segnis ATCC 33393]
gb|EFU68561.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aggregatibacter
segnis ATCC 33393]
Length = 425

Score = 45.1 bits (105), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 96/417 (23%), Positives = 166/417 (39%), Gaps = 43/417 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV + G+K+ + IL A L+ + N+ + +D+ L LR LG+ VE +
Sbjct: 12 LKGTVDISGAKNAALPILFAAILATEPVTLTNVPDLKDIETTLKILRQLGVEVERNAQGV 71

Query: 75 RAVVVGCGGKFP--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ F P E K A + R V+ GG + + R
Sbjct: 72 VRLDASKINHFIAPIYELVKTMRASIWALAPLVARFNQGVSLPGGCS-----IGAR 122

Query: 133 PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSISSQYLSALLMAAP 191
P+ + GL++LGA + G V IG + KV + ++S +++AA
Sbjct: 123 PVDLHISGLERLGAIVLEDGYVKAYVDSRLIGTRIVMEKVSIGATLS-----IMIAAT 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G +I+ P + T + + G K + S D I+G + +++ V
Sbjct: 177 LAKGTT--VIENAAREPEIADTAEFNLKMGAKISGAGS-DAITIEGVDRLTGCEHS-VA 231

Query: 252 GDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D FL AAI+GG + + +L + + L GA+V TE ++T+
Sbjct: 232 PDRIETGTFLVAAAISGGRIVCKNTKANTLDAVI---DKLREAGAQVDVTEDTITLMDLG 288

Query: 312 REPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
P KA+++ P D+ ++ + A+G + I + R + I
Sbjct: 289 NRP-----KAVNIRTAPYPGFPDMDQAQFTLLNMVANGTSIITETIF-----ENRFMHI 337

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPTIRD 424
EL ++G E + I L+ + D R +++ LA C TI D
Sbjct: 338 -PELIRMGGKAEIEGNTAICHGVAHLSGAEV-MATDLRASISLVLAGCIATGETIVD 392

>ref|YP_003606379.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1002]
gb|ADG16868.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1002]

Length = 420

Score = 45.1 bits (105), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 69/263 (26%), Positives = 114/263 (43%), Gaps = 27/263 (10%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      +SG V + G+K+ + IL LS ++N+ + +DV ML L +G+ +EA +
Sbjct: 12  LSGEVVVSGAKNAALPILCAGLLSADPVHLENVPDLQDVRTMLKLLGQMGVRIEAGE--- 68

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMRE 131
      G+ ++ +K + + MR+ + + A G+A L G +
Sbjct: 69  -----GRVALDASKVDNLVAPYEMVKTRASILVLGPLVARFGHARVSLPGGCAIGA 120

Query: 132  RPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      RP+ + GL+ +GA++ G + R L G ++ ++ I+ LLMAA
Sbjct: 121  RPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-VTDMITVTGTENLLMAA 173

Query: 191  PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      LA G+ II+ P V L+ G K E + DR I+G K K+ +
Sbjct: 174  VLAEGET---IIENAAREPEVVDLAHLVAMGAKIEGIGT-DRLVIQGVDKLHGAKHTVI 229

Query: 251  EGDASSASYFLAGAAITGGTVTV 273
      D A FL A GG VT+
Sbjct: 230  P-DRIEAGTFLCAVAAAGGDVTL 251
```

```
>ref|YP_622555.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia AU 1054]
ref|YP_834070.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia HI2424]
ref|ZP_04939852.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia PC184]
gb|ABF77582.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia AU 1054]
gb|ABK07177.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia HI2424]
gb|EAY63023.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
      cenocepacia PC184]
      Length = 449
```

Score = 45.1 bits (105), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 65/280 (23%), Positives = 117/280 (41%), Gaps = 33/280 (11%)

```
Query: 3  GAEIEVLQPIKEISGTVKLPKSGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRT 62
      G +++ ++ +SG + + G+K+ + IL L+ +DN+ N +DV L L
Sbjct: 29  GMDKLAIEGGNRLSGEIVVSGAKNAALPILCAGLLTADPVDLDNVPNLKDVRTTLKVLNQ 88

Query: 63  LGLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
      +G+ E D GC + V + ++++ A++ G
Sbjct: 89  MGVKSETD-----GCRVQLDASRVDNLVAPYE-----LVKTMRASILVLGPLLARF 134

Query: 117  GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
      G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135  GEAKVSLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-VT 187

Query: 176  GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
      I+ LLMAA LA G+ +I+ P V L+ G K + + DR
Sbjct: 188  DMITVTGTENLLMAATLADGET---VIENAAREPEVSDLAHLVAMGAKIDGIGT-DRLV 243

Query: 236  IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
      I+G ++ +++ + D A FL A GG V + G
Sbjct: 244  IQGVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVMLTG 282
```

```
>ref|ZP_08151417.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
      bacterium 4_1_37FAA]
gb|EGC74129.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
      bacterium 4_1_37FAA]
      Length = 430
```

Score = 45.1 bits (105), Expect = 0.020, Method: Compositional matrix adjust.

Identities = 95/428 (22%), Positives = 176/428 (41%), Gaps = 47/428 (10%)

```

Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T +DNL + D++ +L A+ +G
Sbjct: 2  EQYIIKGGSPVLGEVEIGGAKNAALAILAAAIMTDETVTIDNLPDVNDINVLEAMEGIG 61

Query: 65  LSVEADKAAKRAVVVCG--GKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
++ + + V + G F ++ D ++++ A L A+ A
Sbjct: 62  AQIQ--RVDHRHTVKINGSTIGDFSIDYDIKKIR-----ASYLLGALLGKYNKAEV 111

Query: 122  VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RPI + G + LGA+V+ G L V + +I+
Sbjct: 112  ALPGGCNIGSRPIDQHLKGFALGAEEVIEHGKILAEATLKGTHLYFDVSVGATIN-- 169

Query: 182  YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA +A G + I++ + P+V + G + + + D I+G QK
Sbjct: 170  ----VMAAAMADG---LTILENVAKEPHVVDVANFLNSMGANIKGAGT-DVIKIRGVQK 221

Query: 242  YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + + D A F+ AA T G +TV L+ + LE MG +V
Sbjct: 222  LHKTEYSIIP-DQIEAGTFMFAAAATKGDITVLNVIPKHLEATIS--KLEEMGCQVEEF 277

Query: 302  ETSVTVTGPPREFFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD-VASW 356
+ +V V K LK+ V P D+ + V + G + I + +
Sbjct: 278  DDAVRV-----ANKRLKSTQVKTLPPYGFPTDMQPQIGVTLALSKGTSIITESIFEN 330

Query: 357  RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACA 416
R K + EL ++GA ++ + I EK + + + D R A +A A
Sbjct: 331  RFKYLD-----ELARMGAVIKVEGNSATIEGVEKFSGARV-SAPDLRAGAALVIAGLA 382

Query: 417  EVPVTIIRD 424
+TI D
Sbjct: 383  TDGITIVD 390

```

>ref|ZP_07635822.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ruminococcaceae
bacterium D16]
Length = 430

Score = 45.1 bits (105), Expect = 0.020, Method: Compositional matrix adjust.
Identities = 76/299 (25%), Positives = 125/299 (41%), Gaps = 19/299 (6%)

```

Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q K + GT+ + G+K+ + I+ A L +G ++N+ DV +L L+ LG V
Sbjct: 6  IQGGKPLHGTITISGAKNAVAIIPAALLVDGVCRIENIPQISDVTLILQILQELGADV 65

Query: 69  ADKAAKRAVVVCGGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ V + C +V L A L A+ G A L G
Sbjct: 66  T--VNRTVDIDCS-----HIRNRQVPYELARKIRASYLVGALLGRFGWAEVPLPGGCD 118

Query: 129  MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RPI + G +GADV G C +V G G L GG++ L +S +++
Sbjct: 119  LGGRPIDQHIKGFVAMGADVVRNGLIC--AKVPG-GRLSGGQIYLD-MVSVGATMNIML 174

Query: 189  AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
A LA G + II+ P++ + G + + D I+G ++ K +
Sbjct: 175  AGVLADG---MTIENAAKEPHIVDLANFLNSMGANIMGAGT-DVIKIRGVKRLKGGTYS 230

Query: 249  YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A ++A A GG V ++ L D A+++E MG V + +V V
Sbjct: 231  IIP-DQIEAGTYMAAVAAAGGDVLIQNVIPKHL--DCITAKLVE-MGVDVEELDDAVRV 285

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>ref|ZP_02183884.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Carnobacterium
sp. AT7]
gb|EDP69364.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Carnobacterium
sp. AT7]
Length = 436

Score = 45.1 bits (105), Expect = 0.021, Method: Compositional matrix adjust.
Identities = 88/372 (23%), Positives = 156/372 (41%), Gaps = 38/372 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+IV++ K ++G+VK+ G+K+ IL L S+G + + N+ DV + L L
Sbjct: 2 EKIVVRGGKHLTGSVKVEGAKNAVLPIAATILASKGQSKLTNPILSDVFTINEVLSHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
L+V+ D+ K+ +++ + E E V + + M L A + G+A L
Sbjct: 62 NLTVDFDQ-TKKEIILDATKELHFEAPFEYVSKMRASI-VVMGPLLRL----GHAKVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG-GLPGGKVKLSGSISSQY 182
G + RPI + G + +GA+V G + L G + L S
Sbjct: 116 PGGCAIGTRPIDLHLKGFEAMGAEVHIENG-----YIEAFADQLKGAHIYLDLDFP-SVGA 168

Query: 183 LSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA LA G IE + + P + + R G K + + + I+G +
Sbjct: 169 TQNMMAATLAKGTTTTIENVARE---PEIVDLANFLNRMGAKVIGAGT-ESIRIEGVSEL 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+++ + D A F+ AA+T G + +E + + L+ MG +
Sbjct: 225 TGVEHSIIP-DRIEAGTFMIAAAVTQGNIIYIEDA---VAEHNKPLISKLKEMGVQFEDEA 280

Query: 303 TSVTVTGPPREPFGKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDVA---- 354
+ V GP K LKA DV P D+ + + +FA+G + +++
Sbjct: 281 NGLRVIGP-----KKLKATDVKTMPHPGFPTDMQAQMTIAQVFAEGTSTMKETVFENR 333

Query: 355 SWRVKETERMVA 366
++E RM A
Sbjct: 334 YMHMEELRRMNA 345

>ref|YP_001484727.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9215]
gb|ABV51141.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9215]
Length = 456

Score = 45.1 bits (105), Expect = 0.021, Method: Compositional matrix adjust.
Identities = 81/370 (21%), Positives = 154/370 (41%), Gaps = 36/370 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V++ G+K+ + ++ + L+ V+ N+ D+ M L++ LS++ +
Sbjct: 23 KLSGIVEISGAKNSALVMAASLLTNERIVLQNVPRLTIDIEKMGNILKS--LSIKLIQKN 80

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R + P + +++ L N A A+ + G A L G + RP
Sbjct: 81 NRLEI-----DPKNISIKDLPYELVNLGRASFFCIGALLSKYGEAKVPLPGGCDIGSRP 134

Query: 134 IGDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + + GL+ LGA++ G ++ + L G +KL S L+MAA LA
Sbjct: 135 IDEHINGLQALGAEIIIEGIVKAKIK-DKANKLHGTHIKLKCP-SVGATETLIMAASLA 192

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G IE + P ++ +++ + G K + ++ I G + + + D
Sbjct: 193 EGRTTIENAARE---PEIQDLQMLNKMGAKEI-YDSGKEKIIIDGVNELCGCTHKVIP-D 247

Query: 254 ASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
A FL AA T ++T+ L+ L+ G+K+T S+T+ G
Sbjct: 248 RIEAGTFLIAAATSSSITISPVIPCHLEA---VTNKLQESGSKITIKGNSITIKG---- 300

Query: 314 PFGRKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWVRKETERMVAIRT 369
K +K +D+ P D+ + A+G + I ++ RM +
Sbjct: 301 ----KEIKGVDIQTAPFPGFPTDLQAPFTTLMAIANGESKITEIIFEN-----RMNHVHL 351

Query: 370 ELTKLGASVE 379
L K+GA+++
Sbjct: 352 -LNKMGANIK 360

>ref|YP_003940069.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cloacae SCF1]
gb|ADO46785.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter

cloacae SCF1]
Length = 419

Score = 45.1 bits (105), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 99/431 (22%), Positives = 169/431 (39%), Gaps = 61/431 (14%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q + G V + G+K+ + IL A L+E + N+ +D+ + L LG VE
Sbjct: 6 VQGPSRLQGEVSISGAKNAALPILFAALLAEFPVEIQNVPKLKDIDTTMKLLSQLGTVKE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G ++ + +V +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVWIDAS--DVNVFCAPYEL-VKTMRASIWALGPLVARFGGQGV 110

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G II+ P + T + G K + DR I+
Sbjct: 166 TVTIMSAATLAEGTT---IENAAREPEIVDTANFLNAMGAKITGQGT-DRITIEGVARL 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG + +L D A++ E GA
Sbjct: 222 GGGVYR-----VLPDRIETGTFLVAAAIISGGKIVCRHAQPDTL--DAVLAKLRE-AGAD 272

Query: 298 VTWTETSVTVTGPPREPFRGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA++V P D+ ++ + A+G I +
Sbjct: 273 IEVGQDWISLDMHGKRP-----KAVNVRTAPHPGFPTDMQAQFTLLNMVAEGTGVITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
E EL ++GA E + I EKL+ + D R + + LA
Sbjct: 327 I-----FENRFMHLPELIRMGAAHAEIESNTAICHGVEKLGAQV-MATDLRASASLVLA 379

Query: 414 ACAEVPVTIRD 424
C TI D
Sbjct: 380 GCIAEGTTIVD 390

>ref|YP_487950.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris HaA2]
sp|Q2IRX1.1|MURA_RHOP2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABD09039.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris HaA2]
Length = 429

Score = 45.1 bits (105), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 72/310 (23%), Positives = 128/310 (41%), Gaps = 41/310 (13%)

Query: 13 KEISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ GT+ + G+K+ + +++ A LS+ T ++DN+ DV + L G+ + A
Sbjct: 10 NKLHGTPISGAKNAALPLMIAALLSDETLLIDNVPRPADVALLQRIILGNHGVDIMA--- 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRS---LTAAVTAAGGN 118
GK P + + L + I MR+ + A + A
Sbjct: 67 -----AGKRPGDHEYQGQTLHISAKNIIDTTAPYELVSKMRASFWVIAPLLARMHE 117

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-S 177
A L G + RP+ L++ L++LG + L D V GGL G ++ +
Sbjct: 118 AKVSLPGGCAIGTRPVDLLIMALEKLGVE----LSIDAGYVVAKAPGGLKGATIEFPKVT 173

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S +++ LMAA LA G II P + + + G + + + R I+
Sbjct: 174 VSGTHVA--LMAATLAKGTT---IISNAACEPEITDVADCLNKMGARITGAGT-PRILIE 227

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + + +Y +A A+TGG V + G LQ + +VL GA
Sbjct: 228 GVDKLHGARHTVLPDRIETGTYAMA-VAMTGGEVQLSGARPELLQSAL---DVLTAQAGAT 283

Query: 298 VTWTETSVTV 307
+T + V
Sbjct: 284 ITINNDGIKV 293

>ref|YP_003165888.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Accumulibacter phosphatis clade IIA str. UW-1]
gb|ACV33959.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Accumulibacter phosphatis clade IIA str. UW-1]
Length = 421

Score = 45.1 bits (105), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 87/388 (22%), Positives = 157/388 (40%), Gaps = 42/388 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + + G+K+ + IL L+ + N+ D+ ML + +G++V D A
Sbjct: 12 LAGEIAISGAKNAALPILCACLLTAEPHLTNVPRLRDIATMLRLIEQMGVAVTHDGA-- 69

Query: 75 RAVVVGCGGK----FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
VV+ G P + K L + R A V+ GG A +
Sbjct: 70 NGVVLDSGLSNPLAPYDMVKTMRASILVLGPLLARHGEARVSLPGGCA-----IG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ ++GL+ +GA + G G GL G + ++ ++ L+MAA
Sbjct: 121 ARPVEQHILGLQAMGASIHVEHGY-IQAGAGTGKRGRLRGACI-VTDMVTVTGTENLMMAA 178

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G+ II+ P V + G + + + D+ I+G ++ + +
Sbjct: 179 ALADGET---IIENAAREPEVVDLANCLVSMGAQISGAGT-DKIRIRGVERLHGATHRIM 234

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ +Y A AA +GG+V + G L D ++L+ G + ++ + P
Sbjct: 235 ADRIETGTYLCAAAA-SGGSVRLTGTSAAYL--DAVVDKLLD-AGCDIVAERDAIRLKAP 290

Query: 311 PREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
PR LKA+ + + P D+ + A+G IR+ + E M A
Sbjct: 291 PR-----LKAVSIRTSPYPAFPTDMAQFMAINCAEGSAVIRET----IFENRFMHA 339

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLN 394
+ EL +LGA + ++T E+L
Sbjct: 340 V--ELIRLGADIRIDASNAMVTGVERLQ 365

>ref|YP_154801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Idiomarina
loihensis L2TR]
sp|Q5R0J5.1|MURA_IDILO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAV81252.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Idiomarina
loihensis L2TR]
Length = 419

Score = 45.1 bits (105), Expect = 0.022, Method: Compositional matrix adjust.
Identities = 92/380 (24%), Positives = 153/380 (40%), Gaps = 52/380 (13%)

Query: 10 QPIKEISGTVKLPGSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA 69
QP+ SG+V + G+K+ + IL+ + L + N+ + DV L L LG+S
Sbjct: 10 QPL---SGSVTISGAKNAALPILMASLLPSEKITLSNVPDLHDVDTTLELLDCLGIS--H 64

Query: 70 DKAARKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVL 123
+V C + K L + + + A+ G G A L
Sbjct: 65 SNLNNNSV---CIDPTTLNHFKAPYDL-----VKTMRASILVLGPLLAKTGKAEVSL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RP+ + GL+++GA +D G ++ + G L G ++ L ++S
Sbjct: 114 PGGCAIGARPVNLHIEGLRKMGAHIDVENGY----IKASVEGRLQGAEILLD-TVSVTGT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYK 243
L+MAA LA G+ +I+ P V + G + S D +I G K

Sbjct: 169 ENLMAAVLAEGEET---VIENAAREPEVIDLANFLNSLGNVRDAGS-DTIHITGVNKLH 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + V D FL A TGG+V E SL +K LE GA + +

Sbjct: 225 GGEYS-VMPDRIETGTFLVAALATGGSVRCEKTDPAFLDAVLK---KLEEAGATIDKGDN 280

Query: 304 SVTVTGPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ + + GR KA+++ P D+ + A+G IR+

Sbjct: 281 WIAI-----QSHGRP--KAVNIITAPHPAFPTDMAQFCALNAIAEGTAGIRETIFEN-- 331

Query: 360 ETERMVAIRTELTKLGASVE 379
R + I EL ++GA+VE

Sbjct: 332 ---RFMHI-PELRRMGANVE 347

>gb|EFE28162.2| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Filifactor
alocis ATCC 35896]
Length = 429

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 82/319 (25%), Positives = 128/319 (40%), Gaps = 31/319 (9%)

Query: 1 MAGAEIEVLQPIKE---ISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYML 57
M G + + +KE + GTV++ G+K+ I+ L+EG +V+ + N +DV M+

Sbjct: 1 MKGMDSLAYITVKESPSLRGTQISGAKNAVLPIIAATLLAEGISVIKGVPNLKDVQVMV 60

Query: 58 GALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQL---FLGNAGIAMRSLTAAVT 113
L LG E ++ V VE E V FL + R A ++

Sbjct: 61 ELLACLGAELK---GDSLFDASHITSVEAPHELVNKMRSFLVMGALLSRFQRAKIS 117

Query: 114 AAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKV 172
GG A + RPI + G + LGA V+ G + + L GGKV

Sbjct: 118 LPGGCA-----IGSRPIDLHLKGFEALGATVNIIDEGLQSGYIEAHAEYLQGGKV 168

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
L S +LMAA L G + +I+ P + + G + + + +

Sbjct: 169 YLDFP-SVGATENILMAASLTPG---VTVIENAAEEPEIVDLANYLNMMGARVRGAGT-N 223

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDV-KFAEVL 291
I G +K P V D A F+ AA+T G V VE T ++ + K E+

Sbjct: 224 TIRIIGVEKLH-PIEYTVIPDRIEAGTFMVAAMTKGDVLVENVITDHIKPVIAKLTEI- 281

Query: 292 EMMGAKVTWTETSVTVTGP 310
G + + +V V GP

Sbjct: 282 ---GCTIEEYDNAVVRVIGP 297

>ref|YP_001902771.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris str. B100]
sp|B0RQI0.1|MURA_XANCB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAP50715.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. campestris]
Length = 424

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 96/400 (24%), Positives = 160/400 (40%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG

Sbjct: 3 KIVVTGGQALHGEVHISGAKNAVLPILCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG

Sbjct: 63 EVTIDEGLTAKGRSILVDPKSVTHQIAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCF-LGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L GG+ +

Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY----IKATSNRGLKGGRYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRITVQG 224

Query: 239 GKQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAFLP-DRIETGTFLVAAAMTGGSVTVRRARPDTLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA 354
T T SVT+ + P +A+++ P D+ + A+G I +
Sbjct: 281 TTAEESVTLDMHGKRP-----RAVNLTTPAPAFPTDMQAQFMALNCVAEGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|YP_003853064.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium thermosaccharolyticum DSM 571]
gb|ADL69980.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium thermosaccharolyticum DSM 571]
Length = 417

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 78/326 (23%), Positives = 135/326 (41%), Gaps = 30/326 (9%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+I+++ + GTVK+ G+K+ I+ + LS G +D++ +DV+ M+ ++ LG
Sbjct: 5 KIIIVENSALRGTVKISGAKNSVLPIIAASLSYGEVFIDDPVELKDVNVMIELIKFLGA 64

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ V + P E K+ FL + + A G+A L G
Sbjct: 65 HCTFKNGKGLKINVDIKDVEAPYELVKKMRASFL-----VMGPILAKLGHAKISLPG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + G + LGA +D +G R L G KV L S
Sbjct: 116 GCAIGTRPIDLHLKGFQTLGAQID--IGHGYVEARAK---RLVGKKVYLDFF-SVGATEN 169

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQYKSP 245
++MAA A G I I+ P V + + G + + + D I+G ++ K
Sbjct: 170 IMMAAVFADG---ITTENAAEEPEVVDLANFLNKMGANIKGAGT-DTIRIEGVKELKGT 225

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
++ + + +Y +A AA+TGG V +E + ++ + AK+T V
Sbjct: 226 EHTVIPDRIEAGTYMVA-AAMTGGDVLIENV-----IVDHIKPIIAKLTECGIDV 274

Query: 306 TVTGPPREPFGRKHLKAIDVNMNKMP 331
G G+++ KA+DV P
Sbjct: 275 FEETGVRVKGKRNKAYVDVKTLPYP 300

>ref|NP_829044.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydomonas
caviae GPIC]
gb|AAP04922.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydomonas
caviae GPIC]
Length = 444

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 91/381 (23%), Positives = 155/381 (40%), Gaps = 58/381 (15%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ ++ N+ + DV + +LG V DK A+
Sbjct: 12 LQGSVRVSGAKNSTTKLLVASLLSDRKCILRNVPDIGDVRLTVELCESLGSIVHWDKQAE 71

Query: 75 RAVVVGCGGKFPVEDAK---EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + A+ + + L A +A V GG+A +
Sbjct: 72 VIEIHTPEIRMTEVLAQFSRVNRIPILLGALLARCPGEGVVVPCVGGDA-----IG 122

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
ER + GL+QLGA V C D + GL G + L S L++A+

Sbjct: 123 ERTLNFHFEGLEQLGAQVAC----DGQGYQAAAPKGLVGAYITLPYP-SVGATENLILAS 177

Query: 191 PLALGD-----VEIEIIDKLISIPY--VEMTL---RLMERFGVKAHSDSWDRFYIKG 238
A G +E+EI+D ++ + VE+T R +E FG D FY

Sbjct: 178 VRARGRTIIKNAALEVEILDILFLQKAGVEITTDNDRTIEIFGC-----DDFY--- 226

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ +V D A+ F A +TGG V VE + + F + L +G

Sbjct: 227 -----EVDHWVIPDKIEAASFGMAAVLTGGRVVFVENAEQDLM---IPFLKTLRSIGGGF 277

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ TET + EP + DV+ + D +V+ A+G + I +

Sbjct: 278 SVTETGIEFF--YNEPLKGGVLETDVHPGFLTDWQQPFSVLLSQAEGSSVIHETV---- 331

Query: 359 KETERMVAIRTELTKLGASVE 379
R+ +R L ++GAS E

Sbjct: 332 -HENRLGYLRG-LQQMGASCE 350

>ref|YP_003845758.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
ref|ZP_07630266.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
gb|ADL53994.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
cellulovorans 743B]
Length = 420

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 105/440 (23%), Positives = 175/440 (39%), Gaps = 50/440 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
E +V+ + G V + G+K+ + IL A + S+ V+DN+ + ED+ M ++++

Sbjct: 2 ERLVVTGGNPLRGAVDITGAKNAAVAILPAALMASKNVVCVIDNVPDIEDISCMETIMKSI 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV- 122
G VE G F V+ + L MR + A G V

Sbjct: 62 GAKVERK-----GNAFHVDSTELTTTEALIEEMRKMGRSYYLIGALLGRFKKVK 110

Query: 123 --LDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSIS 179
L G + RPI + G + LGA VD G + R L G + L +S

Sbjct: 111 VELPGGCHIGVRPIDQHKGFEALGAKVDIKHGIAEVTADR-----LIGANIYLD-VVS 163

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+++AA LA G+ +E K P+V + G K + + + D I G

Sbjct: 164 VGATINVMLAAALAEGETTLENAAKE---PHVVDVANFLNSMGAKIKGAGT-DVIKILGV 219

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
++ + + D A F+ AA GG VT+ L+ A+++E MG +V

Sbjct: 220 KELSGCDYSVIP-DQIEAGTFMIAAACGGEVTLNNVIPKHLESIT--AKLIE-MGVEVE 275

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVAS 355
+ SVTV +LK ++V P DV + + A G + + + +

Sbjct: 276 ENDDSVTVR-----TNGNLKGVNVKTLPPYGFPTDVQQPMTLLSVAKGRSVVHE-SI 327

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAAC 415
W E EL K+GA+++ I+ E+L + +D R A +A

Sbjct: 328 W-----ESRFKFIDELKKMGANIKVEGRVAIVDGVRLTGATV-VANDLRAGAAMIIAGL 381

Query: 416 -AEVPVTIRDPGCTRKTFPD 434
AE + D G + +P+

Sbjct: 382 MAEGETIVTDIGHIDRGYPN 401

>ref|YP_002647380.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
pyrifoliae Ep1/96]
emb|CAX54101.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
pyrifoliae Ep1/96]
emb|CAY72657.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia
pyrifoliae DSM 12163]
gb|ADP11186.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Erwinia sp.
Ejp617]

Length = 420

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 101/431 (23%), Positives = 169/431 (39%), Gaps = 61/431 (14%)

```

Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      +Q  +SG V + G+K+ + IL A L+E + N+ +D+ + L LG+
Sbjct: 6  VQGPTRLSGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLGQLGV--- 62

Query: 69  ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
      KA + V + A E+ +++++ A++ A G G
Sbjct: 63  --KAERNGSVYLDASNVDIYCAPYEL-----VKTMRASIWALGPLVARFGQGQVS 110

Query: 123  LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
      L G G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 111  LPGGCAIGARPVLDLHITGLGLEQLGAEIKLEEGY---VKASVAGRLKGAHIVMD-KVSVGA 165

Query: 183  LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
      ++ AA LA G +I+ P + T + G K + S DR I+
Sbjct: 166  TVTIMSAATLATGTT---VIENAAREPEIVDTAHFLNTLGAKITGAGS-DRITIEGVDR 221

Query: 238  GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      GG Y+ V D FL AI+GG V +L D A++ E GA
Sbjct: 222  GGGVYR-----VLPDRIETGTFLVAGAISGGKVICRAAQPDTL--DAVLAKLRE-AGAD 272

Query: 298  VTWTETSVTVTGPPREPFGKRHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDV 353
      + E +++ + P KA+++ P D+ +++ L A+G I +
Sbjct: 273  IEVGEDWISLDMHGKRP-----KAVNLRATAPHPGFPTDMQAQFSLNLVAEGTGVITET 326

Query: 354  ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTIAIDTYDDHRMAMAFSLA 413
      + E M EL ++GA E I EKL+ + D R + + LA
Sbjct: 327  ----IFENRFMHV--PELVRMGAAHAEIESHTLICHGVEKLSSAQV-MATDLRASASLVLA 379

Query: 414  ACAEVPVTIRD 424
      C T+ D
Sbjct: 380  GCIAEGTTLVD 390

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>ref|ZP_07739943.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aminomonas
      paucivorans DSM 12260]
gb|EFQ23832.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Aminomonas
      paucivorans DSM 12260]
Length = 434

```

Score = 45.1 bits (105), Expect = 0.023, Method: Compositional matrix adjust.
Identities = 80/314 (25%), Positives = 131/314 (41%), Gaps = 37/314 (11%)

```

Query: 7  IVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTV-VNLLNSEDVHYMLGALRTLGL 65
      +V+Q + G++ G+K+ + ++ A L +G + +D + N D+H M LR LG+
Sbjct: 12  LVIQGGTFLRGLSLTAQAKNAALPVMASALLLKGRRLTLDRVPLNLDIHTMADLLRHLGV 71

Query: 66  SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRS---LTAAVTAAGGNATY 121
      +E G+ D E++Q +A + MR+ + + A G A
Sbjct: 72  QIE-----FKGQRMFLDVPEDLQWETPSALVRKMRASSLVLGPLIARCGRAIL 119

Query: 122  VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG---TDCPPVRVNGIGGLPGGKVKLSGSI 178
      L G + RP+ + GL ++GA D G + P +R G++ L
Sbjct: 120  PLPGGCAIGSRPMDFHLKGLAKMGASFDLVHGAVHAETPRLR-----PGRIYLDFF- 170

Query: 179  SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
      S LLMAA L G+ IE + I + TLR M G + E S ++G
Sbjct: 171  SVGATENLLMAAVLTEGETIIEAAREPEIVNLAETLRAM---GAQVEGEGSGT-LRVEG 226

Query: 239  GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      + + + + +++Y LAG IT G VTV+ ++ LE G +
Sbjct: 227  QKDLQDAEVRIPDRIEASTYLLAG-VITRGRVTVKDIVPDHIEA---LLSKLEEAGVGI 282

Query: 299  TWTETSVTVTGPPR 312
      SVTV P R
Sbjct: 283  QIQGDSVTVQAPDR 296

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>ref|ZP_07469768.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49726]
gb|EFM42878.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
accolens ATCC 49726]
Length = 422

Score = 45.1 bits (105), Expect = 0.024, Method: Compositional matrix adjust.
Identities = 106/438 (24%), Positives = 167/438 (38%), Gaps = 55/438 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTVK+ G+K+ +++ A L+EGTT + N DV M L LG V D +
Sbjct: 13 LAGTVKVDGAKNSVLKMAAALLAEGTTTLTNCPEILDVPLMKKVLGCEVTIDGSTV 72

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAG-----GNATYVLDGVP 127
R AK + NA A+R A+V G G+A L G
Sbjct: 73 RITT-----PAKPQ-----SNADFDAVRQFRASVCVLGPLTSRCGHAKVALPGGD 117

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ GL++LGA G V L G ++L S +L
Sbjct: 118 AIGSRPLDMHQTGLEKLGATTRIEHG-----AVVAEASELRGSTIRLDFP-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G ++ P + +++ G E + I G ++ +P
Sbjct: 172 TAAVLAEGTT---VLHNAAREPEIVDLCEMLKSMGANIE-GEGTSEVTIHGVERL-NPTE 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD A + AA+T G +TV G L + E L+ GA + E V
Sbjct: 227 HEVIGDRIVAGTWAYAAAMTQGDITVGGIAPRHLHLPL---EKLKSAGADIETYENGFRV 283

Query: 308 TGPPREPFGRKHLKAIDVNMNKMMPDVAMTLAVVAL----FADGPTAI-RDVASWRVKETE 362
R A+D P L +A+ A+G T I +V R + +
Sbjct: 284 RMEKRP-----TAVDYQTLFPFGFPTDLQPMAGISAIAGETTVITENVFESRFRFVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
M+ +LGA + + ++ + L+ T + + D A A CA+ T+
Sbjct: 337 EML-----RLGADAQVDGHHVVVRGKDHLSSSTHVSSDIRAGAGLVLSALCADEATTV 389

Query: 423 RDPGCTRKTFPDYFDVLS 440
D + +P + + LS
Sbjct: 390 HDVFHIDRGYPHFVENLS 407

>ref|ZP_05138543.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
gb|EEE40368.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
Length = 457

Score = 45.1 bits (105), Expect = 0.024, Method: Compositional matrix adjust.
Identities = 81/370 (21%), Positives = 154/370 (41%), Gaps = 36/370 (9%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V++ G+K+ + ++ + L+ V+ N+ D+ M L++ LS++ +
Sbjct: 23 KLSGIVEISGAKNSALVMAASLLTNERIVLQNVPRLTIDIEKMGNILKS--LSIKLIQKN 80

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
R + P + +++ L N A A+ + G A L G + RP
Sbjct: 81 NRLEI-----DPKNISIKDLPYELVNLGRASFFCIGALLSKYGEAKVPLPGGCDIGSRP 134

Query: 134 IGDVVGGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + + GL+ LGA++ G ++ + L G +KL S L+MAA LA
Sbjct: 135 IDEHINGLQALGAEIIIEEGIVKAKIK-DKANKLHGTNIKLKCP-SVGATETLIMAASLA 192

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G IE + P ++ +++ + G K + ++ I G + + + D
Sbjct: 193 EGRTTIENAARE---PEIQDLQMLNKMGAKEI-YDSGKEKIIIDGVNELCGCTHKVIP-D 247

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
A FL AA T ++T+ L+ L+ G+K+T S+T+ G
Sbjct: 248 RIEAGTFLIAAAATSSSITISPVIPCHLEA---VTNKLQESGSKITIKGNSITIKG---- 300

Query: 314 PFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
K +K +D+ P D+ + A+G + I ++ RM +
Sbjct: 301 ----KEKKGVDIQTAPFPGFPTDLQAPFTTLMAIANGESKITEIIFEN-----RMNHVHL 351

Query: 370 ELTKLGASVE 379
L K+GA+++
Sbjct: 352 -LNKMGANIK 360

>ref|ZP_05295200.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J1-208]
Length = 407

Score = 45.1 bits (105), Expect = 0.025, Method: Compositional matrix adjust.
Identities = 87/368 (23%), Positives = 145/368 (39%), Gaps = 53/368 (14%)

Query: 38 SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLF 97
S+GT+V+ N+ N DV + L+ L V V V G+ + E V
Sbjct: 13 SKGTSVLKNVPNLSDFVTINEVLKYNADV---SfVNDDEVTVDATGEITS DAPFEYV--- 66

Query: 98 LGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCF 151
R + A++ G G+A L G + RP+ + G + +GA V
Sbjct: 67 -----RKMRA SIVVMGPLLARTGSARVALPGGCAIGSRPVDLHLKGFEAMGAVVKIE 118

Query: 152 LGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYV 211
G L G KV L S ++MAA LA G +I+ + P +
Sbjct: 119 NGYIEATAE-----KLVGAKVYLDFF-SVGATQNIIMMAATLAEGTT---VIENVAREPEI 169

Query: 212 EMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
+ + G + + + + I+G ++ + +++ + D A F+ AAITGG V
Sbjct: 170 VDLANFLNQMGARVIGAGT-EVIRIEGVKELTATEHSIIP-DRIEAGTFMIAAAITGGNV 227

Query: 272 TVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP 331
+E + LE MG ++ E + V GP + LKA+DV P
Sbjct: 228 LIEDAVPEHIS---SLIAKLEEMGVQIIIEENGIRVIGPDK-----LKAVDVKTMPHP 277

Query: 332 ----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCI 386
D+ + V+ + ++G + + + V R E M + ++ G SV I
Sbjct: 278 GFPTDMQSQMMVIQMLSEGTSIMTETVFNRFMHVEEMRRMNADMKIEGHSV-----I 330

Query: 387 ITPPEKLN 394
I+ P KL
Sbjct: 331 ISGPAKLQ 338

>pdb|3KR6|A Chain A, Mura Dead-End Complex With Fosfomycin
Length = 419

Score = 45.1 bits (105), Expect = 0.025, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE D
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLDVDTSMKLLSQLGAKVERD--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + ++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRA SIWALGPLVARFGQGQVSLPGGX 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIEANAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPRIETGTFLVAAAISRKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIET-----VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|YP_003111989.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Catenulispora
acidiphila DSM 44928]
gb|ACU70148.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Catenulispora
acidiphila DSM 44928]
Length = 438

Score = 44.7 bits (104), Expect = 0.026, Method: Compositional matrix adjust.
Identities = 105/408 (25%), Positives = 157/408 (38%), Gaps = 53/408 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD--K 71
++G + + G+K+ + +++ +A L+EG T + + DV M LR LG V D
Sbjct: 11 RLAGEIAVCGAKNSALKLMAVALLAEGRTTELRGVPRILDVELMAELLRRRLGCGVRLDWE 70

Query: 72 AAKRAVVVGCGKGFPE--DAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+R G ++ D E L +R L A++ G G A
Sbjct: 71 GPEREDGPQKGSIAIVIDVPADPGTEADYDL-----VRRLRASICVLGPLLARQGEAKVS 124

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVD---CFLGTDCCPPVRVNGIGGLPGGKVKLSGSIS 179
G + R + + GL++LGAD+ FL P GL G + L S
Sbjct: 125 YPGGDAIGSRGLDMHIDGLQRLGADISQEHGFLVASAPK-----GLTGASILLDFP-S 176

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+LMAA LA G +ID P + L+ G K + S + I+G
Sbjct: 177 VGATENILMAAVLARGTT---VIDNAAREPEIVDICALLASMGAKIDSGT-STLVIEGV 232

Query: 240 QKYK-SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+P V D A F A +T G V V G L+ + + L GA V
Sbjct: 233 DTLSPAPSPHLVVADRIVAGMFAVAATMTRGDVVRVAGGNAHLEIAL---DKLTQAGATV 289

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRV 358
ET V+ R P +A+D+ P A L LFA A+ +A
Sbjct: 290 VPDETGRFVS-MDRRP-----RAVDIVTLPPYGFATDLQ--PLFA----AMNSIAEGTS 336

Query: 359 KETERMVAIR----TELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
TE + R EL +LGASV + I+ E+L+ + D
Sbjct: 337 MVTENLFDARFVFLQELARLGASVRTEGHHAIVRGVERLSGAPVRATD 384

>ref|NP_897726.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Synechococcus
sp. WH 8102]
sp|Q7U5R6.1|MURA_SYNPX RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAE08148.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Synechococcus sp. WH
8102]
Length = 433

Score = 44.7 bits (104), Expect = 0.026, Method: Compositional matrix adjust.
Identities = 103/420 (24%), Positives = 161/420 (38%), Gaps = 60/420 (14%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G +K+ G+K+ + ++ + L+E + N+ N D+ M L LG+ VE
Sbjct: 22 RRLQGVKLVSGAKNSALVMTASLLTEELVELINVPNLTDIAGMGRILSALGVQVEH--- 78

Query: 73 AKRAVVVGCGGKGFPEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
+ V + G E E V SL A+ G G+A L G

Sbjct: 79 SNGVALNAGNLTSHPEPPYELVN-----SLRASFFCIGSLLGRLGHARVPLPGG 127

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGS-----ISS 180
R+ RP+ + + GLK LGA V G V+ G K +L+G+ S

Sbjct: 128 CRIGARPVVEHIRGLKALGAHVSVVEHGIVSACVK-----GSKKRLTGAPIVLDPCSV 179

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G IE P V+ L+ + G + I G +

Sbjct: 180 GATETLLMAAVLATGTTTIE---NAAHEPEVQDLANLLIQMGADISGA-GGPVITIHGVE 235

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ N V D A FL AAIT + VE L + L G ++

Sbjct: 236 RLAGVSNYPVIPDRIEAGTFLIAAAITRSPVRPEVPIEHLA---VLQKLRDCGCQLEI 292

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASW 356
+T +++T P + ++A+D+ P D+ + A G + I +

Sbjct: 293 DQTGISIT--PGD-----IQAVDITTPFPFGFPTDLQAPFMAALMATAQGTSVISE---- 340

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDTYDDHRMAMAFSLAACA 416
K E + EL ++GAS+ I+ +L+ + T D R A A LA A

Sbjct: 341 --KIYENRLQHVLAELQRMGASIRVDGSTAIVEGVAQLSAAPV-TGSDLRAAAAMVLAGLA 397

>ref|YP_003908400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1003]
gb|ADN59109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
CCGE1003]
Length = 420

Score = 44.7 bits (104), Expect = 0.026, Method: Compositional matrix adjust.
Identities = 68/273 (24%), Positives = 121/273 (44%), Gaps = 27/273 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ +SG V + G+K+ + IL + LS +DN+ + +DV ML L +G

Sbjct: 2 DKLVEIEGGYPLSGEVVVSAGAKNAALPILCASLLSAEPVQLDNVPLQDVRTMLKLLGQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+ +E+ + G+ ++ +K + + MR+ + + A G+A

Sbjct: 62 VRIESGE-----GRVSLDASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+

Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-ITDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ +I+ P V L+ + G K E + DR I+G

Sbjct: 164 TGTEENLLMAAVLAEGE---VIENAAREPEVGDALHLLVQMGAKIEGIGT-DRLVIQGV 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
K + + D A FL A GG VT+

Sbjct: 220 KLHGATHVIP-DRIEAGTFLCAVAAAGGDVTL 251

>ref|YP_003336158.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptosporangium
roseum DSM 43021]
gb|ACZ83415.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptosporangium
roseum DSM 43021]
Length = 422

Score = 44.7 bits (104), Expect = 0.026, Method: Compositional matrix adjust.
Identities = 112/424 (26%), Positives = 172/424 (40%), Gaps = 53/424 (12%)

Query: 15 ISGTVKLPKSGKSLSNRI-----LLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ GT + G+K N +L LLAA +G TV+ N+ EDV + +G VE

Sbjct: 12 LRGTAFIQGAK---NAVLPMIGAALLAA--KGRTVLRNVPIIEDVRRRAVELAEAIKAVKE 66

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP- 127
+A + V+ K PV A E + F G+ A+ G A +++GV

Sbjct: 67 LHEAERTLVIDASRLKSPVLPV-EIARRFRGSV-----LFVPALLHRLGEA--IIEGVGG 118

Query: 128 -RMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186

```

      + R +      +G K+LGA VD   G   V+      G G + L + S      L
Sbjct: 119 CNLGSRLNDFHYLGYKRLGAIVDE--GDSVIHVKT---AGFTGATLYLD-TPSHTGTENL 172

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      +MAA L G      +I+      P V + ++ R G + S      F      G +
Sbjct: 173 IMAAALGRGTT---VIENAALEPEVLVDVIEMLTRMGARI--SGGGTGFIITVEGVEELQAV 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      V D A F      AAITGG V + G      L G V++      LE MG V +++
Sbjct: 228 EHTVMPDRDLGAGVFAMAAAITGGEVNLVGADLDHL-GVVRK--LEQMG--VEFSDHGAV 282

Query: 307 VTGPPREPFGFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      +      P      L+ I+V + P      D+ + VA ADG + I +      + +
Sbjct: 283 LHVRDRP-----LRPINVITDTYPGFATDLQSPIMTVACLADGASYIHE-----RIFD 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
      A+ +EL K+GA +E + ++      L T + T D R +A LA A      T+
Sbjct: 332 GRFALASELNKMGADIEVKENSAVVRGATPLTGTEV-TAHDLRSGIALVLAGLAAEGETV 390

Query: 423 RDPG 426
      + G
Sbjct: 391 IESG 394

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>ref|YP_004006518.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase mura [Rhodococcus
equi 103S]
ref|ZP_08153204.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus equi
ATCC 33707]
emb|CBH47833.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA [Rhodococcus
equi 103S]
gb|EGD25205.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus equi
ATCC 33707]
Length = 423

```

Score = 44.7 bits (104), Expect = 0.027, Method: Compositional matrix adjust.
Identities = 104/415 (25%), Positives = 164/415 (39%), Gaps = 63/415 (15%)

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Query: 4 AEEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
      +E ++      + G V + G+K+      +++ A L+EGTTV++N + DV M LR L
Sbjct: 2 SERFLVAGGNRLVGEVSVGGAKNSVLKMAAALLAEGTTVIENCPDILDVPLMADVLRGL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      G V + R +      K+ + A      A+R A+V G
Sbjct: 62 GCDVSLEGDVAR-ITTPAQPKYHADFA-----AVRQFRASVCVLGPLVARCH 107

Query: 118 NATYVLGDGVRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      A L G + RP+      GL+ LGA + G C + L G ++L+
Sbjct: 108 KAVVALPGGDAIGSRPLDMHQSGRLRLGAHSEIEHG--CVVAEAD---DLYGANIRLAFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      S      +LMAA LA G+      IID P +      ++ R G K + S I+
Sbjct: 163 -SVGATENILMAAVLARGET---IIDNAAREPEIVDLNMLNRMGAKVSGAGSTT-LTIR 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G + + P + V GD A+ + AA+T G V V G L + L G++
Sbjct: 218 GVDRLQ-PTSHRVIGDRIVAATWGIAAAMTRGDVLRGVNPKHLS---LVLDKLRAAGSQ 273

Query: 298 VTWTETS---VTVTGPPREPFGFRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPT 348
      +T TE V TG P+      VN +P      D+ +A ADG +
Sbjct: 274 IT-TEADGFRVQGTGRPQA-----VNFATLPYPGFPTDLQPMAGLAAIADGTS 321

Query: 349 AI-RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
      I +V R + E M+      +LGA + +I E+L+ + + D
Sbjct: 322 MITENVFEARFRFVEEMI-----RLGADARTDGHHAVIRGVEELSSAPVWSSD 369

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>ref|ZP_06015902.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
pneumoniae subsp. rhinoscleromatis ATCC 13884]
gb|EEW41090.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
pneumoniae subsp. rhinoscleromatis ATCC 13884]
Length = 419

```


Score = 44.7 bits (104), Expect = 0.027, Method: Compositional matrix adjust.
Identities = 102/421 (24%), Positives = 168/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12 LQGEVITISGAKNAALPILFSALLAEPEVEIQNVPKLKDIDTTMKLLSQLGAKVERNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V + G PV+ +F + +++++ A++ A G G L G
Sbjct: 70 --VWIDAG---PVD-----VFCAPYDL-VKTMRASIWALGPLVARFQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHISGLEQLGAEIKLEEGY---VKASVSGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K S DR I+G Q+
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLNALGAKITGQGS-DRITIEGVQLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A+ L GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAISGGKILCRNAQPDTL--DAVLAK-LRDAGADIETGEDWISL 282

Query: 308 TGPPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P KA++V P D+ ++ L A+G I + R
Sbjct: 283 DMHGHPR-----KAVNVRTAPHPGFPTDMQAQFTLLNLVAEGTGVITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I ++L+ + D R + + LA C TI
Sbjct: 332 FMHI-PELIRMGAAHAEIESNTAICHGVKQLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|YP_001480576.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
proteamaculans 568]
sp|A8GK08.1|MURA_SERP5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABV43448.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
proteamaculans 568]
Length = 419

Score = 44.7 bits (104), Expect = 0.027, Method: Compositional matrix adjust.
Identities = 100/427 (23%), Positives = 172/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E
Sbjct: 6 VQGRTRLSGEVAISGAKNAALPILFAALLAEPEVQLQNVPKLKDIDTTIKLLNQLGTKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ +V V G V F + +++++ A++ A G G
Sbjct: 66 RNG----SVFVDASG-----VNEFCAPYDL-VKTMRASIWALGPLVARFGRGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G +I+ P + T + G K + S DR I+G ++
Sbjct: 166 TVTIMSAATLATGTT---VIENAAAREPEIVDTANFLNTLGAKITGAGS-DRITIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AA++GG V +L D A++ E GA +
Sbjct: 222 GG--GVYRVLPDRIETGTFLIAAAVSGGKVMCRDTRPDTL--DAVLAKLRE-AGADIEVG 276

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWR 357

E +++ + P KA+ + P D+ +++ L A+G I +
Sbjct: 277 EDWISLDMHGKRP-----KAVTIRTAPHPGFPTDMQAQFSLNLVAEGTGVITET---- 326
Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
+ E M EL ++GA E + I E+L+ + D R + + +A C
Sbjct: 327 IFENRFMHV--PELIRMGAAEIESNTVICHGVEQLSGAQV-MATDLRASASLVIAGCIA 383
Query: 418 VPVTIRD 424
VT+ D
Sbjct: 384 DGVTVVD 390

>pdb|3ISS|A Chain A, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|B Chain B, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|C Chain C, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|D Chain D, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|E Chain E, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|F Chain F, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|G Chain G, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|H Chain H, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|I Chain I, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|J Chain J, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|K Chain K, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
pdb|3ISS|L Chain L, Crystal Structure Of Enolpyruvyl-Udp-Glcnac Synthase
(Mura) :udp-N-Acetylmuramic Acid:phosphite From
Escherichia Coli
Length = 418

Score = 44.7 bits (104), Expect = 0.028, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE D
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEPEIQNVPKLKDVDTSMKLLSQLGAKVERD--- 67
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + + + + A+ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRSI WALGPLVARFGQGQVSLPGGC 115
Query: 128 RMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLKGAHIVMD-KVSVGATVTIM 170
Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224
Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++

Sbjct: 225 VYRVLPDRIETGTFVLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E

Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+

Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D

Sbjct: 389 VD 390

>ref|ZP_07389387.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
curdlanolyticus YK9]
gb|EFM09062.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
curdlanolyticus YK9]
Length = 464

Score = 44.7 bits (104), Expect = 0.028, Method: Compositional matrix adjust.
Identities = 92/389 (23%), Positives = 161/389 (41%), Gaps = 41/389 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLNRILLALL--SEGTTVVDNLLNSEDVHYMLGALRTL 64
+I+++ + +SGTV++ G+K+ IL + L SEG +V+ ++ +DV + + +LG

Sbjct: 3 KIIVRGGRRLSGTVRIHGAKNAVLPILAASVLASEGESVIADVPLLDVLTIREVIASLG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
AD ++ + + E+ + + + M L A G L

Sbjct: 63 ----ADVQQGPETMIIRANRLTANEPSELVRKMRASILVMGPLLART---QQVRISLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + R I + G + +GA++ LG +VNG L G K+ L + S

Sbjct: 115 GGCAIGMRAIDQHLKGFEAMGAEIT--LGQGFIESKVNG--RLKGAKIYLDVA-SVGATE 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G IE K P + + G + + D I+G ++ +

Sbjct: 170 NIMMAASLAEGTTTIENTAAKE---PEIVDLANYLNAMGAHVRGAGT-DVIRIEGVERLQG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
++ + + +Y +A AITGG V +EG L L+ MG + T+

Sbjct: 226 VRHTVIPDRVEAGTYMIA-TAITGGDVFIIEGVIADHL---APVISKLQEMGVSIVATDNG 281

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
V VT K LK++DV P D+ + + L +DG + + + + R

Sbjct: 282 VRVTAD-----KPLKSDVKTLPPYGPFTDMQSQMSSLLLVSDGTSVVTETIFENRFM 334

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIIT 388
E E K+ A ++ IIT

Sbjct: 335 HVE-----EFAKMNAQIKVDGRAAIIT 356

>ref|ZP_02330017.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
larvae subsp. larvae BRL-230010]
Length = 370

Score = 44.7 bits (104), Expect = 0.028, Method: Compositional matrix adjust.
Identities = 92/381 (24%), Positives = 153/381 (40%), Gaps = 44/381 (11%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLSEGGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + GTV++ G+K+ + ++ A L+E T +DNL DV L LG V+ D

Sbjct: 10 RPLKGTQISGAKNSAVALIPAAILAETTVTLDNPLLLSDVAIYAEILSDLGADV KWD-- 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI----AMRSLTAAVTAAGGNATYVLDGVPR 128
G + D + + N + A L A+ G A L G

Sbjct: 68 -----GDQMMIDPSHMKAMPMPNGNVKKLRASYLLMGAMLGRFGEAVIGLPGGCN 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + G + LGA++ G +R L G K+ L +S +++

Sbjct: 118 FEPRPIDQHKGFEALGAEISNENGALF--IRAK---QLRGAKIYLD-MVSVGATINIML 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G +I+ P + L+ G K + + + + I+G +++
Sbjct: 172 AASRAKG---FTLIENAAKEPEIIDVATLLNSMGAKIKGAGT-ETIRIEGVDALHGCRHS 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ + +Y +A AA T G VTV+ ++ L+ MG ++ + S+ V
Sbjct: 228 IIPDRIQAGTYMIAAAA-THGDVTVDNIIIPKHMEA---LTAKLQEMGVQIEEMDESIRV- 282

Query: 309 GPPREPFRGKHLKAIDVNMNKMPPDVAMTLA--VVALF--ADGPTAIRD-VASWRVKETER 363
FG H + IDV P A L + +L A G + I D V S R K+
Sbjct: 283 -----FGTPHYEPIDVKALVYPGFATDLQSPMTSLLTQASGVSIITDHVYSNRFKQIPE 336

Query: 364 MVAIRTELTKLGAS--VEEGP 382
++ + ++ G S VE GP
Sbjct: 337 LIRMGAKIKVEGRSAVVEGGP 357

>ref|YP_393070.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfurimonas
denitrificans DSM 1251]
sp|Q30T46.1|MURA_SULDN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABB43835.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfurimonas
denitrificans DSM 1251]
Length = 422

Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 91/409 (22%), Positives = 166/409 (40%), Gaps = 45/409 (11%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD--- 70
++ G +K+ G+K+ + ++ ++ L++ + NL + D+ +L L LG +
Sbjct: 11 KLHGEIKISGAKNAALPLIAMSLAKNIVTIKNLPHVADIKTLKLLSNLGAECSSSWEN 70

Query: 71 --KAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + + + L LG + A G+ L G
Sbjct: 71 YSTTINTSTLNQTKATYDIVKTMRASILVLG-----PILARFGHCEVSLPGGCA 119

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIG--GLPGGKVKLSGSISSQYLSAL 186
+ +RPI + L+Q+GA ++ G ++ I GL G + + I+ + +
Sbjct: 120 IGQRPIDLHLKALEQMGAVINIEAG-----YIHAIAPDGLKGCNI-IFDKITVTGTANI 172

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSP 245
+MAA LA G + I P V ++ GVK E ++ + GG+ +
Sbjct: 173 VMAAALAKG---VTTITNAAREPEVVQLCEILNASGVKIEGIETAVLTIHGTGGELEIA 229

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ + + +Y AGA IT +T++G L LE MG+K T T+ S+
Sbjct: 230 PFSVIPDRIEAGTYLCAGA-ITKSELTGKANAKHLGA---VLSKLEEMGSKFTITDDSI 285

Query: 306 TVTGPPREPFRGKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
T+ P + KH+K + P D+ +A ADG + I + R+ E M
Sbjct: 286 TI--HPSKII--KHVKIVTQEYPAPFTDMQAQFLALATQADGTSIIEE---RLFENRFM 337

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLA 413
+EL ++GA + + + KL+ T + D R + A LA
Sbjct: 338 HV--SELQRMGADISLNGNVATVNGHSLSGTDV-MATDLRASSALVLA 383

>pdb|3KQJ|A Chain A, Mura Binary Complex With Udp-N-Acetylglucosamine
Length = 419

Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE D
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEPEVEIQNVPKLKDVDTSMKLLSQLGAKVERD--- 67

Query: 74 KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 127

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          G   + DA+ +V +F   + +++++ A++ A G       G       L G
Sbjct: 68  -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
          + RP+   + GL+QLGA +   G       V+ +   G L G   + +   +S       ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
          AA LA G       II+       P + T   +   G K       + DR   I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
          Y V D       FL AAI+ G +       +L D   A+ L   GA +   E   ++
Sbjct: 225 VYRVLPDRIETGTFVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          +   + P       KA++V       P   D+       ++ L A+G   I +       V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIET-----VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
          M       EL+++GA E   + I   EKL+   +   D R + +   LA C       T+
Sbjct: 332 FMHV--PELSRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
          D
Sbjct: 389 VD 390

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>ref|YP_571399.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB5]
sp|Q130J1.1|MURA_RHOPS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABE41498.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB5]
Length = 429

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Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 73/310 (23%), Positives = 128/310 (41%), Gaps = 41/310 (13%)

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Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
          ++ GT+ + G+K+ +   +++ A LS+ T ++DN+   DV +   L   G+ + A
Sbjct: 10 NKLHGTTIPISGAKNAALPLMIAAMLSDETLILDNVPRADVALLQRILGNHGV DIMAV-- 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRS---LTAAVTAAGGN 118
          GK P +   + L +   I       MR+   + A + A
Sbjct: 68 -----GKRPGDHEYQGQTLHISAKNIIDTTAPYDLVSKMRASFWVIAPLLARMHE 117

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-S 177
          A   L G   + RP+   L++ L++LGA+   L D   V       GGL G   ++   +
Sbjct: 118 AKVSLPGGCAIGTRPVDLLIMALEKLGAE---LSIDAGYVVAKAPGGLKATIEFPKVT 173

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
          +S   +++ LMAA LA G       II       P +       + + G K   + + R   I+
Sbjct: 174 VSGTHVA--LMAAALAKGTT---IIANAACEPEITDVADCLNKMGAKITGAGT-PRIMIE 227

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
          G K   ++   +   +Y +A   A+TGG V + G       LQ +   +VL   G
Sbjct: 228 GVSKLHGARTHTVLPDRIETGTYAMA-VAMTGGEVQLSGARPELLQSAL---DVLVTQAGVT 283

Query: 298 VTWTETSVTV 307
          +T       + V
Sbjct: 284 ITVNNDGIKV 293

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>ref|YP_002575316.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
lari RM2100]
sp|B9KG80.1|MURA_CAMLR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;

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Short=EPT
gb|ACM64065.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
lari RM2100]
Length = 418

Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 82/379 (21%), Positives = 161/379 (42%), Gaps = 54/379 (14%)

Query: 12 IKEISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
++++SG V + G+K+ + ++ + L++ + NL N D+ +L L+ LG S +
Sbjct: 9 VEKLSGEVIISGAKNAALPLIASSILAKNEAQISNLPNVADICTLLSLKKNLGASYTFEN 68

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDG 125
K +D + + + +R + A++ G GN L G
Sbjct: 69 NF-----AKINTKDLNKTIKY-----DIVRKMRASILTGLPLLARFGNCEVSLPG 114

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ +RPI ++ L+++GA+++ G ++ G L K+ ++GS
Sbjct: 115 GCAIGQRPIDLHLLALEKMGANIEIKQGYVVASGKLG-ADLMFDKITVTGS-----EN 167

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG--VKAHSDSWDRFYIKGGQKYK 243
++MAA LA G + + K P V ++ G +K SD + Y G+ +
Sbjct: 168 IIMAAALAHGKTRLLNVAKE---PEVVQLCEVLAEGLDIKGVGSDELE-IYGTSGELLE 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + +Y AG AIT +T++ L + LE MG +E
Sbjct: 224 FKPFKIIPDRIEAGTYLCAG-AITNSKITLKNVNNHLGAVLA---KLEQMGFSFDISED 279

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
S+++ P +E +K +++ ++ P D+ +AL A+G + I + R+
Sbjct: 280 SISIN-PAKE-----IKPVEILTSEYPGFPTDMQAQFMALALRANGVSIIDE----RLF 328

Query: 360 ETERMVAIRTELTKLGASV 378
E M +EL ++GA +
Sbjct: 329 ENRFMHV--SELLRMGADI 345

>ref|YP_002252270.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase (enolpyruvate
transferase) (udp-n-acetylglucosamine enolpyruvyl
transferase) (ept) protein [Ralstonia solanacearum
MolK2]
emb|CAQ17583.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase (enolpyruvate
transferase) (udp-n-acetylglucosamine enolpyruvyl
transferase) (ept) protein [Ralstonia solanacearum
MolK2]
Length = 451

Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 63/267 (23%), Positives = 117/267 (43%), Gaps = 27/267 (10%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ ++ N+ N +DV ML LR +G VE +
Sbjct: 42 LSGEIRVSGAKNAALPIMCAALLTPEPLMLRNVPNLQDVRTMLKLLRQMG--VEGTQNGH 99

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+ P +A ++ +++++ A++ G +A L G
Sbjct: 100 DVTLDAAADIHAP--EAPYDL-----VKTMRASILVLGPLLARFGHARVSLPGCG 147

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLM
Sbjct: 148 IGARFVDQHIKGLQMGAEIVIEHGY-IEAKLADGAKRLRGARI-VTDMVTVTGTENLLM 205

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ +++ P V L+ + G + E + DR ++G ++
Sbjct: 206 AAVLADGET---VLENAAREPEVTDLANLLVKMGARIEGIGT-DRLVVQGVDAALNGAEHT 261

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEG 275
+ D A FL A GG VT+ G
Sbjct: 262 VI-ADRIEAGTFLCAVAAAGGDVTLRG 287

>ref|ZP_01156460.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanicola
granulosus HTCC2516]
gb|EAR51513.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanicola
granulosus HTCC2516]
Length = 422

Score = 44.7 bits (104), Expect = 0.029, Method: Compositional matrix adjust.
Identities = 91/379 (24%), Positives = 153/379 (40%), Gaps = 35/379 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I+++ K +SG +++ G+K+ + ++ LS+ + N D+ M L +LG
Sbjct: 2 DSIIVRGGKPLSGQIRIAGAKNAALALMPATLLSDEPLTLTNAPRLSDIKTMSQLLES 61

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + + K V+ A E+ + + + L A AT L
Sbjct: 62 CEVTSLQDGK--VIALSSHNLSTRADYEIVRKMRASNVLGLPLAREH----QATVSLP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ V L+ LGA+++ G R GGL G +V L + S
Sbjct: 116 GGCAIGARPMIDHVTALALGAEIELRDGYLHAVAR---GGLNGARVPLRFA-SVGATE 170

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
+LMAA LA G IE + I + LR M G + E + ++G + +
Sbjct: 171 NVLMAATLAKGTTISIENAREPEIVDLARCLRAM---GAQIE-GEGTATITVEGVDRLSA 226

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDKVFAEVLEMMGAKVTWTETS 304
+ V +Y LA I GG V G ++ F E L+ G VT T+
Sbjct: 227 ATRVVSVDRIELGTYMLA-PVIAGGEVECLGGSVDLVRA---FCERLDAAGVSVTETDAG 282

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ V P G +DV P D+ + + A+G + + + R+ E
Sbjct: 283 LKVARNRGRPRG-----VDVATEPFGFPPTDLQAQMMAMLC TAEGDSVLEE----RIFE 332

Query: 361 TERMVAIRTELTKLGASVE 379
M A EL ++GAS++
Sbjct: 333 NRFMHA--PELVRMGASID 349

>gb|EGD20404.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
gardneri ATCC 19865]
Length = 424

Score = 44.7 bits (104), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 93/402 (23%), Positives = 162/402 (40%), Gaps = 49/402 (12%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNIISGAKNAVLPILCATLLADAPVEISNPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
V D+ A R+++V P + L ++++ A++ G
Sbjct: 63 EVTIDEGTLAKGRSILVD-----PRSVTHQVAPYEL-----VKTMRASILVLGPLLARY 111

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
GNA L G + RP+ + GL+ LGAD++ G ++ G L G +
Sbjct: 112 GNAEVSPLPGGCAIGSRPVDQHIKGLQALGADINVENGY----IKATSNGRLKGARYVFD- 166

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+S +LMAA LA G +++ P V + G + E + + R +
Sbjct: 167 MVSVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVV 222

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDKVFAEVLEMMGA 296
+G ++ +A + D FL AA+TGG+VTV +L + L GA
Sbjct: 223 QGVERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETLDA--VLDKLT EAGA 278

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD 352
+T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 279 TITTTADSITLDMHGKRP-----RAVSLTTAPYPAPFTDMQAQFMALNCVADGVGVINE 332

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+

Sbjct: 333 T----IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>pdb|2Z2C|A Chain A, Mura Inhibited By Unag-Cnicin Adduct
pdb|2Z2C|B Chain B, Mura Inhibited By Unag-Cnicin Adduct
pdb|2Z2C|C Chain C, Mura Inhibited By Unag-Cnicin Adduct
pdb|2Z2C|D Chain D, Mura Inhibited By Unag-Cnicin Adduct
Length = 423

Score = 44.7 bits (104), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE D
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKVDVDSMKLLSQLGAKVERD--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|NP_297114.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
muridarum Nigg]
ref|ZP_06194921.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
muridarum Nigg]
ref|ZP_06195840.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
muridarum Weiss]
ref|ZP_07225126.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
muridarum MopnTet14]
sp|Q9PJT7.1|MURA_CHLMU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAF39549.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
muridarum Nigg]
Length = 442

Score = 44.7 bits (104), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 97/436 (22%), Positives = 174/436 (39%), Gaps = 83/436 (19%)

Query: 15 ISGTVKLPGSKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG V+ DK A+
Sbjct: 12 LQGSVRVSGAKNATTKLLVASLLSDKRTILKNVPNIEDVQQTVDLCRALGAIVDWDKQAQ 71

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ +F + + + L A + V GG+A
Sbjct: 72 VIDIHTRILLSKVPPQFSCVN---RIPILLGALLRRCPYGIFVPILGGDA----- 120

Query: 128 RMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLS-----GSIS 179
+ R + + GLK+LGA++ D P + LP V + S+
Sbjct: 121 -IGPRTLHFHLEGLKKLGAEEIIVSDEGYWAAAPDGLIGAHITLPYPSVGATENLILASVG 179

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+Q + + AA +E+EIID ++ +++ GV+ +D+ I G
Sbjct: 180 AQGRTIIKNAA-----LEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIFGC 222

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
Q + S +++ + +AS+ +A A ++ G V VE + + F + L +G +
Sbjct: 223 QDFYSVEHSIIPDKIEAASFGMA-AVVSQGRVFVEHARHEHM---IPFLKALRSIGGGFS 278

Query: 300 WTETSVTVTGPPREPFGKHLKA-----IDVNMNKMPPDVAMTLAVVALFADGPTAIRDVA 354
E + E F K LK DV+ + D AV+ A+G + I +
Sbjct: 279 VQENGI-----EFFYDKPLKGGVLLLETDVHPGFITDWQQPFAVLLSQAEGCSVIHETV 331

Query: 355 SWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVTAI 398
E + + L K+GA S P +I P L T +
Sbjct: 332 H-----ENRLGYLSGLAKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQATHL 385

Query: 399 DTYDDHRMAMAFSLAA 414
D R A+ +AA
Sbjct: 386 -VIPDLRAGFAYVMAA 400

>gb|ADH18157.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia trachomatis G/9768]
gb|ADH20005.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia trachomatis G/11074]
gb|ADH97102.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia trachomatis G/9301]
Length = 444

Score = 44.7 bits (104), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 98/435 (22%), Positives = 173/435 (39%), Gaps = 81/435 (18%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLRCRVLGAIVEWDQQAQ 71

Query: 75 RAVVVG---CGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
++ K P + + + L A + V GG+A +
Sbjct: 72 VIEILTPRILLSKVPPQFSCVNRIPILLGALLRRCYPYGFIFVPI LGDA-----IG 122

Query: 131 ERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
R + + GLK+LGA++ D P GL G + L S L+
Sbjct: 123 PRTLHFHLEGLKKLGAEEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATENLI 174

Query: 188 MAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+A+ A G +E+EIID ++ +++ GV+ +D+ I G Q
Sbjct: 175 LASVGAQGRTIIKNAALEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIFGCQ 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ S +++ + +AS+ +A A ++ G + VE + + F +VL +G +
Sbjct: 224 DFYSVEHSIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGGFSV 279

Query: 301 TETSVTVTGPPREPFGKHLKA-----IDVNMNKMPPDVAMTLAVVALFADGPTAIRDVAS 355
E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 280 HENGI-----EFFYDKPLKGGVLLLETDVHPGFITDWQQPFAVLLSQAEGCSVIHETVH 332

Query: 356 WRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVTAI 399
E + L K+GA S P +I P L T +
Sbjct: 333 -----ENRLGYLKLKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQATDL- 385

Query: 400 TYDDHRMAMAFSLAA 414
D R A+ +AA
Sbjct: 386 VIPDLRAGFAYVMAA 400

>ref|NP_521074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia

solanacearum GM1000]
sp|Q8XV78.1|MURA_RALSO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAD16660.1| probable udp-n-acetylglucosamine 1-carboxyvinyltransferase
(enoylpyruvate transferase) (udp-n-acetylglucosamine
enolpyruvyl transferase) (ept) protein [Ralstonia
solanacearum GM1000]
Length = 421

Score = 44.7 bits (104), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 62/267 (23%), Positives = 118/267 (44%), Gaps = 27/267 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ + N+ N +DV ML LR +G VE +
Sbjct: 12 LSGEIRVSGAKNAALPIMCAALLTPEPFTLHNVPNLQDVRTMLKLLRQMG--VEGTQDGH 69
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+ P +A ++ +++++ A++ G G+A L G
Sbjct: 70 DVTLDAAIDAP--EAPYDL-----VKTMRASILVLGPLLARFGHARVSLPGGCG 117
Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLM
Sbjct: 118 IGARPVDQHIKGLQMGAEIVIEHGY-IEAKLADGAKRLHGARI-VTDMVTVTGTENLLM 175
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ ++ P V L+ + G + + + DR ++G + + ++
Sbjct: 176 AAVLADGET---VLENAAREPEVTDLANLLVKMGARIDGIGT-DRLVVQGV EALRGAEHT 231
Query: 249 YVEGDASSASYFLAGAAITGGTVTVEG 275
+ D A FL A GG VT+ G
Sbjct: 232 VI-ADRIEAGTFLCAVAAAGGDVTLRG 257

>ref|ZP_08038603.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
symbiotica str. Tucson]
gb|EFW13090.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Serratia
symbiotica str. Tucson]
Length = 419

Score = 44.7 bits (104), Expect = 0.031, Method: Compositional matrix adjust.
Identities = 102/425 (24%), Positives = 170/425 (40%), Gaps = 61/425 (14%)

Query: 15 ISGTVKLPKSGKSLNRIILLALASEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E +
Sbjct: 12 LSGEVISGAKNAALPILFAALLAEEPVELQNVPKLKDIDTTIKLLSQLGTKIERNG--- 68
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+V V G V F + +++++ A++ A G G L G
Sbjct: 69 -SVYVDASG-----VNEFCAPYDL-VKTMRASI WALGPLVARFGRGQASLPGGCA 116
Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + L +S ++
Sbjct: 117 IGARPVDLHITGLEQLGAEIKLEEGY---VKASVAGRLKGAHI-LMDKVS VGATVTIMS 171
Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYK 243
AA LA G II+ P + T + G K + S D+ I+ GG Y+
Sbjct: 172 AATLATGTT---IIENAAAREPEIVDTANFLNTLGAKISGAGS-DKITIEGVDR LGGGVYR 227
Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
V D FL AA++GG V +L D A++ E GA + E
Sbjct: 228 -----VLPDRIETGTFLIAAAVSGGKVLCDTRPDTL--DAVLAKLRE-AGADIEVGED 278
Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
+++ + P KA+ V P D+ +++ L A+G I + +
Sbjct: 279 WISLDMHGKRP-----KAVTVRTAPHGFPPTDMQAQFSLNLVAEGTGVTET----IF 328
Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVP 419
E M EL ++GA E + I E+L+ + D R + + +A C
Sbjct: 329 ENRFMHV--PELIRMGAAEVESNTVICHGVEQLSGAQV-MATDLRASASLVVAGCIADG 385

Query: 420 VTIRD 424
+TI D
Sbjct: 386 ITIVD 390

>ref|YP_001337259.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
sp|A6TEK8.1|MURA_KLEP7 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABR78992.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
Length = 419

Score = 44.7 bits (104), Expect = 0.031, Method: Compositional matrix adjust.
Identities = 102/421 (24%), Positives = 168/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12 LQGEVTISGAKNAALPILFSALLAEEPVEIQNVPKLKDIDTMTKLLSQLGAKVERNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V + G PV+ +F + +++++ A++ A G G L G
Sbjct: 70 --VWIDAG---PVD-----VFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHISGLEQLGAEIKLEEGY---VKASVSGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K S DR I+G Q+
Sbjct: 172 AATLAEGTT---IIENAAREPEIVDTANFLNALGAKITGQGS-DRITIEGVQRLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A+ L GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKILCRNAQPDTL--DAVLAK-LRDAGADIETGEDWISL 282

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P KA++V P D+ ++ L A+G I + R
Sbjct: 283 DMHGMRP-----KAVNVRTAPHPGFPPTDMQAQFTLLNLVAEGTGVITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I ++L+ + D R + + LA C TI
Sbjct: 332 FMHI-PELIRMGAAHAEIESNTAICHGVKQLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>dbj|BAA78108.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Escherichia coli]
Length = 419

Score = 44.7 bits (104), Expect = 0.031, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
E+ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 ELQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 127
G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247

AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224
Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281
Query: 307 VTGPPPEPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTITET---VFENR 331
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRGMGAHAIESNTVICHGVEKLSGAQV-MATDLRASASVLGACIAEGTTV 388
Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|YP_367767.2| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp.
383]
Length = 420

Score = 44.7 bits (104), Expect = 0.032, Method: Compositional matrix adjust.
Identities = 65/278 (23%), Positives = 117/278 (42%), Gaps = 33/278 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ +SG + + G+K+ + IL L+ +DN+ N +DV L L +G
Sbjct: 2 DKLVEGGHRLSGEIVVSGAKNAALPILCAGLLTGDPVDLDNVPNLKDVRTTLKVLNQMG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ E D GC + V + +++++ A++ G G
Sbjct: 62 VKSETD-----GCRVQLDASRVNDNLVAPYE-----LVKTMRASILVLGPLLARFGE 107
Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 108 AKVSLPGGCAIGARPVDQHIKGLQAMGAEISIEHGFIEARAKR-----LKGARI-VTDM 160
Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
I+ LLMAA LA G+ +I+ P V L+ G K + + DR I+
Sbjct: 161 ITVTGTENLLMAATLADGET---VIENAAREPEVSDLAHLLVAMGAKIDGIGT-DRLVIQ 216
Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 275
G ++ +++ + D A FL A GG V + G
Sbjct: 217 GVERLHGARHSVIP-DRIEAGTFLCAVAAAGGDVRLTG 253

>ref|ZP_01756491.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp.
SK209-2-6]
gb|EBA14819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp.
SK209-2-6]
Length = 422

Score = 44.7 bits (104), Expect = 0.032, Method: Compositional matrix adjust.
Identities = 97/415 (23%), Positives = 171/415 (41%), Gaps = 54/415 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G + + G+K+ ++ LSE + N D+ M L++LG V + + +
Sbjct: 12 LNGQIPIAGAKNACLTLPATLLSEEPLTLTNAPRLSDIKTMTQLLQSLGAEVSSLQDGQ 71
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V +++ E + +R + A+ G G A L G
Sbjct: 72 ----VQAMSSHNIDNHVAEYDI-----VRKMNASNLVLGPMLARLGQAVVSLPGGCA 119
Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ LGA+++ +L P GL G +++LS + S
Sbjct: 120 IGARPMDLHIHGLEALGAEIELKEGYLHAKAPR-----GLKGAIEIELSFA-SVGATEN 171
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G +I P + +++ G + + S I+G +

Sbjct: 172 IMMAATLAKGTT---VIRNAAREPEIVDLADCLKKMGAHIDGAGSSS-IIIEGVDRHLGA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSV 305
+ V +Y LA AI GG V + G G L G FAE L+ G V+ T+ +

Sbjct: 228 THPVVTDRIELGTMYLA-PAICGGEVELLG-GRMDLVG--AFAEKLDQAGINVSETDKGL 283

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
V+ GR +KA+DV P D+ + + A+G + + + ++ E

Sbjct: 284 LVS----RNNGR--VKAVDVTTEPFGFPTDLQAQMMALMCTAEGTSVLEE----KIFEN 333

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACA 416
M A ELT++GA++E +T E+L + D R +++ LA A

Sbjct: 334 RFMHA--PELTRMGANIEVHGGTATVTGVERLKGAPV-MATDLRASVSLILAGLA 385

>ref|YP_003042495.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Photorhabdus
asymbiotica subsp. asymbiotica ATCC 43949]
emb|CAQ85753.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Photorhabdus
asymbiotica]
Length = 417

Score = 44.7 bits (104), Expect = 0.032, Method: Compositional matrix adjust.
Identities = 101/421 (23%), Positives = 172/421 (40%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG VE +

Sbjct: 12 LSGEVSI SGAKNAA LPILFAALLAEEPVELQNVPELKDIDTTIKLLNRLGTKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G F DA+ EV + + +++++ A++ A G G L G

Sbjct: 68 -----GSVFV--DAR-EVNQYCAPYDL-VKTMRSI WALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++

Sbjct: 117 IGARPVDLHISGLEQLGAEIVLEEGY---VKASVNGRLKGACIVMD-KVSVGATVTIMT 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P +E T + G K + + D I+G ++

Sbjct: 172 AATLAEGTT---VIENAAAREPEIEDTANFLNLTGAKITGAGT-DHIIIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGT VTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AA++GG V +L D A++ E GA + E +++

Sbjct: 226 YRVLPDRIETGTFLIAAAVSGKVVCRAKPDTL--DAVLAKLRE-AGADIEVGEDWISL 282

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ + P D+ +++ L A+G I + R

Sbjct: 283 DMHGKRP-----KAVTLRTAPHPGFPTDMAQFSLNLVAEGAGMITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAIEVPVTIR 423
+ I EL ++GA E + + +KL+ + D R + + LA C VTI

Sbjct: 332 FMHI-PELIRMGAAHAEIESNTVLCGHVKKLSSAQV-MATDLRASASLVLAGCIAEGVTIV 389

Query: 424 D 424
D

Sbjct: 390 D 390

>ref|ZP_01264356.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Pelagibacter ubique HTCC1002]
gb|EAS84843.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Pelagibacter ubique HTCC1002]
Length = 417

Score = 44.7 bits (104), Expect = 0.032, Method: Compositional matrix adjust.
Identities = 89/413 (21%), Positives = 163/413 (39%), Gaps = 51/413 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G +++ GSK+ S IL LS + NL +D+ M+ L++LG +E +K

Sbjct: 11 KLKGQIRISGSKNASLPILAATLLSNKKISLANLPRVKDIETMILLKSLGSIIEDNKK- 69

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTA AVTAAGGNATYVLDGVPRMR 130

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      K  +++ K+      +      MR+  +  + A  G  A  L  G  +
Sbjct: 70  -----KLIINKTKQTKTFAAYSILVKTMRAGILVLGPLLAKFGKAKVSLPGGCAIG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      RP+  +  L  +LG      G      V  N  GL  G  +K  +S      L+++AA
Sbjct: 120 TRPVDIHLQALSCLKGVKYKIIQGY----VHANAPKGLIGANIKFP-KVSVGATENLIIAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKSPKN 247
      LA  G      +S  +E  ++  +  F  +      +  W      I+G  K  +
Sbjct: 175 CLAKGKTT-----LSNCAIEPEIKDLVNFLINMGCNIKWTAKRTVRIEGVNNLKEL-D 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      V  D  A  +L  AA+T  G  +  +  G      +  ++      +L+  +G+K+T  +  +  +
Sbjct: 227 YSVMPPDRIEAGTYLIAAALTEGNLKITGIDPKIISTEI---NILKKVGSKITLKKNEILI 283

Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      G      K  +K  I++  +  P  D+  +  V+  A+  +  I++      +  E
Sbjct: 284 QGS-----KKIKNINIKTSPYPGPFPTDLQAQMMVLLCKANKRSHIKE----EIFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
      M      EL  ++GA  +      +  I  K      +      D  R  +++  LAA  A
Sbjct: 333 MHV--AELNRMGAKISINGNQASIEGNIKFEAAEL-MATDLRASVSLILAALA 382

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>gb|EGB61803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
M863]
gb|EGB74172.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
TW10509]
Length = 419

```

Score = 44.7 bits (104), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 103/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

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Query: 14  EISGTVKLPGSKSLSNRILLLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAA 73
      ++  G  V  +  G+K+  +  IL  A  L+E      +  N+  +DV  +  L  LG  VE  +
Sbjct: 11  KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
      G      +  DA+  EV  +F      +  ++++  A++  A  G      G      L  G
Sbjct: 68  -----GSVHI-DAR-EVNVFCAPYDL-VKTMRASIWALGPLVARFGQGVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      +  RP+  +  GL+QLGA  +      G      V+  +  G  L  G  +  +  +S      ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      AA  LA  G      II+      P  +  T      +  G  K      +  DR  I+G  ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      Y  V  D      FL  AAI+  G  +      +L  D  A+  L  GA  +  E  ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      +      +  P      KA++V      P  D+      ++  L  A+G  I  +      V  E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAIEVPVTI 422
      M      EL+++GA  E      +  I      EKL+      +      D  R  +  +  LA  C      T+
Sbjct: 332 FMHV--PELSRMAHAIEIENSTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
      D
Sbjct: 389 VD 390

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>ref|YP_595156.1| 5-enolpyruvylshikimate-3-phosphate synthase [Lawsonia
intracellularis PHE/MN1-00]
emb|CAJ54835.1| 5-enolpyruvylshikimate-3-phosphate synthase [Lawsonia
intracellularis PHE/MN1-00]
Length = 574

```

Score = 44.7 bits (104), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 91/425 (21%), Positives = 174/425 (40%), Gaps = 63/425 (14%)

Query: 38 SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQL- 96
SEGT + ++L ++ + + A LG S+ +++ ++ F + K+ +Q+
Sbjct: 151 SEGT--LQHVLNDPIIECIKAFNQLGASLHWEESG---CIICSNPNFTRKHKKSIQID 205

Query: 97 ---FLGNAGIAMRSLT-----AAVTAAGGNATYVLDGVPRMRER-IGDLVVGLKQLG 145
+GN +++ L A V G N+ + D P + P IG ++ +
Sbjct: 206 TVIHIGNDTLSLYLLIFFIATCPARVKFIGKNSLKLADFSPLRKFLPMIGSRLINI---- 261

Query: 146 ADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKL 205
G D P+R+ LP ++ + + + AL +AA ++ I+I +
Sbjct: 262 -----IPGQDGLPIRIESSAILPS-EIIIPDLPVDAVIALFIAATRWDKELLIDIKEHP 315

Query: 206 ISIPYVEMTLRLMERFGV---KAEHSDSWDRFYIKGGQKYKSPKN---AYVEGDASSAS 258
++ + L E++ + K + I K P+N YV G A+
Sbjct: 316 NVTYILDKIIPLEFQWQIPFQKIIFNKQVTAISITPN-KITFPENPMIGTYVPGTAT--- 371

Query: 259 YFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGPPREPFGFR 317
LA A GGTVT++ D+ EVL G +T T ++ TG +
Sbjct: 372 -LLALPAFVGGTVTLKR--QYQQHTDICLLIEVLTQFGLNITETADTICCTG-----RQ 422

Query: 318 KHLKAIDVNMNMKMPD----VAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTK 373
L + +N+ +P + +TL + L + ++ + V E+ + + L +
Sbjct: 423 IGLTSSSLNIKLTLPKELFPLILTLCCIPLKSETNLLPELPDY-VDES----ILDSYLAQ 477

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFF 433
LG V G +I+P + + DT+ +A SLAA + + +PGC +P
Sbjct: 478 LGL-VRMGSKVKLISPTQTPWTSPSDTW----GLAISLAALRPQIKLSNPGCVEAIYP 531

Query: 434 DYFDV 438
+Y+ +
Sbjct: 532 NYWKI 536

>ref|YP_004028772.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
rhizoxinica HKI 454]
emb|CBW74628.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
[Burkholderia rhizoxinica HKI 454]
Length = 472

Score = 44.3 bits (103), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 90/389 (23%), Positives = 161/389 (41%), Gaps = 47/389 (12%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+SG + + G+K+ + IL + LS ++N+ N +DV ML L +G+ E +
Sbjct: 45 RLSGEITVSGAKNATLPILCASLLSAEPVQLENVPNLQDVRTMLKLLGQMGVRSEVN--- 101

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130
G ++ ++ + + MR+ + + A G+A L G +
Sbjct: 102 -----GNTVTLDASQVDKPVAPYELVKTMRASILVLGPLVARFGHAQVSLPGGCAIG 153

Query: 131 ERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + GL +GA + G D R L G V ++ I+ LLMA
Sbjct: 154 ARPVDQHIKGLTAMGAQISIEHGFIDARSR-----LKGAVH-ITDMITVTGTENLLMA 206

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G+ +++ P V L+ G + + DR + G + ++A
Sbjct: 207 AVLADGET---VLENAAREPEVTDLANLLVAMGARID-GIGTDRLVVHGVPRHLHGARHAV 262

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+ D A FL AA TGG VT+ G L+ + + L GA+V+ + + +
Sbjct: 263 IP-DRIEAGTFLCAAAATGGDVTLRGVTPILILEAVI---DKLREAGAQVSAGDDWIRLRM 318

Query: 310 PPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR- 368
P R ++A+ ++ P A + A F A+ +A+ + E + R
Sbjct: 319 PGRA-----RAVSFRTSEYP--AFPTDMQAQF----MALNAIATGTSQVVETIFENRF 365

Query: 369 ---TELTKLGASVEEGPDYCIITPPEKLN 394

EL +LGA++ + ++T +KL+
Sbjct: 366 MHVQELNRLGANITIDGNTALVTGVDKLS 394

>ref|NP_949867.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas palustris CGA009]
ref|YP_001993988.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas palustris TIE-1]
sp|Q6N176.1|MURA_RHOPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
sp|B3QA35.1|MURA_RHOPT RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
emb|CAE29973.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas palustris CGA009]
gb|ACF03513.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas palustris TIE-1]
Length = 429

Score = 44.3 bits (103), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 72/310 (23%), Positives = 128/310 (41%), Gaps = 41/310 (13%)

Query: 13 KEISGTVKLPKSKSLSNRILLALASEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
E+ GT+ + G+K+ + +++ A L++ T ++DN+ DV + L G+ + A
Sbjct: 10 NELRGTIPIISGAKNAALPLMIAALLTDETLILDNVPRLADVALLQRILGNHGVDDIMA--- 66
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRS---LTAAVTAAGGN 118
GK P + + L + I MR+ + A + A
Sbjct: 67 -----AGKRPDGEHYQGQTLHISAKTIVDTTAPYDLVSKMRASFWVIAPLVARMHE 117
Query: 119 ATYVLDGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-S 177
A L G + RP+ L++ L++LGA++ D V GGL G + +
Sbjct: 118 AKVSLPGGCAIGTRPVDLLIMALEKLGAETI----DGGYVIAKAPGGLKGATIAFPKVT 173
Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S +++ +MAA LA G IID P + + + G K + + R I+
Sbjct: 174 VSGTHVA--VMAALAKGTT---IIDNAACEPEIVDVADCLNKMGAKITGAGT-PRITIE 227
Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + + +Y +A A+ GG V + G LQ + +VL GA
Sbjct: 228 GVAKLHGARHTVLPDRIETGTYAMA-VAMAGGEVQLSGARPELLQAAL---DVLTQAGAT 283
Query: 298 VTWTETSVTV 307
+T + V
Sbjct: 284 ITVNNDGIKV 293

>ref|ZP_02144758.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Phaeobacter gallaeciensis BS107]
gb|EDQ14295.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Phaeobacter gallaeciensis BS107]
Length = 423

Score = 44.3 bits (103), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 91/415 (21%), Positives = 164/415 (39%), Gaps = 53/415 (12%)

Query: 15 ISGTVKLPKSKSLSNRILLALASEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + + G+K+ ++ LSE + N D+ M L++LG V + +
Sbjct: 12 LKGQIPIAGAKNACLTLMPATMLSEEPLTLNAPRLSDIRMTTLLQSLGAEVSTLQDGQ 71
Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+ ++ + I +R + A++ G G+A L G
Sbjct: 72 VLAM-----SSHINNHTADYDI-VRKMRASILVLGPMPLARDGHAVVSLPGGCA 119
Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + L+ LGA +D ++ P +GGL GG + +S
Sbjct: 120 IGARPVDLHLKALEALGAQLDLKDGYPVHAKAP-----LGGLKGGVIDFP-LVSVGATEN 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LMAA LA G +I+ P + + + G + E + I+G +
Sbjct: 173 ALMAATLAKGTT---LINNAAREPEIVDLAQCLRKMQAIE-GEGTSTITIQGVDRHLGA 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ V +Y LA AI GG V + G + ++ F LE G ++T E S+
Sbjct: 229 THPVVTDRIELGTMYLA-PAICGGEVELLGGKRSLEA---FCNKLEAAGVEITENENSL 284

Query: 306 TVTGGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
TV G +KA+DV P D+ + + A+G + + + ++ E
Sbjct: 285 TVR-----RGDNRVKAVDVVTEPFPGFPTDLQAQMMALMCTAEGTSVLEE---KIFEN 334

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
M A EL ++GA ++ + +T E L + D R +++ LA A
Sbjct: 335 RFMHA--PELIRMGAQIDVQGGHATVTGVEGLKGAPV-MATDLRASVSLILAGLA 386

>ref|ZP_08056149.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
gb|EFX46185.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
Length = 436

Score = 44.3 bits (103), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 92/381 (24%), Positives = 153/381 (40%), Gaps = 44/381 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + GTV++ G+K+ + ++ A L+E T +DNL DV L LG V+ D
Sbjct: 27 RPLKGTVQISGAKNSAVALIPAAILAETTVTLNPLSDVAIYAEILSDLGADV KWD-- 84

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI---AMRSLTAAVTAAGGNATYVLDGVPR 128
G + D + + N + A L A+ G A L G
Sbjct: 85 -----GDQMMIDPSHMKAMPMPNGNVKKLRASYLLMGAMLGRFGEAVIGLPGGCN 134

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + G + LGA++ G +R L G K+ L +S +++
Sbjct: 135 FEPRPIDQHIKGFALGAEISNENGALF--IRAK---QLRGAKIYLD-MVSVGATINIML 188

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G +I+ P + L+ G K + + + + I+G +++
Sbjct: 189 AASRAK---FTLIENAAKEPEIIDVATLLNSMGAKIKGAGT-ETIRIEGVDALHGCRHS 244

Query: 249 YVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ + +Y +A AA T G VTV+ ++ L+ MG ++ + S+ V
Sbjct: 245 IIPDRIQAGTYMIAAAA-THGDVTVDNIIIPKHMEA---LTAKLQEMGVQIEEMDESIRV- 299

Query: 309 GPPREPFGKHLKAIDVNMNKMPPDVAMTLA--VVALF--ADGPTAIRD-VASWRVKETER 363
FG + IDV P A L + +L A G + I D V S R K+
Sbjct: 300 -----FGTPHYEPIDVKALVYPGFATDLQSPMTSLLTQASGVSIITDHVYSNRFKQIPE 353

Query: 364 MVAIRTELTKLGAS--VEEGP 382
++ + ++ G S VE GP
Sbjct: 354 LIRMGAQIKVEGRSAVVEGGP 374

>ref|YP_002835673.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Corynebacterium
aurimucosum ATCC 700975]
ref|ZP_06042966.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
aurimucosum ATCC 700975]
gb|ACP33735.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Corynebacterium
aurimucosum ATCC 700975]
Length = 424

Score = 44.3 bits (103), Expect = 0.034, Method: Compositional matrix adjust.
Identities = 107/452 (23%), Positives = 172/452 (38%), Gaps = 51/452 (11%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M ++ ++ + GTVK+ G+K+ +++ A L+EGTT + N DV M L
Sbjct: 1 MGVKDQFIVSGGARLQGTVKVDGAKNSVLKLMAAALLAEGTTTLTNCPEILDVPLMRKVL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAV-----T 113

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      LG +VE D      R      P E      NA  A+R  A+V      T
Sbjct: 61  EGLGCTVEIDGHTVRITT-----PAE-----LHSNADFDAVRQFRASVCVLGPLT 105

Query: 114 AAGGNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVK 173
      A  G+A  L G  +  RP+      GL+++GA      G      V      L G  ++
Sbjct: 106 ARCGHAKVALPGGDAIGSRPLDMHQSGLEKMGARTRIEHG-----AVVAEADRLHGANIR 160

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
      L  S      +L AA LA G+ ++      P +      +++ G +      +
Sbjct: 161 LDFFP-SVGATENILTA AVLADGETQLH--NAAREPEIVDLCTMLKEMGAIEIS-GEGETST 215

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
      I+G K + P      V GD  A  +  A +T G +TV G      L  +  E L+
Sbjct: 216 ITIQGVDKLQ-PTEHEVIGDRIVAGTWAYAAVMTRGDITVGGIAPKHLHLPL---EKLKS 271

Query: 294 MGAKVT--WTETSVTVTGPPPREPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIR 351
      GA V      V + G P      A+D      P      L  +A+  G +A+
Sbjct: 272 AGADVEDYVNGFRVRMNGRP-----SAVDYQTLPPYPGFPTDLQPIAI---GLSAVA 319

Query: 352 DVASWRVKET-ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAF 410
      + S  +  E      E+ +LGA  +  + +I  E+L+ T + + D  A
Sbjct: 320 EGTSIITENVFESRFRFVDEMLRLGADAQVDGHHVIRGQERLSSTHVWSSDIRAGAGLV 379

Query: 411 SLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
      A CA+  T+ D      + +P++ + L
Sbjct: 380 LSALCADETTTVHDVVFHIDRGYPNFVENLQAL 411

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>ref|NP_219968.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis D/UW-3/CX]
      ref|ZP_05353837.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis 6276]
      ref|ZP_05358815.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis 6276s]
      sp|O84461.1|MURA_CHLTR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
      gb|AAC68055.1| UDP-N-Acetylglucosamine Transferase [Chlamydia trachomatis
      D/UW-3/CX]
      gb|ADH19080.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis G/11222]
      gb|ADI51132.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis D-EC]
      gb|ADI52144.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis D-LC]
      Length = 444

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Score = 44.3 bits (103), Expect = 0.035, Method: Compositional matrix adjust.
Identities = 98/438 (22%), Positives = 173/438 (39%), Gaps = 87/438 (19%)

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Query: 15  ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G+V++ G+K+ + ++L+ + LS+  T++ N+ N EDV  +  R LG  VE D+ A+
Sbjct: 12  LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLRCRVLGAIVEWDQQAQ 71

Query: 75  -----RAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      R ++      +F      + + L  A  +      V      GG+A
Sbjct: 72  VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCYPGIFVPILGGDA----- 120

Query: 128 RMRERPIGDLVVGKQLGADV---DCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
      +  R  +  +  GLK+LGA++  D      P      GL G  + L  S
Sbjct: 121 -IGPRTLHFHLEGLKKLGAEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      L++A+  A G      +E+EIID ++      +++ GV+  +D+  I
Sbjct: 172 NLILASVGAQGRTIKNAALEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G Q  + S +++ +      +AS+ +A A ++ G + VE      +  + F +VL  +G
Sbjct: 221 GCQDFYSVEHSIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

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Query: 298 VTWTETSVTVTGPPREPFGGRKHLKA-----IDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+ E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENG I-----EFFYDKPLKGGVLETDVHPGFITDWQQPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
+ D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

>gb|ADX44916.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
avenae subsp. avenae ATCC 19860]
Length = 434

Score = 44.3 bits (103), Expect = 0.035, Method: Compositional matrix adjust.
Identities = 95/405 (23%), Positives = 161/405 (39%), Gaps = 62/405 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ ++ + +SG V + G+K+ + L A L+ + N+ +DV ML +R +G
Sbjct: 2 DQLQIRGGRALSGDVPISGAKNAALPELCAALLTAEPVTLNVPRLQDVATMLQLIRNMG 61

Query: 65 LSVEADKAAKRA---VVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
++ E + RA V G +A E+ ++++ A+V A G
Sbjct: 62 VAAEHSQGDDRASSGTVRIDAGALSTPEAPYEL-----VKTMRASVLALGPLLAR 111

Query: 117 -GNATYVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLS 175
G AT L G + RP+ + GL +GA++ G I LP G+ +L
Sbjct: 112 FGEATVSLPGGCAIGSRPVDQHIKGLSAMGAIEIVVEHGYM-----IARLPEGRSRLQ 163

Query: 176 GS-ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAE-HS 228
G+ I++ ++ LLMAA LA G+ +++ P V ++ G + E H
Sbjct: 164 GARITDMVTVTGTENLLMAATLADGET---VLENAAQEPEVVDLAEMLIAMGAQIEGHG 220

Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFA 288
S R ++G ++ + V D A FL A TGG + L +
Sbjct: 221 TS--RIRVQGVRLHGCTHRVV-ADRIEAGTFLCAVAATGGEALLRHGRADHLDAVI--- 274

Query: 289 EVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFA 344
+ L G V E + V P G L+A + P D+ + + A
Sbjct: 275 DKLRDAGVTVESVEGGIRVRSP-----GAGQLRAQSFRTTEYPGFPTMQAQFMA LNVA 329

Query: 345 DGPTAIRDVASWRVKET--ERMVAIRTELTKLGASVEEGPDYCI 387
G + RV ET E EL +LGA ++ +I
Sbjct: 330 QGAS-----RVTETIFENRFMHVDELLRLGARIQADGKVAVI 366

>ref|YP_004025746.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor kristjanssonii 177R1B]
gb|ADQ40133.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor kristjanssonii 177R1B]
Length = 419

Score = 44.3 bits (103), Expect = 0.035, Method: Compositional matrix adjust.
Identities = 93/402 (23%), Positives = 164/402 (40%), Gaps = 42/402 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V++ + G V + G+K+ + ++ A +++G +V++NL EDV M L LG
Sbjct: 6 EKLVIIEGGYPLEGEVINGAKNAAVIPAALMADGESVIENLPLIEDVFAMDDILRLG 65

Query: 65 LSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ ++++ A L A+ G A +
Sbjct: 66 AKIEYDNHSLKIDARNLHSYIAPYEVKKIR-----ASYLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RPI + G + LGA+V G ++ L G K+ L +S
Sbjct: 118 GGCNFGSRPIDQHIKGFRLGAEVKIENG-----IKAYA-DRLVGTKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKS 244

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      L++AA  A G      II+      P+V  T   +   G K + + + D   I+G  K
Sbjct: 172 NMLAAVKAKGTT---IIENAAKEPHVVDANFLNSMGAKIKGAGT-DVIRIEGVDKLYP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
      K A +      + +Y +A  A T G V V+      L+      A+++E MGA+V   E S
Sbjct: 228 TKYAIIPDQIEAGTYMIAACA-TKGHVIVKNVIPKHLES LT--AKLVE-MGAEVITYEDS 283

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNKM P----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      +      E  R  L++ +      P   D+   + V+      G + + +   W
Sbjct: 284 I-----EVICRGR LRSASIKTMPYPGFPTDLQPQMTVLLSLCSGTSVVTE-GVW---- 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
      E      EL K+GA+++      ++   E L      V A+D
Sbjct: 332 -ENRYQYVDELKKMGANIKVEGRVAVVEGVESLQGAEEVAVD 372

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>ref|YP_909046.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
      adolescentis ATCC 15703]
dbj|BAF38964.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
      adolescentis ATCC 15703]
Length = 441

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Score = 44.3 bits (103), Expect = 0.035, Method: Compositional matrix adjust.
Identities = 87/376 (23%), Positives = 155/376 (41%), Gaps = 42/376 (11%)

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Query: 13 KEISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++GT+K+ G+K+ ++ ++ A L+ GT+V+ N+   DVH +   LR  G+ V  D A
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGTSVLKNVPEIRDVHVVDLLRLHGVDTVVDGA 74

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
      VV      + D   +V   G++ I +   +   +   G A   G   +   R
Sbjct: 75 --NGVV TIDATNVQLADVA-DVDTLGSSRIPI L-FSGPLLHRLGEAFIPALGGCNIGGR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS---GSISSQYLSALLM 188
      PI   +   L++LGA+VD      + +   GL G K+ L   G+   L+A+L
Sbjct: 131 PIDFHLETLRKLKANVDK---EHKDG IHITAPNGLHGAKIHL PYP SVGATEQTLLAAVLA 187

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247
      L   IE      P +   + ++++ G  A  S   DR F I+G ++ K   +
Sbjct: 188 EGKTELSGAAIE-----PEIMDLVSVLQKMG--AIISVDVDRTFRIEGVKELKGYTH 237

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      + D   A+ + + A  T G + V+G   +   + F  V   +G +   T+   +
Sbjct: 238 TSLT-DRIEAAASWAALATHGDIFVKGATQPEM---MTFLNVFRKIGGEFDITDKGIRF 293

Query: 308 TGPPREPFGRKHLKAI----DVNMNKM P DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      P   +      LK +   DV+   M D   L V   A+G + + +   E
Sbjct: 294 WHPGGD-----LKPVAIETDVHPGFMTDQQQLVVALTQANGLSIVHETVY-----EN 341

Query: 364 MVAIRTELTKLGASVE 379
      L ++GA+++
Sbjct: 342 RFGFTKPLVQMGATIQ 357

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>ref|YP_002888077.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis B/Jali20/OT]
ref|YP_002888959.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis B/TZ1A828/OT]
emb|CAX10018.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis B/TZ1A828/OT]
emb|CAX10911.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
      trachomatis B/Jali20/OT]
Length = 444

```

Score = 44.3 bits (103), Expect = 0.036, Method: Compositional matrix adjust.
Identities = 98/438 (22%), Positives = 173/438 (39%), Gaps = 87/438 (19%)

```

Query: 15 ISGTVKLPGSKSLSNRILL AALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV   +   R LG  VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLCRVLGAIVEWDQQAQ 71

```

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ +F + + L A + V GG+A
Sbjct: 72 VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCYPYGFVPIILGGDA----- 120

Query: 128 RMRERPIGDLVVLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ R + + GLK+LGA++ D P GL G + L S
Sbjct: 121 -IGPRTLHFHLEGLKKLGAIEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
L++A+ A G +E+EIID ++ +++ GV+ +D+ I
Sbjct: 172 NLILASVGAQGRTIIKNAALEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Q + S +++ + +AS+ +A A ++ G + VE + + F +VL +G
Sbjct: 221 GCQDFYSVEHSIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKA-----IDVNMNMKMPDVAMTLAVVALFADGPTAIRD 352
+ E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENG I-----EFFYDKPLKGGVLETDVHPGFITDQQPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
+ D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

>ref|NP_954143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
sulfurreducens PCA]
sp|Q748B3.1|MURA_GEOSL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAR36493.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
sulfurreducens PCA]
gb|ADI85853.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
sulfurreducens KN400]
Length = 417

Score = 44.3 bits (103), Expect = 0.036, Method: Compositional matrix adjust.
Identities = 92/381 (24%), Positives = 153/381 (40%), Gaps = 45/381 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++++ K++ G V + GSK+ + I + L+ G + N+ D++ + L +LG
Sbjct: 2 DKLIKGGKKLIGEVSVSGSKNAALPIFVSTILAPGLNEIRNVPFLRDINTTIKVLESLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
VE + R VE + V+ MR+ + + A G A
Sbjct: 62 AVVEGNGNIVRIDTTHVNN---VEATYDLVK-----TMRASVLVLGPLLARHGRARV 110

Query: 122 VLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RPI + GL LGAD+ G + L G ++ S
Sbjct: 111 SLPGGCAIGARPINLHLKGLAALGADIRLEHGVEAKAK-----KLKGARINFDISTVGG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
L+MAA LA G+ +++ P + ++ + G K + + + D I G K
Sbjct: 166 T-EQLMMAAALAKGET---VLENAAREPEIIDLAETLIKMGAKIDGAGT-DTIRIT-GVK 219

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+P V D A F+ AAITGG + + L V F L+ G ++T
Sbjct: 220 ELAPVAHDVMPDRIEAGTFMVAAAITGGDIKIRNMKLEHLDALV-FK--LQDAGVEITNR 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ V V G PR P KA+++ P D+ + ADG + I S
Sbjct: 277 DNVVRVKG-PRRP-----KAVNIKTRPYPGFPTDMQAQFMALMCVADGASVI----SEN 325

Query: 358 VKETERMVAIRTELTKLGASV 378
+ E M +EL + GA +
Sbjct: 326 IFENRFMHV--SELLRFGADI 344

>ref|YP_928947.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella amazonensis SB2B]
sp|A1SA71.1|MURA_SHEAM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABM01278.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella amazonensis SB2B]
Length = 418

Score = 44.3 bits (103), Expect = 0.036, Method: Compositional matrix adjust.
Identities = 89/400 (22%), Positives = 164/400 (41%), Gaps = 49/400 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ +Q ++GTV + G+K+ + IL+ L+E V+ N+ + DV LR LG
Sbjct: 2 DKLSIQSGGGLAGTVVISGAKNAALPILMAGVLAESPFVLTNVP SLRDVDTCKLLRLCLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V D G + ++ ++ + F+ + +++ A++ G G
Sbjct: 62 AEVTQD-----GDRITIDSSR--IDHFVAPYEL-VKTRASILILGPLLARFGT 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + GL+Q+GA ++ G ++ G L G + + +
Sbjct: 108 ADVSLPGGCAIGARPVNHLHLGLEQMGAKIEVKEGY----IKARVDGRLKGAHIFMD-MV 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S LLMAA LA G + +I+ P V + G + + I G
Sbjct: 163 SVGATENLLMAAALADG---VTVIENAAREPEVIDLANCLVAMGAQISGIGTAT-LKITG 218

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKV 298
++ + V D FL AA+T G + E +SL+ LE GA++
Sbjct: 219 VERLNGC-DYRVMPDRIETGTFVAAAVTRGRIRCENADPSSLE---SVLAKLEDAGAEI 274

Query: 299 TWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
+ + + + P KA+++ P D+ V+ A+G I +
Sbjct: 275 NTGDDWIELDMHGKRP-----KAVNIKTAPYPAFPTDMQAQFCVLNCLAEGTGTITET- 327

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL ++GA++E CI+ E+L+
Sbjct: 328 ---IFENRFMHV--PELMRMGANMELEGHTCIVHGVRLS 362

>ref|YP_001858979.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia phymatum STM815]
sp|B2JHY7.1|MURA_BURP8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACC71933.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia phymatum STM815]
Length = 420

Score = 44.3 bits (103), Expect = 0.036, Method: Compositional matrix adjust.
Identities = 69/273 (25%), Positives = 119/273 (43%), Gaps = 27/273 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ ++++G + + G+K+ + IL LS +DN+ + +DV L L +G
Sbjct: 2 DKLVIEGGQKLAGEIVVSGAKNAALPILCAGLLSAEPVHLDNVDPDQDVRTTLKLLGQMG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+ E+ GK ++ +K + + MR+ + + A G A
Sbjct: 62 VRTES-----ADGKVS LDASKVDNLVAPYELVKTRASILVLGPLVARFGEAKV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA+++ G + R L G ++ ++ I+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAIEINIEHGFIEARAKR-----LKGARI-ITDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ II+ P V L+ G K E + DR I+G

Sbjct: 164 TG TENLLMAAVLADGET---IIENAAREPEVGD LASLLVSMGAKIEGIGT-DRLVIQGV D 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273

K K+ V D A FL A GG VT+

Sbjct: 220 KLHGAKHTVVP-DRIEAGTFLCAVAAAGGDVTL 251

>ref|ZP_07398801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
duerdenii ATCC BAA-1640]
gb|EFM26127.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Peptoniphilus
duerdenii ATCC BAA-1640]
Length = 416

Score = 44.3 bits (103), Expect = 0.037, Method: Compositional matrix adjust.
Identities = 77/328 (23%), Positives = 138/328 (42%), Gaps = 44/328 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL G 64

E I ++ ++GTVK+ G+K+ + IL L T+++ + + +D+ M+ +++LG

Sbjct: 2 ERIYVKKSGPLNGTVKVSGAKNAALPILAATILGTTETILEGVPDLKDISIMIEVIKSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

VE + K + + E + E + MR+ + + V++

Sbjct: 62 --VEVEHLGKHTLKINAKNLNAYETSYELMS-----KMRASSVVMGPLLARMRKVIN 111

Query: 125 GVP---RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181

+P + RPI + G + LG D+ V G + KL G S+

Sbjct: 112 PLPGGCNIGARPIDLHLKGFRALGVDI-----VEEPGKITASAEKLIG--STI 157

Query: 182 YL-----SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233

YL ++MAA +A G+ II+ P + + + G + + +

Sbjct: 158 YLDFPSVGATQNIMMAATMAEGET---IIENAAMEPEIVDLASFLNKMGARIMGAGT-SS 213

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEM 293

IKG + + + D A F+ AA+TGG V VE C + ++ + A+++E

Sbjct: 214 IRIKGVKSLSGATHQIIP-DRIEAGTFMVAAMTGGDVLVENCIPSHMKPII--AKLIE- 269

Query: 294 MGAKVTWTETSVTVTGPP-REPFGRKHL 320

GA+V + SV V G PF K L

Sbjct: 270 AGAEVEVDDDSVRVKGNKIVNPFDIKTL 297

>ref|ZP_04633531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
frederiksenii ATCC 33641]
gb|EEQ13766.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
frederiksenii ATCC 33641]
Length = 421

Score = 44.3 bits (103), Expect = 0.037, Method: Compositional matrix adjust.
Identities = 104/431 (24%), Positives = 171/431 (39%), Gaps = 59/431 (13%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68

+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E

Sbjct: 6 VQGRTRLSGEVTISGAKNAALPILFAALLAEFPVELQNVPKLKDIDTTIKLLSQLGTKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122

D A +V V G V F + ++++ A++ A G G

Sbjct: 66 RD--ASGSVFDASG-----VDEFCAPYDL-VKTMRASIWALGPLVARFGKGQVS 112

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182

L G + RP+ + GL+QLGA++ G V+ + G L + + +S

Sbjct: 113 LPGGCAIGARPVDLHITGLEQLGAIEKLEEGY----VKASVNGRLKAAHIVMD-KVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237

++ AA LA G +I+ P + T + G K + + DR I+

Sbjct: 168 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKITGAGT-DRITIEGVARL 223

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297

GG Y+ V D FL AAI+GG V +L D A++ E GA

Sbjct: 224 GGGVYR-----VLPDRIETGTFLVAAAIISGGKVVCVRQTRPDTL--DAVLAKLRE-AGAD 274

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPP----DVAMTLAVVALFADGPPTAIRDV 353

```

      +   E   +++   + P       KA+       P   D+   +++ L A+G   I +
Sbjct: 275 IEIGEDWISLDMHGQRP-----KAVFTRTAPHPGFPTDMAQFSLNLVAEGTGVITET 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
      + E   M       EL ++GA E   + I   E+L+   +   D R + +   LA
Sbjct: 329 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVQEQLSGAQV-MATDLRASASLVLA 381

Query: 414 ACAEVPVTIRD 424
      C       VTI D
Sbjct: 382 GCIADGVITVD 392

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>ref|ZP_05815359.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
      sp. 3_1_33]
gb|EEW94807.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
      sp. 3_1_33]
      Length = 423

```

Score = 44.3 bits (103), Expect = 0.038, Method: Compositional matrix adjust.
Identities = 71/287 (24%), Positives = 123/287 (42%), Gaps = 24/287 (8%)

```

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
      K+ISG +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKISGELKVDGSKNSTLPIMIATLVKEKGTIYILKNVPDLRDIRTLVALLESGLGLEVEKLDA 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
      + + + G G       D ++++ FL G+       V   GG A       +
Sbjct: 71 NSYKIINNLGSAEASDYDLVKMRASFLVMGGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
      RP+   + G + LGA ++   G       V       GL GG + L   S       ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY----VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYV 250
      A G       I++   P +E       + + G K       + + R I G K       + + + +
Sbjct: 177 VKAKGKT---ILENAAKEPEIEDLCNFLIKMGAKISGAGTG-RIEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      + +Y +A + +   G++ V G       L       F       LE MGAk
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAK 275

```

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>ref|YP_969394.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
      avenae subsp. citrulli AAC00-1]
sp|AlTKY2.1|MURA_ACIAC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|ABM31620.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
      citrulli AAC00-1]
      Length = 434

```

Score = 44.3 bits (103), Expect = 0.038, Method: Compositional matrix adjust.
Identities = 70/281 (24%), Positives = 122/281 (43%), Gaps = 40/281 (14%)

```

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
      +++ ++   + +SG V + G+K+ +   L A L+   + N+   +DV ML +R +G
Sbjct: 2 DQLQIRGGRALSGDVPISGAKNAALPELCAALLTAEPVTLNVPRLQDVATMLQLIRNMG 61

Query: 65 LSVEADKAAKRA---VVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
      ++ E + RA       V       G       +A E+       +++++ A+V A G
Sbjct: 62 VAAEHSQGDDRASSGTVRIDAGALSTPEAPYEL-----VKTMRASVLALGPLLAR 111

Query: 117 -GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLS 175
      G AT L G       + RP+   + GL +GA++   G       I LP G+ +L
Sbjct: 112 FGEATVSLPGGCAIGSRPVDQHIKGLSAMGAIEIVVEHG-----YMIARLPEGRSRLQ 163

Query: 176 GS-ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAE-HS 228
      G+ I++ ++       LLMAA LA G+       +++   P V       ++   G + E H
Sbjct: 164 GARITDMVTVTGTENLLMAATLADGET---VLENAAQEPEVVDLAEMLIAMGAQIEGHG 220

```


Query: 229 DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGG 269
S R ++G ++ + V D A FL A TGG
Sbjct: 221 TS--RIRVQGVRLHGCTHRVV-ADRIEAGTFLCAVAATGG 258

>ref|YP_585391.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cupriavidus metallidurans CH34]
sp|Q1LIA4.1|MURA_RALME RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABF10122.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cupriavidus metallidurans CH34]
Length = 416

Score = 44.3 bits (103), Expect = 0.038, Method: Compositional matrix adjust.
Identities = 67/264 (25%), Positives = 113/264 (42%), Gaps = 25/264 (9%)

Query: 15 ISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L+ T + N+ + +D ML LR +G+ E
Sbjct: 12 LKGEIRISGAKNAALPILCAGLLTADTVTIGNVPLQDTRTMLKLLRQMGMAEMVDGV- 70

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMRE 131
A + G P E + + V+ MR+ + + A G A L G +
Sbjct: 71 -ATLQGADINSP-EASYDLVK-----TMRASILVLGPLVARFGEARVSLPGGCGIGA 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+ +GA++ G R N L G +V ++ I+ LLMAA
Sbjct: 121 RPVDQHIKGLQAMGAEITIEHG--FIHARAN---RLKGARV-VTDMITVTGTENLLMAAT 174

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G+ +++ P V L+ + G K E + DR ++G + ++ V
Sbjct: 175 LAEGET---VLENAAREPEVTDLAELLVKMGAKIEGIGT-DRLVVQGVDRHLGAEHKVV- 229

Query: 252 GDASSASYFLAGAAITGGTVTVEG 275
D A FL AA T G + + G
Sbjct: 230 ADRIEAGTFLCAAAATLGDIVLRG 253

>ref|YP_003145844.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Kangiella koreensis DSM 16069]
gb|ACV26076.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Kangiella koreensis DSM 16069]
Length = 419

Score = 44.3 bits (103), Expect = 0.038, Method: Compositional matrix adjust.
Identities = 95/425 (22%), Positives = 171/425 (40%), Gaps = 52/425 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+++++ + G +K+ G+K+ + IL+ A L +G T + NL + DV L + LG
Sbjct: 2 DKLLIKDAGPLDGAIKISGAKNAALPILMGALLVDGVTIGNLPHLNDVTTTLELMGRLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ D KF VE ++ + + + + A+ + G G
Sbjct: 62 AKLTIDD-----KFNVEIDSRKIHSEAPYEL-VKTRASILVLGPLLARFGE 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSI 178
A L G + RP+ + G++++GAD++ G V+ G L G K+ + +
Sbjct: 109 AVVSLPGGCAIGSRPVNLHIEGMREMGADIEVEAGY---VKAKSNGRLKGAKIVME-MV 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S L+MAA LA G +I+ P V + G K + + I+G
Sbjct: 164 SVGATENLIMAAALADG---TSVIENAAREPEVVDLANFLNSMGAKISGAGT-SVITIEG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGD-VKFAEVLEMMGAK 297
++ + + + +Y +A AA+T G + L VK E GA+
Sbjct: 220 VERMHGHHHDVLPDRIETGYLVA-AAMTRGRIRCRNTDPDILDVAVLKLREA---GAE 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
VT E + + P KA+++ P D+ + ADG I +
Sbjct: 275 VTTGEGWIELDMKGNRP-----KAVNIKTAPYPGFPTDMQAQFCAMNAVADGTGTITET 328

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M + E+ ++GA + + I EKL+ + D R + + LA
Sbjct: 329 ----IFENRFMHVL--EMQRMGADIAIEGNTAICRGVEKLSGAQV-MATDLRASASLVLA 381

Query: 414 A-CAE 417
CAE
Sbjct: 382 GLCAE 386

>ref|YP_003465691.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
seeligeri serovar 1/2b str. SLCC3954]
emb|CBH28609.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
seeligeri serovar 1/2b str. SLCC3954]
Length = 423

Score = 44.3 bits (103), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 99/418 (23%), Positives = 175/418 (41%), Gaps = 50/418 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V+Q K+++GT+++ G+K+ + ++ A L+E V++ L + DV+ + L LG
Sbjct: 3 EKLVIQGGKLAGTLQVDGAKNSAVALIPAAILAESEVVLEGLPDISDVYTLYDILEELG 62

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVL 123
+V +D K AV+ D + + L N + +R+ + A G +
Sbjct: 63 GNVRSN--KTAVI-----DPTNMISMPLPNGNVKLRASYLMGAMLGRFKKAV 110

Query: 124 DGVP---RMREPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISS 180
G+P + RPI + G + LGA V G +R+ + L G ++ L +S
Sbjct: 111 IGLPGGCVLGP RPIDQHIKGFALGAKVTNEQGAIY--LRAD---ELIGARIYLD-VVSV 164

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
+++AA A G II+ P + L+ G + + + D I G +
Sbjct: 165 GATINIMLA AAVRAKGT---IENAAKEPEIIDVATLLSNMGAIKAGT-DTIRITGVE 220

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + D A F+ AA +G V +E T L+G + A++ E MG +
Sbjct: 221 HLGCHHTIIP-DRIEAGTFMVLAAASGKGVRIENVIPTHLEGII--AKLTE-MGVPM DI 276

Query: 301 TETSVTVTGPPREPFGRKHLKAIDVNMNKM P----DVAMTLAVVALFADGP TAIRD-VAS 355
E ++ V + +K ID+ P D+ L + ADG + + D +
Sbjct: 277 EEDAIFVGEVEK-----VKKIDIKTYAYPGFPTDLQQPLTALLTRADGSSVVTDTIYP 329

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
R K EL ++G + +IT P KL + + T D R A +A
Sbjct: 330 SRFKHI-----AELERMGGKFKLEGRSAVITGPAKLQGSKV-TATDLRAGAALVIA 379

>ref|NP_893417.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus subsp. pastoris str. CCMP1986]
sp|Q7V0G1.1|MURA_PROMP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAE19759.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus subsp. pastoris str. CCMP1986]
Length = 457

Score = 44.3 bits (103), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 88/390 (22%), Positives = 160/390 (41%), Gaps = 46/390 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G VK+ G+K+ + +L + L++ ++DN+ D+ M L+ LG+ + +K
Sbjct: 22 KTLRGKVKISGAKNSALVLLAASLLTDEKIIIDNVPLLT DIEKMGNILKNLGVKLH-NKD 80

Query: 73 AKRAVVVGCGGKFPVEDAK----EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
+ + D+K +E+ L N A A+ G A+ L G
Sbjct: 81 HQLII-----DSKNISIQELPYELVNLGRASFFCIGALLTRFGEASIPLPGGCN 129

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLSALL 187
+ ERPI + + GL+ LGA++ + D ++ G ++L+ S L+

Sbjct: 130 IGERPINEHINGLRALGAEI--IIDRDVVKAKLVKKKTKLFGANIRLNCP-SVGATETLI 186

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G +I+ P ++ +++ + G K + ++ I G K +

Sbjct: 187 MAASLAEGRT---VIENAAREPEIQDLCQMLNKMGAKEI-YDSGKEKIIDGVHKLHGCTH 242

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A FL AA T ++TV L+ LE G+K+ S+++

Sbjct: 243 KVIP-DRIEAGTFLIAAAATSSSITVSPVIPNHLEA---VLNKLSESGSKIIKGNISISI 298

Query: 308 TGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
G ++KA+D+ P L + A+ +A R K TE +

Sbjct: 299 KG-----NNIKAVDIKTAPFPGFPTDLQAPFM-----ALMTIAKGRSKITETIFEN 344

Query: 368 RTE----LTKLGASVEEGPDYCIITPPEKL 393
R L ++G+S+ + I +KL

Sbjct: 345 RMNHVDLLNQMGSSITLKNINIAHINGVKKL 374

>ref|ZP_07661296.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseibium sp.
TrichSKD4]
gb|EFO28851.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseibium sp.
TrichSKD4]
Length = 429

Score = 44.3 bits (103), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 47/170 (27%), Positives = 77/170 (45%), Gaps = 13/170 (7%)

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL LGAD++ G V V GGL G +V+ +S ++MAA

Sbjct: 131 RPVDFIDGLAALGADIEIEGGY---VVVKAPGGLKGARVEFP-KVSVGATHTIMMAAT 185

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G+ EI + + + LR M G + E D ++G ++ +A +

Sbjct: 186 LANGETEIVNAAREPEVSDLAACLRAM---GARIE-GDGTSTIRVQGVKRLHGAHHAVLP 241

Query: 252 GDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ +Y +A A+TGG V ++G L + + L GA++T T

Sbjct: 242 DRIETGTYAMA-VAMTGGNVLLKGARADLLDSAL---DTLRQTGAETITET 287

>ref|YP_001456079.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Citrobacter
koseri ATCC BAA-895]
sp|A8AQ80.1|MURA_CITK8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABV15643.1| hypothetical protein CKO_04592 [Citrobacter koseri ATCC BAA-895]
Length = 419

Score = 44.3 bits (103), Expect = 0.041, Method: Compositional matrix adjust.
Identities = 98/421 (23%), Positives = 168/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE +

Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLDIDTTMKLLSQLGTVKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + +V +F + +++++ A++ A G G L G

Sbjct: 68 -----GSVIDAS--QVNIFCAPYEL-VKTMRSIHALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++

Sbjct: 117 IGARPVDLHITGLEQLGAIEIKLEEGY---VKASVNGRLKGAIHVM-DKSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P + T + G K + DR I+G ++

Sbjct: 172 AATLAEGTT---VIENAAREPEIVDTANFLVTLGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A+ L GA + E +++

Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTL--DAVLAK-LRDAGADIETGEDWISL 282

Query: 308 TGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA++V P D+ ++ L A+G I + + E

Sbjct: 283 DMHGQRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTTET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+

Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTLV 389

Query: 424 D 424

D
Sbjct: 390 D 390

>emb|CAM89159.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]
emb|CAM89168.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]
emb|CAM89177.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]
emb|CAM89186.1| 3-phosphoshikimate-1-carboxyvinyltransferase [Brucella melitensis]
Length = 188

Score = 44.3 bits (103), Expect = 0.041, Method: Compositional matrix adjust.
Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 4/101 (3%)

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI--TPPEKL 393
LA+ A FA+G T + + RVKE++R+ A+ L G EG + + L

Sbjct: 88 LAIAASFAEGETVMDGLDELRVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPGGKGL 147

Query: 394 NVTADITYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFP 433
+ T+ DHR+AM+F + A E PVT+ D +FP

Sbjct: 148 GGGTVGTHLDHRIAMSFLVMGLASEKPVTVDDSTMIATSFP 188

>ref|NP_995094.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Microtus str. 91001]
gb|AAS63971.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Microtus str. 91001]
Length = 423

Score = 44.3 bits (103), Expect = 0.043, Method: Compositional matrix adjust.
Identities = 104/439 (23%), Positives = 173/439 (39%), Gaps = 60/439 (13%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGAL 60
M ++ +Q +SG V + G+K+ + IL A L+E + N+ +D+ + L

Sbjct: 1 MVTMDKFRVQGRTRLISGEVTISGAKNAALPILFAALLAEPELVQNVPKLDIDTTIKLL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---- 116
LG +E + G F A E F + +++ A++ A G

Sbjct: 61 SQLGTKIERNN-----GSVFVDASAVNE---FCAPYDL-VKTMRSIWIWALGPLVA 106

Query: 117 --GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKL 174
G L G + RP+ + GL+QLGA++ G V+ + G L G + +

Sbjct: 107 RFGQGQVSLPGGCAIGARPVDLHITGLEQLGAEIKLEEGY----VKASVNGRLKGAHIVM 162

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
+S ++ AA LA G +I+ P + T + G K + + DR

Sbjct: 163 D-KVSVGATVTIMSAATLAEGTT---VIENAREPEIVDTANFLNLTGAKISGAGT-DRI 217

Query: 235 YIK-----GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAE 289
I+ GG Y+ V D FL AAI+GG V +L D A+

Sbjct: 218 TIEGVTRLGGGVYR-----VLPDRIETGTFLVAAAISGGKVVCQRTPDTL--DAVLAK 269

Query: 290 VLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFAD 345
+ E GA + + +++ + P KAI P D+ +++ L A+

Sbjct: 270 LRE-AGADIEVGDDWISLDMQKRP-----KAITFRTAPHPGFPTDMQAQFSLNLVAE 322

Query: 346 GPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHR 405
G I + + E M EL ++GA E + I E+L+ + D R

Sbjct: 323 GTGVITET----IFENRFMHV--PELIRMGAAHAEIESNTVICYGEVQLSGAQV-MATDLR 375

Query: 406 MAMAFSLAACAEVPVTIRD 424

+ + LA C VTI D
Sbjct: 376 ASASLVLAGCIAEGVTIVD 394

>ref|ZP_02441426.1| hypothetical protein ANACOL_00699 [Anaerotruncus colihominis DSM 17241]
>gb|EDS12471.1| hypothetical protein ANACOL_00699 [Anaerotruncus colihominis DSM 17241]
Length = 459

Score = 44.3 bits (103), Expect = 0.043, Method: Compositional matrix adjust.
Identities = 93/386 (24%), Positives = 148/386 (38%), Gaps = 52/386 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ ++Q ++G V + G+K+ + I+ L++G V++N+ N D+ + LR LG
Sbjct: 34 EQFIVQGETHLNGEVTISGAKNAAVAIIPATILAQGKCVIENIPNISDIKVLQILRALG 93

Query: 65 LSVEA-DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
SV+ D+ V VE V L A L A+ A A+ +
Sbjct: 94 ASVQMLDRTT-----VEIDTTHIVEPV---VPYELARYMRASYLLGALLARCNRASVSM 145

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G RPI + G + LGADV G +N L G +S
Sbjct: 146 PGGCNFGVRPIDQHMKGFALGADVSDSGM-----INARADLLLAGAHYFDVVSVGAT 199

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+++A+ A G I I++ P++ + G + + D I G
Sbjct: 200 INVMLASVKAG---ITILENCAKEPHIVDLANFLNSMGADIRGAGT-DVIKIHGVDILH 255

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + +Y +A AA TGG V V L+ E LE GA V +
Sbjct: 256 GTTYPIIPDQIEAGTYMVAAAA-TGGDVLVRNVIPKHLEA---ITEKLEKAGATVIEYDD 311

Query: 304 S--VTVTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVAS 355
S VT TGP + VN+ MP D+ + + A+G T+I
Sbjct: 312 SIRVTRTGPLSK-----VNLKTMHPGPFPTDMQPQMTALLSIANG-TSIVTEGV 359

Query: 356 W--RVKETERMVAIRTELTKLGASVE 379
W R + + EL +LGA ++
Sbjct: 360 WDNRFYVD-----ELRRLGAQIQ 378

>gb|EGD14948.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas perforans 91-118]
Length = 424

Score = 43.9 bits (102), Expect = 0.046, Method: Compositional matrix adjust.
Identities = 95/400 (23%), Positives = 158/400 (39%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNISGAKNAVLPILCATLLADAPVEISNPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSILVDPRSVTHQVAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLGDVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L G + +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY----IKATSHGRLKGARYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRLVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +

Sbjct: 281 TTTADSITLDMQGKRP-----RAVSLTTAPYPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394

+ E M EL +LGA ++ I+ E+L+

Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|YP_001007900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia enterocolitica subsp. enterocolitica 8081]
sp|A1JRA1.1|MURA_YERE8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
emb|CAL13772.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia enterocolitica subsp. enterocolitica 8081]
emb|CBY25544.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia enterocolitica subsp. palearctica Y11]
Length = 422

Score = 43.9 bits (102), Expect = 0.046, Method: Compositional matrix adjust.
Identities = 101/431 (23%), Positives = 171/431 (39%), Gaps = 58/431 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68

+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG+ +E

Sbjct: 6 VQGRTRLSGEVTISGAKNAALPILFAALLAEDPVELQNVPKLKDIDTTIKLLSQLGVKIE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D A+ V G V F + +++ A++ A G G

Sbjct: 66 RDAASGSVFVDASG-----VDEFCAPYDL-VKTMRSI WALGPLVARFVGKQVS 113

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QL A++ G V+ + G L + + +S

Sbjct: 114 LPGGCAIGARPVDLHITGLEQLSAEIKLEEGY---VKASVNGRLKAAHIVMD-KVSVGA 168

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+

Sbjct: 169 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKITGAGT-DRITIEGVARL 224

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA

Sbjct: 225 GGGVYR-----VLPDRIETGTFLVAAAISGGKVVCQRTPDTL--DAVLAKLRE-AGAD 275

Query: 298 VTWTETSVTVTGPPREFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA+ + P D+ +++ L A+G I +

Sbjct: 276 IEVGDDWISLDMHGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGTGVITET 329

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I E+L+ + D R + + LA

Sbjct: 330 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVQLSGAQV-MATDLRASASLVLA 382

Query: 414 ACAEVPVTIRD 424
C VTI D

Sbjct: 383 GCIADGVITVD 393

>ref|YP_003008906.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus sp. JDR-2]
gb|ACS98819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus sp. JDR-2]
Length = 417

Score = 43.9 bits (102), Expect = 0.046, Method: Compositional matrix adjust.
Identities = 88/382 (23%), Positives = 158/382 (41%), Gaps = 47/382 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E++++ + + GTV++ G+K+ + ++ A L+E V+DNL + DV L+ LG

Sbjct: 2 EKLMI RGRPLRGTVQISGAKNSAVALVPAAILAESEVVLDNLP H L S D V V V Y S E I L Q D L G 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
AVV G ++ ++ E + +R+ L A+ G A

Sbjct: 62 -----AVVSWQGDVMKIDPSRLESKPMPNGKVKLLRASYLLMGAMLGRFGGEAII 110

Query: 122 VLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G RPI + G + LGA V G+ +R++ L G K+ L +S
Sbjct: 111 GLPGGCNFEPRIQHIKGFALGATVTNEHGS---MRIHA-KELRGAKIYLD-VVSVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+++AA A G II+ P + L+ G + + + + I+G
Sbjct: 165 ATINIMLAASRAKGST---IIEENAAKEPEIIDVATLLNAMGARIKGAGT-ETIRIEGVDS 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+++ + + +Y +A AA T G VT++ ++ LE MG V
Sbjct: 221 MHGCRHSIIPDRIQAGTYMIAAAA-TRGDVTIDNVIPKHMEA---MTAKLEEMGVTVQEM 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASW 356
+ S+ + G P A+DV P D+ + + A G + + D V S
Sbjct: 277 DESIRIIGAP-----EYTAVDVKALVYPGFATDLQSPMTTLAQAGVLSILSDYVYSN 329

Query: 357 RVKETERMVAIRTELTKLGASV 378
R K EL ++GA++
Sbjct: 330 RFKHV-----PELNRMGANI 344

>ref|NP_667483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
KIM 10]
ref|YP_071996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 32953]
ref|YP_653641.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Antiqua]
ref|YP_649378.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]
ref|YP_001161720.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Pestoides F]
ref|YP_001399447.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis IP 31758]
ref|ZP_02022444.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
CA88-4125]
ref|YP_001605686.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Angola]
ref|ZP_02223945.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. F1991016]
ref|ZP_02226090.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. IP275]
ref|ZP_02232303.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. E1979001]
ref|ZP_02237996.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. B42003004]
ref|ZP_02306059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Antiqua str. UG05-0454]
ref|ZP_02312292.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. MG05-1020]
ref|ZP_02318723.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Mediaevalis str. K1973002]
ref|YP_001719274.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis YPIII]
ref|YP_001874109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia
pseudotuberculosis PB1/+]
ref|YP_002348456.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
CO92]
ref|ZP_04457040.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Pestoides A]
ref|ZP_04459384.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. PEXU2]
ref|ZP_04514931.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
biovar Orientalis str. India 195]
ref|ZP_04519216.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Nepal516]
ref|ZP_06205614.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
KIM D27]
ref|YP_003569370.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
Z176003]
sp|Q8ZB56.1|MURA_YERPE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;

AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|Q665K4.1|MURA_YERPS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|Q1CE02.1|MURA_YERP_N RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|Q1C1H6.1|MURA_YERPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|A4THI5.1|MURA_YERPP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|A7FDW9.1|MURA_YERP3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|B2K403.1|MURA_YERPB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|A9R1S6.1|MURA_YERPG RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

sp|B1JL60.1|MURA_YERPY RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

gb|AAM83734.1|AE013614_8 UDP-N-glucosamine 1-carboxyvinyltransferase [Yersinia pestis KIM 10]

emb|CAH22751.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pseudotuberculosis IP 32953]

gb|ABG19778.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Nepal516]

gb|ABG15696.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Antiqua]

emb|CAL22157.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis CO92]

gb|ABP38747.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Pestoides F]

gb|EDM39061.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis CA88-4125]

gb|ABS49505.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pseudotuberculosis IP 31758]

gb|ABX85341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Angola]

gb|EDR33246.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Orientalis str. IP275]

gb|EDR37188.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Orientalis str. F1991016]

gb|EDR42090.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Antiqua str. E1979001]

gb|EDR51187.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Antiqua str. B42003004]

gb|EDR57366.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Orientalis str. MG05-1020]

gb|EDR61326.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Antiqua str. UG05-0454]

gb|EDR63838.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Mediaevalis str. K1973002]

gb|ACA66821.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pseudotuberculosis YPIII]

gb|ACC90652.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pseudotuberculosis PBI/+]

gb|EEO74328.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Nepal516]
gb|EEO79357.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Orientalis str. India 195]
gb|EEO85638.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Orientalis str. PEXU2]
gb|EEO91827.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Pestoides A]
gb|ACY60092.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis D106004]
gb|EFA47821.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis KIM D27]
gb|ADE66108.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis Z176003]
gb|ADW00683.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis biovar Medievalis str. Harbin 35]
Length = 420

Score = 43.9 bits (102), Expect = 0.046, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 170/431 (39%), Gaps = 60/431 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E
Sbjct: 6 VQGRTRLSGEVTISGAKNAALPILFAALLAEEPVELQNVPKLKIDITTIKLLSQLGKTIE 65

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G F A E F + +++ A++ A G G
Sbjct: 66 RNN-----GSVFVDASAVNE---FCAPYDL-VKTMRASIWALGPLVARFGQGQVS 111

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 112 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGA 166

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+
Sbjct: 167 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNLTGAKISGAGT-DRITIEGVTRL 222

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 223 GGGVYR-----VLPDRIETGTFLVAAISGGKVVCRTQTRPDTL--DAVLAKLRE-AGAD 273

Query: 298 VTWTETSVTVTGPPREPFRGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KAI P D+ +++ L A+G I +
Sbjct: 274 IEVGDDWISLDMQGRKRP-----KAITFRTAPHPGFPTDMQAQFSLNLVAEGTGVITET 327

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I E+L+ + D R + + LA
Sbjct: 328 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGEQLSGAQV-MATDLRASASLVLA 380

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 381 GCIAEGVTIVD 391

>ref|YP_003672859.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp. C56-T3]
gb|ADI28282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp. C56-T3]
Length = 428

Score = 43.9 bits (102), Expect = 0.047, Method: Compositional matrix adjust.
Identities = 93/397 (23%), Positives = 154/397 (38%), Gaps = 49/397 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+ G+K+ + ++ A L++ ++ L + DVH + + +G S D
Sbjct: 12 LRGTIKVSGAKNSAVALIPAAILADSPVTIEGLPDISDVHILGSLIEEIGGSFSD---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI----AMRSLTAAVTAAGGNATYVLDGVPRMR 130
GK V D V + L N + A L A+ A L G +
Sbjct: 68 -----GKEAVIDPTNMVSMPLPNGKVKKLRASYYLGMAMLRGFKKAVVGLPGGCHLG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + G + LGA V G +R L G ++ L +S +++AA
Sbjct: 120 PRPIDQHIKGFETLGATVTNEQG--AIYLRAE---ELRGARIFLD-VVSVGATINIMLAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G II+ P + L+ G K + + + D I G + ++A +
Sbjct: 174 VRAKGR---IENAAKEPEIIDVATLLSNMGAKIKGAGT-DVIRIDGVETLSGCRHAI 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ +Y +A AA T G V V+ ++ L MG +V E + V G
Sbjct: 230 PDRIEAGTYMIAAAA-TNGEVVDNVIPQHVE---SLTAKLREMGVRVETGEDQILVCGT 285

Query: 311 PREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
LKA+DV P D+ + A+G + + D + S R K +
Sbjct: 286 -----DVLKAVDVKTLVYPGFPTDLQQPFTALLTKANGTSVVTDTIYSARFKHVD--- 335

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
EL ++ A+V+ I+T P KL + D
Sbjct: 336 ----ELRRMNANVKVEGRSAIVTGPVKLQGAQKVKASD 368

>ref|YP_001031867.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus
lactis subsp. cremoris MG1363]
emb|CAL97121.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus
lactis subsp. cremoris MG1363]
gb|ADJ59532.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus
lactis subsp. cremoris NZ9000]
Length = 426

Score = 43.9 bits (102), Expect = 0.047, Method: Compositional matrix adjust.
Identities = 98/446 (21%), Positives = 167/446 (37%), Gaps = 62/446 (13%)

Query: 14 EISGTVKLPGSKLSNRILLALLAAL-SEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ G V++ G+K+ +L L SEG V+ N+ DV M + LG S+ D+
Sbjct: 12 KLQGEVEIEGAKNAVLPLLAATLLASEGEVVLTNVPILSDVFMNNLVDHLGTSISFDQE 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
AK+ ++ + E V MR+ + + A G A + G +
Sbjct: 72 AKK-IIAKANSEIKTTAPYEYVS-----KMRASIVVMGPILARNGQARVSMPPGGCSI 122

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL----- 183
RPI + G +Q+GA + G + KL G + YL
Sbjct: 123 GSRPIDLHLRGFEQMGATI-----TQNAGYIEAKADKLKG--AHYILDFPSVG 168

Query: 184 --SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
L++AA LA G + ++ P + L+ + G + + + D IKG +K
Sbjct: 169 ATQNLILAATLAEG---VTTLENAAREPEIVDLANLLNKMGANVKAGT-DTIIKGVKEK 224

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K++ V+ D A F+ AA+T G V ++ + + L MG T
Sbjct: 225 MHGAKHSVVQ-DRIEAGTFMVAAAMTQGDVLKDA---IAEHNRLISKLSSEMGVNFTE 280

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTA-IRDVASW 356
ET + V GP + LKA V P D+ + A G + + V
Sbjct: 281 ETGLRVVGPEK-----LKATSVKTLPHPGFPTDMQSQMTAAQAIAAGESVMVETVFEN 333

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
R + E E+ ++G V+ + +I L A+ + D A L A
Sbjct: 334 RFQHLE-----EMRRMGLEVDITRNTALIQGNSNLQGAQVKTDLRASAAILLGLVA 386

Query: 417 EVPVTIRDPGCTRKTFPDYFDVLSTF 442
+ T+R + + + + L
Sbjct: 387 KGQTTVRRLSHLDRGYKFKHEKLKAL 412

>ref|YP_001488534.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus pumilus
SAFR-032]
gb|ABV63974.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus pumilus
SAFR-032]
Length = 435

Score = 43.9 bits (102), Expect = 0.047, Method: Compositional matrix adjust.
Identities = 86/359 (23%), Positives = 145/359 (40%), Gaps = 45/359 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L S +V+ ++ DV+ + LR L
Sbjct: 2 EKIIIVRGQKLNKGTVEGAKNAVLPIVIAASLLASTEKSVICDVPTLSVDYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V + V V E E V R + A+V G G
Sbjct: 62 GAEVHFEN---NEVSDASHALETEAPFEYV-----RKMRAVSLVMGPLLARTG 107

Query: 118 NATYVLDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + +GA + G V+ G L G K+ L
Sbjct: 108 HARVALPGGCAIGSRPIDQHLKGFEAMGAKIQVGNFIEAEVK---GRLQGAKIYLDLP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G I++ + P + + G K + + I+
Sbjct: 164 -SVGATENIIMAAALAEGETT---ILENVAKEPEIVDLANYINAMGGKVRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + K+ + D A F+ AAIT G V V+G + +E MG +
Sbjct: 219 GVETLHGAKHNIIP-DRIEAGTFMVAAAITEGNVLKGAPEHM---TSLVAKMEEMGIQ 274

Query: 298 VTWTETSVTVTGPPREPFGRKHLKVIDNMNKMP---DVAMTLAVVALFADGPTAIRD 352
+ E + V GP + LK ID+ P D+ + + L A+G + I +
Sbjct: 275 IIEEEGLRVIGPSQ-----LKPIDLKTMPPHGFPTDMQSQMMALLLRANGTSMITE 326

>ref|ZP_07388964.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
curdolanolyticus YK9]
gb|EFM09593.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
curdolanolyticus YK9]
Length = 414

Score = 43.9 bits (102), Expect = 0.048, Method: Compositional matrix adjust.
Identities = 76/315 (24%), Positives = 128/315 (40%), Gaps = 31/315 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTILGLSVEADKA 72
+ + G +++ G+K+ + +L A L+E +DNL DV LR LG VE +
Sbjct: 6 RPLHGEIQISGAKNSAVALLPAAILAESEVTLNLPALISDVAVYSEILRDLGAKVERHED 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPR 128
R D + V + N + M L A+ G A L G
Sbjct: 66 TMRI-----DPSKLVSTAMPNGKVKMLRASYYLMGALLGRFGEAVIGLPGGCN 113

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + G + LGA V G +R++ L G K+ L +S +++
Sbjct: 114 FEPRPIDQHIKGFALGATVTNEHGA---MRISA-KELRGAKIYLD-LVSVGATINIML 167

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA A G II+ P + L+ G K + + + + I+G ++ +++
Sbjct: 168 AAARAKGST---IENAAKEPEIIDVATLLNAMGAKIKGAGT-ETIRIEGVERMHGCRHS 223

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
+ + +Y + AA T G VTVEG ++ L MGA V + + + +
Sbjct: 224 IIPDRIQAGTYMIMAAA-TRGDVTVEGVIPKHEA---VTAKLREMGATVEELDDAIRIV 279

Query: 309 GPPREPFGRKHLKAI 323
G + P+ LKA+
Sbjct: 280 GGDK-PYEAVDLKAL 293

>ref|YP_003023579.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter sp.
M21]
gb|ACT19821.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter sp.
M21]
Length = 421

Score = 43.9 bits (102), Expect = 0.048, Method: Compositional matrix adjust.
Identities = 85/384 (22%), Positives = 155/384 (40%), Gaps = 51/384 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V++ ++SG V + GSK+ + I + L+ G + N+ D++ + L LG
Sbjct: 2 EKLVIKGGNKLSGEVTVSGSKNAALPIFISTILAPGCHTISNVFPLRDINTTIKVLKLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+V+ G G ++ + F + +R++ A+V G G
Sbjct: 62 ATVD-----GRGNVVKIDTTN--LNSFEATYDL-VRTMRASVLVLGPLLARFGQ 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RPI + GL LGA++ G + L G ++ S
Sbjct: 108 ARVSLPGGCAIGARPINLHLKGLAALGAEITLHGYVEAKAK-----KLKGARINFDIST 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
LLMAA A G+ +++ P + ++ + G E + + D IKG
Sbjct: 163 VGGT-EQLLMAAATAQGET---VLENAAREPEIVDLAEILIKMGADIEGAGT-DTIRIKG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ + ++A V D A F+ +AITGG + ++ L + L+ G ++
Sbjct: 218 VEALTAEEHA-VMPDRIEAGTFMIASAITGGDIKIKNMRLDHLDA---LSFKLQDAGVEI 273

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
T + V V GP K ++ +++ P D+ + A+G + I
Sbjct: 274 TNKDNMVRVKGPF-----KKIRNVNIKTRPYPGFPTDMQAQFMALMCIAEGASVI--- 322

Query: 355 SWRVKETERMVAIRTELTKLGASV 378
S + E M +EL + GA +
Sbjct: 323 SENIFENRFMHV--SELLRFGADI 344

>ref|ZP_02330012.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Paenibacillus
larvae subsp. larvae BRL-230010]
ref|ZP_08057836.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
gb|EFX44507.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase-like protein
[Paenibacillus larvae subsp. larvae B-3650]
Length = 418

Score = 43.9 bits (102), Expect = 0.048, Method: Compositional matrix adjust.
Identities = 86/380 (22%), Positives = 154/380 (40%), Gaps = 42/380 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V++ + +SG +++ G+K+ + IL + ++ G + N+ D+ ML + LG
Sbjct: 2 EKLVIIEGGRPLSGAIQIHGAKNAALPILAASLMASGVHTLHNVPPELLDIEVMLSIVEALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
VE G ++ + MRS L + A G+
Sbjct: 62 CRVEQR-----GNTVTLDTTSHSYHIPDDLKMLMRSSIFLMGPLLARFGSVQL 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
G + ER I + GL++LG +++ C R L G + L S
Sbjct: 111 YHPGGCAIGERKIDFHLRGLQELGVEIEESGNRIICKADR-----LQGADIMLDFP-SV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
L+MAA +A G + I P ++ + + G + + + D IKG Q
Sbjct: 164 GATENLMMAAAMAEG---VTTIFNAAREPEIQDLQHFLNKMGAIEIIGAGT-DTITIKGVQ 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ ++ + D A FL AA T GTV++EG L VL+ GA++T
Sbjct: 220 ELRACSYRIIP-DRIVAGTFLVAAAATKGTVSIEGANPVHL---TSLMHVLKRTGAQLTV 275

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP-DVAMTLAVVALFADGPTAIRD-VASWRV 358
+ + V+ P R P + + + P D+ + V+ DG + I++ + R
Sbjct: 276 RDDLIQVSAPYR-PKAVE--RIVTAPYPSFPTDLQSQIMVLLSLTDGHSIIKETIFEGRF 332

Query: 359 KETERMVAIRTELTKLGASV 378
K + EL ++GA +
Sbjct: 333 KHVD-----ELCRMGADI 345

>gb|ACY63808.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis
D182038]

Length = 415

Score = 43.9 bits (102), Expect = 0.049, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 170/431 (39%), Gaps = 60/431 (13%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG +E
Sbjct: 1 MQGRTRLSGEVTISGAKNAALPILFAALLAEFPVELQNVPKLKDIDTTIKLLSQLGKIE 60

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G F A E F + +++ A++ A G G
Sbjct: 61 RNN-----GSVFVDASAVNE---FCAPYDL-VKTMRASIWALGPLVARFGQGQVS 106

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 107 LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGA 161

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+
Sbjct: 162 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNTLGAKISGAGT-DRITIEGVTRL 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 218 GGGVYR-----VLPDRIETGTFLVAAAISGGKVCRQTRPDTL--DAVLAKLRE-AGAD 268

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP---DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KAI P D+ +++ L A+G I +
Sbjct: 269 IEVGDDWISLDMQGRKRP-----KAITFRTAPHPGFPTDMQAQFSLNLVAEGTGIVTET 322

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I E+L+ + D R + + LA
Sbjct: 323 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVEQLSGAQV-MATDLRASASLVLA 375

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 376 GCIAEGVTIVD 386

>ref|ZP_01769920.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 305]
ref|ZP_02491742.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei NCTC 13177]
gb|EBA45507.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 305]
Length = 449

Score = 43.9 bits (102), Expect = 0.049, Method: Compositional matrix adjust.
Identities = 69/280 (24%), Positives = 120/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D R V+ PV A E+ +++ A++ G
Sbjct: 89 MGMREETDGV--RVVLDASRVDPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|YP_001057773.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia

pseudomallei 668]
ref|YP_001065017.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106a]
ref|ZP_02401431.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei DM98]
ref|ZP_02454305.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 9]
ref|ZP_02469916.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei B7210]
ref|ZP_02480324.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 7894]
ref|ZP_02496729.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 112]
ref|ZP_02504743.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei BCC215]
ref|ZP_03792301.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pakistan 9]
ref|YP_002895376.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
ref|ZP_04815556.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
ref|ZP_04894173.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
ref|ZP_04903083.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei S13]
ref|ZP_04963685.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|ABN83941.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 668]
gb|ABN90529.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106a]
gb|EDO83060.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 406e]
gb|EDO91011.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pasteur 52237]
gb|EDS86095.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei S13]
gb|EEH27259.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei Pakistan 9]
gb|ACQ97851.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei MSHR346]
gb|EES26181.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1106b]
Length = 435

Score = 43.9 bits (102), Expect = 0.049, Method: Compositional matrix adjust.
Identities = 55/220 (25%), Positives = 87/220 (39%), Gaps = 32/220 (14%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + GTV LP SK R LL+A L+ TT ++N+ + ALR GL+V
Sbjct: 6 VHPGALKGTVTLPASKPHVQRALLVALLNGATTRIENVSWCAETELQFAALRQFGLTV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-GVP 127
VE + L AG+ T + AAG + + +
Sbjct: 65 -----VERGDASLTLRGAGGV---EATGTIDAAGSGMLFRMSAALA 103

Query: 128 RMRERPI----GDLVVGLKQLGAD-VDCFLGTDCPPVRVN--GIGGLPG-GKVKLSGSIS 179
+ ERP+ D + + D LG D N I P ++ L+ S
Sbjct: 104 SLSERPVTIRCNDLSLFRSDSVFDDGFFSHLGIDARRRAGNLVTISRKPHPERIALTRKS 163

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLME 219
+Q++S L AP + D + + D Y++MT++ M
Sbjct: 164 TQFISFALFVAPFS-ADRTL RVADDGSQAGYIDMTIKAMS 202

>ref|YP_252850.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
haemolyticus JCSC1435]
sp|Q4L7Y1.1|MURA2_STAHI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2

dbj|BAE04244.1| UDP-N-acetylglucosamine 1-carboxyvinyl transferase 1
[Staphylococcus haemolyticus JCSC1435]
Length = 421

Score = 43.9 bits (102), Expect = 0.049, Method: Compositional matrix adjust.
Identities = 95/371 (25%), Positives = 149/371 (40%), Gaps = 35/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV++ ++G VK+ G+K+ +L + L SEG + + N+ + DV + L TL
Sbjct: 2 DKIVIKGGNRLTGEVKEGAKNAVLPLVTASLLASEGQSKLVNVPDLSVVTTINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+VE +K + AV+V E E V + + M L A + G+A L
Sbjct: 62 NANVEYNKE-EGAVLVDASTTLKEEAPYEVVSKMRASI-LVMGPLLARL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA++ G + GL G + L S
Sbjct: 116 PGGAIGARPIEQHIKGFALGAEIHLNGNIYASTK----DGLKGTDIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G IE + K P + + G K + + D I G +K +
Sbjct: 171 QNIIMASLAKGKTVIENVAKE---PEIVDLANYINEMGGKVTGAGT-DTITIHGVEKLR 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+++ + D A + AAIT G V V + LE MG + + E
Sbjct: 227 GVEHSIIP-DRIEAGTLIAAAITRGDVVFVRDAVKEHM---TSLIYKLEEMGVNLDFOED 282

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA---S 355
V VT LK +DV P D+ + + L A+G I +
Sbjct: 283 GVRVT-----AEDELKPVDVKTLPHPGFPTDMQSQMIALLLTAEGHKVITETVTFENRF 335

Query: 356 WRVKETERMVA 366
V E RM A
Sbjct: 336 MHVAEFRMNA 346

>ref|YP_002236399.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
pneumoniae 342]
ref|YP_003437442.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
variicola At-22]
ref|ZP_06550935.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella sp.
1_1_55]
sp|B5XSV2.1|MURA_KLEP3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACI10433.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
pneumoniae 342]
gb|ADC56430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
variicola At-22]
gb|EFD84558.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella sp.
1_1_55]
Length = 419

Score = 43.9 bits (102), Expect = 0.050, Method: Compositional matrix adjust.
Identities = 101/421 (23%), Positives = 169/421 (40%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12 LQGEVTISGAKNAALPILFSALLAEEPVEIQNVPKLDIDTTMKLLSQLGAKVERNGS-- 69

Query: 75 RAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V + G PV+ +F + +++++ A++ A G G L G
Sbjct: 70 --VWIDAG---PVD-----VFCAPYDL-VKTMRSI WALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVLDHISGLEQLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + + DR I+G Q+

Sbjct: 172 AATLAEGTT---IIENAAAREPEIVDTANFLNALGAKIKGQGT-DRITIEGVQRLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A+ L GA + E +++

Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKILCRNAQPDTL--DAVLAK-LRDAGADIETGEDWISL 282

Query: 308 TGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363

P KA++V P D+ ++ L A+G I + R
Sbjct: 283 DMHGNRP-----KAVNVRTAPHPGPFPTDMQAQFTLLNLVAEGTGVITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
+ I EL ++GA E + I ++L+ + D R + + LA C TI

Sbjct: 332 FMHI-PELIRMGAAHAEIESNTAICHGVKQLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424

D
Sbjct: 390 D 390

>ref|ZP_02413233.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 14]
Length = 449

Score = 43.9 bits (102), Expect = 0.050, Method: Compositional matrix adjust.
Identities = 69/280 (24%), Positives = 120/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L

Sbjct: 29 GTDKLAIEGGRRLAGETAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D R V+ PV A E+ +++++ A++ G

Sbjct: 89 MGMREETDGV--RVVLDASVDNPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++

Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEIHIEGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR

Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVTDLAHLLVAMGAKID-GIGTDLRV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEG 275

I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|ZP_07736075.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor lactoaceticus 6A]
gb|EFR13414.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Caldicellulosiruptor lactoaceticus 6A]
Length = 419

Score = 43.9 bits (102), Expect = 0.051, Method: Compositional matrix adjust.
Identities = 93/402 (23%), Positives = 164/402 (40%), Gaps = 42/402 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++V++ + G V + G+K+ + ++ A +++G +V++NL EDV M L LG

Sbjct: 6 EKLVIIEGGYPLEGEVINGAKNAAVAVIPAALMADGESVIENLPLIEDVFAMDDILLRLG 65

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+E D + + ++ +++++ A L A+ G A +

Sbjct: 66 AKIEYDNHSLKIDARNLHSYVAPYESVKKIR-----ASYYLIGALLTRFGRAEVAMP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G RPI + G + LGA+V G ++ L G K+ L +S

Sbjct: 118 GGCNFGSRPIDQHIGFRALGAEVKIENG----IKAYA-DRLVGTKIYLD-VVSVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKS 244
L++AA A G II+ P+V T + G K + + + D I+G K

Sbjct: 172 NLMLAAVKAKGTT---IIENAAKEPHVVDTANFLNSMGAKIKGAGT-DVIRIEGVDKLYP 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
K A + + +Y +A A T G V V+ L+ A+++E MGA+V E S
Sbjct: 228 TKYAIIPDQIEAGTYMIAACA-TKGHVIVKNVIPKHLESLT--AKLVE-MGAEVITYEDS 283

Query: 305 VTVTGPPEPFGGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+ E R L++ + P D+ + V+ G + + + W
Sbjct: 284 I-----EVICRGRRLRSASIKTMPYPGFPTDLQPQMTVLLSLCSGTSVVTE-GVW---- 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAID 399
E EL K+GA+++ ++ E L V A+D
Sbjct: 332 -ENRYQYVDELKKMGANIKVEGRVAVVEGVESLQGAEVVAVD 372

>ref|YP_001060672.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 668]
gb|ABN82382.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
pseudomallei 668]
Length = 449

Score = 43.9 bits (102), Expect = 0.052, Method: Compositional matrix adjust.
Identities = 69/280 (24%), Positives = 120/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEIEVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +DN+ + +DV L L
Sbjct: 29 GTDKLAIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDNVPLDKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D R V+ PV A E+ +++++ A++ G
Sbjct: 89 MGMREETDGV--RVVLDASRVDNPV--APYEL-----VKTMRASILVLGPLLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G
Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|ZP_07519150.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
TA143]
Length = 419

Score = 43.9 bits (102), Expect = 0.052, Method: Compositional matrix adjust.
Identities = 103/427 (24%), Positives = 171/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEFPVEIQNVPKLKDVDTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G + DA+ +V +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 LPGGCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 166 TVTIMCAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +
Sbjct: 222 GG--GVYRVLADRIETGTLVAAAISRGKIICRNAQPDTL--DAVLAK-LRDAGADIEVG 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +
Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIET----- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + LA C
Sbjct: 327 VFENRFMHV--PELSRMGAHAIEISNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
T+ D
Sbjct: 384 EGTTVVD 390

>ref|YP_003134756.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Saccharomonospora viridis DSM 43017]
gb|ACU97929.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Saccharomonospora viridis DSM 43017]
Length = 427

Score = 43.9 bits (102), Expect = 0.053, Method: Compositional matrix adjust.
Identities = 112/437 (25%), Positives = 170/437 (38%), Gaps = 56/437 (12%)

Query: 17 GTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
G V++ G+K+ +++ A L+EGTT + N DV M LR++G VE D R
Sbjct: 15 GEVEVVGAKNSVLKMAAALLAEGTTTIRNCPRI LDVPLMADVLRSVGCEVELDGDVTRI 74

Query: 77 VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPRMR 130
P E L AM L A+V G A L G +
Sbjct: 75 TT-----PAE-----LSHRADSPAMGKLRSVCVLGPLVGRLLKAVVALPGGDAIG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ GL++LGA G C + GL G ++ L S +LMAA
Sbjct: 121 SRPLDMHQNLRLKLGATSTIEHG--CVVAEAD---GLHGAQIWLDFF-SVGATENILMAA 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G +ID P + ++ G + E + + ++G + P + +V
Sbjct: 175 VLAEGTT--VIDNAAREPEIVDLCTMLTEMGARIEGAGT-STLTVEGVDSLRL-PTDHHV 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV-TWTETSVTVTG 309
GD + + AA+T G VTV G L E L + GA V T+ + V
Sbjct: 230 IGDRIVGATWAFAAAMTRGDVTVTGVNPHLD---LVLEKLRLAGADVTTFFDDKGFRVVQ 286

Query: 310 PPREPFGGRKHLKAIDVNMNKMMPDVAMTLA--VVALFA--DGPTAI-RDVASWRVKETERM 364
R +A+D P A L VAL A +G + I +V R + E M
Sbjct: 287 NDRP-----RAVDFVTLPPYGFATDLQPFVAVALSAVSEGTSMITENVYEARFRFIEEM 339

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA-CAEVPTIR 423
V +LGA + ++ E+L+ + D R LA CAE +
Sbjct: 340 V-----RLGADARTDGHHAHVVRGVERLSSAPV-WASDIRAGAGLVLAGLCAEGVTQVW 391

Query: 424 DPGCTRKTFFPDYFDVLS 440
D + +P++ + L+
Sbjct: 392 DVFHIDRGYPEFVENLN 408

>ref|YP_002721901.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brachyspira
hyodysenteriae WA1]
gb|ACN84197.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Brachyspira
hyodysenteriae WA1]
Length = 421

Score = 43.9 bits (102), Expect = 0.053, Method: Compositional matrix adjust.
Identities = 79/312 (25%), Positives = 125/312 (40%), Gaps = 34/312 (10%)

Query: 13 KEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
I G +K+ GSK+ S +L+ + L++ ++ N+ + DVH ++ L LG V D
Sbjct: 6 NNIGGILKVSGSKNASLPLLVASILTDEPVLHNVPLVDVHVLIDILEPLGKKV--DFK 63

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA-----VTAAGGNATYVLDGVP 127
V++ GK E+A ++ + + I + L A V+ GG A
Sbjct: 64 NNTTVIISHNGK--SEEAPYKLVKKMRGSIIVLGPLLAKRKHCRVSYPGGCA----- 113

Query: 128 RMRERPIGDLVVGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA-- 185
RPI + G++ LGA +D G V G L G + LSG L
Sbjct: 114 -FGPRPIDLHLKGMEALGAKIDITAGYIDAKVE---GNLVGADMDLSGKFGPTVLGTDN 168

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G II P + L+ G K S D I+G +
Sbjct: 169 VMMAAALAKGTT--IIRNAAKEPECTNLVDLLNAMGAKIT-GGSTDILTIEGVEALHGA 224

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ + D FLA AA G + +E L ++L +G + TE ++
Sbjct: 225 EFTVIP-DRIETGTFLAIAAAGRGKLENAEPKHL---TYVLDLLSDIGCDIKTTENTI 280

Query: 306 TVTGPPRE--PF 315
+ +E PF
Sbjct: 281 EIDARNKELKPF 292

>ref|ZP_03711484.1| hypothetical protein CORMATOL_02331 [Corynebacterium matruchotii
ATCC 33806]
gb|EEG26162.1| hypothetical protein CORMATOL_02331 [Corynebacterium matruchotii
ATCC 33806]
Length = 396

Score = 43.9 bits (102), Expect = 0.053, Method: Compositional matrix adjust.
Identities = 97/412 (23%), Positives = 149/412 (36%), Gaps = 39/412 (9%)

Query: 35 AALSEGTTVVDNLLNSEDEVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEV 94
A L+EGTT + N DV M LR LG V D R DA +
Sbjct: 4 ALLAEGTTTLTNCPEILDVPLMAEVLRLGCEVSVDHETVRITTPATVSSDADFDAVRQF 63

Query: 95 QLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGKQLGADVDCFLGT 154
+ A + +T+ G A L G + RP+ GL++LGA G
Sbjct: 64 R-----ASVCVLGPLTSRTGRAVVALPGGDAIGSRPLDMHQSGLEKLGATTYIRHGA 115

Query: 155 DCPVVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMT 214
V L G +++L S +L AA LA G +E + I + +
Sbjct: 116 -----VVAEATKLVGAEIELDFP-SVGATENILTAAVLAEGRTVLENAAREPEIVDLCEM 169

Query: 215 LRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
LR M A+ + + G P V GD A + AA+T G +TV
Sbjct: 170 LRQM-----GAQLTGECSPTIVIDGVKLYPTQHEVIGDRIVAGTWAYAAAMTRGDITVS 224

Query: 275 GCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVA 334
G L + E+L+ GA+++ E V P R KA+D P
Sbjct: 225 GIAPRHLHLPL---EMLKFAGAQISSYENGFRVNMHPHP-----KAVDYQTLPPFGFP 274

Query: 335 MTLAVVALFADGPTAIRDVASWRVKETERMVAIR----TELTKLGASVEEGPDYCIITPP 390
L +A+ I +A TE + R E+ +LGA + ++
Sbjct: 275 TDLQPMAL-----GISAIAEGTSVITENIFEARFRFVDEMMLRGADATVDGHHVVLGRV 328

Query: 391 EKLNVTAIDTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDYFDVLSTF 442
E+L+ T + + D A CA+ + D + +P++ + L
Sbjct: 329 EQLSSTPVWSSDIRAGLVLGLCADGETEVHDVYHIDRGYPNFVENLQQL 380

>ref|ZP_02917249.1| hypothetical protein BIFDEN_00525 [Bifidobacterium dentium ATCC
27678]
ref|YP_003359779.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
dentium Bd1]
ref|ZP_07457096.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
dentium ATCC 27679]
ref|ZP_07695964.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
dentium JCVIHP022]
gb|EDT44717.1| hypothetical protein BIFDEN_00525 [Bifidobacterium dentium ATCC
27678]
gb|ADB08955.1| murA UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium dentium Bd1]
gb|EFM40633.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
dentium ATCC 27679]
gb|EFO77794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium

dentium JCVIHMP022]
Length = 441

Score = 43.9 bits (102), Expect = 0.053, Method: Compositional matrix adjust.
Identities = 51/187 (27%), Positives = 87/187 (46%), Gaps = 8/187 (4%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ V+ D A
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVSDDLRLHGVDDVDVGA 74

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ +V K + D +V G++ I + + + G A G + R
Sbjct: 75 --KGIVTIDATKVQLADVA-DVDTLSGSSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI + L++LGA+VD + + GL G K+ L S L+AA L
Sbjct: 131 PIDFHLETLRKLKANVD--KEHKDGIHITAPDGLHGAKIHLPPY-SVGATEQTLLAAVL 186

Query: 193 ALGDVEI 199
A G E+
Sbjct: 187 AEGKTEL 193

>ref|YP_003254471.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
ref|YP_0041133960.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
gb|ACX79989.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC61]
gb|ADU95817.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
Y412MC52]
Length = 428

Score = 43.9 bits (102), Expect = 0.054, Method: Compositional matrix adjust.
Identities = 92/397 (23%), Positives = 157/397 (39%), Gaps = 49/397 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GT+K+ G+K+ + ++ A L++ ++ L + DVH + + +G S D
Sbjct: 12 LRGTIKVSGAKNSAVALIPAAILADSPVTIEGLPDISDVHILGSLIEEIGGSFSFD---- 67

Query: 75 RAVVVVCGCGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVLDGVP---RMR 130
GK V D V + L N + +R+ + A G + G+P +
Sbjct: 68 -----GKEAVIDPTNMVSMPLPNKGKVKLRASYILMGAMLRFKKAVVGLPGGCHLG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + G + LGA V G +R L G ++ L +S +++AA
Sbjct: 120 PRPIDQHIKGFALGATVTNEQG--AIYLRAE---ELRGARIFLD-VVSVGATINIMLAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G II+ P + L+ G K + + + D I G + ++A +
Sbjct: 174 VRAKGR---IIENAAKEPEIIDVATLLSNMGAKIKGAGT-DVIRIDGVETLSGCRHAI 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ +Y +A AA T G V V+ ++ L MG +V E + V G
Sbjct: 230 PDRIEAGTYMIAAAA-TNGEVVDNVPQHVE---SLTAKLREMGVRVETGEDQILVCGT 285

Query: 311 PREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
LKA+DV P D+ + A+G + + D + S R K +
Sbjct: 286 -----DVLKAVDVKTLVYPGFPTDLQQPFTALLTKANGTSVVTDTIYSARFKHVD--- 335

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
EL ++ A+V+ I+T P KL + D
Sbjct: 336 ----ELRRMNANVKVEGRSAIVTGPVKLQGAQVKASD 368

>ref|NP_875930.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
sp|Q7VAC5.1|MURA2_PROMA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2

gb|AAQ00583.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus subsp. marinus str. CCMP1375]
Length = 427

Score = 43.9 bits (102), Expect = 0.056, Method: Compositional matrix adjust.
Identities = 92/414 (22%), Positives = 172/414 (41%), Gaps = 46/414 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+++SG +++ G+K+ S ++ A L++ + + N+ DV M L ++G+ + +K
Sbjct: 7 QKLSGHIRVSGAKNSSLVLMMAAALLADRSVFLSNVPLLTDEVMKSLLVSMGVELRRNK- 65

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
+ ++ G +D E A SL A+ G G A L G
Sbjct: 66 -NQLEIMTSGLSLFSKDLSC-----AFHSLRASFFCIGPLARFGEAKIPLPGG 114

Query: 127 PRMRERPIGDLVVLGKQLGADV----DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
R+ RPI + + LK LGA V D + P + L G +++ + S
Sbjct: 115 CRIGARPIDEHQALKALGARVEIQNDYVVAKAISPQK-----RLIGARIRFNCK-SVGA 168

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+LMAA L+ G I++ P ++ ++ G K + + + + I+G +
Sbjct: 169 TETILMAATLSQGT---ILENTAEPEIQDLATMLNEMGAKIQGAGT-SQITIEGVDR 224

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAKVTWTE 302
K + V D A FL AAIT +T+ L+ + L+ G + ++
Sbjct: 225 KGC-SYTVMPDRIEAGTFLVAAAITRSPLTISPVPVPEHLEAVIL---KLQECGLIEYSG 280

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+++V RK+L+A+D+ P L A F T ++ ++ + E
Sbjct: 281 NTLVS-----IPRKNLQAVDITTRFPFGFPTDLQ--APFMALMTTVKGISKIQTTFE 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
+ EL ++GA++ + ++ L T++ T D R A LA+ A
Sbjct: 332 NRMQHVHGLQRMGATIVLEGNTAVVIGGNNLKATSV-TGGDLRSCAAMVLASLA 384

>ref|ZP_03613993.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
capitis SK14]
gb|EEE48771.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
capitis SK14]
Length = 421

Score = 43.5 bits (101), Expect = 0.057, Method: Compositional matrix adjust.
Identities = 92/371 (24%), Positives = 146/371 (39%), Gaps = 35/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G VK+ G+K+ +L + L SEG + + N+ DV + L TL
Sbjct: 2 DKIVINGGNRLTGEVKVEGAKNAVLPLVLTASLLASEGQSKLVNVPALSDVETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V +K + AV V K E E V + + M L A + G+A L
Sbjct: 62 NADVSYNKE-ENAVKVDATQKLNEEAPYEVSKMRASI-LVMGPLLARL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA++ G + N GL G ++ L S
Sbjct: 116 PGGCAIGSRPIEQHIKGFALGAEIHLNGN----IYANAKNGLKGTQIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ P + + G K + + D I G K
Sbjct: 171 QNIIMASLASGK---SIIENAAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVDKLH 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTSLQGDVKFAEVLEMMGAKVTWTET 303
+++ + + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHSIIPDRIEAGTLLIAG-AITRGDIFVRGAIKEHM---ASLVYKLEEMGVNLDKFED 282

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
+ V+ LK +DV P D+ + + L A+G I +
Sbjct: 283 GIQVS-----AEGDLKPVDVKTLPHPGFPTDMQSQMMALLLTANGHKVITETVFENRF 335

Query: 356 WRVKETERMVA 366
V E RM A

Sbjct: 336 MHVAEFRMNA 346

>gb|EGD09072.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
vesicatoria ATCC 35937]
Length = 424

Score = 43.5 bits (101), Expect = 0.058, Method: Compositional matrix adjust.
Identities = 95/400 (23%), Positives = 160/400 (40%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNISGAKNAVLPLCATLLADAPVEMSNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSILVDPKSVTHQVAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGA++ G ++ G L GG+ +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGAEISVENGY---IKATSNRLKGGRYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLADGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAFLP-DRIETGTFLVAAAMTGGSVTVRRARPDTLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+++ P D+ + ADG I +
Sbjct: 281 TTTADSITLDMHGKRP-----RAVNLTTAPYPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|ZP_04171573.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
mycoides DSM 2048]
ref|ZP_04264856.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus BDRD-ST196]
ref|ZP_04297687.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH621]
gb|EEK70644.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus AH621]
gb|EEL03428.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus BDRD-ST196]
gb|EEL96690.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
mycoides DSM 2048]
Length = 419

Score = 43.5 bits (101), Expect = 0.058, Method: Compositional matrix adjust.
Identities = 69/276 (25%), Positives = 106/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNGRARIALPGGCAIGSRPIDQHLKGFEAMGAKVKVGNF---- 129

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V + G L G K+ L S ++ AA LA G +++ P + +
Sbjct: 130 VEAHVEGELKGAKIYLDFF-SVGATENIMSATLAKGTT---VLENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G+K + + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVEKLYGANHPPIIP-DRIEAGTFMVAAAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNKMP---DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVDIKTMHPGFPPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA---SWRVKETERMVA 366
+ + L ADG + I + V+E RM A
Sbjct: 294 SQMMALLLHADGTSMTTETVFENRFMHVEEFRMNA 329

>ref|YP_004195902.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Desulfobulbus propionicus DSM 2032]
gb|ADW18611.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Desulfobulbus propionicus DSM 2032]
Length = 427

Score = 43.5 bits (101), Expect = 0.059, Method: Compositional matrix adjust.
Identities = 89/383 (23%), Positives = 156/383 (40%), Gaps = 41/383 (10%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ + GTV + G+K+ + +L L+ G + N+ + D ML L LG
Sbjct: 2 DKLVIIEGGFPYLGTVGISGAKNAALPLLAATLLAPGVHTLHNVPDLRDTRTMLKLEILG 61

Query: 65 LSVEADKAAKRA---VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
E R + G + + L LG + RS A V+ GG A
Sbjct: 62 ARWERAGHTVRINSDHLTGVEAPYDLVKTMRASVLVLGP--LLARSGFARVSLPGGCA-- 117

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQ 181
+ RPI + G ++LG G V G G + G + S
Sbjct: 118 -----IGARPINYHLQGFELGVTTHLEQGY---VEARGEGRMRGNTIYFDIP-SVT 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LMA+ +A G+ +I P V + ++ G + E D+ DR ++G +
Sbjct: 166 GTENVLMASVVARGET---VIKNAAKEPEVGNLIDMLVAMGAEIEGKDT-DRLVVQGVDR 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ ++A + + +Y +A AA TGG +T+ C + E L + G ++
Sbjct: 222 LHATESAIIPDRIETGTMYIAVAA-TGGCMTITDCIPAHVSA---LTEKLLLCGVEIEAG 277

Query: 302 ETSVTVTGPPREPFGGRK--HLKAIDVMNMKMP---DVAMTLAVVALFADGPTAIRDVAS 355
TS+TV+ P E GR L+++D+ P D+ + + DG + I +
Sbjct: 278 ATSLTVSCP--EIGGRSLCRLRSVDITTLPPYGPFTDLQAQFMALMVQGDGTSIIHET-- 333

Query: 356 WRVKETERMVAIRTELTKLGASV 378
+ E M EL ++GA +
Sbjct: 334 --IFENRFMHV--AELKRMGADI 352

>ref|YP_001514306.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alkaliphilus oremlandii OhILAs]
gb|ABW20310.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alkaliphilus oremlandii OhILAs]
Length = 420

Score = 43.5 bits (101), Expect = 0.059, Method: Compositional matrix adjust.
Identities = 69/273 (25%), Positives = 119/273 (43%), Gaps = 24/273 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++++ K+++GTVK+ G K+ + IL L+ T V+DNL DV + L +LG
Sbjct: 2 EKLIIEGGKKLNGTVKISGFKNAAVAILPATVLAGDTCVIDNLPQISDVKILADMLSSLG 61

Query: 65 LSVEADKAAKRAV-VVGCGGKFPVEDAKEEVQ--LFLGNAGIAMRSLTAAVTAAGGNATY 121
+V+ + + G F D +E++ +L AG+ R A V GG +
Sbjct: 62 ANVKELRPNTLQINTTAMEGCFADHDLAKELRASYYLLGAGLG-RFKKAKVAYPGGCS-- 118

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGCPVVRVNGIGGLPGGKVKLSGSISSQ 181
+ RPI + G + +GA V G + V L G ++ L +S
Sbjct: 119 -----IGSRPIDQHIKGFAMGASVSIEHGI---ITVEA-DKLVGAIEIYLD-VVSVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+++AA +A G IID P+V + G + + + D IKG +K
Sbjct: 166 ATINIMLAAMAEAGTT---IIDNAAKEPHVVDMANFLNCMGADVKGAGT-DVIKIKGVEK 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
+ + + +Y +A AA GG V ++

Sbjct: 222 LGGCIHTVIPDQIEAGTYMIAAAA-AGGDVLID 253

>ref|ZP_05052591.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Octadecabacter antarcticus 307]
gb|EDY78857.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Octadecabacter antarcticus 307]
Length = 423

Score = 43.5 bits (101), Expect = 0.060, Method: Compositional matrix adjust.
Identities = 95/422 (22%), Positives = 167/422 (39%), Gaps = 47/422 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ IV++ K +SG +++ G+K+ + ++ LS+ + N D+ M L +LG
Sbjct: 2 DSIVVRGGKALSGQIEIAGAKNAALALMPATLLSDEPLTLTNTPRLSDIKMTVLLES 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ + + K + C G + V+ A + + A G+A L
Sbjct: 62 AEISSLDGK-VQTMSCHGSINTTADYDIVRKM-----ASNVLGPLLAREGHAIIVSLP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSI----- 178
G + RP+ GL ++GA +D G + GG KL G++
Sbjct: 116 GGCAIGARPMDIHTDGLTKMGAQIDLRNGY----LHAKAEGG-----KLKGAVIDFPFA 165

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++MAA LA G +I+ P + + + G + + D I+G
Sbjct: 166 SVGATENIMMAATLAKGTT---VINNAAREPEIVDLASCLRKMGQAID-GDGTSTITIQG 221

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOGDVKFAEVLEMMGAKV 298
+ + V +Y LA I GG V G G L G FAE L+ +G V
Sbjct: 222 VDRHLGATHPVVTDRIELGTYMLA-PVIAGGEVECIG-GRMELVG--AFAEKLDVGVSV 277

Query: 299 TWTETSVTVTGPPREPFRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVA 354
T+ + V P +A++V P D+ + + FADG + + +
Sbjct: 278 EETKVGLKVKLNGDRP-----RAVNVKTEPFPGFPTDLQAQMMAMLCFADGTSVLEE-- 329

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAA 414
++ E M A EL ++GA++E +T +K+ + D R +++ LA
Sbjct: 330 --KIFENRFMHA--PELVRMGANIEVHGGTATVTGVDKMKGAPV-MATDLRASVSLILAG 384

Query: 415 CA 416
A
Sbjct: 385 LA 386

>ref|ZP_01223692.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [marine gamma proteobacterium HTCC2207]
gb|EAS48251.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [marine gamma proteobacterium HTCC2207]
Length = 420

Score = 43.5 bits (101), Expect = 0.060, Method: Compositional matrix adjust.
Identities = 93/417 (22%), Positives = 168/417 (40%), Gaps = 66/417 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ +Q + G V + GSK+ + IL LSEG V NL + +DV + L +LG
Sbjct: 2 EKLKIQGGGPLKGEVWISGSKNAALPILSATLLSEGLATVSNLPHLQDVTTTIELLGS 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG 116
++V D +++QL + N+ + ++++ A++ G
Sbjct: 62 VTVSID-----DKLQLEVDNSTLHVSHTAPYELVKTMRASILVLG 100

Query: 117 -----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGG 170
G A G + RP+ + GL+ +GA ++ D ++ G L G
Sbjct: 101 PLLSRYGEANVSFPGGCAIGSRPVDLHLRGLEAMGATIEI----DEGYIKARSSGRLVGC 156

Query: 171 KVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
+ L +S L+MAA LA G +I+ P + + +G + S
Sbjct: 157 HI-LMDVVSVGATENLMAAVLAEGQT---VIENAAAREPEIVDLANCLNAWGADIQGIGS 212

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOGDVKFAEV 290

R I G + K + + V D + L A A T G V V + S L + +
Sbjct: 213 -ARLVINGVEKI-TGGHFKVMPDRIETGTYLAAAVATRGKVVTQTDPSSEAVLLK--- 267

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADG 346
LE GA++T E + + + P KA+++ P D+ + + A+G

Sbjct: 268 LEEAGAQITQGEDWIELDMQGRP-----KAVNIKTAPYPAFPTDMAQVTAINAVAEG 321

Query: 347 P-TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402

I + R+ + + EL ++GA++ + ++T E+LN + D
Sbjct: 322 TGVVIETIFENRLMQVQ-----ELNRMGATITVEGNTALVTGVERLNAAAPVMASD 371

>gb|ABC00789.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 25

Score = 43.5 bits (101), Expect = 0.060, Method: Compositional matrix adjust.
Identities = 21/24 (87%), Positives = 22/24 (91%)

Query: 89 DAKEEVQLFLGNAGIAMRSLTAAV 112

DAKEEV+LFLGNAG AMR LTAAV

Sbjct: 1 DAKEEVKLFLGNAGTAMRPLTAAV 24

>ref|ZP_03756298.1| hypothetical protein CLOSTASPAR_00281 [Clostridium asparagiforme
DSM 15981]

gb|EEG57478.1| hypothetical protein CLOSTASPAR_00281 [Clostridium asparagiforme
DSM 15981]
Length = 447

Score = 43.5 bits (101), Expect = 0.061, Method: Compositional matrix adjust.
Identities = 71/309 (22%), Positives = 130/309 (42%), Gaps = 21/309 (6%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E+ V++ + G V + G+K+ + IL + +++ ++DNL + D++ +L A+ +G

Sbjct: 19 EQYVIKGGNPLVGDVTISGAKNAALGILAASIMTDDDLIDNLPDVRDINVLEAIEEIG 78

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

VE + + V + V E ++ A A+ +A L

Sbjct: 79 ARVE--RIDRHTVRINGSNIKEVAVDDEYIRRIR----ASYFIGALLGKYKSAQVPLP 131

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G + RPI + G + LGA+V+ G V + I L + L +S

Sbjct: 132 GGCNIGSRPIDQHLKGFRALGAENVIERGA----VIAHAI-DLVAAHIYLD-VVSVGATI 185

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

++MAA LA G I++ P+V + G + + + D I+G +

Sbjct: 186 NIMMAAALAEQQT---ILENAAKEPHVVDVANFLNSMGANIKGAGT-DTIRIRGVNRLHG 241

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

+ + + D A F+ AA+T G V V+ L+ A+++E MG +V +

Sbjct: 242 TEYSIIP-DQIEAGTFMCAAAVTRGDMVMKNVIPKHLEAIT--AKLME-MGCEVIEFDDE 297

Query: 305 VTVTGPPRE 313

V V G P +

Sbjct: 298 VRVVGKPAQ 306

>ref|ZP_05347124.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]

gb|EET60067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bryantella
formatexigens DSM 14469]
Length = 437

Score = 43.5 bits (101), Expect = 0.062, Method: Compositional matrix adjust.
Identities = 91/384 (23%), Positives = 147/384 (38%), Gaps = 49/384 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G V + G+K+ + ++ A L GTTV+ DV YM G LR LG +V +

Sbjct: 12 LCGEVTIQGAKNAALPLMAAAVLHRTTTLHRCQPQILDVEYMSGILRGLGCTVRRE---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFL-GNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130

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          G+  + DA+E      +      +R+  L  ++      G A      G  +
Sbjct: 68  -----GQTLIIDAREISDFCVAAQPATCLRASVLLMGSLLGRCGCARLPYPGGCTIG 119

Query: 131 ERPIGDLVVGLKQLGAD-----VDCFLGTDCP--PVRVNGIGGLPGGKVKLSG-SISS 180
          ERPI  +   +++GA      +  + G  C  P      G  P  +  +L G S+
Sbjct: 120 ERPIDLHLQVFERMGAQILPEEEGIGVYAGKGCakePGCARADGAAPPDRARLQGCsRLR 179

Query: 181 QYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
          + S      ++ A LA G  E  +D  + P  +      R  +  + G K E      R
Sbjct: 180 SFPSVGATENAILGAVLAEGTTE---LDGCATEPEIAELCRFLNQKGAKIE-GVGRQRLV 235

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
          I G      +  +  +      +Y LA AA T G ++V G      L      EVL+  G
Sbjct: 236 ITGVTCLQDSQYTLMPDRIVAGTYLLA-AAGTRGRISVRGVCPEHLGA---LTEVLQKSG 291

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMpdVAMTL-AVVALFADGPTAIRDVA 354
          AK+      +  +      RE  +      L  V      P      L  +  + +F G      R V+
Sbjct: 292 AKLKTGRDVICMDA--REAY----LPVSSVRTEPYPGFPTDLQSQLMVFLTGA---RGVS 342

Query: 355 SWRVKETERMVAIRTELTKLGASV 378
          +  +  E      I  EL K+GA  +
Sbjct: 343 TLEERLFESRFLIAGELQKMGAE 366

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>ref|YP_383350.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
metallireducens GS-15]
gb|ABB30625.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
metallireducens GS-15]
Length = 428

```

Score = 43.5 bits (101), Expect = 0.063, Method: Compositional matrix adjust.
Identities = 91/389 (23%), Positives = 156/389 (40%), Gaps = 61/389 (15%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTL 64
          +++++ K+++G V + GSK+ +  +  +  L+ G  + N+  D++  +  L +LG
Sbjct: 13  DKLIKGGKLTGDVSVSGSKNAALPVFISTILAPGLNEIRNVPFLRDINTTIKVL 72

Query: 65  LSVEADKAAKRAVVVGCGGKFPVE-----DAKEEVQLFLGNAGIAMRSLTAAVTAAG--- 116
          AVV G G  ++      D  +      L      +++++ A+V  G
Sbjct: 73  -----AVVEGNGNIVKIDTTHVNDVEATYDL-----VKTMRASVLVLGPLL 113

Query: 117 ---GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVK 173
          G A  L G  +  RPI  + GL  LGAD+  G  +      L G ++
Sbjct: 114 ARHGRARVSLPGGCAIGARPINLHLKGLAALGADIRLEHGYVEAKAK-----KLKGARIN 168

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
          +      L+MAA LA G+  I++      P  +      ++ R G  +  +  +  D
Sbjct: 169 FDIATVGGT-EQLMMAAALAKGET---ILENAAREPEIIDLADILNRMGARIDGAGT-DT 223

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
          I G K  +P  V  D  A  F+  AAITGG  +  +      L  V F  L+
Sbjct: 224 IRII-GVKELAPVVHDVMPDRIEAGTFMVA AAITGGDIKIHNMKLEHLDALV-FK--LQD 279

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMp----DVAMTLAVVALFADGPTA 349
          G ++  +  V V G PR P      +AI++      P  D+  +  ADG  +
Sbjct: 280 AGVEIINRDNVVRVKG-PRRP-----RAINIKTRPYPGFPTDMQAQFMALMCVADGASV 332

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASV 378
          I  S  + E  M      +EL  + GA  +
Sbjct: 333 I----SENIFENRFMHV--SELLRFGADI 355

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>ref|YP_001717572.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Desulforudis audaxviator MP104C]
gb|ACA59940.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Desulforudis audaxviator MP104C]
Length = 417

```

Score = 43.5 bits (101), Expect = 0.064, Method: Compositional matrix adjust.
Identities = 101/429 (23%), Positives = 164/429 (38%), Gaps = 54/429 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E I+++ + GT+ + G+K+ IL + L G + + N+ N +DV M+ L LG
Sbjct: 2 ERIIKGGNRLKGTITVSGAKNAVLPLGASLLYGGESFIKNVPLNQDVEVMVELLEYLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQ---LFLGNAGIAMRSLTAAVTAAGGNATY 121
+ + R + ED +++ L LG + R T ++ GG
Sbjct: 62 ARINREDHCLRIDNRNVASREIGEDLMRKMRASNLVLGP--LLGRFRTVLISQPGG---- 115

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVD---CFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ RP+ + G++ LGA ++ F+ D L G + L
Sbjct: 116 -----CNIGSRPMDLHLRGMRALGARIEERAGFIKADAAR-----LVGADIYLDVP- 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++MAA LA G + P V + + G K + + D I+G
Sbjct: 162 SVGATENIMMAASLARGRTTLR---NAAREPEVVDLQSYLNQMGAKISGAGT-DVIRIEG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ +P V D A +L AAITGG VTVE E +E + AK+
Sbjct: 218 VESL-NPCRHTVIPDRIEAGTYLVAAAITGGEVTVESI-----IPEHVEPVIAKL 266

Query: 299 TWTETSVTVTGPPREPFGKRLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-V 353
VTG + L+AIDV P D+ + ADG + + + +
Sbjct: 267 REAGAEFEVTDGAVHIRCPERLRAIDVRTLPYPGFPTDMQPQFVALLSLADGTSTVTETI 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLA 413
R K +EL +LGA + + II + L+ ++ D R A LA
Sbjct: 327 FENRFKHV-----SELRLGADIRLEGNTAIKGGKSLSGALVEA-SDLRAGAALVLA 378

Query: 414 ACAEVPVTI 422
T+
Sbjct: 379 GLGAENTTV 387

>ref|ZP_08069594.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
vestibularis ATCC 49124]
gb|EFX96231.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
vestibularis ATCC 49124]
Length = 423

Score = 43.5 bits (101), Expect = 0.065, Method: Compositional matrix adjust.
Identities = 77/267 (28%), Positives = 120/267 (44%), Gaps = 30/267 (11%)

Query: 15 ISGTVKLPKSGKSLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+SG V + G+K N +L LLAA SEG T + N+ DV+ M +R L ++V+ D
Sbjct: 13 LSGEVVIEGAK---NAVLPLLAATILASEGQTTLTNPILSDVYTMNNVVRGLDIAVDFD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127
+ K VVV G+ + E V MR+ + + A G+A + G
Sbjct: 70 E-EKNTVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNGHAKVSMPPGCC 120

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + GL+ +GA + +G D N L G + + S L+
Sbjct: 121 TIGSRPIDLHLKGLEAMGAKI-TQVGGDITATAEN----LKGATIIYMDFP-SVGATQNL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G IE + I V++ L L+ G + + + + IKG + K+
Sbjct: 175 MAATLADGVTTIENAREPEI--VDLAL-LLNEMGADVKGAGT-ETLVIKGVKALHGTHK 230

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVE 274
A V+ D A F+ AA+T G V ++
Sbjct: 231 AVVQ-DRIEAGTFMVAAAMTSGDVLIK 256

>emb|CBI81343.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bartonella sp.
1-1C]
Length = 430

Score = 43.5 bits (101), Expect = 0.065, Method: Compositional matrix adjust.
Identities = 95/420 (22%), Positives = 166/420 (39%), Gaps = 55/420 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRT--LGLSVEADKA 72

Sbjct: 12 ++G + + G+K+ + +++ A L+EGT + + + DV +L L +G +VE +
LNGVIPISGAKNAALPLMVAALLTEGTLTLKYIPHLVDVELLLRILNHHGIGYAVEGRTS 71

Query: 73 -----AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
AK+ V P E + F + R A V+ GG A

Sbjct: 72 HQESGYSRTIHFTAKKITTVAH----PYELVTKMRASFWVIGPLLARCREAYVSLPGGCA 127

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
+ RP+ ++ GLK LGA + G VR GL GG+ + ++

Sbjct: 128 -----IGTRPVDFILEGLKSLGAQIVIEQGY----VRAKAPNGLQGGRYRFP-KVT 173

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
LLMAA +A G I+D P V ++ ++ G + + I G

Sbjct: 174 VGGTHVLLMAAVMAKGT---ILDNAACEPEVTNLIQALKAMGARIS-GEQTTLTIHGV 229

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
+K S K + + +Y +A A+TGG V ++ L + E L+ G ++

Sbjct: 230 EKLHSAKVQVIPDRIEAGTYAMA-VAMTGGDVFLKNANPHHL---TEVLECLKKTGLEIE 285

Query: 300 WTETSVTVTGPPEPFGGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
+ V P + K + V++ P A + A F T R + +

Sbjct: 286 IKPEGINVRRNAQ-----KIMPVDIKTGPFPAFPTDLQAQFMALMT--RAQGNAHIT 336

Query: 360 ET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
ET R + ++ EL +LGA + ++ E L + D R +++ +AA A

Sbjct: 337 ETVFENRFMHVQ-ELIRLGAQITLNGQTALVCGTENLQGAQV-MATDLRASVSLVIAALA 394

>ref|ZP_07723059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
vestibularis F0396]
gb|EFQ59882.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
vestibularis F0396]
Length = 423

Score = 43.5 bits (101), Expect = 0.065, Method: Compositional matrix adjust.
Identities = 77/267 (28%), Positives = 120/267 (44%), Gaps = 30/267 (11%)

Query: 15 ISGTVKLPGSKSLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+SG V + G+K N +L LLAA SEG T + N+ DV+ M +R L ++V+ D

Sbjct: 13 LSGEVVIEGAK---NAVLPLLAATILASEGQTTLTNPILSDVYTMNNVVRGLDIAVDFD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS--LTAAVTAAGGNATYVLDGVP 127
+ K VVV G+ + E V MR+ + + A G+A + G

Sbjct: 70 E-EKNTVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNGHAKVSMPPGC 120

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + GL+ +GA + +G D N L G + + S L+

Sbjct: 121 TIGSRPIDLHLKLEAMGAKI-TQVGGDITATAEN----LKGAAIYMDFP-SVGATQNLN 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G IE + I V++ L L+ G + + + + IKG + K+

Sbjct: 175 MAATLADGVTTIENAAREPEI--VDLAL-LLNEMGADVKGAGT-ETLVIKGVKALHGTKH 230

Query: 248 AVEGDASSASYFLAGAAITGGTVTVE 274
A V+ D A F+ AA+T G V ++

Sbjct: 231 AVVQ-DRIEAGTFMVAAAMTSGDVLIK 256

>ref|ZP_02900958.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
albertii TW07627]
gb|EDS94224.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
albertii TW07627]
Length = 419

Score = 43.5 bits (101), Expect = 0.066, Method: Compositional matrix adjust.
Identities = 105/422 (24%), Positives = 164/422 (38%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +

Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEFVEIQNVPKLKDVDTSMKLLSQLGAKVERNGSV 70

Query: 74 K---RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYVLDGVP 127
R V V C P E K MR+ A + A G L G
Sbjct: 71 HIDARDVNVFCA---PYELVK-----TMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREFFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|ZP_06748712.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 1_1_41FAA]
gb|EFG28043.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 1_1_41FAA]
Length = 423

Score = 43.5 bits (101), Expect = 0.066, Method: Compositional matrix adjust.
Identities = 70/286 (24%), Positives = 124/286 (43%), Gaps = 24/286 (8%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKA 72
+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L++LGL VE D
Sbjct: 12 KIAGELKVDGSKNSTLPIMIATLVEKGTIYILRNVPDLRDIRTLVALLQSLGLEVEKLDAN 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRE 131
+ + + G G D ++++ FL G+ A V GG A +
Sbjct: 72 SYKIIINGLSGAEASYDLVKKMRASFLVMGGMLAIEKKAKVALPGGCA-----IGA 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 123 RPVDLHLKGFEALGAKINIEHGY----VEATTENGLIGGNIIIDFP-SVGATENIIMAAV 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G I++ P +E + + G K + R I G +K + + + +
Sbjct: 178 KAKGKT---ILENAAKEPEIEDLCNFLIKMGAKI-NGVGTSRLEIDGVEKLTACEYSIIA 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK
Sbjct: 234 DRIVAGTYIIA-SILFDGSIKVGSIIPDHLSS---FLLKLEEMGAK 275

>ref|ZP_05808171.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mesorhizobium
opportunism WSM2075]
gb|EEW35387.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mesorhizobium
opportunism WSM2075]
Length = 418

Score = 43.5 bits (101), Expect = 0.066, Method: Compositional matrix adjust.
Identities = 98/409 (23%), Positives = 170/409 (41%), Gaps = 45/409 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ G V + G+K+ + + A LS + NL + DV MLG +R G E ++
Sbjct: 10 HRLQGAVNISGAKNAALPQIAAALLSPYPLELTNLPDVTDVENMLGVVRLHG--AEVTRS 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A A + E + + V+ MR+ + A + A G+A L G +
Sbjct: 68 AH-AATIDTNAAVSKETSYDTRV-----KMRATVVLAPLLARFGHARVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ V L LGA + G+ + + GL G ++ LS S S +MA
Sbjct: 119 GARPVDMHVSALAALGARIAIENG-----IVASAPNGLTGTRIVLS-SPSVGATETAMMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A A G+ EI + + + L M G + E + + R I G +++ ++
Sbjct: 174 ATTAGGETEILNAAREPEVADLAACLNAM---GARVEGAGT-HRILIAGDTSWQAARHDI 229

Query: 250 VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+ + +Y +A AAITGG + + L+ ++LE G V + + V+
Sbjct: 230 IPDRIEAGTYAIA-AAITGGQLELT---HARLEHMASVVQLEATGVSVWPGDRGLIVS- 284

Query: 310 PPREFPGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
RE + LKA+D+ P D+ + ADG + +R+ + E M
Sbjct: 285 --RE----RPLKAVDLATEPYPGFPTDLQAQFMALMCCADGASLLRET----IFENRFMH 334

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
EL +LGA+++ ++ E L+ + D R +++ LAA
Sbjct: 335 V--PELMRLGANIKLQGTMALVRGGETLHGAQV-MATDLRASVSLVLAA 380

>ref|YP_003368037.1| UDP-N-acetylglucosamine L-carboxyvinyltransferase [Citrobacter
rodentium ICC168]
emb|CBG91326.1| UDP-N-acetylglucosamine L-carboxyvinyltransferase [Citrobacter
rodentium ICC168]
Length = 419

Score = 43.5 bits (101), Expect = 0.067, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 170/427 (39%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPGSKLSNRILLALLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEPEVEIQNVPKLKDVDTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ + + DA+ V +F + +++++ A++ A G G
Sbjct: 66 RNGSVRI-----DAR-NVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 LPGGCTIGARPVDLHITGLEQLGATIRLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 166 TVTIMCAATLAEGTT---IIENAAREPEIVDTANFLIALGAKISGQGT-DRITIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +
Sbjct: 222 GG--GVYRVLPDRIETGTFLVAAAISRGKIVCRNAQPDTL--DAVLAK-LRDAGADIEVG 276

Query: 302 ETSVTVTGPPREFPGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +
Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFTITET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + LA C
Sbjct: 327 VFENRFMHV--PELSRMGAHAIEISNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
T+ D
Sbjct: 384 EGTTVVD 390

>ref|ZP_03241130.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
HPKX_438_AG0C1]
Length = 230

Score = 43.5 bits (101), Expect = 0.067, Method: Compositional matrix adjust.
Identities = 35/137 (25%), Positives = 62/137 (45%), Gaps = 5/137 (3%)

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VT 306
+ D SSA +F AIT + + ++ + ++ E L+ MGA + + S +
Sbjct: 68 IANDPSSAFFFALACAITPKSRLLLKNVLLNPTR--IEAFEALKKMGASIEYAIQSKDLE 125

Query: 307 VTGPPREPFGRKHLKAIDVNMNMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G +ID N+ + D L++ LFA G + +R+ R KE++R+ A
Sbjct: 126 IIGDIYIEHAPLKAISIDQNIASLIDEIPALSIAMLFAGKGSVMVRNAKDLRAKESDRIKA 185

Query: 367 IRTELTKLGASVEEGPD 383
+ + LG EE D
Sbjct: 186 VISNFKALGIECEEFEED 202

>ref|ZP_07162908.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 116-1]
ref|ZP_07168119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 175-1]
gb|EFJ67107.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 175-1]
gb|EFK15268.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 116-1]
Length = 419

Score = 43.5 bits (101), Expect = 0.068, Method: Compositional matrix adjust.
Identities = 104/424 (24%), Positives = 166/424 (39%), Gaps = 47/424 (11%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVE 65

Query: 69 ADKAAK---RAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ + R V V C V+ + + A+ SL A G L G
Sbjct: 66 RNGSVHIDARDVNVFCAPYDLVKTMRASIW-----ALGSLVARF---GQGQVSLPG 113

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 114 GCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVT 168

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++ AA LA G IL+ P + T + G K + DR I+G ++
Sbjct: 169 IMCAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG- 223

Query: 246 KNAY-VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
Y V D FL AAI+ G + +L D A+ L GA + E
Sbjct: 224 -GVYRVLDPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDW 279

Query: 305 VTVTGPPEPFGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
+++ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 280 ISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---VFE 329

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
M EL+++GA E + I EKL+ + D R + + LA C
Sbjct: 330 NRFMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGT 386

Query: 421 TIRD 424
T+ D
Sbjct: 387 TVVD 390

>sp|Q39YP9.2|MURA_GEOMG RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
Length = 417

Score = 43.5 bits (101), Expect = 0.068, Method: Compositional matrix adjust.
Identities = 91/389 (23%), Positives = 156/389 (40%), Gaps = 61/389 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTL 64
+++++G V + GSK+ + + + L+ G + N+ D++ + L +LG
Sbjct: 2 DKLIIGGGKLTGDVSVSGSKNAALPVFISTILAPGLNEIRNVPFLRDINTTIKVLESLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-----DAKEEVQLFLGNAGIAMRSLTAAVTAAG--- 116
AVV G G ++ D + L +++++ A+V G
Sbjct: 62 -----AVVEGNGNIVKIDTTHVNDVEATYDL-----VKTMRASVLVLGPLL 102

Query: 117 ---GNATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGLPGGKVK 173
G A L G + RPI + GL LGAD+ G + L G ++
Sbjct: 103 ARHGRARVSLPGGCAIGARPINLHLKGLAALGADIRLEHGYVEAKAK-----KLKGARIN 157

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ L+MAA LA G+ I++ P + ++ R G + + + D
Sbjct: 158 FDIATVGGT-EQLMMAALAKGET---ILENAAREPEIIDLADILNRMGARIDGAGT-DT 212

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
I G K +P V D A F+ AAITGG + + L V F L+
Sbjct: 213 IRII-GVKELAPVVHDVMPDRIEAGTFMVAATAITGGDIKHNMKLEHLDALV-FK--LQD 268

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNMP-----DVAMTLAVVALFADGPTA 349
G ++ + V V G PR P +AI++ P D+ + ADG +
Sbjct: 269 AGVEIINRDNVVRVKG-PRRP-----RAINIKTRYPGFPPTDMQAQFMALMCVADGASV 321

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASV 378
I S + E M +EL + GA +
Sbjct: 322 I----SENIFENRFMHV--SELLRFGADI 344

>ref|YP_001654787.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis 434/Bu]
ref|YP_001653799.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis L2b/UCH-1/proctitis]
ref|ZP_07224183.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis L2tet1]
gb|AAD32216.1|AF142781_1 UDP-N-acetylglucosamine enolpyruvyl transferase [Chlamydia
trachomatis]
emb|CAP04154.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis 434/Bu]
emb|CAP07108.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis L2b/UCH-1/proctitis]
Length = 444

Score = 43.5 bits (101), Expect = 0.068, Method: Compositional matrix adjust.
Identities = 98/438 (22%), Positives = 172/438 (39%), Gaps = 87/438 (19%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDEVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLCRVLGAIVEWDQQAQ 71

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ +F + + L A + V GG+A
Sbjct: 72 VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCYPYGFVPI LGGA----- 120

Query: 128 RMRERPIGDLVVGLKQLGADV---DCFLGTDCCPPVRVNGIGLPGGKVKLSGSISSQYLS 184
+ R + + GLK+LGA++ D P GL G + L S
Sbjct: 121 -IGPRTLHFHLEGLKKLGAIEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
L++A+ A G +E+EIID ++ +++ GV+ +D+ I
Sbjct: 172 NLILASVGAQGRITIIKNAALEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Q + S ++ + +AS+ +A A ++ G + VE + + F +VL +G
Sbjct: 221 GCQDFYSVEHFIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

Query: 298 VTWTETSVTVTGPPREPFGKHLKA-----IDVNMNMPDVAMTLAVVALFADGPTAIRD 352
+ E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENG I-----EFFYDKPLKGGVLETDVHPGFITDWQQPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
 E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
 + D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

>gb|EFW78574.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. glycinea str. B076]
gb|EFW86037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. glycinea str. race 4]
Length = 421

Score = 43.5 bits (101), Expect = 0.069, Method: Compositional matrix adjust.
Identities = 93/398 (23%), Positives = 153/398 (38%), Gaps = 63/398 (15%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-----LS 66
 + G +++ G+K+ + IL L++G V NL + D+ M+ +G LS
Sbjct: 12 LDGEIRISGAKNSALPILATLLADGPVTVQNLPHLHDITTMIELFGRMGIEPVIDEKL 71

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVL 123
 VE D + +V P E K MR+ + + A G A L
Sbjct: 72 VEIDPRTIKTLVA-----PYELVK-----TMRASILVLGPMVARFGAEVAL 113

Query: 124 DGVPFRMRPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
 G + RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 114 PGGCAIGSRPVDLHIRGLEAMGAIIDVEGGYIKAKAPE-----GGLRGANFFFD-TVSV 166

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 ++MAA LA G ++ P V + G K H D I G +
Sbjct: 167 TGTENIMMAASLANGR---SVLQNAAREPEVVDLANFLIAMGAKI-HGAGTDTITIDGVK 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
 + P V D +L AA+TGG V V+ T L+ + L+ GA+VT
Sbjct: 223 RL-GPATYNVMPDRIETGYTLVAAAVTGGRVKVKDPTDPTILEAVLL---KLQEAGAEVTT 278

Query: 301 TETSVTVTGPPREPFGKRHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
 E + + + P KA++V P D+ + A+G A+ +
Sbjct: 279 GEDWIELNMHGKRP-----KAVNVRTAPYPAPFTDMQAQFISLNAIAEGTGAVIET--- 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
 + E M E+ ++GA ++ + I+T E L
Sbjct: 330 -IFENRFMHVY--EMHRMGAQIQVEGNTAIVTGTEVLK 364

>ref|YP_237203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. syringae B728a]
ref|YP_276261.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. phaseolicola 1448A]
ref|ZP_05637521.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. tabaci ATCC 11528]
ref|ZP_07006533.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 savastanoi pv. savastanoi NCPPB 3335]
ref|ZP_07261973.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. syringae 642]
sp|Q4ZNV7.1|MURA_PSEU2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
sp|Q48EC7.1|MURA_PSE14 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
gb|AAZ39165.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. syringae B728a]
gb|AAZ33832.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. phaseolicola 1448A]
gb|EFH97934.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 savastanoi pv. savastanoi NCPPB 3335]

Length = 421

Score = 43.5 bits (101), Expect = 0.069, Method: Compositional matrix adjust.
Identities = 93/398 (23%), Positives = 153/398 (38%), Gaps = 63/398 (15%)

Query: 15 ISGTVKLPGSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTL-----LS 66
+ G +++ G+K+ + IL L++G V NL + D+ M+ +G LS
Sbjct: 12 LDGEIRISGAKNSALPILAAATLLADGPVTVQNLPHLHDIT'TMIELFGRMGIEPVIDEKL 71

Query: 67 VEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTA AVTAAGGNATYVL 123
VE D + +V P E K MR+ + + A G A L
Sbjct: 72 VEIDPRTIKTLVA-----PYELVK-----TMRASILVLGPMVARFGEAEVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
G + RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 114 PGGCAIGSRPVDLHIRGLEAMGAIIDVEGGYIKAKAPE-----GGLRGANFFFD-TVSV 166

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G ++ P V + G K H D I G +
Sbjct: 167 TGTENIMMAASLANGR---SVLQNAAREPEVVDLANFLIAMGAKI-HGAGTDTITIDGVK 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ P V D +L AA+TGG V V+ T L+ + L+ GA+VT
Sbjct: 223 RL-GPATYKVPMDRIETGTYLVAAAVTGGRVKVKDTDPITLEAVLL---KLQEAGAEVTT 278

Query: 301 TETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASW 356
E + + + P KA++V P D+ + A+G A+ +
Sbjct: 279 GEDWIELNMHGKRP-----KAVNVRTAPYPAPPTMQAQFISLNAIAEGTGAVIET--- 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M E+ ++GA ++ + I+T E L
Sbjct: 330 -IFENRFMHVY--EMHRMGAQIQVEGNTAIVTGTEVLK 364

>ref|ZP_05441356.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. D11]
ref|ZP_06524860.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. D11]
gb|EFD81049.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. D11]
Length = 423

Score = 43.5 bits (101), Expect = 0.073, Method: Compositional matrix adjust.
Identities = 70/287 (24%), Positives = 123/287 (42%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPGSKSLNRIILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKIAGELKVDGSKNSTLPIMIATLVEKGTYILKNVPDLRDIRTLVALLESLEVEKLD 70

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + G G D +++ FL G+ V GG A +
Sbjct: 71 NSYKIINNGLSGAEASYDLVKMKRASFLVMGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G I++ P +E + + G K + + R I G K + + + +
Sbjct: 177 VKAKGKT---ILENAAKEPEIEDLCNFLIKMGAKISGAGTG-RIEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAK 275

>ref|ZP_03054973.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus pumilus
ATCC 7061]
gb|EDW21400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus pumilus
ATCC 7061]
Length = 435

Score = 43.5 bits (101), Expect = 0.073, Method: Compositional matrix adjust.
Identities = 97/410 (23%), Positives = 160/410 (39%), Gaps = 53/410 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L S +V+ ++ DV+ + LR L
Sbjct: 2 EKIIIVRGQKLNKGTVEGAKNAVLPIAASLLASTEKSVIDCVPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G V + V V E E V R + A+V G G
Sbjct: 62 GAEVHFEN---NEVSDASHALETEAPFEYV-----RKMRAVLVMGPELLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
+A L G + RPI + G + +GA + G V+ G L G K+ L
Sbjct: 108 HARVALPGGCAIGSRPIDQHLKGFEAMGAKIQVGNGFIEAEVQ---GRLKGAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++MAA LA G I++ + P + + G K + + I+
Sbjct: 164 -SVGATENIIMAAALAEETT---ILENVAKEPEIVDLANYINAMGGKVRGAGTGT- IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + K+ + D A F+ AAIT G V V+G + +E MG +
Sbjct: 219 GVETLHGAKHNIP-DRIEAGTFMVAAAITEGNVLVKGAVPEHM---TSLVAKMEEMGIQ 274

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRD- 352
+ E + V GP LK ID+ P D+ + + L A+G + I +
Sbjct: 275 IIEEEELRVIGPSE-----LKPIDLKTMHPGFPTDMQSQMALLLRANGTSMITET 327

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
V R E + ++ G SV II P +L + D
Sbjct: 328 VFENRFMAEEFRMNGDIKIEGRSV-----IINGPVQLQGAEVSATD 370

>ref|NP_931225.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Photorhabdus
luminescens subsp. laumondii T101]
sp|Q7N068.1|MURA_PHOLL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAE16400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate
transferase) (UDP-N-acetylglucosamine
enolpyruvyltransferase) (EPT) [Photorhabdus luminescens
subsp. laumondii T101]
Length = 421

Score = 43.1 bits (100), Expect = 0.075, Method: Compositional matrix adjust.
Identities = 102/421 (24%), Positives = 167/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12 LSGEVTISGAKNAALPILFAALLAEPELVQNVPELKDIDTTIKLLNRLGKVERNGSVF 71

Query: 74 --KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYVLDGVPR 128
R V C P E K MR+ A + A G L G
Sbjct: 72 VDARDVNQYCA---PYELVK-----TMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHISGLEQLGAEIVLEEGY---VKASVNGRLKGACIVMD-KVSVGATVTIMT 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P +E T + G K + + D I+G ++
Sbjct: 172 AATLAEGTT---VIENAAAREPEIEDTANFLNLGAKITGAGT-DHITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG V +L D A++ E GA + + V++
Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKVVCRHAQPNTL--DAVLAKLRE-AGADIAIGKDWVSL 282

Query: 308 TGPPREPFGKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ + P D+ +++ L A+G I + R
Sbjct: 283 DMHGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGAGMITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
+ I EL ++GA E + + +KL+ + D R + + LA C VT+
Sbjct: 332 FMHI-PELIRMGAAHAEIESNTVLCHGVKKLSAQV-MATDLRASASLVLAGCIAEGVTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|ZP_05276290.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-064]
Length = 328

Score = 43.1 bits (100), Expect = 0.076, Method: Compositional matrix adjust.
Identities = 51/214 (23%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G +I+ + P + + + G + + + + I+G ++ +
Sbjct: 68 IMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIEGVKELTAT 123

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+++ + D A F+ AAITGG V +E + LE MG ++ E +
Sbjct: 124 EHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQIIIEENGI 179

Query: 306 TVTGPPPREPFGKRHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V GP + LKA+DV P D+ + V+ + ++G + + + V R
Sbjct: 180 RVIGPDK-----LKAVDVKTMPHPGFPTDMQSQMMVIQMLSEGTSIMTETVFENRFMH 232

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
E M + ++ G SV II+ P KL
Sbjct: 233 VEEMRRMNADMKIEGHSV-----IISGPAKLQ 259

>ref|ZP_05380835.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis 70]
ref|ZP_05381758.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis 70s]
ref|ZP_05382685.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis D(s)2923]
emb|CBJ14977.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis Sweden2]
gb|ADH17234.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis E/150]
gb|ADH20929.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
trachomatis E/11023]
Length = 444

Score = 43.1 bits (100), Expect = 0.078, Method: Compositional matrix adjust.
Identities = 97/438 (22%), Positives = 173/438 (39%), Gaps = 87/438 (19%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEVDHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLRCVLGAIVEWDQQAQ 71

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ +F + + L A + V GG+A
Sbjct: 72 VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCYPYGFVPILGGDA----- 120

Query: 128 RMRERPIGDLVVGLKQLGADV---DCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ R + + GLK+LGA++ D P GL G + L S
Sbjct: 121 -IGPRTLHFHLEGLKKLGAEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
L++A+ A G +E+EIID ++ +++ G++ +D+ I
Sbjct: 172 NLILASVGAQGRTIKNAALEVEIIDLIV-----FLQKAGMEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Q + S +++ + +AS+ +A A ++ G + VE + + F +VL +G
Sbjct: 221 GCQDFYSVEHSIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

Query: 298 VTWTETSVTVTGPPREPFGKHLKA-----IDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+ E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENGIGI-----EFFYDKPLKGGVLETDVHPGFITDWQQPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
+ D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

>ref|ZP_06460536.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. aesculi str. NCPPB3681]
ref|ZP_06478351.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. aesculi str. 2250]
Length = 421

Score = 43.1 bits (100), Expect = 0.080, Method: Compositional matrix adjust.
Identities = 93/398 (23%), Positives = 153/398 (38%), Gaps = 63/398 (15%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL-----LS 66
+ G +++ G+K+ + IL L++G V NL + D+ M+ +G LS
Sbjct: 12 LDGEIRISGAKNSALPILAATLLADGPVTVQNLPHLHDITTMIELFGRMGIEPVIDEKL 71

Query: 67 VEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVL 123
VE D + +V P E K MR+ + + A G A L
Sbjct: 72 VEIDPRTIKTLVA-----PYELVK-----TMRASILVLGPMVARFGAEVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
G + RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 114 PGGCAIGSRPVDLHIRGLEAMGAIIDVEGGYIKAKAPE-----GGLRGANFFFD-TVSV 166

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G ++ P V + G K H D I G +
Sbjct: 167 TG TENIMMAASLANGR---SVLQNAAREPEVVDLANFLIAMGAKI-HGAGTDTITIDGVK 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ P V D +L AA+TGG V V+ T L+ + L+ GA+VT
Sbjct: 223 RL-GPATYKVMPPRIETGTYLVA AAVTGGRVKVKDTPDPTILEAVLL---KLQEAAGAEVTT 278

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASW 356
E + + + P KA++V P D+ + A+G A+ +
Sbjct: 279 GEDWIELNMHGKRP-----KAVNVRTAPYPAPFTDQAQFISLNAIAEGTGAVIET--- 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M E+ ++GA ++ + I+T E L
Sbjct: 330 -IFENRFMHVY--EMHRMGARIQVEGNTAIVTGTEVLK 364

>ref|YP_346601.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas fluorescens Pf0-1]
sp|Q3KHZ4.1|MURA_PSEPF RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABA72612.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas fluorescens Pf0-1]
Length = 421

Score = 43.1 bits (100), Expect = 0.080, Method: Compositional matrix adjust.
Identities = 86/393 (21%), Positives = 155/393 (39%), Gaps = 53/393 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L +G V NL + D+ M+ +G+ D+
Sbjct: 12 LDGEIRISGAKNSALPILAATLLCDGPVTVGNLPHLHDITTMIELFGRMGIEPVIDE--- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K VE ++ + +++++ A++ G G A L G
Sbjct: 69 -----KLSVEIDPRTIKTLIAPYEL-VKTMRASILVLGPMVARFGAEVALPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 119 IGSRPVDLHIRGLEAMGAVIDVEGGYIKAKAPE-----GGLRGAHFFFD-TVSVTG TEN 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G ++ P V + G K + + D I G ++ S
Sbjct: 172 IMMAAALAKGR---SVLQNAAREPEVVDLANFLNAMGAKVSGAGT-DTITIDGVERLGSA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ + +Y +A AA+TGG V V+ T L+ E L GA++T E +
Sbjct: 228 FYKVPMDRIETGTYLVA-AAVTGGRVKVKDTPITLEA---VLEKLREAGAEITCGEDWI 283

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + P KA++V P D+ + A+G A+ + + E
Sbjct: 284 ELNMHGKRP-----KAVNVRTAPYPAFPTDMAQAFISLNAIAEGTGAVIET----IFEN 333

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
M EL ++GA ++ + I+T E L
Sbjct: 334 RFMHVY--ELHRMGAHIQVEGNTAIVTGIETLK 364

>pdb|1A2N|A Chain A, Structure Of The C115a Mutant Of Mura Complexed With The
Fluorinated Analog Of The Reaction Tetrahedral
Intermediate
Length = 419

Score = 43.1 bits (100), Expect = 0.080, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRSI WALGPLVARFGQGQVSLPGGA 115

Query: 128 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFIET----VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEPVITI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMGAHAIEISNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|ZP_07029714.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
sp. MP5ACTX8]
gb|EF157201.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidobacterium
sp. MP5ACTX8]
Length = 426

Score = 43.1 bits (100), Expect = 0.082, Method: Compositional matrix adjust.
Identities = 91/385 (23%), Positives = 157/385 (40%), Gaps = 44/385 (11%)

Query: 17 GTVKLPGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA--DKAAK 74
 GT+K+ G+K+ + A L+E +++N+ D+ L ++G VE +A
 Sbjct: 14 GTIKISGAKNSALPCMAAAILTEDEVILENIPQVHDIETERKLLESMGAQVELGYGRAQH 73

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
 R + PV AK E+ + + + L A G A + G + RPI
 Sbjct: 74 RTSIQCAVLSDPV--AKYEIVKTMRASSLVLGPLIART----GMARVAMPGGCAIGGRPI 127

Query: 135 GDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
 + GL+ +GA + G + R+ G + K+ ++G+ LLMAA LA
 Sbjct: 128 DLHIKGLEAMGATITQEHGYLEARADRLKGT-HIVFDKITVTGT-----EDLLMAATLA 180

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
 G+ + + P V L+ G + E + + IKG K ++ + D
 Sbjct: 181 EGE---SLFCAREPEVTDLAALLNMGAEQIEGAGT-SVIRIKGVAKLHGARGH-RINPD 235

Query: 254 ASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTTTETSVTVTGPPRE 313
 A FL AITGG + V+ C L LE G K+ + +V V +
 Sbjct: 236 RIEAGTFLIAGAITGGDLNVCCNPEHLGA---LLGKLEQCGVKLEIGKENVRVHSGGK- 291

Query: 314 PFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAI-RDVASWR---VKETERM- 364
 L+A+D++ + P D+ + A+G + + ++ R V E RM
 Sbjct: 292 -----LQAVDISTEEYPGFPTDMQAQFMALLTQAEGTSVVTENIFENRFMHVGEINRMG 345

Query: 365 ----VAIRTELTKLGASVEEGPDYC 385
 V+ RT + GA ++ C
 Sbjct: 346 ANISVSGRTATIRGGAGLQSAAVMC 370

>ref|YP_911282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
 phaeobacteroides DSM 266]
 sp|A1BEN1.1|MURA_CHLPD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
 gb|ABL64858.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
 phaeobacteroides DSM 266]
 Length = 424

Score = 43.1 bits (100), Expect = 0.082, Method: Compositional matrix adjust.
 Identities = 103/414 (24%), Positives = 168/414 (40%), Gaps = 60/414 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
 +++V+ + ISGTV GSK+ S I+ L+E GT + + D+ L+ L
 Sbjct: 2 DKLVIHGRRISGTVAAASGSKNSSLPIIAATLLAEKGTFTLHRIPELHDIETFTQLLQHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
 G+ + R + E VQ L + + + A++ G G
 Sbjct: 62 GVETTFNNNTLRV-----STENVQSILAPYEL-VKKMRASIYVLGPLLARFG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGG----LPGGKVK 173
 A L G RPI ++ ++LGA++ G V+ + G P V
 Sbjct: 108 EAKVSLPGGCAFGPRPIDLHLMAMEKLGAEIKIETGFITASVKGKKLRGAHIDFPVSSVG 167

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
 +G+ LMAA LA G I + P +E + G + + + +
 Sbjct: 168 ATGNA-----LMAAVLAKGTT---TITNAAAEPIETLCHFLSAMGACIDGTGT-TK 215

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDV-KFAEVLE 292
 I+G ++ + V D A+ LA AAITGG++T+ G + L+ + KF
 Sbjct: 216 LVIEGVATLQAEFTNV-FDRIEAAATLLAAAAITGGSITLNGVEPSQLKAVLKKFVHA-- 272

Query: 293 MMGAKVTTTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVA--MTLAVVALF--ADGPT 348
 G +++ SVT+ P + L DV P M +AL A G +
 Sbjct: 273 --GCQISTQSDSVTLISP-----EQLLPDVTAKPYPSFPTDMQAQWIALMTQASGKS 323

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
 I D RV ER I EL +LGA +E + ++ P KL+ T + + D
 Sbjct: 324 LITD---RVYH-ERFNHI-PELNRLGAHIEIKNNQAVVHGPRKLSGTTVMSTD 371

```
>ref|YP_002384263.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
    fergusonii ATCC 35469]
sp|B7LR56.1|MURA_ESCF3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
    AltName: Full=Enoylpyruvate transferase; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
    Short=EPT
emb|CAQ90659.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
    fergusonii ATCC 35469]
gb|EGC96629.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
    fergusonii ECD227]
    Length = 419
```

Score = 43.1 bits (100), Expect = 0.082, Method: Compositional matrix adjust.
Identities = 103/425 (24%), Positives = 166/425 (39%), Gaps = 59/425 (13%)

```
Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
    ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEFPVEIQNVPKLKDVDTSMKLLSQLGAKVERNGSV 70

Query: 74 K---RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLD 124
    R V V C P E +++++ A++ A G G L
Sbjct: 71 HIDARDVNVFCA---PYE-----LVKTMRAIWLGLPLVARFGQGQVSLP 112

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
    G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 113 GGCSIGARPVDLHISGLEQLGATIKLEEGY---VKASVEGRLKGAHIVMD-KVSVGATV 167

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
    ++ AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 168 TIMCAATLAEGTT--IIENAAREPEIVDTANFLVTLGAKISGQGT-DRITIEGVERLGG 223

Query: 245 PKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
    Y V D FL AAI+ G + +L D A+ L GA + +
Sbjct: 224 --GVYRVLPDRIETGTFLVAAAIISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIETGDD 278

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
    +++ + P KA++V P D+ ++ L A+G I + V
Sbjct: 279 WISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTTET---VF 328

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVP 419
    E M EL+++GA E + I EKL+ + D R + + LA C
Sbjct: 329 ENRFMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEG 385

Query: 420 VTIRD 424
    TI D
Sbjct: 386 TTIVD 390
```

```
>ref|YP_328277.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
    trachomatis A/HAR-13]
sp|Q3KLP3.1|MURA_CHLTA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
    AltName: Full=Enoylpyruvate transferase; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
    Short=EPT
gb|AAX50729.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydia
    trachomatis A/HAR-13]
    Length = 444
```

Score = 43.1 bits (100), Expect = 0.082, Method: Compositional matrix adjust.
Identities = 97/438 (22%), Positives = 173/438 (39%), Gaps = 87/438 (19%)

```
Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
    + G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLRCRVLGAIVEWDQQAQ 71

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
    R ++ +F + + L A + V GG+A
Sbjct: 72 VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCPYGIFVPILGGDA----- 120

Query: 128 RMRERPIGDLVVGLKQLGADV---DCFLGTCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
```



```

      + R + + GLK+LGA++ D P GL G + L S
Sbjct: 121 -IGPRTLHFHLEGLKKLGAEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      L++A+ A G +E+EIID ++ +++ G++ +D+ I
Sbjct: 172 NLILASVGAQGRRTIIKNAALEVEIIDLIV-----FLQKAGMEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G Q + S +++ + +AS+ +A A ++ G + VE + + F +VL +G
Sbjct: 221 GCQDFYSVEHSIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

Query: 298 VTWTETSVTVTGPPREPFRGRHLKA----IDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
      + E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENG-----EFFYDKPLKGGVLETDVHPGFITDWQQPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
      E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACHDLFHECLSAKSCRYSTGNHPHSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
      + D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

```

>ref|ZP_08118552.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudonocardia
sp. P1]
Length = 421

Score = 43.1 bits (100), Expect = 0.085, Method: Compositional matrix adjust.
Identities = 104/444 (23%), Positives = 172/444 (38%), Gaps = 43/444 (9%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      E ++ +SG+V + G+K+ +++ A L+EG T ++N DV M LR+LG
Sbjct: 2 EHFAVRGGARLGSVDVVGAKNSVLKLMMAALLAEGRTTLENCPEILDVPLMADVLRSLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAG-IAMRSLTAAVTAAGGNATYVL 123
      +V + V G + +++ + G + R A V GG+A
Sbjct: 62 CAVAIEGGTVHIDVPANPGAADYRSVSKLRASVCVLGPLVARCRRRAVVPLPGGDA---- 117

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
      + RP+ GL++LGA D G+ + L G ++ L S
Sbjct: 118 -----IGSRPLDMHQNLRLKLGATTDIEHGSVTASAQ-----DLHGAQIWLDFP-SVGAT 166

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
      +LMAA LA G +ID P + ++++ G K E S + G +
Sbjct: 167 ENILMAAVLAEGTT---VIDNAAREPEIVDLQVMQMGAKLEGVGS-STLTVHGVGTGLQ 222

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
      P V GD + + AA+T G VTV G + + L GA+++ E
Sbjct: 223 -PTTHRVIQDRIVGATWAFAAAMTRGEVTVRGVDPHID---LVLDKLRSAEISTGEE 278

Query: 304 SVTVTGPPREPFRGRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      +V P R +A+D P A L +A+ A+ VA TE
Sbjct: 279 EFSVAMPGRP-----EAVDFVTLPYPGFATDLQPMI-----ALSVAEGTSMITEN 325

Query: 364 MVAIR----TELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAA-CAEV 418
      + R E+ +LGA + ++ E+L+ + D R LA CA
Sbjct: 326 VFEARFRFVDEMVR LGADARTDGHHAVVRGREELSSAPV-WASDIRAGAGLVLAGLCARG 384

Query: 419 PVTIRDPGCTRKTRTFPDYFDVLSTF 442
      + D + +P + + LS
Sbjct: 385 TTEVWDVAHIDRGYPFRFVENLSAL 408

```

>ref|YP_004111016.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris DX-1]
gb|ADU46283.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris DX-1]
Length = 429

Score = 43.1 bits (100), Expect = 0.085, Method: Compositional matrix adjust.

Identities = 71/311 (22%), Positives = 129/311 (41%), Gaps = 41/311 (13%)

Query: 13 KEISGTVKLPKSGSKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
E+ GT+ + G+K+ + +++ A L++ T ++DN+ DV + L G+ + A
Sbjct: 10 NELRGTIPIGAKNAALPLMIAALLTDETLILDNVPRADVALLQRILGNHGVDDIMA--- 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRS---LTAAVTAAGGN 118
GK P + + L + I MR+ + A + A
Sbjct: 67 -----AGKRPGDHEYQGQTLHISAKTIVDTTAPYDLVSKMRASFWVIAPLVARMHE 117

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG-S 177
A L G + RP+ L++ L++LGA++ D V GGL G + +
Sbjct: 118 AKVSLPGGCAIGTRPVDLLIMALEKLGAEITI---DGGYVIAPGGLKGTATIPFPKVT 173

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S +++ +MAA LA G IID P + + G + + R I+
Sbjct: 174 VSGTHVA--VMAAALANGTT---IIDNAACEPEIVDVADCLNKMGARITGAGT-PRIIE 227

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G K ++ + +Y +A A+ GG V + G LQ + +VL GA
Sbjct: 228 GVAKLHGARHTVLPDRIETGTYAMA-VAMAGGEVQLSGARPELLQAAL---DVLTEAGAT 283

Query: 298 VTWTETSVTVT 308
+T + V+
Sbjct: 284 ITVNNDGIKVS 294

>ref|ZP_03166422.1| hypothetical protein RUM_LAC_00068 [Ruminococcus lactaris ATCC 29176]
gb|EDY34170.1| hypothetical protein RUM_LAC_00068 [Ruminococcus lactaris ATCC 29176]
Length = 430

Score = 43.1 bits (100), Expect = 0.085, Method: Compositional matrix adjust.
Identities = 96/426 (22%), Positives = 175/426 (41%), Gaps = 43/426 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E+ +++ + G V++ G+K+ + IL A +++ +++NL + D++ ML A+ +G
Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALGILAAAIMADEPVLINLPDVNDINVMLEAIEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ + G F ++ D ++++ A L A+ A L
Sbjct: 62 AMVQRIDRHTVKINGSTIGDFSIDYDIKKIR-----ASYLLGALLGKYKRAEVAL 113

Query: 124 DGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV G L V + +I+
Sbjct: 114 PGGCNIHSRPIDQHLKGFRALGADVIEYKGIVAAEHLKGTHLYFDVVTGATIN---- 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA +A G I I++ + P+V + G + + D I+G +
Sbjct: 170 --VMAAAMADG---ITIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVKSLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + + D A F+ AA T G VTV L D +++++ +G +V +
Sbjct: 224 KAEYSIIP-DQIEAGTFMFAAAATRGDVTVLNVIPKHL--DATISKID-IGCEVEEFDD 279

Query: 304 SVTVTGPPEPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRV 358
+V V R LK+ V P D+ + VV A G + I + + R
Sbjct: 280 AVRVAKGR-----LKSTQVKTLPPGYPTDMQPQIGVVLALASGTSTITESIFENRF 332

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEV 418
K + EL ++GA+++ + I EK + + + D R A +A A
Sbjct: 333 KYLD-----ELARMGANIKVEGNSATIEGVEKFSARV-SAPDLRAGAALCIAGLATD 384

Query: 419 PVTIRD 424
+TI D
Sbjct: 385 GITIVD 390

>ref|YP_872416.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidothermus cellulolyticus 11B]

gb|ABK52430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidothermus
cellulolyticus 11B]
Length = 456

Score = 43.1 bits (100), Expect = 0.086, Method: Compositional matrix adjust.
Identities = 106/416 (25%), Positives = 164/416 (39%), Gaps = 71/416 (17%)

Query: 7 IVLQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
I ++P + ++G V + G+K+ +++ A L+ G TV+ N+ + DV M LR LG
Sbjct: 6 IQVRPSR-LAGRVAVTGAKNSVLKMAAALLAPGRTVLRNVPDILDVQIMAALLRRLGCD 64

Query: 67 VEADKAAKRAVVVGCGGKFPVE---DAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
VE GG+ V+ + E L +R L A++ G G
Sbjct: 65 VEP-----AGGELVVDVPDTPVRHEADYDL-----VRRLRASICVLGPLLVRCG 107

Query: 118 NATYVLDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
L G + R + + GL +LGA+V G + GL G V L
Sbjct: 108 ETKVALPGGDNIGSRGLDLHIAGLCRLGAETVSEHGY----LVARAPHGLSGATVWLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S LLMAA LA G +ID P + +++ G K E + + +
Sbjct: 164 -SVGATENLLMAAVLAQG---TTVIDNAAREPEIVDLATMLQEMGAKIEGAGTST--LVV 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGA- 296
G SP D A F GA +TGG VTV C L+ VL+ +G+
Sbjct: 218 HGVDTLSPVTHATVPDRIVAGTFAFGAVMTGGAVTVTRCRPEHLE-----IVLDRLGSC 271

Query: 297 ----KVWTETSVTVTGPPREPFGKRLKKAIDVNMNMKMPDVA-----MTLAVVALFADGP 347
V E V + G PR A+DV P A M +A+ A+ ADG
Sbjct: 272 GAEIAGVDGEFHVAMYGRPR-----AVDVVTLPPYGFATDFLPMVIAMNAV-ADGV 321

Query: 348 TAI-RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
+ +V R + + EL +LGA + + ++ +L+ ++ D
Sbjct: 322 AMVTENVFEGFRFIQ-----ELVRLGADIRTDGHHAVVRGRPRLSGAPVEATD 370

>ref|ZP_04574348.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 7_1]
gb|EEO43110.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 7_1]
Length = 423

Score = 43.1 bits (100), Expect = 0.087, Method: Compositional matrix adjust.
Identities = 94/408 (23%), Positives = 163/408 (39%), Gaps = 41/408 (10%)

Query: 13 KEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKIAGELKVDGSKNSTLPIMIATLVEKGTIILKNVPDLRDIRTLVALLESLEVEKLD 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMR 130
+ + + G G D ++++ FL G+ V GG A +
Sbjct: 71 NSYKIINNGLSGAEASYDLVKKMRASFLVMGGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY----VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G I++ P +E + + G K + + R I G K + + + +
Sbjct: 177 VKAKGKT---ILENAAKEPEIEDLCNFLIKMGAKISGAGTG-RIEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ +Y +A + + G++ V G L F LE MGAK + V
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAKFNIEGNKLEVLTK 288

Query: 311 PREPFGKRLKKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ LKA V P D+ + + +G + I++ + E M
Sbjct: 289 LSD-----LKAAKVTTMPHPGFPTDLQSPMMLMCLVNGTSEIKET----IFENRFMHV 338

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAA 414
EL ++GA +E IT E + + D R + LAA

Sbjct: 339 --PELNRMGAKIEIDSSTAKITGVENFSSAEV-MASDLRAGASLILAA 383

>ref|NP_643274.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas axonopodis pv. citri str. 306]
sp|Q8PID3.1|MURA_XANAC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAM37810.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas axonopodis pv. citri str. 306]
Length = 424

Score = 43.1 bits (100), Expect = 0.087, Method: Compositional matrix adjust.
Identities = 95/400 (23%), Positives = 158/400 (39%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVHISGAKNAVLPILCATLLADAPVEISNPHLDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSMLVDPRSVTHQVAPYELVKTMRASILVLGPELLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L G + +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY---IKATSNGLKRGARYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGARIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPREPFRGKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 281 TTTADSIITLDMQGKRP-----RAVSLTAPYPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|YP_004050374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Calditerrivibrio nitroreducens DSM 19672]
gb|ADR18211.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Calditerrivibrio nitroreducens DSM 19672]
Length = 420

Score = 43.1 bits (100), Expect = 0.088, Method: Compositional matrix adjust.
Identities = 67/275 (24%), Positives = 110/275 (40%), Gaps = 48/275 (17%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G VK+ G+K+ IL L+ G ++DN N DV ML L+ +G++ E
Sbjct: 12 LNGKVKVSGAKNSCLPILAATLLASGEYLIDNTPNLMDVTRTMLKLLKGMGINYEF----- 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG-----GNA 119
++ ++FL N+ ++++ A+V G G A
Sbjct: 67 -----QDNRVFLTNSDDNDLWTAPYDLVKTMRASVVVLGPELLAKKGKA 109

Query: 120 TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
L G + ERP+ + L Q+GA +D G + L G ++ ++
Sbjct: 110 KVSLPGGCAIGERPVDQHIKALAQMGAKIDIEHGYYIAEAQ-----KLKGCEIYFD-LVT 163

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
++MAA LA G+ I+ P V R ++R G + + IKG
Sbjct: 164 VTGTENIMMAATLAEGET---ILYNAAQEPEVVDLARFLKRMGANIS-GEGTNVIKIKGV 219

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274

+ +P + V D A L A TGG V VE
Sbjct: 220 SEL-NPADYTVMTDRIEAGTILCAVAGTGGDVVVE 253

>pdb|3KQA|A Chain A, Mura Dead-End Complex With Terreic Acid
pdb|3KQA|B Chain B, Mura Dead-End Complex With Terreic Acid
pdb|3KQA|C Chain C, Mura Dead-End Complex With Terreic Acid
pdb|3KQA|D Chain D, Mura Dead-End Complex With Terreic Acid
pdb|3LTH|A Chain A, E. Cloacae Mura Dead-End Complex With Unag And Fosfomycin
Length = 419

Score = 43.1 bits (100), Expect = 0.088, Method: Compositional matrix adjust.
Identities = 99/421 (23%), Positives = 166/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE D
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNPVKLKDIDTTMKLLTQLGKTKVERD---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + V F + +++ A++ A G G L G
Sbjct: 68 -----GSVWIDASN--VNNFSAPYDL-VKTMRSIWLGLPLVARFGQGQVSLPGGXA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL++LGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVLDLHIFGLEKLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A++ E GA + E +++
Sbjct: 226 YRVLDPRIETGTFLVAAISGGKIVCRNAQPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGKRP-----KAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|YP_003744447.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum CFBP2957]
emb|CBJ41803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
solanacearum CFBP2957]
Length = 453

Score = 43.1 bits (100), Expect = 0.090, Method: Compositional matrix adjust.
Identities = 63/267 (23%), Positives = 116/267 (43%), Gaps = 27/267 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ ++ N+ N +DV M LR +G VE +
Sbjct: 44 LSGEIRVSGAKNAALPIMCAALLTPEPLMLRNVPNLQDVRTMFKLLRQMG--VEGTQNGH 101

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
+ P +A ++ +++ A++ G G+A L G
Sbjct: 102 DVTLDAAADIHAP--EAPYDL-----VKTMRASILVLGLPLARFGHARVSLPGGCG 149

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+Q+GA++ G +G L G ++ ++ ++ LLM
Sbjct: 150 IGARPVQHIKGLQMGAEIVIEHGY-IEAKLADGAKRLRGARI-VTDMVTVTGTEENLLM 207

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G+ +++ P V L+ + G E + DR ++G K ++
Sbjct: 208 AAVLADGET---VLENAAREPEVTDLANLLVKMGACIEGIGT-DRLVVQGVDAIKGAEHT 263

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEG 275
 + D A FL A GG VT+ G
 Sbjct: 264 VI-ADRIEAGTFLCAVAAAGGDVTLRG 289

>ref|NP_417656.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli str. K-12 substr. MGL655]
 ref|NP_708988.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella flexneri 2a str. 301]
 ref|NP_755813.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli CFT073]
 ref|NP_838698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella flexneri 2a str. 2457T]
 ref|YP_312145.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella sonnei Ss046]
 ref|AP_003732.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli str. K-12 substr. W3110]
 ref|YP_542598.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli UTI89]
 ref|YP_671159.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 536]
 ref|YP_690575.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella flexneri 5 str. 8401]
 ref|YP_858805.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli APEC 01]
 ref|YP_001464665.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli E24377A]
 ref|YP_001459991.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli HS]
 ref|YP_001723515.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli ATCC 8739]
 ref|YP_001745461.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli SMS-3-5]
 ref|ZP_03003257.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 53638]
 ref|ZP_03030407.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B7A]
 ref|ZP_03035982.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli F11]
 ref|ZP_03046405.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli E22]
 ref|ZP_03051280.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli E110019]
 ref|ZP_03061625.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B171]
 ref|ZP_03066733.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella dysenteriae 1012]
 ref|ZP_03071286.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 101-1]
 ref|YP_002294748.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli SE11]
 ref|YP_002330936.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O127:H6 str. E2348/69]
 ref|YP_002388672.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli IAI1]
 ref|YP_002393172.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli S88]
 ref|YP_002399691.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli ED1a]
 ref|YP_002404561.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 55989]
 ref|YP_002409587.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli IAI39]
 ref|YP_002414328.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli UMN026]
 ref|ZP_04005715.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 83972]
 ref|YP_003034808.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli BL21-Gold(DE3)pLySS AG]
 ref|ZP_04872412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia sp.]

1_1_43]

ref|YP_003046239.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B str. REL606]

ref|ZP_05432757.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella sp. D9]

ref|ZP_05438101.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia sp. 4_1_40B]

ref|YP_003223780.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O103:H2 str. 12009]

ref|YP_003231207.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O26:H11 str. 11368]

ref|YP_003236342.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O111:H- str. 11128]

ref|ZP_06650724.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli FVEC1412]

ref|ZP_06655283.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B354]

ref|ZP_06659257.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B185]

ref|ZP_06663943.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli B088]

ref|ZP_06992136.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli FVEC1302]

ref|ZP_07097773.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 107-1]

ref|ZP_07103970.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 119-7]

ref|ZP_07116332.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 198-1]

ref|ZP_07122228.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 84-1]

ref|ZP_07135505.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 115-1]

ref|ZP_07141889.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 182-1]

ref|ZP_07145326.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 187-1]

ref|ZP_07152878.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 21-1]

ref|ZP_07174815.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 200-1]

ref|ZP_07179370.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 45-1]

ref|ZP_07186016.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 69-1]

ref|ZP_07189397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 196-1]

ref|ZP_07195009.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 185-1]

ref|ZP_07207885.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 124-1]

ref|ZP_07219742.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 78-1]

ref|ZP_07244872.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 146-1]

ref|ZP_07450601.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli NC101]

ref|ZP_07499231.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H736]

ref|ZP_07504098.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli M605]

ref|ZP_07509581.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli M718]

ref|ZP_07514045.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli TA206]

ref|ZP_07524086.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli TA271]

ref|ZP_07592732.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli W]

ref|ZP_07615141.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H591]

ref|ZP_07620615.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli

TA280]

ref|ZP_07625687.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H299]

ref|ZP_07688194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 145-7]

ref|ZP_07782682.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 2362-75]

ref|ZP_07786711.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli 1827-70]

sp|P0A749.1|MURA_ECOLI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|P0A750.1|MURA_ECOL6 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|P0A751.1|MURA_SHIFL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|Q3YX52.1|MURA_SHISS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|Q0T095.1|MURA_SHIF8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|Q0TCS1.1|MURA_ECOL5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|Q1R6E7.1|MURA_ECOUT RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|A1AG91.1|MURA_ECOK1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|A7ZS86.1|MURA_ECO24 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|A8A504.1|MURA_ECOHS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B1IQ74.1|MURA_ECOLC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B6I1R2.1|MURA_ECOSE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B7MBV8.1|MURA_ECO45 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B7NKQ6.1|MURA_ECO7I RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B7M095.1|MURA_ECO8A RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

sp|B7NDH3.1|MURA_ECOLU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName:


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Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B1LGF5.1|MURA_ECOSM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B7UJS9.1|MURA_ECO27 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B7LHP8.1|MURA_ECO55 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B7N0X1.1|MURA_ECO81 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
pdb|1UAE|A Chain A, Structure Of Udp-N-Acetylglucosamine Enolpyruvyl
Transferase
gb|AAN82387.1|AE016767_147 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
CFT073]
gb|AAA24187.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Escherichia coli]
gb|AAA57990.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Escherichia coli
str. K-12 substr. MG1655]
gb|AAC76221.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
str. K-12 substr. MG1655]
dbj|BAA78107.1| UDP-N-acetylglucosamine enolpyruvoyl transferase [Escherichia coli]
gb|AAN44695.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella flexneri 2a
str. 301]
gb|AAP18509.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella flexneri 2a
str. 2457T]
gb|AAZ89910.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella sonnei Ss046]
dbj|BAE77233.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
str. K12 substr. W3110]
gb|ABE09067.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli
UTI89]
gb|ABG71258.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
536]
gb|ABF05270.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella flexneri 5
str. 8401]
gb|ABJ02681.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli APEC
O1]
gb|ABV07608.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
HS]
gb|ABV17317.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E24377A]
gb|ACA76188.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
ATCC 8739]
gb|ACB15605.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
SMS-3-5]
gb|EDU66289.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
53638]
gb|EDV61086.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B7A]
gb|EDV64876.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
F11]
gb|EDV81598.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E22]
gb|EDV86856.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E110019]
gb|EDX29112.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B171]
gb|EDX33361.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
dysenteriae 1012]
gb|EDX37907.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
101-1]
dbj|BAG78997.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
SE11]
emb|CAS11016.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Escherichia coli
O127:H6 str. E2348/69]

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emb|CAU99831.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
55989]
emb|CAR00151.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
IAI1]
emb|CAR04799.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
S88]
emb|CAR19800.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
IAI39]
emb|CAR09989.2| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
ED1a]
emb|CAR14823.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
UMN026]
emb|CAP77649.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
LF82]
gb|EEH71999.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia sp.
1_1_43]
gb|EEJ45772.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
83972]
emb|CAQ33522.1| UDP-N-acetylglucosamine enolpyruvoyl transferase [Escherichia coli
BL21(DE3)]
gb|ACT27623.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
'BL21-Gold(DE3)pLysS AG']
gb|ACT40703.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B str. REL606]
gb|ACT44858.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
BL21(DE3)]
dbj|BAI27467.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O26:H11 str. 11368]
dbj|BAI32646.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O103:H2 str. 12009]
dbj|BAI37791.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O111:H- str. 11128]
gb|ACX38206.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
DH1]
dbj|BAI56561.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
SE15]
gb|ADA75556.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
flexneri 2002017]
emb|CBG36305.1| UDP-N-acetylglucosamine L-carboxyvinyltransferase [Escherichia coli
O42]
gb|EFE62041.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B088]
gb|EFE99836.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
FVEC1412]
gb|EFF04957.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B185]
gb|EFF11822.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
B354]
gb|ADE88182.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
IHE3034]
gb|EFI19195.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
FVEC1302]
gb|EFI88143.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 196-1]
gb|EFJ56581.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 185-1]
gb|EFJ62418.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 200-1]
gb|EFJ74174.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 198-1]
gb|EFJ81224.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 69-1]
gb|EFJ87192.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 84-1]
gb|EFJ90532.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 45-1]
gb|EFJ97202.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 115-1]
gb|EFK01236.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 182-1]
gb|EFK20360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli

MS 21-1]
gb|EFK25663.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 187-1]
gb|EFK44683.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 119-7]
gb|EFK50917.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 107-1]
gb|EFK70492.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 124-1]
gb|EFK74702.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 78-1]
gb|EFK91560.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 146-1]
gb|EFM50493.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
NC101]
gb|EFN37525.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
W]
gb|ADN48057.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
ABU 83972]
gb|ADN69516.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
UM146]
gb|EFO59987.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 145-7]
emb|CBJ02955.1| UDP-N-acetylglucosamine L-carboxyvinyltransferase [Escherichia coli
ETEC H10407]
gb|EFQ01119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
1827-70]
gb|EFR14602.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
2362-75]
gb|ADR28573.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O83:H1 str. NRG 857C]
gb|EFS13010.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
flexneri 2a str. 2457T]
gb|ADT76822.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
W]
dbj|BAJ44934.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
DH1]
gb|EFU37084.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 85-1]
gb|EFU48411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 110-3]
gb|EFU54187.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 153-1]
gb|EFU57215.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
MS 16-3]
gb|EFU97881.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
3431]
gb|EFW69304.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
WV_060327]
gb|EFW76678.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
EC4100B]
gb|EFZ40604.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
EPECa14]
gb|EFZ48716.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E128010]
gb|EFZ50940.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella sonnei
53G]
gb|EFZ59180.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
LT-68]
gb|EFZ64211.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
1180]
gb|EFZ68541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
1357]
gb|ADX49185.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
KO11]
gb|EGB32411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E1520]
gb|EGB37890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
E482]
gb|EGB42973.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
H120]

gb|EGB47167.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H252]
gb|EGB53378.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H263]
gb|EGB56770.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli H489]
gb|EGB65519.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli TA007]
gb|EGB77919.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 57-2]
gb|EGB81387.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 60-1]
gb|EGB87578.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli MS 117-3]
gb|EGC13436.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli E1167]
Length = 419

Score = 43.1 bits (100), Expect = 0.090, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVLDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFPGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTMQAQTLLNLVAEGTGFITET----VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|ZP_03265448.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp. H160]
gb|EEA03037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp. H160]
Length = 420

Score = 43.1 bits (100), Expect = 0.093, Method: Compositional matrix adjust.
Identities = 67/263 (25%), Positives = 114/263 (43%), Gaps = 27/263 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL LS ++N+ + +DV ML L +G+ +EA +
Sbjct: 12 LSGEVVVSGAKNAALPILCAGLLSADPVHLENVPDLQDVRTMLKLLGQMGVRIEAGE--- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMRE 131
G+ ++ +K + + MR+ + + A G+A L G +
Sbjct: 69 -----GRVALDASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARVSLPGGCAIGA 120

Query: 132 RPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
 RP+ + GL+ +GA++ G + R L G ++ ++ I+ LLMAA
 Sbjct: 121 RPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-VTDMITVTGTENLLMAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
 LA G+ +I+ P V L+ G K + + DR I+G K K+ +
 Sbjct: 174 VLAEGET---VIENAAAREPEVVDLAHLLVAMGAKIDGIGT-DRLVIQGVDKLHGAKHTVI 229

Query: 251 EGDASSASYFLAGAAITGGTVTV 273
 D A FL A GG VT+
 Sbjct: 230 P-DRIEAGTFLCAVAAAGGDVTL 251

>pdb|1RYW|A Chain A, C115s Mura Liganded With Reaction Products
 pdb|1RYW|B Chain B, C115s Mura Liganded With Reaction Products
 pdb|1RYW|C Chain C, C115s Mura Liganded With Reaction Products
 pdb|1RYW|D Chain D, C115s Mura Liganded With Reaction Products
 pdb|1RYW|E Chain E, C115s Mura Liganded With Reaction Products
 pdb|1RYW|F Chain F, C115s Mura Liganded With Reaction Products
 pdb|1RYW|G Chain G, C115s Mura Liganded With Reaction Products
 pdb|1RYW|H Chain H, C115s Mura Liganded With Reaction Products
 Length = 419

Score = 43.1 bits (100), Expect = 0.093, Method: Compositional matrix adjust.
 Identities = 99/421 (23%), Positives = 166/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G V + G+K+ + IL A L+E + N+ +D+ + L LG VE D
 Sbjct: 12 LQGEVITISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERD---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
 G ++ + V F + +++++ A++ A G G L G
 Sbjct: 68 -----GSVIDASN--VNNFSAPYDL-VKTMRSI WALGPLVARFGQGVSLPGGSA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 + RP+ + GL++LGA++ G V+ + G L G + + +S ++
 Sbjct: 117 IGARPVDLHIFGLEKLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
 AA LA G II+ P + T + G K + DR I+G ++
 Sbjct: 172 AATLAEGTT---IIENAAAREPEIVDTANFLVALGAKISGGQT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
 Y V D FL AAI+GG + +L D A++ E GA + E +++
 Sbjct: 226 YRVLPDRIETGTFLVAAAIISGKIVCRNAQPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
 + P KA+ V P D+ ++ L A+G I + + E
 Sbjct: 283 DMHGKRP-----KAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
 M EL ++GA E + I EKL+ + D R + + LA C T+
 Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
 D
 Sbjct: 390 D 390

>ref|ZP_04587072.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
 syringae pv. oryzae str. 1_6]
 Length = 421

Score = 43.1 bits (100), Expect = 0.094, Method: Compositional matrix adjust.
 Identities = 92/398 (23%), Positives = 155/398 (38%), Gaps = 63/398 (15%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 66
 + G +++ G+K+ + IL L++G V NL + D+ M+ +G LS
 Sbjct: 12 LDGEIRISGAKNSALPILAAATLLADGPVTVQNLPHLHDITTMIELFGRMGIEPVIDEKLS 71

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVL 123

VE D + +V P E K MR+ + + A G A L
Sbjct: 72 VEIDARTIKTLVA-----PYELVK-----TMRASILVLGPMVARFGEAEVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
G + RP+ + GL+ +GA +D ++ P GGL G ++S

Sbjct: 114 PGGCAIGSRPVDLHIRGLEAMGAIIDVEGGYIKAKAPE-----GGLRGAHFFFD-TVSV 166

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G ++ P V + G K H D I G +

Sbjct: 167 TGTENIMMAASLANGR---SVLQNAAREPEVVDLANFLIAMGAKI-HGAGTDTITIDGVK 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ S + + +Y +A AA+TGG V V+ T L+ + L+ GA+VT

Sbjct: 223 RLGSATYKVMPPRIETGTYLVA-AAVTGGRVKVKTDPITLEAVLL---KLQEAGAEVTT 278

Query: 301 TETSVTVTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
E + + + P KA++V P D+ + A+G A+ +

Sbjct: 279 GEDWIELNMHGKRP-----KAVNVRTAPYPAPFTDMAQAFISLNAIAEGTGAIVET--- 329

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M E+ ++GA ++ + I+T E L

Sbjct: 330 -IFENRFMHV--EMHRMGAQIQVEGNTAIVTGTEVLK 364

>ref|ZP_06486109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. vasculorum NCPPB702]
Length = 424

Score = 43.1 bits (100), Expect = 0.096, Method: Compositional matrix adjust.
Identities = 94/402 (23%), Positives = 162/402 (40%), Gaps = 49/402 (12%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG

Sbjct: 3 KIVVTGGQALHGEVNISGAKNAVLPILCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
V D+ A R+++V P + L +R++ A++ G

Sbjct: 63 EVTIDEGTLAKGRSILVD-----PRSVTHQIAPYEL-----VRTMRASILVLGPLLARY 111

Query: 117 GNATYVLGDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSG 176
G A L G + RP+ + GL+ LGAD+ G ++ G L G +

Sbjct: 112 GTAEVSLPGGCAIGSRPVDQHIKGLQALGADISVENGY----IKATSNGLKGSRYVFD- 166

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+S +LMAA LA G +++ P V + G + E + + R +

Sbjct: 167 MVSVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLNALGAQIEGAGT-PRIVV 222

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+G ++ +A + D FL AA+TGG+VTV +L D ++ E GA

Sbjct: 223 QGVERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETL--DAVLDKLTE-AGA 278

Query: 297 KVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
+T T S+T+ + P +A+ + P D+ + ADG I +

Sbjct: 279 IITTTADSITLDMQGKRP-----RAVSLTTAPYPAPFTDMAQFMALNCVADGVGVINE 332

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+

Sbjct: 333 T----IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|ZP_02825910.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC508]
gb|EDU95262.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC508]
Length = 419

Score = 43.1 bits (100), Expect = 0.096, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +

Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEFPVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++++ A++ A G G L G

Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++

Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G II+ P + T + G K + DR I+G ++

Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++

Sbjct: 225 VYRVLDPRIETGTFLVAAAISRGKIICRNTQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREFPFRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E

Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+

Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D

Sbjct: 389 VD 390

>ref|NP_794195.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000]

ref|ZP_03394750.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato T1]

ref|ZP_07231527.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato Max13]

ref|ZP_07250193.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato K40]

ref|ZP_07259819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato NCPPB 1108]

sp|Q87WV2.1|MURA_PSESM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

gb|AA057890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000]

gb|EEB61993.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato T1]

Length = 421

Score = 43.1 bits (100), Expect = 0.096, Method: Compositional matrix adjust.
Identities = 86/393 (21%), Positives = 157/393 (39%), Gaps = 53/393 (13%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L++G V NL + D+ M+ +G+ D+

Sbjct: 12 LDGEIRISGAKNSALPILAATLLADGPVTVQNLPHLDITTMIELFGRMGIEPVIDE--- 68

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K VE ++ + + +++++ A++ G G A L G

Sbjct: 69 -----KLSVEIDPRTIKTLIAPYEL-VKTMRASILVLGPMVARFGEAEVALPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ +GA +D ++ P GGL G ++S

Sbjct: 119 IGSRPVDLHIRGLEAMGAIIDVEGGYIKAKAPE-----GGLRGAHFFFD-TVSVTGTEN 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G +++ P V + G K H D I G ++ S

Sbjct: 172 IMMAASLANGR---SVLENAAREPEVVDLANFLIAMGAKI-HGAGTDTITIDGVKRLGSA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTTWTETSV 305

+ + +Y +A AA+TGG V V+ T L+ + L+ GA+VT E +
Sbjct: 228 TYKVMPIRIETGTYLVA-AAVTGGRVKVKTDPITLAVLL---KLQEAGAEVTTGEDWI 283

Query: 306 TVTGPPEPFPGRKHLKAIDVNMNKM---DVAMTLAVVALFADGPTAIRDVASWRVKET 361

+ + P KA++V P D+ + A+G A+ + + E
Sbjct: 284 ELNMHGKRP-----KAVNVRTAPYPAPFTDMAQAFISLNAIAEGTGAVIET----IFEN 333

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394

M E+ ++GA ++ + I+T E L
Sbjct: 334 RFMHVY--EMHRMGAQIQVEGNTAIVTGTEVLK 364

>ref|ZP_04209462.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock4-18]
ref|ZP_04230646.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-29]
gb|EEL37642.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-29]
gb|EEL58897.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock4-18]
Length = 419

Score = 43.1 bits (100), Expect = 0.097, Method: Compositional matrix adjust.
Identities = 70/276 (25%), Positives = 106/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G

Sbjct: 74 VRKMRASVQVMGPLLARNRRIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +

Sbjct: 134 VE----GELKGAKIYLDFFP-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G +K ++ + D A F+ AAITGG + +E

Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVKLYGNHSHIIP-DRIEAGTFMVAIAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPPEPFRKHLKAIDVNMNKM---DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+

Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVIDIKTMPHPGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA---SWRVKETERMVA 366

+ + L ADG + I + V+E RM A
Sbjct: 294 SQMMALLLQADGTSMITETVFENRFMHVEEFRRMNA 329

>ref|YP_409520.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella boydii Sb227]
ref|YP_001881896.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella boydii CDC 3083-94]
sp|Q31W66.1|MURA_SHIBS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
sp|B2U1Y8.1|MURA_SHIB3 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
gb|ABB67692.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella boydii Sb227]
gb|ACD07542.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella boydii CDC 3083-94]
gb|EFW49690.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella dysenteriae CDC 74-1112]
gb|EFW61400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella flexneri CDC 796-83]
Length = 419

Score = 43.1 bits (100), Expect = 0.097, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73


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      ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
      G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFQQQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      + RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIEANAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      + + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTITET----VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
      M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRGAHAIEISNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
      D
Sbjct: 389 VD 390

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>ref|ZP_04148600.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar tochigiensis BGSC 4Y1]
gb|EEM19704.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar tochigiensis BGSC 4Y1]
Length = 339

Score = 42.7 bits (99), Expect = 0.098, Method: Compositional matrix adjust.
Identities = 73/285 (25%), Positives = 110/285 (38%), Gaps = 35/285 (12%)

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Query: 105 MRSLTAAVTAAG-----GNATYVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
      +R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
      V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE----GELKGAKIYLDFF-SVGATENIMSAA TLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
      G K + + I+G K ++ + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAAAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKM-----DVA 334
      L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIIEENEGVRVIGPDK-----LKAVDIKTMPHPGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA-IRTELTKL 374
      + + L ADG + I + V+E RM A I+ E+ L
Sbjct: 294 SQMMALLLQADGTSMITETVFENRFMHVVEEFRMNADIKIEVVLL 338

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>ref|YP_889184.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium smegmatis str. MC2 155]
gb|ABK72461.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium smegmatis str. MC2 155]
Length = 418

Score = 42.7 bits (99), Expect = 0.098, Method: Compositional matrix adjust.
Identities = 101/402 (25%), Positives = 150/402 (37%), Gaps = 67/402 (16%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E V+ +SG V + G+K+ +++ A L+EGT+ + N + DV M LR L
Sbjct: 2 SERFVVTGGNRLSGEVAVGGAKNVSLKMAAALLAEGTSTITNCPDILDVPLMAEVLRL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D A R P DA A+R A+V G
Sbjct: 62 GATVELDGATVRIT----SPDEPKYDADFA-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L
Sbjct: 108 KARVALPGGDAIGSRPLDMHQAGLRQLGA--TCNIEHGCVVAEAD---HLHGAIEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW----- 231
S +LMAA +A G + I P V ++ G + + +
Sbjct: 163 -SVGATENILMAAVVAEG--VTTIHNAAREPDVVDLCAMLNEMGAQISGAGTSTLTITG 218

Query: 232 -DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
DR Y P V GD A+ + AA+T G +TV G LQ
Sbjct: 219 VDRLY-----PTEHRVIGDRIVAATWGIAAAMTRGDITVTGVDPQHLQ---LVLHK 266

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPPDVAMTLAVVAL----FADG 346
L GA VT + V R KA++V P L +A+ ADG
Sbjct: 267 LHDAGATVTQNDNGFRVVQYERP-----KAVNVATLPFGFPPTDLQPMAGLAAIADG 319

Query: 347 PTAI-RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 387
+ I +V R + E M+ +LGA + ++
Sbjct: 320 TSMITENVFEARFRFVEEMI-----RLGADARTDGHHAVV 354

>emb|CAN72374.1| hypothetical protein VITISV_019596 [Vitis vinifera]
Length = 381

Score = 42.7 bits (99), Expect = 0.100, Method: Compositional matrix adjust.
Identities = 85/341 (24%), Positives = 132/341 (38%), Gaps = 31/341 (9%)

Query: 56 MLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTA 115
M LR+LG +EA + V G VE E++ G + + A
Sbjct: 1 MASILRSLGAIEIA---CNGEMWVNADGVGSVEPCPEDIGKIRGGFFV-----IGPLLAR 52

Query: 116 GGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ LGA V+ LG + GL GG+ KL
Sbjct: 53 FGEAVVALPGGCDIGTRPVDLYIRGLRALGAIVE--LGDGKVRAQAANGRLVGGGRFKLD 110

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S L+MAA +A G + ++ + P V R + G E + S D Y
Sbjct: 111 HP-SVGATETLMAACMADG---VTVLSNVAKEPEVIDLARFLTGSACVEGAGS-DTLY 165

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
IKG + V D A F+ AA+T +++ + + L G
Sbjct: 166 IKGKNQLHG-SECIVPPDRIEAGTFMLAAAVTRSSISMSPVIPSHV---ACLIDKLLAAG 221

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGP TAIR 351
K+T ++ V+ P + +L+ DV P D+ V+ DG + +
Sbjct: 222 CKITCAHDTLEVASVPDDV--GHNLQGFVDVTCPPFGFPPTDLQPMVLLTTCDGSSIVE 279

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEK 392
+ RM +R EL KLGA + +I EK
Sbjct: 280 ETVF-----ENRMGHVR-ELQKLGARIRVCGSTAVICGKEK 314

>ref|ZP_04536540.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia sp.
3_2_53FAA]
gb|EEH85358.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia sp.
3_2_53FAA]
Length = 419

Score = 42.7 bits (99), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 103/427 (24%), Positives = 171/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE

Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEELVEIQNVPKLKDVDTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G + DA+ +V +F + +++++ A++ A G G

Sbjct: 66 RN-----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S

Sbjct: 111 LPGGCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + DR I+G ++

Sbjct: 166 TVTIMCAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +

Sbjct: 222 GG--GVYRVLDPRIETGTFVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVG 276

Query: 302 ETSVTVTGPPREFPGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +

Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTITET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + LA C

Sbjct: 327 VFENRFMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
T+ D

Sbjct: 384 EGTTVVD 390

>ref|ZP_03645634.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium bifidum NCIMB 41171]
ref|YP_003938018.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium bifidum S17]
ref|YP_003970382.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
[Bifidobacterium bifidum PRL2010]
ref|ZP_07801653.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Bifidobacterium
bifidum NCIMB 41171]
gb|ADO52444.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium bifidum S17]
gb|ADP35345.1| MurA UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium bifidum PRL2010]
gb|EFR49587.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Bifidobacterium
bifidum NCIMB 41171]
Length = 441

Score = 42.7 bits (99), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 25/72 (34%), Positives = 43/72 (59%), Gaps = 2/72 (2%)

Query: 1 MAGAEIIVLQPI--KEISGTVKLPGSKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLG 58
MA +E VL + K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH +

Sbjct: 1 MAESENDVLHVVGKPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVD 60

Query: 59 ALRTLGLSVEAD 70
LR G+ VE D

Sbjct: 61 LLRLHGVVDVEVD 72

>ref|YP_107313.1| putative 3-phosphoskimimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei K96243]
ref|YP_332316.1| putative 3-phosphoskimimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 1710b]
ref|ZP_02410002.1| putative 3-phosphoskimimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 14]
ref|ZP_02446037.1| putative 3-phosphoskimimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 91]
ref|ZP_02488612.1| putative 3-phosphoskimimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei NCTC 13177]
ref|ZP_03451571.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia
pseudomallei 576]

ref|ZP_04951920.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710a]
emb|CAH34677.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei K96243]
gb|ABA49068.1| putative 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710b]
gb|EEC37385.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 576]
gb|EET08939.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1710a]
Length = 435

Score = 42.7 bits (99), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 54/221 (24%), Positives = 87/221 (39%), Gaps = 34/221 (15%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + GTV LP SK R LL+A L+ TT ++N+ + ALR GL+V
Sbjct: 6 VHPSGALKGTVTLPASKPHVQRALLVALLNGATTRIENVSWCAETELQFAALRQFGLTV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-GVP 127
VE + L AG+ T + AAG + + +
Sbjct: 65 -----VERGDASLTLRGAGAGV---EATGTIDAAGSGMLFRMSAALA 103

Query: 128 RMRERPI----GDLVVGLKQLGAD-VDCFLGTDCPPVRVNGI----GGLPGGKVKLSGSI 178
+ ERP+ D + + D LG D N + P ++ L+
Sbjct: 104 SLSERPVTIRCNDLSFRSDSVFDDGFFSHLGDARRRAGNLVTISRKAHP-ERIALTRK 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLME 219
S+Q++S L AP + D + + D Y++MT++ M
Sbjct: 163 STQFISFALFVAPFS-ADRTL RVADDGSQAGYIDMTIKAMS 202

>ref|ZP_04888326.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1655]
gb|EDU09310.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia pseudomallei 1655]
Length = 435

Score = 42.7 bits (99), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 54/221 (24%), Positives = 87/221 (39%), Gaps = 34/221 (15%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+ P + GTV LP SK R LL+A L+ TT ++N+ + ALR GL+V
Sbjct: 6 VHPSGALKGTVTLPASKPHVQRALLVALLNGATTRIENVSWCAETELQFAALRQFGLTV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-GVP 127
VE + L AG+ T + AAG + + +
Sbjct: 65 -----VERGDASLTLRGAGAGV---EATGTIDAAGSGMLFRMSAALA 103

Query: 128 RMRERPI----GDLVVGLKQLGAD-VDCFLGTDCPPVRVNGI----GGLPGGKVKLSGSI 178
+ ERP+ D + + D LG D N + P ++ L+
Sbjct: 104 SLSERPVTIRCNDLSFRSDSVFDDGFFSHLGDARRRAGNLVTISRKAHP-ERIALTRK 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLME 219
S+Q++S L AP + D + + D Y++MT++ M
Sbjct: 163 STQFISFALFVAPFS-ADRTL RVADDGSQAGYIDMTIKAMS 202

>ref|YP_003501381.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O55:H7 str. CB9615]
gb|ADD58397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli O55:H7 str. CB9615]
Length = 419

Score = 42.7 bits (99), Expect = 0.10, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEFPVKIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
 G + DA+ +V +F + +++++ A++ A G G L G
 Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGLDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
 + RP+ + GL+QLGA + G V+ + G L G + + +S ++
 Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
 AA LA G II+ P + T + G K + DR I+G ++
 Sbjct: 171 CAATLAEGTT---IENAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
 Y V D FL AAI+ G + +L D A+ L GA + E ++
 Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIICRNTQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
 + + P KA++V P D+ ++ L A+G I + V E
 Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
 M EL+++GA E + I EKL+ + D R + + LA C T+
 Sbjct: 332 FMHV--PELSRMAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
 D
 Sbjct: 389 VD 390

>ref|ZP_08131360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
 D5]
 gb|EGB91577.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium sp.
 D5]
 Length = 430

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
 Identities = 97/411 (23%), Positives = 172/411 (41%), Gaps = 37/411 (9%)

Query: 17 GTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRA 76
 G V++ G+K+ + IL A +++ T ++DNL + D++ ML A+ +G +V+
 Sbjct: 14 GEVEIGGAKNAALAILAAAIMTDETVLIDNLPDVNDINVMLEAIAIGIGATVQRMDRHTVK 73

Query: 77 VVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVPRMRERPIG 135
 + G F +E D ++++ A L A+ A L G + RPI
 Sbjct: 74 INGSTIGDFNIEYDIKKIR-----ASYLLGALLGKYKRAEVALPGGCNIGSRPID 125

Query: 136 DLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALG 195
 + G + LGADV G V L V + +I+ ++MAA +A G
 Sbjct: 126 QHLKGFALGADVVDIEHGKIVAEAEVLRGTHLYFDVTVGATIN-----VMMAAAMADG 179

Query: 196 DVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDAS 255
 + I++ + P+V + G + + + D I+G + + + + D
 Sbjct: 180 ---LTIMENVAKEPHVVDVANFLNSMGANIKAGT-DVIKIRGVKSLHKTEYSIIP-DQI 234

Query: 256 SASYFLAGAAITGGTIVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPF 315
 A F+ AA T G VTV L D +++++ +G +V + +V V R
 Sbjct: 235 EAGTFMFAAAATLGDTVTLNVIPKHL--DATISKLVLD-IGCEVEEFDDAVRVVAKSRLCS 291

Query: 316 GR-KHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRD-VASWRVKETERMVAIRTELTK 373
 + K L + P + +TLA A G + I + + R K + EL +
 Sbjct: 292 TQVKTLPPYPGYPTDMQPQIGVTLA----LAKGTSTITESIFENRFKYLD-----ELAR 340

Query: 374 LGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIRD 424
 +GA ++ + I EK + + + D R A +A A +TI D
 Sbjct: 341 MGAVIKVEGNSATIEGVEKFSGARV-SAPDLRAGAALCIAGLATDGITIID 390

>ref|YP_004200846.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter sp.
 M18]
 gb|ADW15570.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter sp.
 M18]

Length = 421

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 89/385 (23%), Positives = 154/385 (40%), Gaps = 53/385 (13%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
      E++V++ ++SG V + GSK+ + I + L+ G + N+ D++ + L LG
Sbjct: 2  EKLVIKGGNKLSGEVTVSGSKNAALPIFISTILAPGCHTISNVPFLRDINTTIKVLEKLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKE-EVQLFLGNAGIAMRSLTAAVTAAG-----G 117
      V+ K VV K D E L +R++ A+V G G
Sbjct: 62  AKVD----GKGNVV-----KIDTTDLNSWEATYDL-----VRTMRASVLVLGPLLARFG 106

Query: 118 NATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
      A L G + RPI + GL LGA++ G + L G ++ S
Sbjct: 107 QARVSLPGGCATGARPINLHLKGLAAGAEITLHGYVEAKAK-----KLKGARINFDIS 161

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
      LLMAA A G+ I++ P + ++ + G E + + D IK
Sbjct: 162 TVGGT-EQLLMAAATAQGET---ILENAAREPEIVDLADILTKMGANIEGAGT-DTIRIK 216

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G ++ +P V D A F+ +AITGG + ++ L + F L+ G +
Sbjct: 217 GVEQL-TPAEHAVMPDRIEAGTFMIASAITGGDIKIKNMRLEHLDA-LTFK--LQDAGVE 272

Query: 298 VTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
      + + V V GP + +++++ P D+ + A+G + I
Sbjct: 273 IINKDNVVRVKGP-----RKIRSVNIKTRPYPGFPTDMQAQFMALMCIAEGASVI--- 322

Query: 354 ASWRVKETERMVAIRTELTKLGASV 378
      S + E M +EL + GA +
Sbjct: 323 -SENIFENRFMHV--SELLRFGADI 344
```

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>ref|YP_002228009.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
      enterica subsp. enterica serovar Gallinarum str. 287/91]
sp|B5REQ5.1|MURA_SALG2 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
emb|CAR38995.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
      enterica subsp. enterica serovar Gallinarum str. 287/91]
      Length = 419
```

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 101/421 (23%), Positives = 165/421 (39%), Gaps = 53/421 (12%)

```
Query: 15  ISGTVKLPKSKLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
Sbjct: 12  LQGEVTISGAKNAALPILFAALLAEPEVEIQNVPKLKDVDTSMKLLSQLGAKVERNGS-- 69

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
      V +V +F + +++++ A++ A G G L G
Sbjct: 70  -----VHIDASQVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCT 116

Query: 129 MRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      + RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLEQLGATIKLEEGY---VKASVEGRLKGAHIVMD-KVSVGATVTIMC 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      AA LA G II+ P + T + G K + DR I+G ++ S
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVTLGAKIAGQGT-DRITIEGVERLGS--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      Y V D FL AAI+ G + +L D A+ L GA + E +++
Sbjct: 226 YRVLDPDIETGTFLVAAAIISRGKILCRNAQPDTL--DAVLAK-LRDAGADIEVGEDWISL 282

Query: 308 TGPPREPFRGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      + P KA++V P D+ ++ L A+G I + V E
Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTITET---VFENRF 332
```

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIR 423

M EL+++GA E + I E L+ + D R + + LA C TI
Sbjct: 333 MHV--PELSRMGARAEIESNTVICHGIETLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424

D
Sbjct: 390 D 390

>ref|NP_289763.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 EDL933]
ref|NP_312095.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. Sakai]
ref|ZP_02776617.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4113]
ref|ZP_02779178.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4401]
ref|ZP_02794052.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4486]
ref|ZP_02806340.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4076]
ref|ZP_02811082.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC869]
ref|ZP_03085427.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4024]
ref|ZP_03251103.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4206]
ref|ZP_03255773.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4045]
ref|ZP_03259572.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4042]
ref|YP_002272659.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4115]
ref|ZP_03443194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14588]
ref|YP_003079975.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14359]
ref|ZP_05942481.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. FRIK2000]
ref|ZP_05947589.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. FRIK966]
sp|Q8X9J9.1|MURA_EC057 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|B5YS78.1|MURA_EC05E RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAG58323.1|AE005547_9 first step in murein biosynthesis;UDP-N-glucosamine
1-carboxyvinyltransferase [Escherichia coli O157:H7 str.
EDL933]
dbj|BAB37491.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. Sakai]
gb|EDU52483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4113]
gb|EDU69955.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4076]
gb|EDU76813.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4401]
gb|EDU80226.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4486]
gb|EDU92199.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC869]
gb|EDZ78168.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4206]
gb|EDZ84408.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4045]
gb|EDZ87057.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC4042]
gb|ACI38630.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli

O157:H7 str. EC4115]
gb|ACI77386.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli]
gb|ACI77387.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli]
gb|ACI77388.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli]
gb|ACI77389.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli]
gb|ACI77390.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Escherichia coli]
gb|EEC27903.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14588]
gb|ACT73899.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. TW14359]
gb|EFW64201.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. EC1212]
gb|EFX09832.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. G5101]
gb|EFX14566.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H- str. 493-89]
gb|EFX19324.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H- str. H 2687]
gb|EFX24160.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. 3256-97 TW 07815]
gb|EFX29346.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O55:H7 str. USDA 5905]
Length = 419

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KLQGEVTISGAKNAALPILFAALLAEPEVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPN 247
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFVLAAAISRGKIICRNTQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTMQAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|YP_001975520.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Wolbachia
endosymbiont of Culex quinquefasciatus Pel]
sp|B3CLV0.1|MURA_WOLPP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAQ54868.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Wolbachia
endosymbiont of Culex quinquefasciatus Pel]
Length = 425

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.

Identities = 85/382 (22%), Positives = 155/382 (40%), Gaps = 55/382 (14%)

Query: 13 KEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSV----E 68
K + G +K+ GSK+ I+ + S + + N+ + DVH M L++LG V
Sbjct: 11 KPLIGKIKINGSKNAVLPIMAASLFSNSSITLHNVPDLIDVHLMSELLKSLGAEVNFICN 70

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D A + + C + L + IA R L A+ G G + V
Sbjct: 71 KDYKANHTLEIDCSN-----INNHLISHEIASR-LRASFLMLGPMLSRFGRVSTV 119

Query: 123 LDGVPRMRERPIGDLVVLGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G + +RP+ + L+ +GA ++ D + G L G ++ +S
Sbjct: 120 FPGGCNIGKRPVDIHIKALEAMGAKIE----IDSCNITATTGKGLQKEITFE-KVSVGA 174

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++M+A LA G + I+ + P V + ++ G E +++ + I+G +
Sbjct: 175 TENIIMSATLAEG--VTTINNAATEPEVLDLIEFLKIMGANIEVNNT--KITIEGVEAL 229

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
++ + + +Y LA A IT G + +EG + ++ A L+ +GA+V +
Sbjct: 230 NGCEHKIIPDRIEAGTYALA-AIITDGELKLEGVSLSDIEC---IANELKTIGARVELHD 285

Query: 303 TSVTVTGPPREPFPGRKH--LKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
+ ++ RK+ +K+ V N P D+ L A G + I +
Sbjct: 286 DGIIS-----RKNKSIKSAHVATNPYPNFPSPMQPQLMSAMSIAGGISIIEE---- 333

Query: 357 RVKETERMVAIRTELTKLGASV 378
E A EL KLGA++
Sbjct: 334 --NVFESRFAHANELRKLGANI 353

>ref|YP_001530432.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Desulfococcus
oleovorans Hxd3]
sp|A8ZWM4.1|MURA_DESOH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABW68355.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Desulfococcus
oleovorans Hxd3]
Length = 417

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 86/398 (21%), Positives = 156/398 (39%), Gaps = 47/398 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGL 64
+ I+++ + ++GTV++ G+K+ + IL + L+ GT N+ + D+ + L LG
Sbjct: 2 DRIIVEGGRRLTGTVVEISGAKNAALPILASSLLTNGTCTYTNVPDLRDIQSIKELLTHLG 61

Query: 65 LSVEADKAAKRAVVVGCGG-KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
+E + G + P E ++ L + R A V+ GG A
Sbjct: 62 AKIECQGTTVQVDASGVNNHEAPYELVRKMRASILVLCPLVARLGRARVSLPGGCA---- 117

Query: 124 DGVPRMRERPIGDLVVLGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
+ ERPI + GL+ +GAD+ ++ P L GG + S
Sbjct: 118 -----IGERPIDFHLKGLEAMGADIALEHGYVNASAPK-----LTGGSIFYDVP-SV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G I P V + ++ + G + + + I+G
Sbjct: 164 TGTEENLLMAAALADGTTR---IGNAAACEPVTALVDVLNQMGANITGAGTPE-ITIQGVP 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+P + + D F+ AA+T G +T+ + L+G + K+
Sbjct: 220 SL-NPVSVSIIIPDRIETGTFMVAAALTKGDITITNAEPSHLKGQLD-----KLAQ 268

Query: 301 TETSVTVTGPPREPFPGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASW 356
T + V G G +K++DV P D+ V+ A G + I +
Sbjct: 269 TGARIEVNGKVIRVVGDTIKSVVDVKTLPYPGFPTMQAQFVLMVSVASGLSIITETIFE 328

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
R + + +EL ++GA + + ++ KL+
Sbjct: 329 -----NRFIHV-SELKRMGADITISGNTAMVAGAPKLS 360

```
>ref|YP_560589.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
    xenovorans LB400]
sp|Q13TQ2.1|MURA_BURXL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
    AltName: Full=Enoylpyruvate transferase; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
    Short=EPT
gb|ABE32537.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
    xenovorans LB400]
    Length = 420
```

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 68/273 (24%), Positives = 118/273 (43%), Gaps = 27/273 (9%)

```
Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
    +++V++ +SG V + G+K+ + IL LS ++N+ + +DV ML L +G
Sbjct: 2 DKLVEGGYPLSGEVVSGAKNAALPILCAGLLSAQPVHLENVPDLQDVRTMLKLLQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
    + +E+ G+ + +K+ + MR+ + + A G+A
Sbjct: 62 VQIESGD-----GRVSLNASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
    L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGTRI-VTDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
    LLMAA LA G+ +I+ P V L+ G K E + DR I+G
Sbjct: 164 TGTEENLLMAAVLAEGET---VIENAAAREPEVGDLAHLLVEMGAKIEGIGT-DRLVIQGV 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
    K K+ + D A FL A GG VT+
Sbjct: 220 KLHGAKHTVIP-DRIEAGTFLCAVAAAGGDVTL 251
```

```
>ref|ZP_04579893.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oxalobacter
    formigenes OXCC13]
gb|EEO30866.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oxalobacter
    formigenes OXCC13]
    Length = 417
```

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 89/394 (22%), Positives = 145/394 (36%), Gaps = 61/394 (15%)

```
Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
    + G + + G+K+ + IL + L+ + N+ +DV ML L +G+ +
Sbjct: 12 LEGEIAISGAKNAALPILCTSLTSDDIELTNVPELKDVQTMNLNLEQMGVIR----- 65

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRSLTAAV-----TAAGGNAT 120
    KE+ +L L + + +++++ AA+ A G A
Sbjct: 66 -----KEDDKLILNGSAVNNFYAPYEMVKTMRAAILVLCPLVARFGEAK 109

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
    L G + RP+ + GL+ LGA+V G + L G ++ ++ I+
Sbjct: 110 VSLPGGCAIGSRPVEQHIKGLRALGAEVQIEGGYILARAK-----KLKGTRI-VTDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
    LLMAA LA G+ II P V L+ + G K E + DR I G
Sbjct: 164 TGTEENLLMAATLAEGET---IKNAAAREPEVTDLALLIKMGAKIEGIGT-DRLVIHGV 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVT 299
    + K+ + D FL A TGG VT+ L+ + K E+ + +
Sbjct: 220 RLHGAKHEVIP-DRIETGTFLCAVAATGGDVTLTKTRDNILESALNKIREMGAEIASGTD 278

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVK 359
    W + P F +M A +AV L D I + R
Sbjct: 279 WIHIKMN-QRPKGVNFRTEYPGFPTDMQ-----AQFMAVNCLAEDASHVIETIFENRFM 332

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
    + EL +LGA ++ + IT KL
```

Sbjct: 333 HVQ-----ELNRLGARIKTEGNTAFITGVGKL 359

>ref|YP_002870557.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas fluorescens SBW25]
sp|C3K8X4.1|MURA_PSEFS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAY47161.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas fluorescens SBW25]
Length = 421

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 86/393 (21%), Positives = 153/393 (38%), Gaps = 53/393 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L +G V NL + D+ M+ +G+ D+
Sbjct: 12 LDGEIRISGAKNSALPILAAATLLCDGPVTVANLPHLHDITTMIELFGRMGIEPVIDE--- 68
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K VE ++ + + +++++ A++ G G A L G
Sbjct: 69 -----KLSVEIDPRTIKTLIAPYEL-VKTMRASILVLGPMVARFGEAEVALPGGCA 118
Query: 129 MRERPIGDLVVLGKQLGADVDC---FLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 119 IGSRPVDLHIRGLEAMGATIDVEGGYIKAKAPE-----GGLRGANFFFD-TVSVTGTEN 171
Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G ++ P V + G + + D + G ++ P
Sbjct: 172 IMMAAALANGR---SVLQNAAREPEVVDLANFLIAMGANITGAGT-DTITVDGVKRLH-P 226
Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSV 305
V D +L AA+TGG V V+ T L+ E L GA++T E +
Sbjct: 227 ATYKVMPPRIETGTYLVAAAVTGGRVKVKDTPDPTILEA---VLEKLEAGAEITTGEDWI 283
Query: 306 TVTGGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
+ + P KA++V P D+ + A+G A+ + + E
Sbjct: 284 ELNMHGKRP-----KAVNVRTAPYPAPFTDMAQAFISLNAIAEGTGAVIET----IFEN 333
Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
M EL ++GA ++ + I+T EKL
Sbjct: 334 RFMHVY--ELHRMGAKIQVEGNTAIVTGTEKLK 364

>ref|YP_265898.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus Pelagibacter ubique HTCC1062]
sp|Q4FNE4.1|MURA_PELUB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAZ21295.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus Pelagibacter ubique HTCC1062]
Length = 417

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 90/410 (21%), Positives = 164/410 (40%), Gaps = 45/410 (10%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G +++ GSK+ S IL LS + NL +D+ M+ L++LG +E +
Sbjct: 11 KLKGQIRISGSKNASLPILAAATLLSNKKISLANLPRVKDIETMILLKSLGSIIEDN--- 67
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
K+ +++ + A V+ AGI + + A G A L G + RP
Sbjct: 68 KKELIINKTKQTKTFAAYSLVKTM--RAGIL---VLGPLLAKFGKAKVSLPGGCAIGTRP 122
Query: 134 IGDVLVVLGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L +LG G V N GL G +K +S L++AA LA
Sbjct: 123 VDIHLQALSGLGVKYKIIQGY----VHANAPKGLIGANIKFP-KVSVGATENLIIAACL 177
Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD---RFYIKGGQKYKSPKNAYV 250

G +S +E ++ + F + + W I+G K + V
Sbjct: 178 KGKTT-----LSNCAIEPEIKDLVNFLINMGCNIKWTAKRTVRIEGVNNLKEL-DYSV 229
Query: 251 EGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D A +L AA+T G + + G + ++ +L+ +G+K+T + + + G
Sbjct: 230 MPDRIEAGTYLIAAALTEGNLKITGIDPKIISTEI---NILKKVGSKITLKKNEILIQGS 286
Query: 311 PREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
K +K I++ + P D+ + V+ A+ + I++ + E M
Sbjct: 287 -----KIKNINIKTSPYPGFPTDLQAQMMVLLCKANKRSHIKE---EIFENRFMHV 335
Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
EL ++GA + + I K + D R +++ LAA A
Sbjct: 336 --AELNRMGAKISINGNQASIEGNIKFEAAEL-MATDLRASVSLILAALA 382

>ref|YP_001897176.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
phytofirmans PsJN]
sp|B2SZ71.1|MURA_BURPP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACD17952.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia
phytofirmans PsJN]
Length = 420

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 68/273 (24%), Positives = 119/273 (43%), Gaps = 27/273 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++V++ +SG V + G+K+ + IL + LS ++N+ + +DV ML L +G
Sbjct: 2 DKLVIEGGYPLSGEVVSGAKNAALPILCASLLSAEPVHLENVVDLQDVRTMLKLLGQMG 61
Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+ +E+ G+ + +K+ + + MR+ + + A G+A
Sbjct: 62 VQIESGD-----GRVSLNASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110
Query: 122 VLDGVPRMRERPIGDLVVLGKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGARI-VTDMITV 163
Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ +I+ P V L+ G K E + DR I+G
Sbjct: 164 TGTEENLLMAAVLAEGET---VIENAAAREPEVGDLAHLVLVAMGAKIEGIGT-DRLVIQGV 219
Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
K K+ + D A FL A GG VT+
Sbjct: 220 KLHGAKHTVIP-DRIEAGTFLCAVAAAGGDVTL 251

>ref|ZP_07654793.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylobacter
tundripaludum SV96]
gb|EFO05404.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylobacter
tundripaludum SV96]
Length = 421

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 90/391 (23%), Positives = 159/391 (40%), Gaps = 51/391 (13%)

Query: 15 ISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + IL LSE V N+ + D+ + L +G+ + D+
Sbjct: 12 LSGELRISGAKNAALPILAATLLSESPVSVGNIPHLHDITTTMELLGRMGVHLTVDE--- 68
Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K +E + F+ + +R++ A++ G G A L G
Sbjct: 69 -----KMNIEVDSSTINSFVAPYEL-VRTMRASILVLGPLVARFGAEHVSPLGGCA 118
Query: 129 MRERPIGDLVVLGKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL ++GAD+ G R+ G L ++ ++G+ LL
Sbjct: 119 IGSRPVDIHLGLMKMGADITVENGFIHAKATRLKGC-RLVLEQITVTGT-----ENLL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G II+ P V + + G K D I+G +K
Sbjct: 172 MAAALAEGETT---IIENAAKEPEVTDLAHFLNKMGAKIT-GIGTDVLVIEGVEKLGVESI 227

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
Y + D +L AAITGG++ ++ L D +++E GA++T E +
Sbjct: 228 HYDILPDRIETGTYLIAAAITGGSIKLKNTRPDIL--DAVLEKLVE-AGAEITTGEDWIK 284

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ +P KA+ V + P D+ + ADG I +
Sbjct: 285 LDMHGNKP-----KAVSVRTSPYPAFPTDMAQFTAMNAIADGVGIITETVF-----EN 333

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
R + ++ EL ++GA ++ + I T +KL
Sbjct: 334 RFMHVQ-ELQRMGADIKLESNTAICTGVKKL 363

>ref|YP_004221522.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JCM 1217]
dbj|BAJ67430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JCM 1217]
Length = 441

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 52/194 (26%), Positives = 85/194 (43%), Gaps = 22/194 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ V+ D A
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVSDLLRLHGVDDVDVGA 74

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+V + + D + L L + + R A + A GG A
Sbjct: 75 --NGIVTVDASRVQLADVADVDTLSGSSRIPILFSGPLVHRLGEAFIPALGGCA----- 126

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + L++LGA VD + + GL G K+ L S
Sbjct: 127 ---IGGRPIDFHLETLRKLKLGATVD---KEHKDGIHITAPNGLHGAHIHLPYP-SVGATEQ 179

Query: 186 LLMAAPLALGDVEI 199
L+AA LA G E+
Sbjct: 180 TLLAAVLAEGKTEL 193

>ref|YP_003006081.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dickeya zeae
Ech1591]
gb|ACT08602.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dickeya zeae
Ech1591]
Length = 420

Score = 42.7 bits (99), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 98/427 (22%), Positives = 171/427 (40%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++G V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 6 VQGPTRLAGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTTMKLLSQLGARVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G V+ + V +F + +++ A++ A G G
Sbjct: 66 RN-----GSVHVDAST--VNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHINGLEQLGAHITLEEGY---VKATVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA+G II+ P + T + G K + S D+ I+G ++
Sbjct: 166 TVTIMSAATLAVGKT---IIENAAAREPEIVDTANFLNTLGAKISGAGS-DKIVIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AA++GG V +L D +++ E GA +
Sbjct: 222 GG--GVYRVLPRIETGTFLVAAAVSGGKVVCRHTRPDTL--DAVLSKLRE-AGADIEIG 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWR 357
+ +++ R P KA++V + P D+ +++ L A+G I +
Sbjct: 277 DDWISLDMHGRRP-----KAVNVRTSPHPGFPTDMQAQFSLNLVAEGTGVITETIF-- 328

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
R + I EL ++GA E + I +L+ + D R + + LA C
Sbjct: 329 ---ENRFMHI-PELIRMGAQAEIESNTVICHGVSRLSGAQV-MATDLRASASLVLAGCLA 383

Query: 418 VPVTIRD 424
T+ D
Sbjct: 384 EGTTLVD 390

>gb|AAT48249.1| chloroplast CP4-EPSPS fusion protein precursor [Glycine max]
Length = 141

Score = 42.7 bits (99), Expect = 0.11, Method: Composition-based stats.
Identities = 20/50 (40%), Positives = 31/50 (62%)

Query: 15 ISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+SGTV++PG KS+S+R + L+ G T + LL EDV A++ +G
Sbjct: 90 LSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMG 139

>ref|XP_003190361.1| udp-n-acetylglucosamine enolpyruvyl transferase [Aspergillus oryzae
RIB40]
Length = 308

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 74/299 (24%), Positives = 119/299 (39%), Gaps = 28/299 (9%)

Query: 13 KEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++++G V++ GSK+ ++ L+ G + + L D+ M L+ LG V
Sbjct: 11 RDVTGNVRVSGSKNAGLPLMAATLLAPGPSTLHGLPPVSDIKNMGSILQYLGADVSVQVSD 70

Query: 73 AKRAVVVGCGGKF-PVE--DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
+F P + D+ LFLG + A G+A G +
Sbjct: 71 NFTIDTDTVTSRFVPAQLTDSLRLASILFLG-----PLLARFGHACLSFPGGCSI 119

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + + GL++LGA C TD + + L G + + + ++ L+MA
Sbjct: 120 GNRPVEEHINGLRKLGA---CITVTDT-YIEAHA-SQLQGATIDMQTPSVTGTMN-LIMA 173

Query: 190 APLALGDVEIEIIDKLISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNA 248
A LA G + I P V + + GV H D+ I G SP
Sbjct: 174 ACLARG---VTHIHNAAREPEVGDLINFLVLMGVDI-HGAGTDQLVIHGCHSTPLSPCQY 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V D FL AI G +TV C + V + L+ +GA+V ++ SVTV
Sbjct: 230 GVMEDRIEVGTFLILGAICGNPLTVYPCHP---EQHVMLIKNLKAVGARVDISDDSVTV 285

>ref|YP_955107.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
vanbaalenii PYR-1]
gb|ABM15101.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
vanbaalenii PYR-1]
Length = 417

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 100/402 (24%), Positives = 152/402 (37%), Gaps = 67/402 (16%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E V+ +SG V + G+K+ +++ A L+EGT+ + N + DV M LR L
Sbjct: 2 SERFVVTGGGRLSGEVAVGGAKNSVLKMAAALLAEGTSTITNCPDILDVPLMAEVLRLGL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE D R ++ K + A+R A+V G
Sbjct: 62 GATVELDGDVVIRIT-----SPDEPKYDADF-----AAVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177

```

      A  L  G  +  RP+      GL+QLGA  C  +  C      +  L  G  +++L
Sbjct: 108 KAKVALPGGDAIGSRPLDMHQAGLRQLGA--RCNIEHGCVVAEAD---HLRGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSW----- 231
      S      +LMAA LA G  +  I      P V      ++ + G +  + S
Sbjct: 163 -SVGATENILMAAVLAEG---VTTIHNAAREPDVVDLCTMLNQMQAQVTGAGSSTLTITG 218

Query: 232 -DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
      DR Y      P      V GD  A+ +  AA+T G ++V G      LQ
Sbjct: 219 VDRLY-----PTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAPHLQ---LVLHK 266

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVAL----FADG 346
      L  GA VT T+      V  R      KA++V      P      L  +A+      ADG
Sbjct: 267 LHDAGATVTQTDDGFRVVQYERP-----KAVNVATLPFPGFPTDLQPMAGLAADVADG 319

Query: 347 PTAI-RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 387
      + I  +V  R  +  E M+      +LGA      +  ++
Sbjct: 320 TSMITENVFEARFRFVEEMI-----RLGADARTDGHHAVV 354

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>ref|ZP_01995869.1| hypothetical protein DORLON_01864 [Dorea longicatena DSM 13814]
gb|EDM62839.1| hypothetical protein DORLON_01864 [Dorea longicatena DSM 13814]
Length = 116

Score = 42.7 bits (99), Expect = 0.12, Method: Composition-based stats.
Identities = 18/60 (30%), Positives = 35/60 (58%)

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Query: 9  LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
      + P + + G V +PG KS+S+R ++L +++ GTT + + L  D      +  R +G+ +E
Sbjct: 6  IAPTRGLKGEVTPGDKSISHRSIMLGSIALGTTEITHFLEGADCLSTIDCFRKMGEVEIE 65

```

>gb|EFX33752.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
O157:H7 str. LSU-61]
Length = 419

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 102/422 (24%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

```

Query: 14  EISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      ++ G V + G+K+ +  IL  A L+E      + N+      +DV      +  L  LG  VE +
Sbjct: 11  KLQGEVTISGAKNAALPILFAALLAEPEVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
      G      + DA+ +V +F      + +++++ A++ A G      G      L  G
Sbjct: 68  -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
      +  RP+      + GL+QLGA +      G      V+ +  G L G  +  +  +S      ++
Sbjct: 116 TIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLLKAHIVMD-KVSVGATVTIM 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
      AA LA G      II+      P  +  T      +  G K      + DR  I+G ++
Sbjct: 171 CAATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224

Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      Y V  D      FL  AAI+ G +      +L  D  A+ L  GA +  E  ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAISRGKIIICRNTQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      +      + P      KA++V      P      D+      ++ L A+G  I  +      V  E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAPFTDMQAQFTLLNLVAEGTGFIETET---VFENR 331

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPVTI 422
      M      EL+++GA  E  +  I      EKL+      +  D R + +  LA C      T+
Sbjct: 332 FMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388

Query: 423 RD 424
      D
Sbjct: 389 VD 390

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>ref|ZP_07666170.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gardnerella vaginalis ATCC 14018]
Length = 452

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 89/374 (23%), Positives = 152/374 (40%), Gaps = 38/374 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G +K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G++V+ D A
Sbjct: 26 KPLNGAIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVDLLRLHGVNVDVDGA 85

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A VV + D +V G++ I + + + G A G + R
Sbjct: 86 A--GVVSIDASNVLADVA-DVDTLSGSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 141

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS---GSISSQYLSALLM 188
PI + L++LGA+VD + + GL G K+ L G+ L+A+L
Sbjct: 142 PIDFHLETLRKLGANVDK---DHEDGIHITAPNGLHGTKIHLPPYPSVGATEQTLLAAVLA 198

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247
L IE P + + +++ G A S DR F I+G K + N
Sbjct: 199 EGKTELSGAAIE-----PEIMDLVAVLQKMG--AIISVDVDRTFRIEGVDKLQG-YN 247

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
D A+ + + A T G V ++G + + F V +G + T+ +
Sbjct: 248 HTALTDRIEAASWASALATHGDVFIKATQPEM---MTFLNVFRKVGQDFDVTNNGIRF 304

Query: 308 TGPPREPFGKHLKAI--DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P G H AI DV+ M D L V A G + + + E
Sbjct: 305 W----HPGGDLHPVAIETDVHPGFMTDWQQLVVALTQAKGLSIVHETV-----YENRF 354

Query: 366 AIRTELTKLGASVE 379
L ++GA ++
Sbjct: 355 GFTKPLVQMGAMIQ 368

>ref|ZP_06842366.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp. Ch1-1]
gb|EFG70044.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia sp. Ch1-1]
Length = 420

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 68/273 (24%), Positives = 118/273 (43%), Gaps = 27/273 (9%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
+++V++ +SG V + G+K+ + IL LS ++N+ + +DV ML L +G
Sbjct: 2 DKLVIEGGYPLSGEVVSGAKNAALPILCAGLLSAEPVHLENVPDLQDVRTMLKLLGQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
+ +E+ G+ + +K+ + MR+ + + A G+A
Sbjct: 62 VQIESGD-----GRVSLNASKVDNLVAPYEMVKTMRASILVLGPLVARFGHARV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA++ G + R L G ++ ++ I+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLQAMGAETIEHGFIEARAKR-----LKGTRI-VTDMITV 163

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ +I+ P V L+ G K E + DR I+G
Sbjct: 164 TGTENLLMAAVLAEGET---VIENAAREPEVGDLAHLLVEMGAKIEGIGT-DRLVIQGV 219

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273
K K+ + D A FL A GG VT+
Sbjct: 220 KLHGAKHTVIP-DRIEAGTFLCAVAAAGGDVTL 251

>pdb|1EJC|A Chain A, Crystal Structure Of Unliganded Mura (Type2)
pdb|1EJD|A Chain A, Crystal Structure Of Unliganded Mura (Type1)
pdb|1EJD|B Chain B, Crystal Structure Of Unliganded Mura (Type1)
pdb|1EYN|A Chain A, Structure Of Mura Liganded With The Extrinsic Fluorescence

Probe Ans
pdb|1YBG|A Chain A, Mura Inhibited By A Derivative Of 5-Sulfonoxy-Anthranilic
Acid
pdb|1YBG|B Chain B, Mura Inhibited By A Derivative Of 5-Sulfonoxy-Anthranilic
Acid
pdb|1YBG|C Chain C, Mura Inhibited By A Derivative Of 5-Sulfonoxy-Anthranilic
Acid
pdb|1YBG|D Chain D, Mura Inhibited By A Derivative Of 5-Sulfonoxy-Anthranilic
Acid
Length = 419

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 99/421 (23%), Positives = 166/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE D
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERD---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + V F + +++ A++ A G G L G
Sbjct: 68 -----GSVWIDASN--VNNFSAPYDL-VKTMRSIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL++LGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARFVDLHIFGLEKLGAIEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A++ E GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAISGGKIVCRNAQPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFGKRLKKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGKRP-----KAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|ZP_03298160.1| hypothetical protein COLSTE_02082 [Collinsella stercoris DSM 13279]
gb|EEA89720.1| hypothetical protein COLSTE_02082 [Collinsella stercoris DSM 13279]
Length = 427

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 86/380 (22%), Positives = 148/380 (38%), Gaps = 41/380 (10%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I G V + G+K+ + +++ L+ G T ++N+ N DVH M L+ +G +E +
Sbjct: 12 IEGRVCVSGAKNSALKLMAATLLAPGKTTLENVPNISDVHVMGKVLKRMGAVIEV--VDE 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYVLDGVPRMRE 131
+++ E V MR+ TA + G A + G +
Sbjct: 70 HTLIIDTSAVDSWEAPYELVA-----KMRASTAVMGPLLGRFGCAKIAMPGGCNLGA 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
R I ++GL+ LG + D TD + GL G V L + S L+MA+
Sbjct: 122 RKIDMHILGLEALGVEFD---TDHGYIHATAPQGLEGTSVTLEFA-SVGATENLIMASV 176

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G +ID P + ++ G + + + I+G + P V
Sbjct: 177 KARGTT---VIDNAAREPEIVDLANMLNEMGARITGAGT-PVVTIEGVDELH-PVTHRVV 231

Query: 252 GDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311

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      GD  A  F+  AA+  G  VE  G      +  +  E MG ++  +  V  V
Sbjct: 232 GDRIEAGTFIVAAALMAGPAGVEVVGFPNPHLGMVKK-FETMGIQIERIDNGVRV---- 286

Query: 312 REPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
      F  +  +D+  P  D+  + V++  A G + I +  +  E  M  A
Sbjct: 287 ---FRCEQFAPVDIQTLPFGFPTDMQAQVMVLSALAQQGNSIITE----NIFENRFMFA- 338

Query: 368 RTELTKLGASVEEGPDYCI 387
      +EL ++GA +  + +I
Sbjct: 339 -SELVRMGAEIRVEGGHAMI 357

```

>ref|ZP_01386237.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium ferrooxidans DSM 13031]
gb|EAT58894.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium ferrooxidans DSM 13031]
Length = 423

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 99/413 (23%), Positives = 164/413 (39%), Gaps = 58/413 (14%)

```

Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALS-EGTTVDNLLNSEDVHYMLGALRTL 63
      +++V++ + ISG+V  GSK+ S  I+  LS  GT ++ ++ + +D+  L  L
Sbjct: 2  DKLVIIRGGRRISGSVSASGSKNSSLPIIASLTLSGNGTFILHHIPDLQDIKFTTQLLHHL 61

Query: 64  GLSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
      G      +  + V  G  +  E V+  MR+  +  + A  G+A
Sbjct: 62  GAET---SFGSNTLNVTTGNVTSILAPYELVK-----KMRASIYVLGPLLARFGHAR 110

Query: 121 YVLDGVPVRMRERPIGDLVVGLKQLGADVDC---FLGTDCTPPVRVNGIG-GLPGGKVKLSG 176
      L G      RPI  ++ +++LGA +  F+  P  +++G  P  V  +G
Sbjct: 111 VSLPGGCAFGPRPIDLHLMAMEKLGARITIEITGFIDATAPGGKLHGAHIDFPISSVGATG 170

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
      +  LMAA LA G  I  + P +  +  G  + + +  I
Sbjct: 171 NA-----LMAASLAEGTT---TISNAAEPEIVTLCHFLTAMGATIRGTGTTE-LEI 218

Query: 237 KGGQKYKSP--KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDV-KFAEVLEM 293
      +G Q  +  +NA+  D  A  LA AAITGG +TV  L+  + KF
Sbjct: 219 EGSQSLNAAEFQNAF---DRIEAGTLLAAAAITGGEITVNDVEPEQLKSVLKKFVHA--- 272

Query: 294 MGAKVTWTETSVTVTGPPREPFGKRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTA 349
      G  V  TE SVT+  +  L  D+  P  D+  +  A+G +
Sbjct: 273 -GCTVETTENSVTLKSSGK-----LIPTDITAKPYPAFPTDMQAQWIALMTQAEGTSH 324

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYD 402
      I D      ER  I  EL +LGA++E  +  ++  P  L+  T  + + D
Sbjct: 325 ITDKIYH-----ERFNHI-PELNRLGANIEIRKNQAVVHGPRTLSGTKVMSTD 371

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>ref|ZP_01071728.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni HB93-13]
ref|YP_001000542.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 81-176]
ref|ZP_02271234.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 81-176]
ref|ZP_03223121.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni CG8421]
ref|YP_002344265.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]
sp|Q9PP65.1|MURA_CAMJE RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
sp|A1VZK1.1|MURA_CAMJJ RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|EAQ60461.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni HB93-13]
gb|EAQ72300.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter

jejuni subsp. jejuni 81-176]
emb|CAL34986.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni NCTC 11168]
gb|EDZ32379.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni CG8421]
gb|EFV05878.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni DFVF1099]
Length = 418

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 88/405 (21%), Positives = 168/405 (41%), Gaps = 68/405 (16%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V
Sbjct: 6 IEGTNHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GN 118
F A N IA +R + A++ G G+
Sbjct: 65 -----NFQNSALLNTNTL--NQTIAKYDIVRKMRSILTLGPLLARFGH 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + +RPI ++ L+++GA++ G V G L G ++ L I
Sbjct: 108 CEVSLPGGCAIGQRPIDLHLLALEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKI 160

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISII---PYVEMTLRLMERFG--VKAHSDSWDR 233
+ ++MAA LA G KL+++ P V +++ G +K +D +
Sbjct: 161 TVTGSENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDAGLEIKGIGTDELE- 213

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
Y G+ + + + + +Y AG AIT +T++ T L L
Sbjct: 214 IYGSDGELLEFEKFSVIPDRIEAGTYLCAG-AITNSKITLDKVNATHLSA---VLAKLHQ 269

Query: 294 MGAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTA 349
MG + TE S+T+ P +E +K +++ ++ P D+ +AL A+G +
Sbjct: 270 MGFETLITEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMALALKANGTSI 322

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
I + R+ E M +EL ++GA ++ I ++LN
Sbjct: 323 IDE----RLFENRFMHV--SELLRMGADIKLNIGHIATIVGGKELN 361

>ref|ZP_05297647.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Listeria
monocytogenes FSL J2-003]
Length = 284

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 51/214 (23%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G +I+ + P + + + G + + + + I+G ++ +
Sbjct: 24 IMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIEGVKELTAT 79

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+++ + D A F+ AAITGG V +E + LE MG ++ E +
Sbjct: 80 EHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQIIIEEENGI 135

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V GP + LKA+DV P D+ + V+ + ++G + + + V R
Sbjct: 136 RVIGPDK-----LKAVDVKTMPHPGFPTMQSQMMVIQMLSEGTSIMTETVFENRFMH 188

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
E M + ++ G SV II+ P KL
Sbjct: 189 VEEMRRMNADMKIEGHSV-----IISGPAKLQ 215

>ref|ZP_07871794.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Listeria
marthii FSL S4-120]
gb|EFR86704.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Listeria
marthii FSL S4-120]
Length = 284

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 51/214 (23%), Positives = 92/214 (42%), Gaps = 27/214 (12%)

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G +I+ + P + + + G + + + + I+G ++ +
Sbjct: 24 IMMAATLAEGTT---VIENVAREPEIVDLANFLNQMGARVIGAGT-EVIRIEGVKELTAT 79

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+++ + D A F+ AAITGG V +E + LE MG ++ E +
Sbjct: 80 EHSIIP-DRIEAGTFMIAAAITGGNVLIEDAVPEHIS---SLIAKLEEMGVQIIIEENGI 135

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V GP + LKA+DV P D+ + V+ + ++G + + + V R
Sbjct: 136 RVIGDPK-----LKAVDVKTMPHPGFPTMQSQMMVIQMLSEGTSIMTETVFENRFMH 188

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
E M + ++ G SV II+ P KL
Sbjct: 189 VEEMRRMNADMKIEGHSV-----IISGPAKLQ 215

>ref|ZP_06696044.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecium E1636]
gb|EFF22481.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Enterococcus
faecium E1636]
Length = 152

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 41/148 (27%), Positives = 72/148 (48%), Gaps = 13/148 (8%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALS-EGTTVVDNLLNSEDVHYMLGALRTL 63
EEI+++ +++GTV++ G+K+ IL + L+ EG T +DN+ DV M +R L
Sbjct: 2 EEIIVRGGNQLNGTVRIEGAKNAVLPIAASLLAEEGITTLDNVPIILSDVFTMNQVIRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ V+ D+ K V + + +E E V MR+ + + A G+A
Sbjct: 62 NVDVDFDE-QKNQVTIDASRQLEIEAPYEYVS-----QMRASIVVMGPLLARNGHAK 112

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADV 148
+ G + +RPI + G + LGA +
Sbjct: 113 VAMPGGCAIGKRPIDLHLKGFQALGAKI 140

>ref|ZP_03289868.1| hypothetical protein CLONEX_02075 [Clostridium nexile DSM 1787]
gb|EEA81971.1| hypothetical protein CLONEX_02075 [Clostridium nexile DSM 1787]
Length = 430

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 79/345 (22%), Positives = 148/345 (42%), Gaps = 40/345 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T ++NL + D++ +L A+ +G
Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALAILAAAIMTDETVTIENLPDVNDINVLEAMAGIG 61

Query: 65 LSVE-ADKAAKRAVVVGCGGK-FPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+V+ D+ R + G G + F +E D ++++ A L A+ A
Sbjct: 62 ATVQRIDRHTVR--INGAGVQDFSIEYDYIKKIR-----ASYLLGALLGKYRRAEV 111

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS---- 177
L G + RPI + G + LGA+V+ G KL G+
Sbjct: 112 ALPGGCNIGSRPIDQHLKGFALGAEEIEYKIIAEAE-----KLEGTHLYF 159

Query: 178 --ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
+S ++MAA +A G + I++ + P+V + G + + + D
Sbjct: 160 DVVSVGATINVMMAAAMAEG---VTILENVAKEPHVVDVANFLNSMGANIKGAGT-DVIK 215

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
IKG +K + + + D A F+ AA+T G VTV L+ + LE +G
Sbjct: 216 IKGVEKLHKTEYSIIP-DQIEAGTFMFAAAVTKGDVTVLNVIPKHLEATIA---KLEEIG 271

Query: 296 AKVTWTETSVTVTGPPPREPFGR-KHLKAIDVNMNKMPPDVAMTLAV 339
++ + +V V R + K L + P + +TLA+

Sbjct: 272 CEIEEFDDAVRVVAKTRLKHTQVKTLPPYGFPTDMQPQIGVTAL 316

```
>ref|YP_081035.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
    licheniformis ATCC 14580]
ref|YP_093465.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
    licheniformis ATCC 14580]
ref|ZP_08002335.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 [Bacillus sp.
    BT1B_CT2]
sp|Q65DU2.1|MURA2_BACLD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
    AltName: Full=Enoylpyruvate transferase 2; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
    Short=EPT 2
gb|AAU25397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
    licheniformis ATCC 14580]
gb|AAU42772.1| MurAB [Bacillus licheniformis ATCC 14580]
gb|EFV70563.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 [Bacillus sp.
    BT1B_CT2]
    Length = 429
```

Score = 42.7 bits (99), Expect = 0.12, Method: Compositional matrix adjust.
 Identities = 87/397 (21%), Positives = 162/397 (40%), Gaps = 48/397 (12%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
    ++GTV + G+K+ + ++ L++ T ++ L + D+ + LR +G +V +K
Sbjct: 12  LNGTVHISGAKNSAVALIPATILADSTVTLEGLPHISDILTLRDLLREIGGNVHFEKGEM 71

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVLDGVP---RMR 130
    V D ++ L N + +R+ + A G + G+P +
Sbjct: 72  -----VVDPAPMISMPLPNGKVKQLRASYYLMGAMLRFRKKAIVIGLPGGCHLG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
    RPI + G + LGA+V G +R L G ++ L +S +++AA
Sbjct: 120 PRPIDQHIGKFEALGAEVTNEQGAIY--LRAE---ELKGARIYLD-VVSVGATINIMLAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
    LA G +I+ P + L+ G K + + + D I+G + +++ +
Sbjct: 174 VLAKGRT--VIENAAKEPEIIDVATLLTSMGAKIKGAGT-DVIRIEGVESLHGCRHSII 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
    D A F+ AA G V ++ T L+ L MG ++ + + + G
Sbjct: 230 P-DRIEAGTFMIAAASMGQEVLDNVPITHLE---SLIAKLREMGVRIEESSEQILMVG- 284

Query: 311 PREPFGKRHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
    G+K LK +D+ P D+ + + A+G + + D + S R K +
Sbjct: 285 -----GQKELKPVLDKTLVYPGFPTDLQQPMTSLLTKANGTSVVTDTIYSARFKHID--- 336

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
    EL ++GAS++ IIT P L + D
Sbjct: 337 ----ELRRMGASMKVEGRSAIITGPAPLQGAQKVKASD 369
```

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>ref|YP_002921441.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
    pneumoniae NTUH-K2044]
dbj|BAH65374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella
    pneumoniae subsp. pneumoniae NTUH-K2044]
    Length = 419
```

Score = 42.7 bits (99), Expect = 0.13, Method: Compositional matrix adjust.
 Identities = 102/421 (24%), Positives = 167/421 (39%), Gaps = 53/421 (12%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
    + G V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12  LQGEVTISGAKNAALPILFSALLAEPEVIQNPVKLKDIDTTMKLLSQLGAKVERNGS-- 69

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
    V + G PV+ +F+ + + + + A++ A G G L G
Sbjct: 70  --VWIDAG---PVD-----VFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
    + RP+ + GL+QLGA++ G V+ + G L G + + +S ++
```

Sbjct: 117 IGARPVDLHISGLEQLGAEIKLEEGY----VKASVSGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K S DR I+G Q+

Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLNALGAKITGQGS-DRITIEGVQRLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A+ L GA + E +++

Sbjct: 226 YRVLDPRIETGTFLVAAAISGGKILCRNAQPDTL--DAVLAK-LRDAGADIETGEDWISL 282

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P KA++V P D+ ++ L A+G I + R

Sbjct: 283 DMHGNNR-----KAVNVRTAPHPGFPTDMQAQFTLLNLVAEGTGVITETIF-----ENR 331

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIR 423
+ I EL ++GA E + I + L+ + D R + + LA C TI

Sbjct: 332 FMHI-PELIRMGAAHAEIESNTAICHGVKLLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
D

Sbjct: 390 D 390

>ref|YP_865138.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Magnetococcus
sp. MC-1]

sp|A0L6Y9.1|MURA_MAGSM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT

gb|ABK43732.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Magnetococcus
sp. MC-1]
Length = 419

Score = 42.7 bits (99), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 91/375 (24%), Positives = 153/375 (40%), Gaps = 49/375 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I+++ + GT+ + G+K+ L L+E T + N+ + DV ML L G

Sbjct: 2 DKILVRGGNTLKGITIPISGAKNACLPELAATLLTETDVTLRNVPHLRDVTMTLELLGQHG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
++ D+ K V + C +++ L +R++ A+V G G+

Sbjct: 62 AAITIDE--KLGVSIDCK---SIQNTMAPYDL-----VRTMRASVLVMGPLVARCGH 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RPI + GL+ +GA V G VR+ G L G + +

Sbjct: 109 AEISLPGGCAIGSRPINLHLRGLEMMGAHVTLLEDGY---VRIKA-GRLKGAHIVFD-LV 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ LLMAA LA G I I+D + P V L+ G K + + + R

Sbjct: 163 TVTGTEENLLMAATLADG---ITILDNAAAEPEVVDLANLLMAMGAKIDGAGT--RTITIE 217

Query: 239 GKQYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAK 297
G K + + D F+ AA+TGG +T+ G L+ + K E G +

Sbjct: 218 GVKNLHGTSHDILDPRIETGTFMVAAAVTGGDITMTGTYPALLEAHIAKMREA---GCQ 273

Query: 298 VWTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + ++ V R G L+A+D+ P D+ + V+ A G I++

Sbjct: 274 IDEMDRAIRV---RAEAGT--LRAVDITTLPHPGFPTDLQAQMMVLLTVAKGAAQIKET 327

Query: 354 A----SWRVKETERM 364
V E +RM

Sbjct: 328 IFENRFMHVSELQRM 342

>ref|YP_002522434.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermomicrobium
roseum DSM 5159]

gb|ACM05065.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermomicrobium
roseum DSM 5159]
Length = 424

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 104/441 (23%), Positives = 173/441 (39%), Gaps = 54/441 (12%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + + A L+E V++N+ EDV M LR LG V+ D
Sbjct: 18 LRGRVAIGGAKNAALPMAAALLTEEECVLENVPLEDDVVMTPELLRALGAEDLDTERH 77

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 131
R + +E + +L MR+ +T + A G A + G ++
Sbjct: 78 RVRIRAA----DIESFEPPPELV-----ARMRASFLVTGPLLARFGRARSIPPGGCQLGS 128

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI---GGLPGGKVKLSGSISSQYLSALL 187
RP+ + G ++ GA V+ V +G G L G ++ + S LL
Sbjct: 129 RPVDVLRGFRKFGAQVE-----VTESGFELRSGRLRGCEIYMDYP-SHTGTENLL 178

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G I + P + +++++ G + + R ++G + + +
Sbjct: 179 MAACLAQGT---TILNAAEPEIVNLGQILQDMGARI-NGLGTSRIVVQGVDRLRGYR- 233

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
A V D A AAIT G V ++ + L GA+V W+E+S+ V
Sbjct: 234 ASVLPDRLEAGTLAIAAAITHGEVILDHVREADM---APLTHKLREAGAEVWSESSMLV 290

Query: 308 TGPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
P L A ++ P D+ AV+ A G + I + V + R++ T
Sbjct: 291 RAP-----GLYATEIQALPFPFGFTDLQAAFAVLMTQAQGRSRIFERFVNDRLRYT- 342

Query: 363 RMVAIRTELTKLGASVEE-GPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVT 421
+EL ++GA +E II P KL TA+ D A AE
Sbjct: 343 -----SELQRMGARIELIDRQQAIEGPKVLQGTAVRALDIRSGACLVLAGLVAEGETI 396

Query: 422 IRDPGCTRKTFPDYFDVLSTF 442
+ + R+ + D L+
Sbjct: 397 VLEAHHLRRGYEDLVGKLAAL 417

>ref|YP_219597.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydomonas
abortus S26/3]
sp|Q5L6U5.1|MURA_CHLAB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAH63626.1| putative peptidoglycan synthesis protein [Chlamydomonas abortus
S26/3]
Length = 444

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 91/381 (23%), Positives = 154/381 (40%), Gaps = 58/381 (15%)

Query: 15 ISGTVKLPKSGKSLSNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ V+ N+ + DV + R+LG V DK A+
Sbjct: 12 LEGSVRVSGAKNSTTKLLVASLLSDRKCVRNVPDIDGVRVLTVELCRSLGSIVHWKQAE 71

Query: 75 RAVVVGCGGKFPVEDAK---EEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ A+ + + L A +A V GG+A +
Sbjct: 72 VIEIHTPEIHMSEVSAQFSRVNRIPILLGALLARCPEGVVVPCVGGDA-----IG 122

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
ER + GL+QLGA V D + GL G + L S L++A+
Sbjct: 123 ERTLNFHFEGLEQLGAKV---AYDGHGYQAAAPKGLIGAYITLPPY-SVGATENLILAS 177

Query: 191 PLALGD-----VEIEIIDKLISIPY--VEMTL---RLMERFGVKAHSDSWDRFYIKG 238
A G +E+EI+D ++ + VE+T R +E FG + FY
Sbjct: 178 VRAQGRITIKNAALEVEILDILFLQKAGVEITTDNDRTIEIFGC-----EDFY--- 226

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKV 298
+ +V D A+ F A +TGG V VE + + F + L +G
Sbjct: 227 -----EVDHWVIPDKIEAASFGMAAVLTGGRVFVENAEQHLM---IPFLKTLRSIGGGF 277

Query: 299 TWTETSVTVTGPPEPFGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRV 358
+ TET + EP + DV+ + D +V+ A+G + I +

Sbjct: 278 SVTETGIEFF--YNEPLKGGVLETDVHPGFLTDWQQPFVSVLLSQAEGSSVIHETV---- 331

Query: 359 KETERMVAIRTELTKLGASVE 379
R+ +R L K+GA+ E

Sbjct: 332 -HENRLGYLRG-LQKMGANCE 350

>ref|ZP_04081432.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
ref|ZP_04093299.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1]
ref|ZP_04099366.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar andalousiensis BGSC 4AW1]
ref|ZP_04225469.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-42]
ref|ZP_04286905.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus ATCC 4342]
ref|ZP_04292166.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus R309803]
gb|EEK76146.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus R309803]
gb|EEK81600.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus ATCC 4342]
gb|EEL42823.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-42]
gb|EEM68923.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar andalousiensis BGSC 4AW1]
gb|EEM75004.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1]
gb|EEM86804.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
Length = 419

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 70/276 (25%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G

Sbjct: 74 VRKMRAVQVMGPLLARNGRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +

Sbjct: 134 VE----GELKGAKIYLDFFP-SVGATENIMSAAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGT 278
G K + + I+G K ++ + D A F+ AAITGG + +E

Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAIAITGGDILLENAPV 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTTWETSVTVTGPPREPFGKRHLKAIDVNMNKMP----DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+

Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVDIKTMHPGPFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
+ + L ADG + I + V+E RM A

Sbjct: 294 SQMMALLLQADGTSMTETVFENRFMHVEEFRRMNA 329

>ref|YP_003985434.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gardnerella vaginalis ATCC 14019]
gb|ADP38411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gardnerella vaginalis ATCC 14019]
Length = 459

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 89/374 (23%), Positives = 152/374 (40%), Gaps = 38/374 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72

K ++G +K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G++V+ D A

Sbjct: 33 KPLNGAIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVSDLLRLHGVNVVDVGA 92

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132


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      A  VV      + D  +V  G++ I +  +  +  G A  G  +  R
Sbjct: 93  A--GVVSIDASNVLADVA-DVDTLGSSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 148

Query: 133  PIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS----GSISSQYLSALLM 188
      PI  +  L++LGA+VD      +  +  GL G K+ L  G+  L+A+L
Sbjct: 149  PIDFHLETLRKLKANVDK---DHEDGIHITAPNGLHGTKIHLPPYPSVGATEQTLLAAVLA 205

Query: 189  AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247
      L  IE      P +  +  +++++ G A S  DR F I+G K +  N
Sbjct: 206  EGKTELSGAIE-----PEIMDLVAVLQKMG--AIISVDVDRTFRIEGVDKLQG-YN 254

Query: 248  AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      D  A+ + + A  T G V ++G  +  + F V  +G +  T+  +
Sbjct: 255  HTALTDRIEAASWASALATHGDVFIKQATQPEM---MTFLNVFRKVGQFDVTDNGIRF 311

Query: 308  TGPPREPFGGRHLKAI--DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
      P G H AI DV+  M D  L V  A G + + +  E
Sbjct: 312  W----HPGGDLHPVAIETDVHPGFMTDQQPLVVALTQAKGLSIVHETV-----YENRF 361

Query: 366  AIRTELTKLGASVE 379
      L ++GA ++
Sbjct: 362  GFTKPLVQMGAMIQ 375

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>ref|ZP_08096119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Planococcus
donghaensis MPAlU2]
gb|EGA88255.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Planococcus
donghaensis MPAlU2]
Length = 432

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Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 93/400 (23%), Positives = 161/400 (40%), Gaps = 47/400 (11%)

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Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
      ++I+++  +++ G V++ G+K+  +L A L S G +++  + N DV+  +  LR+L
Sbjct: 2  DQIIVKGGQKLKGVKVRVEGAKNAVLPLVLAGALLASNGKSIIEKVPNLADVYTIQEVLRSL 61

Query: 64  GLSVEADKAAKRAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
      ++VE  K  +++  E  E V+  MR+  +  V A G A
Sbjct: 62  NVTVEY-FPEKNEMMIDASATLSSEAQFEYVR-----KMRASILVMGPVLARNGFAR 112

Query: 121  YVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
      L G  +  RPI  + G + +GA +  G  +  N G L G K+ L  S
Sbjct: 113  VALPGGAIGSRPIDQHLKGFEAMGASIT--FGNGFVEAKTN--GRLRGAKIYLDFF-SV 167

Query: 181  QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      ++MAA LA G  II+  P +  +  G +  + + D  I+G +
Sbjct: 168  GATENINMAAALAEGTT---IENAAKEPEIVDVANYINEMGGRVIGAGT-DTMRIEGVE 223

Query: 241  KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVT 299
      +  + Y+  D  A F+  AAIT G V +E  +  + K E  MG  +
Sbjct: 224  EMHGATH-YIIPDRVEAGTFMVAAAITEGDVVIENAVPEHMAALISKMG-----MGVDIK 278

Query: 300  WTETSVTVTGPPREPFGGRHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD-VA 354
      TE  +  +  + L++ID+  P  D+  +  + L A G  + + V
Sbjct: 279  ETEEGLRIR-----SNRPLRSIDIKTMPHPGFPTDMQSQMMSLMLTATGNGILTETVF 331

Query: 355  SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
      R  E  E  ++ ASV+  I+  P KL
Sbjct: 332  ENRFMHVE-----EFRRMNASVKIEGRSVIMEGPSKLQ 364

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>ref|YP_003245915.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
sp. Y412MC10]
gb|ACX68108.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
sp. Y412MC10]
Length = 449

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Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 89/348 (25%), Positives = 143/348 (41%), Gaps = 39/348 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
K ++G+VK+ G+K+ I+ + L E G +V+ + +DV + L +LG +
Sbjct: 11 KRLTGSVKVSGAKNSVLPPIAASLLGEVGESVIIDAPPLDDVITISKVLES LGAGITYQD 70

Query: 72 AAKRA---VVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
R + C + P E ++ FL + R ++ GG A
Sbjct: 71 EVIRVNAEHITTC--EAPYEWVRKMRASFLVMGPLLARCGRTRISLPGGCA----- 119

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RPI + G + LGA++ LG + NG L G KV L + S ++M
Sbjct: 120 IGRPIDQHLKGFALGAEIS--LGQGYIEAKSNG--RLRGAKVYLDVA-SVGATENIMM 174

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G +I+ P + + G K + + I+G +K K+
Sbjct: 175 AATLAEGTT---VIENAAKEPEIVDLANYLNAMGAKVRGAGT-GVIRIEGVEKMHGVKHN 230

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D A F+A AAITGG V VEG L G V +E MG V E + V
Sbjct: 231 VIP-DRIEAGTFMAAAAITGGDVYVEGAIAIDLH-GPV--ISKMEEMGITVEPDENGIRV- 285

Query: 309 GPPREPFGGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD 352
K LK++DV P D+ + + L ++G + + +
Sbjct: 286 -----IADKPLKSDVKTLPPPGFPTDMQSQMMALLLVSEGTTSVTE 327

>ref|ZP_00121228.1| COG0766: UDP-N-acetylglucosamine enolpyruvyl transferase
[Bifidobacterium longum DJO10A]
ref|NP_696432.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum NCC2705]
ref|YP_001955543.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum DJO10A]
ref|YP_003662100.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JDM301]
ref|YP_004001123.1| mura [Bifidobacterium longum subsp. longum BBMN68]
ref|ZP_07941977.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
sp. 12_1_47BFAA]
ref|YP_004209753.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis 157F]
gb|AAN25068.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum NCC2705]
gb|ACD99045.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Bifidobacterium
longum DJO10A]
gb|ADH01270.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. longum JDM301]
gb|ADQ02554.1| MurA [Bifidobacterium longum subsp. longum BBMN68]
gb|EFV36998.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
sp. 12_1_47BFAA]
dbj|BAJ71975.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis 157F]
Length = 441

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 52/194 (26%), Positives = 85/194 (43%), Gaps = 22/194 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ V+ D A
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVSDLLRLHGVDDVDGA 74

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+V + + D + L L + + R A + A GG A
Sbjct: 75 --NGIVTIDASRVQLADVADVDLTSGSSRIPLFSGPLVHRLGEAFIPALGGCA----- 126

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + L++LGA VD + + GL G K+ L S
Sbjct: 127 ---IGGRPIDFHELETLRKLGA TVD---KEHKDGIHITAPNGLHGAHILPYP-SVGATEQ 179

Query: 186 LLMAAPLALGDVEI 199
L+AA LA G E+
Sbjct: 180 TLLAAVLAEGKTEL 193

>ref|YP_003933214.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Pantoea vagans
C9-1]
gb|AD011765.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Pantoea vagans
C9-1]
Length = 419

Score = 42.4 bits (98), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 99/422 (23%), Positives = 167/422 (39%), Gaps = 53/422 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTL 64
E+ +Q +SG V + G+K+ + IL A L+E + N+ D+ + L LG
Sbjct: 2 EKFRVQGPTRLSGEVTISGAKNAALPILFAALLAEEPVEIQNPVKLRDIDTTMKLLSQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE + G V+ + V +F + +++ A++ A G G
Sbjct: 62 AKVERN-----GSVHVDASA--VDVFCAPYDL-VKTMRASIWALGPLVARFGQ 106

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + RP+ + GL+QLGA++ G V+ + G L G + + I
Sbjct: 107 GQVSLPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGALIVMD-KI 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++ AA LA G +I+ P + T + G K + S D+ I+G
Sbjct: 162 SVGATVTIMSAATLATGTT---VIENAAREPEIVDTANFLNLTGAKISGAGS-DKITIEG 217

Query: 239 GQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVVKFAEVLEMMGAK 297
++ Y V D FL AAI+GG V +L D A+ L GA
Sbjct: 218 VERLGG--GVYTVLPDRIETGTFLVAAISGGKVMCHKTQPDTL--DAVLAK-LRDAGAD 272

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA++V P D+ ++ + A+G I +
Sbjct: 273 IETGEDWISLDMHGKRP-----KAVNVRTAPHPGFPTDMQAQFTLLNMVAEGTGVITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
R + I EL ++G E + I E L+ + D R + + LA
Sbjct: 327 IF-----ENRFMHI-PELIRMGGHAEIESNTAICHGVETLSGAQV-MATDLRASASLVLA 379

Query: 414 AC 415
C
Sbjct: 380 GC 381

>ref|ZP_04067878.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis IBL 4222]
ref|ZP_04074933.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis IBL 200]
ref|ZP_04104971.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar berliner ATCC 10792]
ref|ZP_04129402.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar sotto str. T04001]
ref|ZP_04135922.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar thuringiensis str. T01001]
ref|ZP_04142296.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis Bt407]
gb|EEM26036.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis Bt407]
gb|EEM32371.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar thuringiensis str. T01001]
gb|EEM38912.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar sotto str. T04001]
gb|EEM63361.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar berliner ATCC 10792]
gb|EEM93338.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis IBL 200]
gb|EEN00393.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis IBL 4222]
Length = 419

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 70/276 (25%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVP RMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE----GELKGAKIYLDFFP-SVGATENIMSAAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G K ++ + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAAAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTTTETSVTVTGPPREPFRKHLKAIDVNMNKMP----DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVIDIKTMPHPGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
+ + L ADG + I + V+E RM A
Sbjct: 294 SQMALLLQADGTSMTETVFENRFMHVEEFRRMNA 329

>ref|YP_002361756.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylocella
silvestris BL2]
sp|B8ESQ9.1|MURA_METSB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACK50394.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylocella
silvestris BL2]
Length = 429

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 101/423 (23%), Positives = 176/423 (41%), Gaps = 58/423 (13%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVDNLLNSEVDHYMLGALRTLGLSVEADKA 72
+E++G +++ G+K+ + +++ + L+ T +DNL N DV+ +L L G+ D
Sbjct: 10 QELNGVIQISGAKNAALPLMIASLLTAETLTLDNLPNLADVNMMLLRILGHHGVDHSVD-- 67

Query: 73 AKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIA-MRS---LTAAVTAAGGNATYVLDGVP 127
R + PV A++ V ++ MR+ + A + A G A L G
Sbjct: 68 -GRRLLGAAPNASRPVHLTARDIVDTTAPYELVSKMRASFWVIAPLLARMGEAKVSLPGGC 126

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ L++ L++LGA V+ G V GL G ++K ++ L
Sbjct: 127 AIGTRPVDLLIMALEKLGASVEIEAGY---VHAKAPKGLRGAEIKFP-KVTVGGTHTAL 181

Query: 188 MAAPLALGDVEI-----EIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
MAA LA G I E++D ++ V+M R +K D ++G
Sbjct: 182 MAASLAHGHTIRIVNAAREPEVVD--LAECLVKMGAR-----IKGAGQSVID---VEGVA 230

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
+ + + +Y +A AA+ GG V +EG LQ + +VL GA V
Sbjct: 231 RLNGASHRVLPDRIEAGTYAIA-AAMAGGDMLEGAEGLLQSAL---DVLVEAGATVNV 286

Query: 301 TETSVTVTGPPREPFRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASW 356
+ V R G L +D+ P D+ + A G +
Sbjct: 287 VNEGIRVQ---RNGAG---LMPVDIVTAPFPGFPTDLQAQFMALMTKAKGQS----- 332

Query: 357 RVKET---ERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
R+ ET R + ++ EL +LGA + D ++ E+L + D R +++ +A
Sbjct: 333 RITETIFENRFMHVQ-ELARLGAHIRLDGDVALVDGVERLEGAPV-MATDLRASVSLVIA 390

Query: 414 ACA 416
A A
Sbjct: 391 ALA 393

>ref|YP_250171.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
jeikeium K411]
sp|Q4JXA4.1|MURA_CORJK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:

Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAI36553.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
jeikeium K411]
Length = 418

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 103/439 (23%), Positives = 165/439 (37%), Gaps = 53/439 (12%)

Query: 15 ISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+ G+K+ +++ A L+ GTT++ N DV YM LR LG VE D
Sbjct: 13 LQGAIKVSGAKNSVLKLSAALLAPGTTMLTNCPEIADVPYMAEVLRLGCEVELDGDVV 72

Query: 75 RAVV---VCGGKFPVEDAKEEVQLFLGNAGI----AMRSLTAAVTAAGGNATYVLDGVP 127
R + F E V+ F + + R A V GG+A
Sbjct: 73 RITTPESIEYNADF-----EAVRQFRASVAVLGPLTSRCHKARVALPGGDA----- 118

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ GL+ LGA G V L G ++KL S +L
Sbjct: 119 -IGSRPLDMHQSGLELLGATTKIEHG-----CLVAEAEELRGAQIKLDFFP-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G +D P + ++ G K + + S + ++G + +P +
Sbjct: 172 TAAVLAEGTT---TLDNAAREPEIVDLNMLVAMGAKIDGAGS-NTITVEGVDR-LNPVD 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD A + AA+T G +TV G L E L++ GA+V T V
Sbjct: 227 HEVVGDRIVAGTWAYAAAMTRGDITVGGIDPQHLH---LVLEKLKLAGAQVETPTGFRV 283

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
R KA+D P L +A+ A+ V+ TE +
Sbjct: 284 VQNERP-----KAVDYQTLFPFGFPTDLQPMIA-----ALCTVSEGMSVITENIFES 330

Query: 368 R---TELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
R E+ +LGA + +I E+L+ + + D A A+ +
Sbjct: 331 RFRFVDEMMLRGADASIDGHHVVIRGREQLSSAPVWSSDIRAGAGLVLAGLVADGKTEVH 390

Query: 424 DPGCTRKTFFPDYFDVLSTF 442
D + +P++ + L +
Sbjct: 391 DVYHIDRGYPEFPEQLRSL 409

>gb|EGC09171.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia
fergusonii B253]
Length = 419

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 101/427 (23%), Positives = 167/427 (39%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEFPVEIQNVPKLKDVDTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ + V +V +F + +++++ A++ A G G
Sbjct: 66 RNGS-----VHIDAHDVNVFCAPYEL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 LPGGCSIGARPVDLHISGLEQLGATIKLEEGY---VKASVEGRKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K DR I+G ++
Sbjct: 166 TVTIMCAATLAEGTT---IINAAREPEIVDTANFLVTLGAKIS-GQGTDRITIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +
Sbjct: 222 GG--GVYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTL--DAVLAK-LRDAGADIETG 276

Query: 302 ETSVTVTGPPREPFPGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWR 357
+ +++ + P KA++V P D+ ++ L A+G I +

Sbjct: 277 DDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFIETET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + LA C

Sbjct: 327 VFENRFMHV--PELSRMGAHAIEISNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
TI D

Sbjct: 384 EGTITVD 390

>ref|ZP_05785274.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
gb|EEX08390.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
Length = 421

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 96/409 (23%), Positives = 163/409 (39%), Gaps = 42/409 (10%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G + + G+K+ ++ LSE + N D+ M L++LG V A + +
Sbjct: 12 LHGQIPIAGAKNACLTLMPTLLSEEPLTLTNAPRLSDIKTMTALLQSLGAEVSALQDQG 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
V+ A E+ + + + L A G A L G + RP+
Sbjct: 72 --VLAMSSHDLTSTADYEIVRKMRASNVLGLPLARF----GQAVVSLPGGCAIGARPM 125

Query: 135 GDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
+ GL+ LGA++ D +L P GGL G ++ + S ++MAA
Sbjct: 126 DLHIEGLEALGAEIELKDGYLHAKAP-----GGLKAVHEMRFA-SVGATENIVMAAT 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G ++ P + ++ + + G + + + I+G + + V
Sbjct: 178 LAKGTT---VLKNAAREPEIVDLVQCLRKMGAIQI-GEGETSTIEIQVDRHLGHATHQVVT 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
+Y LA AI GG V + G G SL F E L G V TE + V+
Sbjct: 234 DRIELGTMYLA-PAICGGEVELLG-GRSLVES--FVEKLTAAGVDVEETEAGLKVS--- 286

Query: 312 REPFGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
GR ++A+DV P D+ + + ADG + + + R+ E M A
Sbjct: 287 -RRNGR--VRAVDVVTEFPFGFPTDLQAQMMALMCTADGVSVEE----RIFENRFMHA- 338

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACA 416
EL ++GA +E +T E+L + D R +++ LA A
Sbjct: 339 -PELVRMGAQIEVHGGTATVTGVERLKGAPV-MATDLRASVSLILAGLA 385

>ref|ZP_06488982.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
campestris pv. musacearum NCPPB4381]
Length = 424

Score = 42.4 bits (98), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 95/400 (23%), Positives = 160/400 (40%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNIISGAKNAVLPILCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E + L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSILVDPVSVTHQIAPYELVRTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGAD+ G ++ G L G + +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGADISVENGY----IKATSNRLKGSRYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L D ++ E GA +
Sbjct: 225 VERLGGGHHAFLP-DRIETGTFLVAAAMTGGSVTVRRARPETL--DAVLDKLTE-AGATI 280

Query: 299 TWTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 281 TTTADSITLDMQGRP-----RAVSLTTAPYPAFPTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>gb|ADZ43948.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia enterocolitica subsp. palearctica 105.5R(r)]
Length = 422

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 100/431 (23%), Positives = 171/431 (39%), Gaps = 58/431 (13%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG+ +E
Sbjct: 6 VQGRTRLSGEVTISGAKNAALPILFAALLAEDPVELQNVPKLKDIDTTIKLLSQLGVKIE 65

Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
D A+ V G V F + +++ A++ A G G
Sbjct: 66 RDAASGSVFVDASG-----VDEFCAFYDL-VKTRASIWALGPLVARFVGKQVS 113

Query: 123 LDGVPVRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QL A++ G V+ + G L + + +S
Sbjct: 114 LPGGCAIGARPVDLHITGLEQLSAEIKLEEGY---VKASVNGRLKAAHIVMD-KVSVGA 168

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIK----- 237
++ AA LA G +I+ P + T + G K + + DR I+
Sbjct: 169 TVTIMSAATLAEGTT---VIENAAREPEIVDTANFLNLTGAKITGAGT-DRITIEGVARL 224

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AAI+GG V +L D A++ E GA
Sbjct: 225 GGGVYR-----VLPDRIETGTFLVAAAISGGKVVCQRTPDTL--DAVLAKLRE-AGAD 275

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA+ + P D+ +++ L A+G I +
Sbjct: 276 IEVGDDWISLDMHGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGTGVTET 329

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLA 413
+ E M EL ++GA E + I ++L+ + D R + + LA
Sbjct: 330 ----IFENRFMHV--PELIRMGAAHAEIESNTVICYGVKQLSGAQV-MATDLRASASLVLA 382

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 383 GCIADGVTVTD 393

>ref|ZP_03324899.1| hypothetical protein BIFCAT_01708 [Bifidobacterium catenulatum DSM 16992]
gb|EEB21050.1| hypothetical protein BIFCAT_01708 [Bifidobacterium catenulatum DSM 16992]
Length = 467

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 51/187 (27%), Positives = 84/187 (44%), Gaps = 8/187 (4%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ GT+V+ N+ DVH + LR G+ V D
Sbjct: 41 KPLNGTIKVRGAKNFVSKAMVAALLAPGTSVLKNVPEIRDVHVSDLLRLHGVDTVTD-- 98

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPVRMRER 132
VV + D +V G++ I + + + G A G + R
Sbjct: 99 GDHGVVTIDATNVQLADVA-DVDTLSSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 156

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI + L++LGA+VD + + GL G K+ L S L+AA L
Sbjct: 157 PIDFHLETLRKLGANVD---KEHKDGIHITAPNGLHGAKIHLPPY-SVGATEQTLLAAVL 212

Query: 193 ALGDVEI 199
A G E+
Sbjct: 213 AEGKTEL 219

>gb|EFX83906.1| hypothetical protein DAPPUDRAFT_315300 [Daphnia pulex]
Length = 412

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 80/337 (23%), Positives = 134/337 (39%), Gaps = 52/337 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTL 64
+++ +Q + G + + G+K+ + ++ L+E + V+DNL D +T
Sbjct: 2 DKVRIQKGKASLHGVISIEGAKNAALPLMAACLLTEDSVVLDNLPYLHDK-----KTAS 54

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ K ++ P + ++ L + RS A V+ GG A
Sbjct: 55 FQAQTKTSQA-----PYDIVRKMRASILVLGPLLARSGEAIVSLPGGCA----- 99

Query: 125 GVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ RP+ + GL+ LGA++ D ++ P GL G + IS
Sbjct: 100 ----IGARPVDIHIRGLEALGAEITLEDGYIQARAPR-----GLQGRRYTFP-KISVT 147

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
LLMA+ LA G E+ + P V + G + E + D I+G +
Sbjct: 148 GTENLLMASVLAKGTTELIHAARE---PEVVDLAHFLNHMGARIEGIGT-DTLVIEGVSR 203

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
+ + + +Y +A AAITGG + +EG TSL + VLE MG ++
Sbjct: 204 LHGTTYSVLPDIETGTYLIA-AAITGGELFLEG---TSLNLLPSVSSVLERMGIQLEER 259

Query: 302 ETSVTVTG-PPREPFGRKHLKAIDVNMNKMPPDVAMTL 337
+ + V PPRE G ID+ P A L
Sbjct: 260 QGGIWKSPPPRELLG-----IDIVTEPFPGFATDL 290

>ref|ZP_03977045.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 55813]
ref|ZP_04663940.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis CCUG 52486]
gb|EEI80417.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 55813]
gb|EEQ56037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis CCUG 52486]
Length = 447

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 52/194 (26%), Positives = 85/194 (43%), Gaps = 22/194 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ V+ D A
Sbjct: 21 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVDLLRLHGVDDVDGA 80

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+V + + D + L L + + R A + A GG A
Sbjct: 81 --NGIVTIDASRVQLADVADVDTLSGSSRIPILFSGPLVHRLGEAFIPALGGCA----- 132

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + L++LGA VD + + GL G K+ L S
Sbjct: 133 ---IGGRPIDFHLETLRKLATVD---KEHKDGIHITAPNGLHGAKIHLPPY-SVGATEQ 185

Query: 186 LLMAAPLALGDVEI 199
L+AA LA G E+
Sbjct: 186 TLLAAVLAEGKTEL 199

>ref|ZP_03305252.1| hypothetical protein ANHYDRO_01690 [Anaerococcus hydrogenalis DSM

7454]
gb|EEB35506.1| hypothetical protein ANHYDRO_01690 [Anaerococcus hydrogenalis DSM
7454]
Length = 426

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 68/278 (24%), Positives = 115/278 (41%), Gaps = 21/278 (7%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E +V++ + G V + G+K+ + IL + L+ ++D + +D+ M+ L
Sbjct: 1 MNNEEILVVRKNGPLHGEVYISGAKNSALPILAASLLASEEVILDEVPKLDIEVMVEIL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
R+L VE + KF P E + F+ G + AVT A G
Sbjct: 61 RSLNAKVEYLTETTLKIDSSNVNKFETPFELMDKMRASFI-VMGPLLSKFGHAVTKAPGG 119

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ +RPI + G + LGA + + GL G + L
Sbjct: 120 CN-----IGKRPIDLHLKGFEALGAKTTM---NNEEISSKAKNGLKGEVIYLDFFP- 166

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++MAA LA G+ +I+ P + + + G K + + + IKG
Sbjct: 167 SVGATENIMMAATLAEGET---VIENAAKEPEIVDLASFLSKMGAKITGAGTSN-IIIKG 222

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC 276
+K + ++ V +A+Y LA AAITGG +TV+
Sbjct: 223 VEKLRGTRHTIIVPDRIEAAATYMLA-AAITGGDITVKNV 259

>ref|YP_001619798.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sorangium
cellulosum 'So ce 56']
sp|A9GD73.1|MURA_SORC5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAN99318.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sorangium
cellulosum 'So ce 56']
Length = 422

Score = 42.4 bits (98), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 95/377 (25%), Positives = 156/377 (41%), Gaps = 50/377 (13%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K +SG +++ G+K+ + IL LS+G +++ N+ D+ LR LG +VE
Sbjct: 10 KPLSGKIRISGAKNAALPILCATLLSDGESLLRNVLPALRDIETTSALLRFLGRNVE---T 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
A V VG G E E V+ + + + A G A L G ++ R
Sbjct: 67 APPLVKVGAGDNVRPEAPYELVKQMRASVMV-----LGPLLARFGRKAVSLPGGCQIGTR 121

Query: 133 PIGDLVVLKQLGADVDC---FLGTDCPPVR-VNGIGGLPGGKVKLSGSISSQYLSALLM 188
P+ + GL+ LGA + ++ +C +R + LP ++G+ L+M
Sbjct: 122 PVDQHLKGLEALGATIRLSRGYIVAECKRLRGAEVVDLP----TVTGT-----ENLMM 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + P VE R++ + G + + + D +I+G + + P +
Sbjct: 172 AAALAKGRT---TLVNCAREPEVEELGRVLNKMGARVSGAGT-DVIHIEGADELE-PFDH 226

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVTVT 308
+ D A ++ AA GG V +E L+ A L G +V V V
Sbjct: 227 AIISDRIEAGTYMVAAAAAGDVLIEENAPLEDLEA---VAAKLRQAGVEVGREGDCVRVR 283

Query: 309 GPPREPFGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVKET--E 362
RE GR L+A+DV P D+ V+ A G + R+ ET E
Sbjct: 284 ---RE---GRP-LRAVDVTTAPHPGFPTDMQAQFMVLMCLAQG-----TSRIVETIFE 329

Query: 363 RMVAIRTELTKLGASVE 379
EL ++GA ++
Sbjct: 330 NRFMHVPELARMGAHID 346

>ref|ZP_03927904.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces urogenitalis DSM 15434]
gb|EEH65244.1| possible 3-phosphoshikimate 1-carboxyvinyltransferase [Actinomyces urogenitalis DSM 15434]
Length = 180

Score = 42.4 bits (98), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 47/146 (32%), Positives = 68/146 (46%), Gaps = 24/146 (16%)

Query: 99 GNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTD--- 155
G AG MR + AA +A + DG R RP+ L+ L QLGA + +LG +
Sbjct: 22 GLAGTVMRFVPP--LAALADAPVLFDDGDDGARLRPLSPLLDSTQLGASL-TYLGREGHL 78

Query: 156 ----CP-PVRVN-----GIG-----GLPGGKVKLSGSISSQYLSALLMAAPLALGDV 197
P PVR + G G G+P V + S SSQ+LSALL+ L G +
Sbjct: 79 PVVVSPAPVRPHPAATAPLGQGAESSPGVPTTCVSVDasGSSQFLSALLLVGSLLPGGL 138

Query: 198 EIEIIDKLISIPYVEMTLRLMERFGV 223
+ + S+P+V MT+ + G+
Sbjct: 139 SVTPTGAVPSLPHVAMTVASLRERGL 164

>ref|ZP_04326074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus m1293]
gb|EEK42276.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus m1293]
Length = 419

Score = 42.4 bits (98), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 70/276 (25%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE----GELKGAKIYLDFF-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G K ++ + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAIAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLMMGAKVTTTETSVTVTGPPREPFGKRHLKAIDVNMNKMP----DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVDIKTMPHPGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
+ + L ADG + I + V+E RM A
Sbjct: 294 SQMMALLLQADGTSMITETVFENRFMHVEEFRMNA 329

>ref|ZP_04236505.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-28]
gb|EEL31789.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock3-28]
Length = 419

Score = 42.4 bits (98), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 72/283 (25%), Positives = 104/283 (36%), Gaps = 48/283 (16%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE----GELKGAKIYLDFF-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHS-----DSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTV 271
G K + + D+ Y GG P D A F+ AAITGG +

Sbjct: 186 NAMGAKVRGAGTGTIRIEGVDKLY--GGNHSIIP-----DRIEAGTFMVAAAITGGDI 236

Query: 272 TVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKP 331
+E L+ +E MG K+ V V GP + LKA+D+ P

Sbjct: 237 LIENAVPEHLR---SITAKMEEMGVKIIIEENEGVVRVIGPDK-----LKAVDIKTMPHP 286

Query: 332 ----DVAMTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
D+ + + L ADG + I + V+E RM A

Sbjct: 287 GFPTDMQSQMMALLQADGTSMITETVFENRFMHVEEFRMNA 329

>ref|YP_004097013.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
cellulosilyticus DSM 2522]
gb|ADU32282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
cellulosilyticus DSM 2522]
Length = 441

Score = 42.4 bits (98), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 94/404 (23%), Positives = 165/404 (40%), Gaps = 41/404 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ + ++GTV++ G+K+ ++ + L S+G + + ++ DV+ + LR L

Sbjct: 2 EKIIIVRGRRRLNGTVRVEGAKNAVLPIAASILASKGKSNIYDVPALADVYTINEVLRNL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE D + V E E V+ + + M L A V G+A L

Sbjct: 62 NAEVEYDNHG---ITVDAEKTLNTEAPFEYVRKMRASF-LVMGPLLARV----GHARIAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + +GA+V+ +G +V G L G K+ L S

Sbjct: 114 PGGCAIGSRPIDQHLKGFEAMGA EVE--IGNGYIEAKV--AGRLEGTKIYLDFFP-SVGAT 168

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA A G II+ P + + G K + + I+G +

Sbjct: 169 ENIMMAASTAKGST---IIENAAQEPEIVCLATYLNLMGAKVRGAGTGT-IRIEGVDELV 224

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AAI+GG V VE ++ + A++ E MG +

Sbjct: 225 GADHTIIP-DRIEAGTFMIAAAISGGNVLVENVLPEHIRPLI--AKMTE-MGVDIKEESN 280

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRD-VASWRV 358
+ V GP + LKA+D+ P D+ + + L A+G I + V R

Sbjct: 281 GLRVKGP-----ETLKAVDIKTMHPGFPPTDMQSQMMALLLRAEGSGVITETVFENRF 333

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
E E ++ +++ I+T P +L + D

Sbjct: 334 MHVE-----EFRMNGNIKIEGRSAIVTGPSELQGA EVRATD 370

>ref|ZP_02027983.1| hypothetical protein BIFADO_00393 [Bifidobacterium adolescentis
L2-32]
gb|EDN83484.1| hypothetical protein BIFADO_00393 [Bifidobacterium adolescentis
L2-32]
Length = 456

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 86/376 (22%), Positives = 154/376 (40%), Gaps = 42/376 (11%)

Query: 13 KEISGTVKLPKSGSKLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G +K+ G+K+ ++ ++ A L+ GT+V+ N+ DVH + LR G+ V D A

Sbjct: 30 KPLNGAIKVRGAKNFVSKAMVAALLAPGTSVLKNVPEIRDVHVSDLLRLHGVDTVVDGA 89

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV + D +V G++ I + + + G A G + R

Sbjct: 90 --NGVVTIDATNVQLADVA-DVDTLSGSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 145

Query: 133 PIGDLVVGLKQLGADVDCFLGTDPPVRVNGIGGLPGGKVKLS----GSISSQYLSALLM 188
PI + L++LGA+VD + + GL G K+ L G+ L+A+L

Sbjct: 146 PIDFHLETLRLKLGANVDK---EHKDGIIHITAPNGLHGAKIHLPPYPSVGATEQTLLAAVLA 202

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247

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          L   IE           P +   + +++++ G A S   DR F I+G ++ K   +
Sbjct: 203 EGKTELSGAAIE-----PEIMDLVSVLQKMG--AIISVDVDRTFRIEGVKELKGYTH 252

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
          + D   A+ + + A T G + V+G   +   + F V   +G +   T+   +
Sbjct: 253 TSLT-DRIEAAASWASALATHGDIFVKGATQPEM---MTFLNVFRKIGGEFDITDKGIRF 308

Query: 308 TGPPREPFPGRKHLKAI----DVNMNMPDVMATLAVVALFADGPTAIRDVASWRVKETER 363
          P +           LK +   DV+   M D   L V   A+G + + +   E
Sbjct: 309 WHPGGD-----LKPVAIETDVHPGFMTDWQQPLVVALTQANGLSIVHETV-----YEN 356

Query: 364 MVAIRTELTKLGASVE 379
          L ++GA+++
Sbjct: 357 RFGFTKPLVQMGATIQ 372

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>ref|YP_001406481.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
          hominis ATCC BAA-381]
sp|A7I1U0.1|MURA_CAMHC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
          AltName: Full=Enoylpyruvate transferase; AltName:
          Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
          Short=EPT
gb|ABS52384.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
          hominis ATCC BAA-381]
          Length = 418

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Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 82/377 (21%), Positives = 153/377 (40%), Gaps = 51/377 (13%)

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Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
          +++G VK+ G+K+ + ++ ++ L+   + N+ N D+ +   LR LG S E
Sbjct: 11 KLNKVKVIGSAKNAALPLIAMSILAGNDIKISNVPNVADIKTLAQLLRNLGASAEFLNEN 70

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
          +           + K   +           +R + A++   G   G+   L G
Sbjct: 71 SLKINTN-----DINSTKATYDI-----VRKMRASILVLGPLLARFGHCEVSLPGGC 117

Query: 128 RMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
          + RPI   + L+++GA++D   G   ++ G   + K+ ++G+   ++
Sbjct: 118 AIGARPIDLHLSALEKMGAEIDIKDGYVVCKGKLG-ATISFDKITVTGT-----ENIV 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD-RFYIKGGQKYKSPK 246
          MAA LA G +I   K   P V   ++ + GVK E   + D   Y GG+ K
Sbjct: 171 MAAALAEKGKTKIINAAKE---PEVVQLCEMINKSGVKIEGIGTDDLTIIYGSGKLLKFSD 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
          + +           + Y AG AIT   +T+   L V   MG   + +T
Sbjct: 228 FSVIPDRIEAGTYLCAG-AITKSKITITNANPNHL---VSVLAKFNMDMGFNFEINDDEIT 283

Query: 307 VTGPPREPFPGRKHLKAIDVNMNMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          + PP           K +K ++ ++ P   D+   +A ADG + I +   R+ E
Sbjct: 284 II-PP-----KTIKPTIITSEYPGFPTDMQAQFMALACVADGVSVIDE----RLFENR 332

Query: 363 RMVAIRTELTKLGASVE 379
          M   +EL+++GA ++
Sbjct: 333 FMHV--SELSRMGADIK 347

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>ref|YP_002140495.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
          bemidjensis Bem]
gb|ACH40699.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
          bemidjensis Bem]
          Length = 421

```

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 85/384 (22%), Positives = 155/384 (40%), Gaps = 51/384 (13%)

```

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
          E++V++ ++SG V + GSK+ + I +   L+ G   + N+   D++ + L LG
Sbjct: 2 EKLVIKGGNKLSGEVTVSGSKNAALPIFISTILAPGCHTISNVPFLRDINTTIKVLEKLG 61

```

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+V+ G G ++ + F + +R++ A+V G G
Sbjct: 62 ATVD-----GRGNVVKIDTTN--LNSFEATYDL-VRTMRASVLVLGPLLARFGQ 107

Query: 119 ATYVLGDVPMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RPI + GL LGA++ G + L G ++ S
Sbjct: 108 ARVSLPGGCAIGARPINLHLKGLAALGAEITLEHGYVEAKAK-----KLKGARINFDIST 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
LLMAA A G+ I++ P + ++ + G + + + D IKG
Sbjct: 163 VGGT-EQLLMAAATAQGET---ILENAAREPEIVDLAEILIKMGADIDGAGT-DTIRIKG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+ + ++A V D A F+ +AITGG + ++ L + L+ G ++
Sbjct: 218 VEGLVAAEHA-VMPDRIEAGTFMIAASAITGGDIKIKNMRLDHLDA---LSFKLQDAGVEI 273

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
T + V V GP K ++ +++ P D+ + A+G + I
Sbjct: 274 TNKDNMVRVKGPP-----KKIRNVNIKTRPYPGFPTDMQAQFMALMCIAEGASVI---- 322

Query: 355 SWRVKETERMVAIRTELTKLGASV 378
S + E M +EL + GA +
Sbjct: 323 SENIFENRFMHV--SELLRFGADI 344

>ref|YP_002250527.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dictyoglomus
thermophilum H-6-12]
gb|ACI19808.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dictyoglomus
thermophilum H-6-12]
Length = 438

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 98/423 (23%), Positives = 161/423 (38%), Gaps = 41/423 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ V++ ++ G +++ GSK+ S I+ + L+ G ++DN+ +D M L+ LG
Sbjct: 15 DKFVIEGGHKLGEIEIWGSKNASLPIMAASVLNSGDLILDNVPPVKDNITMAEILKFLG 74

Query: 65 LSVEADKAAKRAVVVG--CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
+ VE R + G G + P E + F L + A G A
Sbjct: 75 MEVEF-LGGDRLHIKGEKGRAPYELVSKMRASF-----ELMGPLLARFGEAEIP 124

Query: 123 LDGVPMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
G R+ RP+ + G + LGA+V G C + GL G K+ L S
Sbjct: 125 YPGGCRIGLRPVDLHIKGFESLGAEVTVKEGYVCARAK----KGLKGTKIHLDKP-SVGA 179

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++MAA +A G+ +I+ P V + G + E + YIKG ++
Sbjct: 180 TRNIMMAAVMAEGET---VIENAAACEPEVVDLGNFLRMMAEIEGLGT-STIYIKGKKEL 235

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
K V D +A F+ + G + ++ LQ F ++ E E
Sbjct: 236 KPVDYYKVIPDRIAAGTFIIAGVMLGKDLIIKNVEPEHLQS--LFIKLKEAGVESFQIKE 293

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRV 358
V V K+ K I+V P D+ + V A G + I +
Sbjct: 294 REVRVKAA-----KNWKGIEVTTMPYPGFPTDLQPQMMVFLSLAQSSSLIVETVF--- 343

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
R + + EL +LGA + +I EKL ++ D R A LA
Sbjct: 344 --ENRFLHV-GELLRLGAKISIDGRTALIQGVEKLGAPVEA-TDLRAGAALVLAGLVAE 399

Query: 419 PVT 421
+T
Sbjct: 400 GIT 402

>ref|YP_404852.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
dysenteriae Sd197]
ref|ZP_07680148.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
dysenteriae 1617]

sp|Q32BE4.1|MURA_SHIDS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABB63361.1| UDP-N-glucosamine 1-carboxyvinyltransferase [Shigella dysenteriae
Sd197]
gb|EFP72113.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella
dysenteriae 1617]
Length = 419

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 101/422 (23%), Positives = 169/422 (40%), Gaps = 53/422 (12%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE +
Sbjct: 11 KIQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERN--- 67
Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
G + DA+ +V +F + +++++ A++ A G G L G
Sbjct: 68 -----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGC 115
Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 116 TIGARPVLDLHISGLEQLGATIKLEEGY----VKASVDGRLLKGAHIVMD-KVSVGATVTIM 170
Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
+A LA G II+ P + T + G K + DR I+G ++
Sbjct: 171 CSATLAEGTT---IIENAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERLGG--G 224
Query: 248 AY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVWTETSVT 306
Y V D FL AAI+ G + +L D A+ L GA + E ++
Sbjct: 225 VYRVLPDRIETGTFLVAAAIISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVGEDWIS 281
Query: 307 VTGPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
+ + P KA++V P D+ ++ L A+G I + V E
Sbjct: 282 LDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET----VFENR 331
Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDHRMAMAFSLAACAEVPVTI 422
M EL+++GA E + I EKL+ + D R + + LA C T+
Sbjct: 332 FMHV--PELSRGMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTV 388
Query: 423 RD 424
D
Sbjct: 389 VD 390

>ref|ZP_01810241.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni CG8486]
gb|EDK22347.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni CG8486]
Length = 418

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 88/405 (21%), Positives = 168/405 (41%), Gaps = 68/405 (16%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V
Sbjct: 6 IEGTNHLSGNTVISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKV- 64
Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GN 118
F A N IA +R + A++ G G+
Sbjct: 65 -----NFQNNALLNTNTL--NQTIAKYDIVRKMRASILTGLPLLARFGH 107
Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + +RPI ++ L+++GA++ G V G L G ++ L I
Sbjct: 108 CEVSLPGGCAIGQRPIDLHLLALEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKI 160
Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFG--VKAHSDSWDR 233
+ ++MAA LA G KL+++ P V +++ G +K +D +
Sbjct: 161 TVTGENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDAGLEIKGIGTDEVE- 213

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
Y G+ + + + + +Y AG AIT +T++ T L L
Sbjct: 214 IYGSDELLEFKEFSVIPDRIEAGTYLCAG-AITNSKITLTKVNDTHLSA---VLAKLHQ 269

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTA 349
MG + TE S+T+ P +E +K +++ ++ P D+ +AL A+G +
Sbjct: 270 MGFETLITEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMALALKANGTSI 322

Query: 350 IRDVASVRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
I + R+ E M +EL ++GA ++ I ++LN
Sbjct: 323 IDE---RLFENRFMHV--SELLRMGADIKLNHGIATIVGGKELN 361

>ref|YP_003015882.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. carotovorum PC1]
sp|C6DIP6.1|MURA_PECCP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACT11346.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. carotovorum PC1]
Length = 420

Score = 42.0 bits (97), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 101/431 (23%), Positives = 171/431 (39%), Gaps = 61/431 (14%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++G V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 6 VQGPTRLAGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTTMKLLGQLGARVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G V+ + V +F + +++ A++ A G G
Sbjct: 66 RN-----GSVHVDASN--VNVFCAPYDL-VKTRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHIYGLEQLGAQIVLEEGY---VKATVDGRLLKAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G II+ P + T + G K + S D+ I+
Sbjct: 166 TVTIMSAATLAEGTT---IIEAAREPEIVDTANFLNLGAKISGAGS-DKITIEGVARL 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AA++ G + +L D A++ E GA+
Sbjct: 222 GGGVYR-----VVPDRIETGTFVAAAVSRGQIICRNRPTDL--DAVLAKLRE-AGAE 272

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA+ V + P D+ +++ L A+G I +
Sbjct: 273 IEIGEDWISLDMHGKRP-----KAVTVRTSPHPGFPTDMQAQFSLNLVAEGTGVITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I +KL+ + D R + + LA
Sbjct: 327 ----IFENRFMHV--PELIRMGAEIESNTVICHGVDKLSGAQV-MATDLRASASLVLA 379

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 380 GCIAEGVTIVD 390

>ref|ZP_04087298.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar huazhongensis BGSC 4BD1]
ref|ZP_04117537.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar kurstaki str. T03a001]
ref|ZP_04123160.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
thuringiensis serovar pakistani str. T13001]
ref|ZP_04205954.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus F65185]
ref|ZP_04214965.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus Rock4-2]
ref|ZP_04242235.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus
cereus Rock1-15]

ref|ZP_04281629.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus m1550]
ref|ZP_04308861.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 172560W]
ref|ZP_04320483.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus ATCC 10876]
gb|EEK47801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus ATCC 10876]
gb|EEK59398.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus 172560W]
gb|EEK86706.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus m1550]
gb|EEL26139.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock1-15]
gb|EEL53457.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus Rock4-2]
gb|EEL62354.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus F65185]
gb|EEM45171.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar pakistani str. T13001]
gb|EEM50770.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar kurstaki str. T03a001]
gb|EEM80877.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus thuringiensis serovar huazhongensis BGSC 4BD1]
Length = 419

Score = 42.0 bits (97), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 70/276 (25%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPLLARNRRIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE---GELKGAKIYLDFFP-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G K ++ + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAAAITGGDILIEHAVP 243

Query: 279 TSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNKMPP---DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIIEENEGVRVIGPDK-----LKAVDIKTMPHPGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
+ + L ADG + I + V+E RM A
Sbjct: 294 SQMMALLLQADGTSMITETVFENRFMHVEEFRMNA 329

>ref|ZP_05846245.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium jeikeium ATCC 43734]
gb|EEW16773.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium jeikeium ATCC 43734]
Length = 418

Score = 42.0 bits (97), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 98/399 (24%), Positives = 151/399 (37%), Gaps = 53/399 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +K+ G+K+ +++ A L+ GTT + N DV YM LR LG VE D
Sbjct: 13 LQGAIVKSGAKNSVLKLSAALLAPGTTTLTNCPEIADVPYMAEVLRLGLGCEVELDGDVV 72

Query: 75 RAVV---VCGCGKFPVEDAKEEVQLFLGNAGI----AMRSLTAAVTAAGGNATYVLDGVP 127
R + F E V+ F + + R A V GG+A
Sbjct: 73 RITTPESIEYNADF-----EAVRQFRASVAVLGPLTSRCHKARVALPGGDA----- 118

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RP+ GL+ LGA G V L G ++KL S +L
Sbjct: 119 -IGSRPLDMHQSGLELLGATTKIEHG-----CLVAEAEELRGAQIKLDFFP-SVGATENIL 171

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G +D P + ++ G K + + S + ++G + +P +
Sbjct: 172 TAAVLAEGTT---TLDNAAREPEIVDLNMLVAMGAKIDGAGS-NTITVEGVDR-LNPVD 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V GD A + AA+T G +TV G L E L++ GA+V T V
Sbjct: 227 HEVVGDRIVAGTWAYAAAMTRGDITVGGIDPQHLH---LVLEKLKLAGAQVETYPGFRV 283

Query: 308 TGPPREPFGFRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
R KA+D P L +A+ A+ V+ TE +
Sbjct: 284 VQNERP-----KAVDYQTLPPFGFTDLQPMAL-----ALCTVSEGMSVITENIFES 330

Query: 368 R---TELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
R E+ +LGA + +I E+L+ + + D
Sbjct: 331 RFRFVDEMMRLGADASIDGHHVVIRGREQLSSAPVWSSD 369

>ref|YP_001566541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Delftia
acidovorans SPH-1]
sp|A9BX80.1|MURA_DELAS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABX38156.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Delftia
acidovorans SPH-1]
Length = 422

Score = 42.0 bits (97), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 93/416 (22%), Positives = 167/416 (40%), Gaps = 62/416 (14%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ + + G V + G+K+ + L A LS + N+ +DV ML +R +G
Sbjct: 2 DKLLIRGGRALHGEVTVSGAKNAALPELCAALLSSEPVTLRNVPRLQDVATMLKLIRNM 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+S E D + V + G E E V +++ A+V A G G
Sbjct: 62 VSAEHDDSG--TVRINAGSLNPEAPYELV-----KTMRASVLALGPLLARFGQ 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI--GGLPGGKVKLSG 176
A L G + RP+ + GL+ +GA++ V NG LPG +L G
Sbjct: 109 ARVSLPGGCAIGSRPVDQHIKGLQAMGAEI-----VVENGYMNACLPGLKRLQG 158

Query: 177 S-ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
+ I++ ++ LMAA LA G+ +++ P + ++ + G + E
Sbjct: 159 ARITTDMTVTGTENFLMAAVLAEGE---VLENAAMEPEIGDLAEMLIKMGARIE-GHG 214

Query: 231 WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEV 290
R I+G ++ ++ V D A FL A TGG + L + +
Sbjct: 215 TGRIVIQGVERLGGCEHQVV-ADRIEAGTFLCAVAATGGNALLRNGRADHLGAVI---DK 270

Query: 291 LEMMGAKVTWTETSVTVTGPPREPFGFRKHLKAIDVNMNKMP---DVAMTLAVVALFADG 346
L+ GA+V+ + + V + LKA + P D+ + L A+G
Sbjct: 271 LKDAGAEVSAEDGGIRVRAAGK-----LKAQSFRTTEYPGFPTMQAQMALNLVAEG 323

Query: 347 PTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
+ + + + E M E+ +LGA + IT + L+ A+ D
Sbjct: 324 CSMVTET----IFENRFMHV--DEMLRLGAQITTDGRVATITGSQSLSGAAVMATD 373

>ref|YP_515753.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydomonas
reinkei Fe/C-56]
dbj|BAE81608.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlamydomonas
reinkei Fe/C-56]
Length = 444

Score = 42.0 bits (97), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 90/383 (23%), Positives = 158/383 (41%), Gaps = 62/383 (16%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ V+ N+ + DV + ++LG V DK A+
Sbjct: 12 LQGSVRVSGAKNSTTKLLVASLLSDRKCVLRNVPDIDGVRILTVELCQSLGSIVHWDKQAE 71

Query: 75 RAVVVGCGGKFPVEDAKEE-----VQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V+ + V + + + L A +A V GG+A
Sbjct: 72 --VIEIHTPEIRVSEVSTQFSRVNRIPILLGALLARCPGVVPCVGGDA----- 120

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ ER + GL+QLGA V D + + GL G + L S L++
Sbjct: 121 IGERTLNFHFEGLEQLGAKVS----YDGHGYQASASKGLVGAYITLPYP-SVGATENLIL 175

Query: 189 AAPLALGD-----VEIEIIDKLISIPY--VEMTL---RLMERFGVKAHSDSWDRFYI 236
A+ A G +E+EI+D ++ + VE+T R +E FG D FY
Sbjct: 176 ASVRAQRTIIKNAALEVEILDILFLQKAGVEITTDNDRTIEIFGC-----DDFY- 226

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
+ +V D A+ F A +TGG V VE + + F + L +G
Sbjct: 227 -----EVDHWVIPDKIEASFGMAAVLTGGRVVFVENAEQDLM---IPFLKTLRSIGG 275

Query: 297 KVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASW 356
+ TE+ + EP + DV+ + D +V+ A+G + I +
Sbjct: 276 GFSVTESGIEFF--YNEPLRGGVVLETDVHPGFLTQWQPFSVLLSQAEGSSVIHETV-- 331

Query: 357 RVKETERMVAIRTELTKLGASVE 379
R+ +R L ++GA+ E
Sbjct: 332 ---HENRLGYLRG-LQQMGANCE 350

>ref|ZP_03742236.1| hypothetical protein BIFPSEUDO_02803 [Bifidobacterium
pseudocatenulatum DSM 20438]
gb|EEG71911.1| hypothetical protein BIFPSEUDO_02803 [Bifidobacterium
pseudocatenulatum DSM 20438]
Length = 441

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 51/187 (27%), Positives = 84/187 (44%), Gaps = 8/187 (4%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ GT+V+ N+ DVH + LR G+ V D
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGTSVLKNVPEIRDVHVVSDDLRLHGVDTVTD-- 72

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
VV + D +V G++ I + + + G A G + R
Sbjct: 73 GDHGVVTIDATNVQLADVA-DVDTLSGSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 130

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
PI + L++LGA+VD + + GL G K+ L S L+AA L
Sbjct: 131 PIDFHLETLRKLGANVD---KEHKDGIHITAPNGLHGAKIHLPPYP-SVGATEQTLLAAVL 186

Query: 193 ALGDVEI 199
A G E+
Sbjct: 187 AEGKTEL 193

>ref|YP_001900785.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
pickettii 12J]
gb|ACD28353.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ralstonia
pickettii 12J]
Length = 454

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 65/274 (23%), Positives = 112/274 (40%), Gaps = 43/274 (15%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG +++ G+K+ + I+ A L+ + N+ N +DV ML LR +G
Sbjct: 45 LSGQIRVSGAKNAALPIMCAALLTAEPALSNVPLNQDVRTMLKLLRQMG----- 94

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIA-----MRSLTAAVTAAG-----GNAT 120
VE + L L A I +++++ A++ G G+A
Sbjct: 95 -----VEGVLDGHNLTLDAAAIHTPEASYDLVKTMRASILVLGPLLARFGHAR 142

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP+ + GL+ +GA++ G +G L G ++ ++ ++

Sbjct: 143 VSLPGGCGIGARPVDQHIKGLQLMGAEIVIEHGY-IEAKLADGAKRLRGARI-VTDMVTV 200

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
LLMAA LA G+ +++ P V L+ + G + E + DR I+G Q

Sbjct: 201 TGTEENLLMAAALADGET--VLENAAREPEVTDLANLLVKMGARIEGIGT-DRLVIQGVQ 256

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
+ + D A FL A GG VT+

Sbjct: 257 ALHGAHTVI-ADRIEAGTFLCAVAAAGGDVTLR 289

>ref|YP_002323757.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 15697]
gb|ACJ53379.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis ATCC 15697]
dbj|BAJ69973.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
longum subsp. infantis JCM 1222]
Length = 441

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 51/194 (26%), Positives = 85/194 (43%), Gaps = 22/194 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ V+ D
Sbjct: 15 KPLAGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVDLLRLHGVDDVD-- 72

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
++ +V + D + L L + + R A + A GG A
Sbjct: 73 GEKGIVTIDASHVQLADVADVDTLGSSSRIPILFSGPLVHRLGEAFIPALGGCA----- 126

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDGPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + L++LGA VD + + GL G K+ L S
Sbjct: 127 ---IGGRPIDFHLETTLRKLGLATVD---KEHKDGIHITAPNGLHGAHLPYP-SVGATEQ 179

Query: 186 LLMAAPLALGDVEI 199
L+AA LA G E+
Sbjct: 180 TLLAAVLAEGKTEL 193

>ref|YP_591183.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Koribacter versatilis Ellin345]
sp|Q1IPU1.1|MURA ACIBL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABF41109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Koribacter versatilis Ellin345]
Length = 433

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 73/296 (24%), Positives = 122/296 (41%), Gaps = 28/296 (9%)

Query: 17 GTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA-AKR 75
G V++ G+K+ + + A L+E +++N+ D+ L+ +G VE A
Sbjct: 14 GNVRVSGAKNAALPAMAAALLTEEPVILENIPQVRDIITERNLLQAMGAEEVELGYGRAHH 73

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLT---AAVTAAGGNATYVLDGVPRMRER 132
+ C E + E V+ MR+ T + A G A L G + R
Sbjct: 74 RTTLCCRNLVNPEASYELVK-----TMRAS TLVLGPLVARTGEARVSLPGGCAIGAR 125

Query: 133 PIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
PI + GL++LGA++ G R+ G + K+ ++G+ LLMAA
Sbjct: 126 PIDLHIKGLEKLGAEITQEHEGYIKAKATRLKG-NHIVFEKITVTGT-----EDLLMAAT 178

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G+ +++ P V L+ + G K E I G +K K+ +
Sbjct: 179 LADGET---VMENCAREPEVTDLAHLLVKMGAKIE-GIGTSTLKITGVEKLHGAKHRIIP 234

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ ++ +AGA +TGG + V+ C + L LE G K+ SV V
Sbjct: 235 DRIEAGTFIIAGA-LTGDDL MVQNCDP SHLGA---LLAKLEENGVKIRSNGDSVRV 286

>ref|ZP_02151795.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanibulbus indolifex HEL-45]
gb|EDQ05662.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanibulbus indolifex HEL-45]
Length = 423

Score = 42.0 bits (97), Expect = 0.19, Method: Compositional matrix adjust.
Identities = 107/433 (24%), Positives = 172/433 (39%), Gaps = 56/433 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ I+++ E++G + + G+K+ ++ LSE + N D+ M LR+LG
Sbjct: 2 DSILVRGGGELNGQIPIAGAKNACLALMPATLLSEEPPLTNAPRLSDIRTMTTELLRSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATY 121
V + + K V+ P+ + + E + MR+ + + A G+A
Sbjct: 62 AEVASMQDGK---VITMASHGPI-NTRAHEYDIVR-----KMRASNVLGPLLAREGHAEV 112

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI--- 178
L G + RP+ GL ++GA++D G + GG KL G++
Sbjct: 113 SLPGGCAIGARPMIDIHTDGLAKMGAIEDLRDGY----LYAKADGG-----KLKGAVIDF 162

Query: 179 ---SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
S +LMAA LA G I + I + LR M G + E D
Sbjct: 163 PFASVGATENILMAATLAKGTTVINNAAREPEIVDLADCLRAM---GAQIE-GDGTSSIT 218

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
I+G + V +Y LA A GG V + G LQ F E L+ G
Sbjct: 219 IQGVDSLHGATHKVVTDRIELGTYMLA-PAFCGGEVELLGGRIDLLQA---FCEKLDAA 274

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKVIDNMNKMP----DVAMTLAVVALFADGPFAIR 351
+VT TE + V GR + A+DV P D+ + + A+G + +
Sbjct: 275 IEVTETEAGLKVA---RRNGR--ISAVDVTTEPFPGFPTDLQAQMMALLCTAEGTSVLE 328

Query: 352 DVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAM 408
+ ++ E M A EL ++GA ++ +T EKL V A D + +
Sbjct: 329 E----KIFENRFMHA--PELIRMGARIDVHGGTAKVTGVEKLKGAPVMATDLRASISLIL 382

Query: 409 AFSLAACAEVPVT 421
A LAA E V+
Sbjct: 383 A-GLAATGETTVS 394

>ref|YP_004066396.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni ICDCJ07001]
gb|ADT66207.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni ICDCJ07001]
Length = 248

Score = 42.0 bits (97), Expect = 0.20, Method: Compositional matrix adjust.
Identities = 32/124 (25%), Positives = 56/124 (45%), Gaps = 9/124 (7%)

Query: 25 KSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGK 84
KS+S+R + + L++ N L ++D L ++ LG +E + + +
Sbjct: 21 KSISHRFAIFSLTQEENKAQNYLLAQDTLNTLEIKNLGAKIEQKDSVCVKIIP----- 74

Query: 85 FPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQL 144
P E L GN+G AMR + + AG + +VL G + RP+ + L Q+
Sbjct: 75 -PKEILSPNCILDCGNSGTAMRLMIGFL--AGISGFFVLSGDKYLNRRPMRRISKPLTQI 131

Query: 145 GADV 148
GA +
Sbjct: 132 GARI 135

>ref|ZP_07829359.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Selenomonas sp. oral taxon 137 str. F0430]
ref|ZP_08030539.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Selenomonas artemidis F0399]
gb|EFR40691.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Selenomonas sp.

oral taxon 137 str. F0430]
gb|EFW30311.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Selenomonas
artemidis F0399]
Length = 425

Score = 42.0 bits (97), Expect = 0.20, Method: Compositional matrix adjust.
Identities = 48/173 (27%), Positives = 78/173 (45%), Gaps = 19/173 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E++V+ + + G VK+ G+K+ I+ A L S G +V+D++ EDV+ + LR+L
Sbjct: 2 EQLVIHGGRLCGRVKIGGAKNAVLPIIAAALLGSRGVSVLDDVPALEDVYTISAVLRSL 61

Query: 64 GLSVEADKAAKR----AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNA 119
G+S + A R A +G P E ++ FL + R A ++ GG A
Sbjct: 62 GVSADYAAAHERLKDATRIGTTS-PYELVRKMRASFLIMGPLLAREGRAEISLPGGCA 120

Query: 120 TYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKV 172
+ RPI + G + LGA VD G + + GL G +
Sbjct: 121 -----IGTRPIDLHLKGFEALGAQVDITQGA----IHASAPNGLKGANI 160

>ref|ZP_01744961.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Sagittula stellata
E-37]
gb|EBA09189.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Sagittula stellata
E-37]
Length = 423

Score = 42.0 bits (97), Expect = 0.20, Method: Compositional matrix adjust.
Identities = 95/417 (22%), Positives = 165/417 (39%), Gaps = 57/417 (13%)

Query: 15 ISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG + + G+K+ ++ LSE + N D+ M L++LG V A A K
Sbjct: 12 LSGEIPIAGAKNACLTLMPTLLSEEPLTLTNAPRLSDIRMTLLQLSLGA EVTAMNAGK 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V+ + A+ ++ +R + A++ G G A L G
Sbjct: 72 --VLAMSSHALTSQRAEYDI-----VRKMRASILVLGPLLARYGYAEVSLPGGCA 119

Query: 129 MRERPIGDLVVLGKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + ++ +GA++D ++ P GGL GG V +S
Sbjct: 120 IGARPVLDHLKAMEAMGAEMDLRDGYVHAKAPA-----GGLKGGVDFP-FVSVGATEN 172

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LMAA LA G ++ P + +++ G + + ++G ++
Sbjct: 173 ALMAATLAKGTT---VLKNAAREPEIVDLAHCLQKMQAIS-GEGTSTIEVQGVRELGG 228

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
++ V +Y LA AI GG VT G L+ F E L+ G V T+ +
Sbjct: 229 THSVVTDRIELGTYMLA-PAICGGEVTCGLGRIDLLEA---FCERLDAAGVSVEETDKGL 284

Query: 306 TVTGPPPREPFGRKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
V RK+ +KA+DV P D+ + + ADG + + ++
Sbjct: 285 KVA-----RKNAVKAVDVVTEPPPGFPTDLQAQMMALMCTADGKAVLEE---KIF 332

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
E M A EL ++GAS++ +T E+L + D R +++ LA A
Sbjct: 333 ENRFMHA--PELIRMGASIDVHGATVTGVERLKGAPV-MATDLRASVSLILAGLA 386

>ref|ZP_05970492.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cancerogenus ATCC 35316]
gb|EFC54220.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cancerogenus ATCC 35316]
Length = 419

Score = 42.0 bits (97), Expect = 0.20, Method: Compositional matrix adjust.
Identities = 99/421 (23%), Positives = 167/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSKSLSNRILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEPEVIQNVPKLKDIDTMTKLLAQLGTVKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + +V F + +++++ A++ A G G L G
Sbjct: 68 -----GSVWIDAS--QVNNFSAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL++LGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHIFGLEKLGAIEKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IIENAAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG +T +L D A+ L GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKITCRNAQPDTL--DAVLAK-LRDAGADIEIGEDWISL 282

Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
P KA++V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGNRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFTITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|ZP_07841530.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
caprae C87]
gb|EFS16835.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus
caprae C87]
Length = 421

Score = 42.0 bits (97), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 91/371 (24%), Positives = 145/371 (39%), Gaps = 35/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
++IV+ ++G VK+ G+K+ +L + L SEG + + N+ DV + L TL
Sbjct: 2 DKIVINGGNRLTGEVKEGAKNAVLPLVTASLLASEGQSKLVNVPALSDVETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGNATYVL 123
V +K + AV V E E V + + M L A + G+A L
Sbjct: 62 NADVSYNKE-ENAVKVDATQNLNEEAPYEVSKMRASI-LVMGPLLRL----GHAIVAL 115

Query: 124 DGVPMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA++ G + N GL G ++ L S
Sbjct: 116 PGCAIGSRPIEQHIKGFALGAEIHLNGN----IYANAKNGLKGTQIHLDFP-SVGAT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA LA G II+ P + + G K + + D I G K
Sbjct: 171 QNIIMAASLASGK---SIIENAAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVDKLH 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+++ + + +AG AIT G + V G + LE MG + + E
Sbjct: 227 GVEHSIIPDRIEAGTLLIAG-AITRGDILVRGAIKEHM--ASLVYKLEEMGVNLD FKED 282

Query: 304 SVTVTGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA----S 355
+ V+ LK +DV P D+ + + L A+G I +
Sbjct: 283 GIQVS-----AEGDLKPVDVKTLPHPGFPTMQSQMMALLLTANGHKVITETVTFENRF 335

Query: 356 WRVKETERMVA 366
V E RM A
Sbjct: 336 MHVAEFRMNA 346

>ref|ZP_04969447.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. polymorphum ATCC 10953]
gb|EDK87531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium

nucleatum subsp. polymorphum ATCC 10953]
 Length = 423

Score = 42.0 bits (97), Expect = 0.21, Method: Compositional matrix adjust.
 Identities = 69/287 (24%), Positives = 122/287 (42%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
 K+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D
 Sbjct: 11 KKIAGELKVDGSKNSTLPIMIATLVEKGTIILRNVPDLRDIRTLVALLESGLGLEVEKLDA 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
 + + + G G D ++++ FL G+ V GG A +
 Sbjct: 71 NSYKIINNGLSGAEASYDLVKKMRASFLVMGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
 RP+ + G + LGA ++ G V GL GG + L S ++MAA
 Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
 A G +++ P +E + + G K + R I G K + + + +
 Sbjct: 177 VKAKGKT--VLENAAKEPEIEDLCNFLIKMGAKI-NGVGTSLRLEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAK 297
 + +Y +A + + G++ V G L F LE MGAK
 Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIGVPEHLS--SFLKLEEMGAK 275

>ref|YP_286592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dechloromonas
 aromatica RCB]
 sp|Q47AK9.1|MURA_DECAR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enolpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
 gb|AAZ48122.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dechloromonas
 aromatica RCB]
 Length = 417

Score = 42.0 bits (97), Expect = 0.21, Method: Compositional matrix adjust.
 Identities = 90/394 (22%), Positives = 165/394 (41%), Gaps = 40/394 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
 ++++++ K +SG V + G+K+ + IL + L+ N+ + D+ ML L +G
 Sbjct: 2 DKLLIEGGKVLSEGEVAMSGAKNAALPILCASLLTSDPVHFTNVPHLNDISTMLRLLGDMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 + V D V+ G G PV A E+ + + + L A G A L
 Sbjct: 62 VGVMTD-GIDGIVLNGGGLNNPV--ASYEMVKTMRASILVLGPLVARC----GEARVSLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
 G + RP+ + GL+ +GA+V G R+ G + V ++G+
 Sbjct: 115 GGCAIGARPVDQHIKGLQAMGAEVKVEQGYVHAKATRLKG-ARICTDMVTVTGT----- 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
 L+MAA LA G+ +I+ P V + G + + + D I+G K
 Sbjct: 168 ENLMMAACLAEGEET---VIENAAAREPEVVDLANCLVSMGARISGAGT-DVIRIQGVDKLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGCGTTSLQGDVKFAEVLEMMGAKVWTET 303
 +A + + +Y A AA TGG + + T++ D ++++ G ++T
 Sbjct: 224 GATHAIMPDIETGTYLCAAAA-TGGDIRL--LKTSAAYLDTVVDKLM-DAGCEITVERD 279

Query: 304 SVTVTGPPREPFGKRLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVK 359
 ++ + P R LKA+ + P D+ + ADG IR+ +
 Sbjct: 280 AIRLVAPKR-----LKAIVSLRTAPYPAFPTDMQAQFMAINCIADGVATIRET----IF 328

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKL 393
 E M EL +LGA+++ + I+ ++L
 Sbjct: 329 ENRFMHV--NELMRLGANIQIEGNNIVRGVDRL 360

>ref|YP_003075109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Teredinibacter
 turnerae T7901]

sp|C5BSW4.1|MURA_TERTT RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACR13037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Teredinibacter
turnerae T7901]
Length = 420

Score = 42.0 bits (97), Expect = 0.21, Method: Compositional matrix adjust.
Identities = 92/382 (24%), Positives = 162/382 (42%), Gaps = 42/382 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++Q ISG +++ GSK+ IL L++ + NL + D+ ML LR +G
Sbjct: 2 DKLIIQGGTRISGEIRISGSKNSGLPILAACLLADSPMDICNPLHNDITTMLALLRCMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ V ++ K V V E E V+ + + +L A G A
Sbjct: 62 VGVTTINE--KMCVEVDPTTLTDTEAPYELVKTMRASILVLGPTL-----AKYGKADVSPF 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ + GL+ +GA++ G +R GL G + ++
Sbjct: 115 GGCAIGSRPVDIHLGLSGLAMGAIEIAVEGGY----IRAPAPNGLKGAHFVMD-KVTVGGE 169

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
LLMAA LA G +++ P + + G K DR I+G ++
Sbjct: 170 NLLMAAVLAKGKT---VLENAAREPEIDVLADCLVAMGAKI-GGIGTDRLEIEGVERLHG 225

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFA--EVLEMMGAKVTWTE 302
+ + +Y +A AA TGG+V + + D+ A + LE GA++ E
Sbjct: 226 CTYTVMPDRIETGTYLVA AAA-TGGSVKLR-----DTRADILTAVLQKLEEAGAELEIGE 279

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVA--SWRVKE 360
+++++ + P KA VN+ P A + + F TA+ VA + V E
Sbjct: 280 STISLDMHGKRP-----KA--VNLRTAPYPAPFTDMQSQF----TAMNAVAEGTGAVTE 327

Query: 361 T---ERMVAIRTELTKLGASVE 379
T R+V + EL ++GA+++
Sbjct: 328 TIFENRLVQV-NELNRMGANIK 348

>ref|ZP_06439928.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerobaculum
hydrogeniformans ATCC BAA-1850]
gb|EFD24781.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerobaculum
hydrogeniformans ATCC BAA-1850]
Length = 431

Score = 41.6 bits (96), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 55/208 (26%), Positives = 89/208 (42%), Gaps = 29/208 (13%)

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
LLMAA LA G+ +I+ P ++ +R ++ G E + ++G QK +P
Sbjct: 176 LLMAAVLAEGET---LIENAAREPEIDNLVRALKSMGAAIE-GEGTGILRVRG-QKELNP 230

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ D A+ +L AITGG VTV+G L L+ G +V E +
Sbjct: 231 ATIDIIPDRIEAATYLLAGAITGGDVTVKGVVAEHLNA---LLAKLDEAGIEVINKENEL 287

Query: 306 TVTGPPEPFGGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASWRVK 359
V P R P G + + MP D+ + + A+G + I + +
Sbjct: 288 RVNSPDR-PRG-----LTVKTPYPGPFSTDLQPQMMALLSLAEGTSVIHET----IF 334

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCI 387
E+ + A +EL K+GA +E + II
Sbjct: 335 ESRFLHA--SELQKMGAIQELQGNTAII 360

>ref|YP_003257754.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pectobacterium
wasabiae WPP163]
gb|ACX86147.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pectobacterium
wasabiae WPP163]
Length = 420

Score = 41.6 bits (96), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 101/431 (23%), Positives = 171/431 (39%), Gaps = 61/431 (14%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++G V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 6 VQGPTRLAGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTTMKLLGQLGARVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G V+ + EV +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVHVDAS--EVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHIYGLEQLGAQIVLEEGY---VKATVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G II+ P + T + G K + S D+ I+
Sbjct: 166 TVTIMSAATLAEGTT---IIENAAREPEIVDTANFLNTLGAKISGAGS-DKITIEGVARL 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AA++ G + +L D A++ E GA+
Sbjct: 222 GGGVYR-----VVPDRIETGTFLVAAAVSRGQIICRNTRPDTL--DAVLAKLRE-AGAE 272

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA+ V + P D+ +++ L A+G I +
Sbjct: 273 IEIGEDWISLDMHGKRP-----KAVTVRTSPHPGFPTDMQAQFSLNLVAEGTGIVTET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I +KL+ + D R + + LA
Sbjct: 327 ----IFENRFMHV--PELIRMGQAQAEIESNTVICHGVDKLSGAQV-MATDLRASASLVLA 379

Query: 414 ACAEVPVTIRD 424
C VT D
Sbjct: 380 GCIAEGVTTVD 390

>ref|ZP_03778898.1| hypothetical protein CLOHYLEM_05967 [Clostridium hylemonae DSM
15053]
gb|EEG73962.1| hypothetical protein CLOHYLEM_05967 [Clostridium hylemonae DSM
15053]
Length = 430

Score = 41.6 bits (96), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 96/427 (22%), Positives = 173/427 (40%), Gaps = 45/427 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
E+ +++ + G V++ G+K+ + IL A +++ T ++DN+ + DV+ +L A+ +G
Sbjct: 2 EQYIIKGGHPLVGEVEIGGAKNAALAILAAAIMTDDTVLIDNIPDVNDVNVLLDAITGIG 61

Query: 65 LSVEADKAAKRAVVVGCGG--KFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
V + + V + G + VE D +++++ A L A+ A
Sbjct: 62 AKVH--RVDRHTVKINGSGIRNYDVEYDIKKIR-----ASYLLGALLGKYKRAEV 111

Query: 122 VLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RPI + G + LGADV G L G V
Sbjct: 112 ALPGGCNIGSRPIDQHLKGFRALGADVIEHGKVVAEAE-----KLVGRHVYFDVVTGVA 166

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++ ++MAA +A G I I++ + P+V + G + + D I+G +
Sbjct: 167 TIN-VMAATMAEG---ITIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVHR 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTW 300
+ + + D A F+ AA T G VTV L+ + K E+ G +V
Sbjct: 222 LHGTEYSVIP-DQIEAGTFMFAAAATKGDVTVLNVIPKHLEATIAKLTEI----GCEVEE 276

Query: 301 TETSVTVTGPPREPFGKHLKAI---DVNMNKMPDVAMTLAVVALFADGPTAIRDVASWR 357
+ +V V + H+K + + P + +TL AL T + R
Sbjct: 277 FDDAVRVV--SKGDLTSTHVKTLPYPGFPTMQPQIGVTL---ALCKGTSTITESIFENR 331

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417

K + EL ++GA+++ + I E+ + + + D R A +A A
Sbjct: 332 FKYL-----ELARMGANIKVEGNSATIEGVEQFSGARV-SAPDLRAGAALCIAGLAT 383

Query: 418 VPVTIRD 424
+TI D

Sbjct: 384 DGITIVD 390

>ref|YP_002153336.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Proteus mirabilis HI4320]
ref|ZP_03842615.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Proteus mirabilis ATCC 29906]
sp|B4EXL1.1|MURA_PROMH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
emb|CAR47146.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Proteus mirabilis HI4320]
gb|EEI46647.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Proteus mirabilis ATCC 29906]
Length = 420

Score = 41.6 bits (96), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 98/420 (23%), Positives = 167/420 (39%), Gaps = 51/420 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LSGEVTISGAKNAALPILFAAILAEPEVELTNVPKLKDIDTTIKLLNRLGTKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G F DA+ + F + +++ A++ A G G L G
Sbjct: 68 -----GSVFV--DAR-HINEFCAPYEL-VKTMRASIWALGPLVARFGRGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA++ D V+ G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLEQLGAEITL----DEGYVKARVDGRLKGAIHIVMD-KVSVGATTITIMT 171

Query: 189 AAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P +E T + G K + + D I+G ++
Sbjct: 172 AAVLAEGKT---IIENAAREPEIEDTANFLNTLGAKISGAGT-DSITIEGVERLGGGTYQ 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ D FL AA++ G V +L D A++ E GA + E +++
Sbjct: 228 ILP-DRIETGTFLVAAAVSRGRVVCNRNAKPDTL--DAVLAKLRE-AGADIETGEDWISLD 283

Query: 309 GPPREPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA+ + P D+ +++ L ADG I + R
Sbjct: 284 MHGKR-----KAVTLRTAPHPGFPTDMQAQFSLNLVADGAGMITETIF-----ENRF 332

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIRD 424
+ I EL ++GA E + + +KL+ + D R + + LA C TI D
Sbjct: 333 MHI-PELIRMGAAHAEIESNTVLCHGVDKLSGAQV-MATDLRASASLVLAGCIAEGTTIVD 390

>ref|YP_003844500.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium cellulovorans 743B]
ref|ZP_07631746.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium cellulovorans 743B]
gb|ADL52736.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium cellulovorans 743B]
Length = 419

Score = 41.6 bits (96), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 102/419 (24%), Positives = 163/419 (38%), Gaps = 43/419 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ G++K+ +K+ I+ L++ TV+ N +DV + LR+LG + D+
Sbjct: 10 KKLQGSIKVNSAKNSVLPPIAACILNKDITVIKNAPMLDDVIVICDVLRLGADISVDRE 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
K + + F E E ++ MR+ + + A G L G +

Sbjct: 70 QK-VIKIDTRELQCEPPSEMI-----KMRASFLIMGPMIARFGGFKISLPGGCNI 120

Query: 130 RERPIGLDLVGLKQLGADVDCFLGTDCPPVRVNGIGLPGGKVKLSGSISSQYLSALLMA 189
RPI + G K LGA+V+ G R L G +V L S ++MA

Sbjct: 121 GTRPIDLHLKGFKALGAEVNPQFGV--VEARAE---KLKGNRVYLDFFP-SVGATENIMMA 174

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A LA G+ +I+ P +E + G K + + I+G +K K +

Sbjct: 175 AVLADGET--VIENAAEPEIEDLANFLRTMGAKIIGAGTGT-IVIEGVKKLKGVEYTP 230

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMGAKVTWTETSVTVT 308
+ D A F+ AAIT + +E ++ K AE MG +T E + V

Sbjct: 231 M-FDRIEAGTFMVAAAITSKIKLENVNEKHKSMTAKLAE---MGIGITSGEDYIIVE 285

Query: 309 GPPREPFGGRKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ LK ID+ P M ++AL T + + E

Sbjct: 286 AS-----EELKPIDIKTMPYPGFPTDMAQIMALL---TTVTGTSIITETIFENRFM 334

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAA-CAEVPVTIRD 424
ELT++GA+++ II E L+ + D R A LA AE TI D

Sbjct: 335 HVNELTRMGANIKIDGRNAIEGIESLSGCEVKA-TDLRAGAALILAGLVAEGSTTIVD 392

>ref|YP_002603455.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Desulfobacterium autotrophicum HRM2]
sp|C0QDM7.1|MURA_DESAH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACN15291.1| MurA [Desulfobacterium autotrophicum HRM2]
Length = 417

Score = 41.6 bits (96), Expect = 0.23, Method: Compositional matrix adjust.
Identities = 93/398 (23%), Positives = 159/398 (39%), Gaps = 60/398 (15%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I ++ K ++G V++ G+K+ + +L + L +G N+ + DV + LR LG

Sbjct: 2 DKIEIRGGKRLTGEVRISGAKNAALPLLASSILVDGAMTFTNVPDLVDVRSIKMLLRDLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
E + V++ G +E A E V R + A++ G G+

Sbjct: 62 AGCEEGBGT---VLIDGSGIHKIEAAYELV-----RKMRA SILVLGPLVARFGH 107

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGI-GGLPGGKVKL 174
A L G + RP+ + GLK LGA + + ++ ++ N I +P +

Sbjct: 108 ARVSLPGGCAIGARPVDMHLKGLKALGATITITENG YIEAKADRLKGNEIYFDIP----TV 163

Query: 175 SGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRF 234
+G+ L+MAA LA G + + I + L LM A + +

Sbjct: 164 TGT-----ENLMAATLAKGTTVLRNCAREPEITALANALNM-----GARVTGAGTAV 212

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
G SP +V D A F+ AA TGG V V GC ++ G + L

Sbjct: 213 IRINGVDGLSPATIHVIPDRIEAGTFMVAAAATGGDVLVTGCEPENMGGIIN---KLRQT 269

Query: 295 GAKVTWTETSVTVTGPPEPFGGRKHLKAIDVNMNKMPPDVA--MTLAVVALFADGPTAI 350
GA V + V V+G K + + D+ P D+ V+ + G + I

Sbjct: 270 GALVEIIDHGKVKVSGG-----KSILSTDIKTLPPYGFPTDMAQFMVLMMAISQGN SVI 322

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVE-EGPDYCI 387
+ + E M EL ++GA + G +Y ++

Sbjct: 323 HET----IFENRFMHV--NELQRMGADISISGGNYAMV 354

>gb|AAN28945.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Chlamydia trachomatis]
Length = 444

Score = 41.6 bits (96), Expect = 0.23, Method: Compositional matrix adjust.
Identities = 97/438 (22%), Positives = 171/438 (39%), Gaps = 87/438 (19%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G+V++ G+K+ + ++L+ + LS+ T++ N+ N EDV + R LG VE D+ A+
Sbjct: 12 LRGSVRVSGAKNATTKLLVASLLSDQRTILKNVPNIEDVRQTVDLRCRVLGAIVEWDQQAQ 71

Query: 75 -----RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
R ++ +F + + L A + V GG+A
Sbjct: 72 VIEIHTPRILLSKVPPQF---SCVNRIPILLGALLRRCYPGIFVPILGGDA----- 120

Query: 128 RMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
+ R + + G K+LGA++ D P GL G + L S
Sbjct: 121 -IGPRTLHFHLEGWKKLGAEIVISDEGYWASAP-----NGLVGAHITLPYP-SVGATE 171

Query: 185 ALLMAAPLALGD-----VEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
L++A+ A G +E+EIID ++ +++ GV+ +D+ I
Sbjct: 172 NLILASVGAQGRITIIKNAALEVEIIDLIV-----FLQKAGVEIT-TDNDKTIEIF 220

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G Q + S ++ + +AS+ +A A ++ G + VE + + F +VL +G
Sbjct: 221 GCQDFYSVEHFIIPDKIEAASFGMA-AVVSQGRIFVEQARHEHM---IPFLKVLRSIGGG 276

Query: 298 VTWTETSVTVTGPPREPFGKHLKA----IDVNMNKMPPDVAMTLAVVALFADGPTAIRD 352
+ E + E F K LK DV+ + D AV+ ++G + I +
Sbjct: 277 FSVHENG-----EFFYDKPLKGGVLETDVHPGFITDWQPPFAVLLSQSEGCSVIHE 329

Query: 353 VASWRVKETERMVAIRTELTKLGA-----SVEEGPDYCIITPPEKLNVT 396
E + L K+GA S P +I P L T
Sbjct: 330 TVH-----ENRLGYLKGLVKMGACHDLFHECLSAKSCRYSTGNHPSAVIHGPTPLQAT 383

Query: 397 AIDTYDDHRMAMAFSLAA 414
+ D R A+ +AA
Sbjct: 384 DL-VIPDLRAGFAYVMAA 400

>ref|YP_081000.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
licheniformis ATCC 14580]
ref|YP_093429.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
licheniformis ATCC 14580]
ref|ZP_08002299.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus sp.
BT1B_CT2]
sp|Q65DX8.1|MURAI_BACLD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
AltName: Full=Enoylpyruvate transferase 1; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
Short=EPT 1
gb|AAU25362.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
licheniformis ATCC 14580]
gb|AAU42736.1| MurAA [Bacillus licheniformis ATCC 14580]
gb|EFV70527.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus sp.
BT1B_CT2]
Length = 436

Score = 41.6 bits (96), Expect = 0.23, Method: Compositional matrix adjust.
Identities = 87/359 (24%), Positives = 143/359 (39%), Gaps = 45/359 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E+I+++ ++++GTVK+ G+K+ ++ + L SE +V+ ++ DV+ + LR L
Sbjct: 2 EKIIIVRGGKRLNGTVKVEGAKNAVLPIAASLLASEEKSVIDCVPTLSDVYTINEVLRHL 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G SV + V V E E V R + A+V G G
Sbjct: 62 GASVHFE---NNTVTVDASRTLSTEAPFEYV-----RKMRAVSLVMGPELLARTG 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
++ L G + RPI + G + +GA + G V G L G K+ L
Sbjct: 108 HSRVALPGGCAIGSRPIDQHLKGFEAMGAKIKVGNGFIEATVE----GRLQAKIYLDFF 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S L+MAA LA G +E K P + + G K + + I+
Sbjct: 164 -SVGATENLIMAAALAEGTTTLENAKE--PEIVDLANYINAMGGKIRGAGTGT-IKIE 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G + K+ + D A F+ AAIT G V V+G L +E MG +

Sbjct: 219 GVKALHGAKHTIIP-DRIEAGTFMVAAAITEGNVLVKGAVPEHL---TSLIAKMEEMGVQ 274

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKVIDNMNKMPP---DVAMTLAVVALFADGPTAIRD 352

+ + + GP LK ID+ P D+ + + + A+G + I +

Sbjct: 275 ILEEGDGLRIIGPSE-----LKPIDLKTMHPGFPDMDQSQMALLMRANGTSMITE 326

>ref|ZP_02089276.1| hypothetical protein CLOBOL_06845 [Clostridium bolteae ATCC BAA-613]

gb|EDP12904.1| hypothetical protein CLOBOL_06845 [Clostridium bolteae ATCC BAA-613]

Length = 430

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 87/422 (20%), Positives = 172/422 (40%), Gaps = 35/422 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E+ +++ + G V + G+K+ + IL + +++ V+DNL + D++ +L A++ +G

Sbjct: 2 EQYIIKGGNPLVGDVTISGAKNAALGILASIMTDDDDVIDNLPDVRDINVLEAIQEIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124

V D+ + V + V E ++ A A+ +A L

Sbjct: 62 ARV--DRIDRHTVKINGSNISEVSVDEYIRIR----ASYFFIGALLGKYKSAQVPLP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184

G + RPI + G + LGA+V G V + I L + L +S

Sbjct: 115 GGCNIGSRPIDQHIKGFALGAEVTTIERGA----VIAHAI-DLVASHIYLD-VVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244

++MAA LA G I++ P++ + G + + + D I+G +

Sbjct: 169 NIMMAAALAEQGT--ILENAAKEPHIVDVANFLNSMGANIKGAGT-DTIRIRGVNRLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304

+ + + D A F+ AA T G + V+ L+ + L +G +V + +

Sbjct: 225 TEYSIIP-DQIEAGTFMCAAAATRGDIMVKNVIPKHLEA---ISAKLTEIGCEVIEFDDA 280

Query: 305 VTVTGPPREPFGGRKHLKVIDNMNKMPP-DVAMTLAVVALFADGPTAIRD-VASWRVKETE 362

V V G P ++H + P D+ ++V + A+G + + + + R K +

Sbjct: 281 VRVVGKP---AQRHTDIKTLPPYGFPTDMPQMSVALVLANGTSMVTESIFENRFKYVD 336

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTI 422

EL ++G++++ + +I + L ++ D R A +A A T+

Sbjct: 337 -----ELARMGSNIKVEGNVAIDGVKGLTGAQVNA-PDLRAGAALVIAGLAADGYTV 388

Query: 423 RD 424

D

Sbjct: 389 VD 390

>ref|ZP_01070396.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 260.94]

ref|YP_004066373.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni ICDCCJ07001]

gb|EAQ58219.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 260.94]

gb|ADT66184.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni ICDCCJ07001]

Length = 418

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 89/409 (21%), Positives = 168/409 (41%), Gaps = 68/409 (16%)

Query: 13 KEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72

+SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V

Sbjct: 10 NHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKV----- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GNATYV 122

F A N IA +R + A++ G +

Sbjct: 65 -----NFQNSALLNTNTL--NQTIKAYDIVRKMRASILTGLPLLARFGHCEVS 111

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182

```

      L G  + +RPI  ++ L+++GA++      G      V      G L G ++ L  I+
Sbjct: 112 LPGGCAIGQRPIDLHLLALEKMGANIQIKQG-----YVVASGKLGNEI-LFDKITVTG 164

Query: 183 LSALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFG--VKAHSDSDWDRFYIK 237
      ++MAA LA G      KL+++  P V      +++  G  +K  +D  +  Y
Sbjct: 165 SENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDGAGLEIKGIGTDELE-IYGT 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLEMMGAK 297
      G+  +  +  +  +  +Y AG AIT  +T++  T L      L MG +
Sbjct: 218 DGELLEFEKFSVIPDRIEAGTYLCAG-AITNSKITLTKVNATHLSA---VLAKLHQMGE 273

Query: 298 VTWTETSVTVTGPPREPFGGRKHLKVIDNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
      TE S+T+  P +E      +K +++  ++ P  D+      +AL A+G + I  +
Sbjct: 274 TLITEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMALALKANGTSIIDE- 325

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
      R+ E  M  +EL ++GA ++      I  ++LN  +  D
Sbjct: 326 ---RLFENRFMHV--SELLRMGADIKLNHGIATIVGGKELNAADVMATD 369

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>ref|YP_004149926.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Staphylococcus pseudintermedius HKU10-03]
gb|ADV06290.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Staphylococcus pseudintermedius HKU10-03]
gb|ADX76047.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus pseudintermedius ED99]
Length = 421

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 67/262 (25%), Positives = 108/262 (41%), Gaps = 36/262 (13%)

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Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVK 173
      G A  L G  +  RPI  + GL+ LGA++      ++  + P      GL G ++
Sbjct: 109 GRAKVALPGGCAIGSRPIEQHLKGLEALGAEIHQEAAGYIYAEAPQ-----GLVGNEIH 161

Query: 174 LSGSISQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFG-VKAHSDSDW 232
      S      ++MAA LA G  IE + +  I  V++  + E  G +K  +D+
Sbjct: 162 FDFP-SVGATQNMMAASLAKGRTVIENVAREPEI--VDLANYINEMGGDIKGAGTDT-- 216

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTGTVEGCGTTSLQGDVKFAEVLE 292
      I G  +  K  K+A +  D  A  +  AAIT G V V+G      +      LE
Sbjct: 217 -VIINGVESLKGVKHAIIP-DRIEAGTLMIAAAITRGDVLVKGAIKEHM---TSLVYKLE 271

Query: 293 MMGAKVTWTETSVTVTGPPREPFGGRKHLKVIDNMNMKMP----DVAMTLAVVALFADGPT 348
      MG ++ +TE  + VT P +      L+ +D+  P  D+  +  + L A+G
Sbjct: 272 EMGVELDYTEEGIRVTAPEK-----LQPVDIKTLPHPGFPTDMQSQMALLLTAECHK 324

Query: 349 AIRDVA----SWRVKETERMVA 366
      +  +      V E +RM A
Sbjct: 325 VVTETVFENRFMHVAFKRMNA 346

```

>ref|ZP_02242425.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas oryzae pv. oryzicola BLS256]
Length = 424

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 93/385 (24%), Positives = 155/385 (40%), Gaps = 45/385 (11%)

```

Query: 6  EIVLQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
      +IV+  +  + G V + G+K+  IL  L++  + N+ +  DV  +  L  LG
Sbjct: 3  KIVVTGGQALQGEVNISGAKNVLPILCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66  SVEADK---AAKRAVVVG----CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
      V  D+  A  R+++V      P E K      L  +  R  TA V+  GG
Sbjct: 63  EVTIDEGTLAKGRSILVDPKSVTHQIAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      A      +  RP+  + GL+ LGA++  G      ++  G L GG+  +
Sbjct: 123 A-----IGSRPVDQHIKGLQALGAEISVENGY----IKATSRGRLKGGRYVFD-MV 168

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Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L D ++ E GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETL--DAVLDKLTE-AGATI 280

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 281 TTTADSITLDMQGKRP-----RAVSLTTAPYPAPFTDMQAQFMALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVE 379
+ E M EL +LGA ++
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQ 353

>ref|ZP_01292174.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [delta
proteobacterium MLMS-1]
gb|EAT01411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [delta
proteobacterium MLMS-1]
Length = 419

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 103/426 (24%), Positives = 168/426 (39%), Gaps = 58/426 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV+ + + G +++ G+K+ + +L L+ G ++DN+ + D ML L LG
Sbjct: 2 DKIVITGGRPLHGEIRISGAKNAALPLLATLLAPGPHILDNPDLRDRTRTMLALLAALG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
E + +++ E + + V R++ A+V G G
Sbjct: 62 AKWERQ---EERLIIDTSALHSHEASYDLV-----RTMRASVLVLGPLLARLGQ 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A L G + RPI ++GL+QLG V+ L RV GL GG +
Sbjct: 108 ARVSLPGGCAIGARPINFHLLGLQQLG--VEHELDQGYVDARVTA-KGLRGGDICFDIP- 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G I+ P + + ++ G K D ++G
Sbjct: 164 SVTATENILMAAVLAQGTTHIK---NAAREPEIGNLIDMLTGMGAKIS-GRGRDTIVVEG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKV 298
+K + P + D FL AA TGG +++ C + L F E +M A V
Sbjct: 220 VKKLRL-PAKIRIVPDRIETGTFLIAAAATGGELSLSNCDASLLP---SFFE--KMRAAGV 273

Query: 299 TWTE----TSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI 350
T E V GP L+ +D+ P D+ + + FA G + I
Sbjct: 274 TIREDGERLQVVRNGP-----LRGVDIKTMPYPGPFTDLQAQMMLMCFASGLSLI 324

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAF 410
+ + E M EL ++GA + I+ P KL + A D R + +
Sbjct: 325 TET----IFENRFMHV--AELRRMGADIRIDGHSSIVNGPGKL-LGAKVMATDLRASASL 377

Query: 411 SLAACA 416
+AA A
Sbjct: 378 VIAALA 383

>ref|YP_003297836.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermomonospora
curvata DSM 43183]
gb|ACY95798.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermomonospora
curvata DSM 43183]
Length = 430

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 100/402 (24%), Positives = 162/402 (40%), Gaps = 47/402 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILL--AAL--SEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+++ GTV + G+K N +L + AAL ++G TV+ N+ EDV + + +G E
Sbjct: 15 RKLQGTTFIQGAK---NAVLPMIGAALMATKGRTVLRNPPIIEDVRRAVELAQAVGAKAE 71

Query: 69 ADKAAKRAVVVCGCGKFPV---EDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
+ A + V + PV E A FL + R A + GG
Sbjct: 72 LHEAERTLVIDASTLSSPVLPAEIASRFRGSFLFVPALLHRLGEAVIEGVGG----- 123

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ R + G K++GA V + D V G L G + + S
Sbjct: 124 -CNLGSRNLDHFYNGFKRMGATVTEQVDGDNGVVIYIKAGDLRGATLYCD-TPSHTGTEN 181

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+MA LA G +I P V + ++R G + S F G + +
Sbjct: 182 LVMAGALAKGTT---LIKNCALPEVLDNIEFLQRMGARI--SGGGTGFIITVEGVEELAA 236

Query: 246 KNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
V D A F+ AAITG +++ G SL+ A+ LE MG + +
Sbjct: 237 VEHTVMPDRIDAGVFIMAAITGSELSLVGA---SLEHLGVAADKLEQMGVEFHQEGAVL 293

Query: 306 TVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRVKE 360
V RE + L+ I+V ++ P D+ + V+ ADGP+ I + + R K
Sbjct: 294 QVR---RE---RPLRPINVTDEYPGFATDLQSPIMAVSCLADGPSYIYERIFDGRFK- 345

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
+ ELTK+GA++E + + P L+ + +D
Sbjct: 346 -----LAGELTKMGANIEVNGNRKAVFGPTPLHGAEVVAHD 381

>ref|ZP_06703939.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
fuscans subsp. aurantifolii str. ICPB 11122]
ref|ZP_06730665.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
fuscans subsp. aurantifolii str. ICPB 10535]
gb|EFF44521.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
fuscans subsp. aurantifolii str. ICPB 11122]
gb|EFF48197.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
fuscans subsp. aurantifolii str. ICPB 10535]
Length = 424

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 94/400 (23%), Positives = 158/400 (39%), Gaps = 45/400 (11%)

Query: 6 EIVLQPIKEISGTVKLPKSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + + G V + G+K+ IL L++ + N+ + DV + L LG
Sbjct: 3 KIVVTGGQALHGEVNISGAKNAVLPILCATLLADAPVEISNVPHLHDVITTVKLLSELGA 62

Query: 66 SVEADK---AAKRAVVVG---CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
V D+ A R+++V P E K L + R TA V+ GG
Sbjct: 63 EVTIDEGTLAKGRSILVDPRSIVTHQVAPYELVKTMRASILVLGPLLARYGTAEVSLPGGC 122

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A + RP+ + GL+ LGA++ G ++ G L G + +
Sbjct: 123 A-----IGSRPVDQHIGLQALGAEISVENGY----IKATSNGLKLGARYVFD-MV 168

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S +LMAA LA G +++ P V + G + E + + R ++G
Sbjct: 169 SVTGTENVLMAAVLAEGTT---VLENAAMEPEVTDLADCLIALGAQIEGAGT-PRIVVQG 224

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKV 298
++ +A + D FL AA+TGG+VTV +L + L GA +
Sbjct: 225 VERLGGGHHAVLP-DRIETGTFLVAAAMTGGSVTVRRARPETLDA---VLDKLTEAGATI 280

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
T T S+T+ + P +A+ + P D+ + ADG I +
Sbjct: 281 TTTADSITLDMHGKRP-----RAVSLTTAPYPAFPTDMAQFMAALNCVADGVGVINET- 333

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+
Sbjct: 334 ---IFENRFMHV--NELLRLGADIQVEGHTAIVRGAERLS 368

>ref|YP_783388.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisA53]
sp|Q07I26.1|MURA_RHOP5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;

AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABJ08408.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisA53]
Length = 429

Score = 41.6 bits (96), Expect = 0.24, Method: Compositional matrix adjust.
Identities = 72/312 (23%), Positives = 131/312 (41%), Gaps = 47/312 (15%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+++GT+ + G+K+ + +++ A LS+ T ++DN+ DV + R LG
Sbjct: 11 QLNGTIPISGAKNAALPLMIAALLSDETLILDNVPRADVAQL---QRILG----- 58

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRS---LTA AVTAAGGNA 119
V + GK P + + L + I MR+ + A + A A
Sbjct: 59 NHGVDILSAGKRPGDHEYQGQTLHISAKNIIDTTAPYELVSKMRASFVVIAPLLARMHVA 118

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSG 176
L G + RP+ L++ L++LGA + ++ CP GGL G +++
Sbjct: 119 KVS LPGGCAIGTRPVDDLIMALEKLGASITIDGGYVVASCP-----GGLKGAEIEFPK 171

Query: 177 -SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
++S +++ LMAA LA G I P + + + G K + + R
Sbjct: 172 VTVSGTHVA--LMAATLAKGTT--FIGNAACEPEIVDVADCLNKMGA KILGAGT-PRIT 225

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMG 295
++G K ++ + + +Y +A A+TGG V + G LQ + +VL G
Sbjct: 226 VEGVAKLHGARHTVLPDRIETGTYAMA-VAMTGGDVQLSGARPELLQSAL---DVLTEAG 281

Query: 296 AKVTWTETSVTV 307
A +T + V
Sbjct: 282 ATITVNNDGIRV 293

>ref|ZP_07902948.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
vortex V453]
gb|EFU38047.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
vortex V453]
Length = 448

Score = 41.6 bits (96), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 87/348 (25%), Positives = 144/348 (41%), Gaps = 39/348 (11%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTLGLSVEADK 71
K ++G+VK+ G+K+ I+ + L E G +V+ + +DV + L +LG +
Sbjct: 10 KRLTGSVKVSGAKNSVLPPIAASLLGEVGESVIIDAPPLDDVITISKVLES LGAGITYQD 69

Query: 72 AAKRA---VVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
R + C + P E ++ FL + R ++ GG A
Sbjct: 70 EVIRVNAEHITTC--EAPYEWVRKMRASFVLMGPLLARCGRTRISLPGGCA----- 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RPI + G + LGA++ LG + NG L G KV L + S ++M
Sbjct: 119 IGTRPIDQHLKGFEALGAEIS--LGQGYIEAKSNG--RLRGAKVYLDVA-SVGATENIMM 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + +I+ P + + G K + + I+G +K ++
Sbjct: 174 AATLAEG---VTVIENAAKEPEIVDLANYLNAMGAKVRGAGT-GVIRIEGVEKMHGVEHN 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVWTETSVTVT 308
+ D A F+A AAITGG V VEG L G V +E MG + E + V
Sbjct: 230 VIP-DRIEAGTFMAAAAITGGDVYVEGAIADHL-GPV--ISKMEEMGITIEPDENGIRV- 284

Query: 309 GPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD 352
K LK++DV P D+ + + L ++G + + +
Sbjct: 285 -----IADKPLKSVDVKTLPPYPGFPTMQSQMMALLLVSEGTSVVTE 326

>ref|ZP_06873821.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus
subtilis subsp. spizizenii ATCC 6633]

ref|YP_003868008.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii str. W23]
gb|EFG92341.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii ATCC 6633]
gb|ADM39699.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis subsp. spizizenii str. W23]
Length = 429

Score = 41.6 bits (96), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 93/432 (21%), Positives = 171/432 (39%), Gaps = 56/432 (12%)

Query: 15 ISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++GTV + G+K+ + ++ L+ ++ L D+ + L+ +G +V +
Sbjct: 12 LNGTVHISGAKNSAVALIPATILANSEVTIEGLPEISDIETLRDLLKEIGGNVHFENGEM 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGI-AMRSLTAAVTAAGGNATYVLDGVP---RMR 130
V D + + L N + +R+ + A G + G+P +
Sbjct: 72 -----VVDPTSMISMLPNGKVKKLRSYLLMGAMLRFRKQAVIGLPGGCHLG 119

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + G + LGA+V G +R L G ++ L +S +++AA
Sbjct: 120 PRPIDQHIKGFALGAEVTNEQGAIY--LRAE---RLRGARIYLD-VVSVGATINIMLAA 173

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G II+ P + L+ G K + + + + I G ++ K+ +
Sbjct: 174 VLAEGKT---IENAAKEPEIIDVATLLTSMGAKIKGAGT-NVIRIDGVKELHGCKHTII 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
+ ++ +AGAA+ G V ++ T L+ L MG + ++ + + G
Sbjct: 230 PDRIEAGTFMIAAGAM-GKEVIIDNVIPHTLE---SLTAKLREMGYHIETSDQQLLIVG- 284

Query: 311 PREPFGKRHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASWRVKETERMV 365
G+KHLK +DV P D+ + + A G + + D + S R K +
Sbjct: 285 -----GQKHLKPVVDKTLVYPGFPTDLQQPMTALLTRAKGTSVVTDTIYSARFKHID--- 336

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPTIRDP 425
EL ++GA+++ IIT P L + D AC V + D
Sbjct: 337 -----ELRRMGANMKVEGRSAIITGPVALQGAKVKASD-----LRAGACLVVAGLMAD- 384

Query: 426 GCTRKTFFPDYFD 437
G T T ++ D
Sbjct: 385 GVTEITGLEHID 396

>ref|ZP_04904861.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia pseudomallei S13]
gb|EDS87873.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Burkholderia pseudomallei S13]
Length = 449

Score = 41.6 bits (96), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 68/280 (24%), Positives = 120/280 (42%), Gaps = 33/280 (11%)

Query: 3 GAEEIVLQPIKEISGTVKLPKSGKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRT 62
G +++ ++ + ++G + + G+K+ + IL LS +D++ + +DV L L
Sbjct: 29 GTDKLAIIEGGRRLAGEIAVSGAKNAALPILCAGLLSAEPVRLDSVPDLKDVRTTLALLGQ 88

Query: 63 LGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+G+ E D R V+ PV A E+ +++++ A++ G
Sbjct: 89 MGMREETDGV--RVVLDASRVDPV--APYEL-----VKTMRASILVGLPLARF 134

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLS 175
G A L G + RP+ + GL+ +GA++ G + R L G ++ ++
Sbjct: 135 GYAKVSLPGGCAIGARPVDQHIKGLQAMGAIEHIEHGYIEARAKR-----LSGARI-VT 187

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
I+ LLMAA LA G+ +I+ P V L+ G K + DR
Sbjct: 188 DMITVTGTENLLMAATLADGET---VIENAAAREPEVTDLAHLLVAMGAKID-GIGTDRLV 243

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEG 275
I+G ++ +A + D A FL A GG VT+ G

Sbjct: 244 IQGVERLHGATHAVIP-DRIEAGTFLCAVAAAGGDVTLTG 282

>ref|ZP_00144234.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. vincentii ATCC 49256]
ref|ZP_04573103.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 4_1_13]
gb|EAA24158.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. vincentii ATCC 49256]
gb|EEO40482.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 4_1_13]
Length = 423

Score = 41.6 bits (96), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 70/287 (24%), Positives = 121/287 (42%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I G +K+ GSK+ + I++ + +GT V+ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKIEGELKVDGSKNSTLPIMIATLVEKGTYYVLRNVPDLRDIRTLVALLESGLVEVEKLDA 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + G G D ++++ FL G+ V GG A +
Sbjct: 71 NSYKIINNGLSGAEASYDLVKKMRASFLVMGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +++ P +E + + G K + R I G K + + + +
Sbjct: 177 VKAKGKT--VLENAAKEPEIEDLCNFLIKMGAKISGVGTG-RLEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLCLKLEEMGAK 275

>ref|YP_004067519.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Pseudoalteromonas sp. SM9913]
gb|ADT67367.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Pseudoalteromonas sp. SM9913]
Length = 419

Score = 41.6 bits (96), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 96/390 (24%), Positives = 154/390 (39%), Gaps = 45/390 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++ V+Q ++G V + G+K+ + IL A L+G + N+ + D+ L+TLG
Sbjct: 2 DQFVIQGGTSLAGEVTISGAKNAALPILFAALLADGKSTFTNPVPHLRDIITTEALLKTLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA--VTAAGGNATY 121
V+ G ++ A L + MR+ A + A G A
Sbjct: 62 ADVQWQ-----GDSLIIIDGATVNSTLAPYDLVKQMRASVLALGPLVARFGEAQV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RP+ + GL+++GA + G V G L G +V + IS
Sbjct: 111 SLPGGCAIGARPVDIHIQGLERMGAQITVENGYINAKVD---GRLKGAEVFME-MISVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
LLMAA LA G +++ P + + G K + S R I+G ++
Sbjct: 166 ATENLLMAATLADGKT--VLENAAREPEIIDLANCLIAMGAKITGAGS-SRIEIEGVER 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
++ + D FL AA+ GG V C T E L A +
Sbjct: 222 LSGCEHRILP-DRIETGTFLVAAAMAGGEVL---CKMTDFHSLEPVIEKLRATNALLEVH 277

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPATIRDVASWRVKET 361
+ S+ + RE LKA VN+ MP + A F TA+ VA+ T
Sbjct: 278 DDSIYLDMRGRE-----LKA--VNIKTMHPGFPPTDMAQF----TALNVVANGSATIT 325

Query: 362 ERMVAIR----TELTKLGASV--EEGPDYC 385

E + R EL ++GA++ E +C
Sbjct: 326 ETIFENRFMHVPELQRMGANIRLEGNTAFC 355

>gb|EFZ74474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
RN587/1]
Length = 419

Score = 41.6 bits (96), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 170/427 (39%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAGLLAEEPVEIQNVPKLKDVTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G + DA+ +V +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 LPGGCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 166 TVTIMCAATLAEGTT---IIEAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +
Sbjct: 222 GG--GVYRVLPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVG 276

Query: 302 ETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +
Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTMDQAQFTLLNLVAEGTGFTITET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + LA C
Sbjct: 327 VFENRFMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383

Query: 418 VPVTIRD 424
T+ D
Sbjct: 384 EGTTVVD 390

>gb|EFW56382.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shigella boydii
ATCC 9905]
Length = 419

Score = 41.6 bits (96), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 102/427 (23%), Positives = 170/427 (39%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPKSKLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++ G V + G+K+ + IL A L+E + N+ +DV + L LG VE
Sbjct: 6 VQGPTKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVTSMKLLSQLGAKVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G + DA+ +V +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVS 110

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ + G L G + + +S
Sbjct: 111 LPGGCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 166 TVTIMCAATLAEGTT---IIEAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERL 221

Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+ G + +L D A+ L GA +
Sbjct: 222 GG--GVYRVLPDRIETGTFLVAAAISRGKIIICRNAQPDTL--DAVLAK-LRDAGADIEVG 276

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +
Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---- 326

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAE 417
V E M EL+++GA E + I EKL+ + D R + + L C
Sbjct: 327 VFENRFMHV--PELSRMGAHAIESENTVICHGVEKLSGAQV-MATDLRASASLVLGCGCIA 383

Query: 418 VPVTIRD 424
T+ D
Sbjct: 384 EGTTVVD 390

>ref|YP_752039.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
frigidimarina NCIMB 400]
sp|Q07XR4.1|MURA_SHEFN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABI73200.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Shewanella
frigidimarina NCIMB 400]
Length = 419

Score = 41.6 bits (96), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 92/398 (23%), Positives = 160/398 (40%), Gaps = 44/398 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++ ++ ++G V + G+K+ + IL+ L+E +V N+ + DV LR LG
Sbjct: 2 DKLTIKASNPLAGEVVISGAKNAALPILMAGVLAETDFIVSNVPSLRDVITSCELLRCLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYV 122
VE ++ + ++ P + K L + R TA V+ GG A
Sbjct: 62 AEVEDLGGSRIRISTTNLNEYCAPYDLVKTMRASILILGPLLARYGTADVSLPGGCA--- 118

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+ +GA ++ G ++ G L G + + +S
Sbjct: 119 -----IGARPVNLHLHGLELMGAKIEVKEGY----IKARVDGRLKGTHIFMD-MVSVGA 167

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
LLMAA LA G +I+ P V + G K + I+G ++
Sbjct: 168 TENLLMAAALADGTT--VIENAAAREPEVTDLAHCLIAMGAKITGIGTAT-LKIEGVERL 223

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAKVTWTE 302
S V D FL AA+T G + ++L+ LE GA++T E
Sbjct: 224 -SGCEYRVMPDRIETGSFLVAAAVTRGKIRCVSADPSALEA---VLSKLEDAGAEITTGE 279

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRV 358
+ + + P K++++ P D+ V+ A+G + RV
Sbjct: 280 DWIELDMKGQRP-----KSVNIKTAPYPAFPTDMQAQFCVLNALAEG-----TGRV 325

Query: 359 KET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
ET E EL ++GA +E+ + CII ++LN
Sbjct: 326 TETIFENRFMHVPELIRMGADIEQEGNTCIIHGIDRLN 363

>ref|ZP_06837441.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
ammoniagenes DSM 20306]
gb|EFG81218.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
ammoniagenes DSM 20306]
Length = 422

Score = 41.6 bits (96), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 109/442 (24%), Positives = 167/442 (37%), Gaps = 59/442 (13%)

Query: 15 ISGTVKLPKSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+ G+K+ +++ A L+EG+T + N DV M L LG +V+ D
Sbjct: 13 LQGAVKVDGAKNSVLKLMMAALLAEGSTTLTNCPEILDVPLMQKVLEGLGCTVDIDG--- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV-----TAAGGNATYVLDGVPR 128
V P DA + A+R A+V TA G A L G
Sbjct: 70 -TTVTIDTPAVPRSDADFD-----AVRQFRASVCVLGPLTARCGKARVALPGGDA 118

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ GL++LGA G V L G K+KL S +L
Sbjct: 119 IGSRPLDMHQSGLEKLGATTHIEHG-----AVVTEASELVGAKIKLDFP-SVGATENILT 172

Query: 189 AAPLALGDVEIEIIDKLISIP-YVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
AA LA G ++D P V++ L+E + A+ S + G P N
Sbjct: 173 AAVLAKGTT---VLDNAAREPEIVDLCSMLLE---MGADISGAGTSTITINGVDKLYPTN 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--V 305
V GD A + A +T G +TV G L + L GA + E V
Sbjct: 227 HEVIGDRIVAGTWAYAAVMTQGDITVSGIAPRHLHLPLS---KLRSAGADIETYENGFRV 283

Query: 306 TVTGPPPREPFGRKHLKAIDVNMKMPDVAMTLAVVAL----FADGPTAI-RDVASWRVKE 360
+ G P K++D P L +A+ A+G I +V R +
Sbjct: 284 RMDGRP-----KSVDYQTLPPFPFPTDLQPMAGLSAIAEGTAVITENVFESRFRF 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDHRMAMAFSLAACAEVPV 420
+ M+ +LGA + + ++ EKL+ T + + D A A CA+
Sbjct: 335 VDEML-----RLGADAQVDGHHVLRGQEKLSSTHVWSSDIRAGAGLVLSAFCADEV 387

Query: 421 TIRDPGCTRKTFPDYFDVLSTF 442
T+ D + +P + + L
Sbjct: 388 TVHDVFHIDRGYPHFVENLQAL 409

>ref|YP_001775384.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa M12]
sp|B0U6N8.1|MURA_XYLFM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACA11754.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa M12]
Length = 425

Score = 41.6 bits (96), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 68/263 (25%), Positives = 109/263 (41%), Gaps = 17/263 (6%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV---EADK 71
+ G V++ G+K+ IL L++ + N+ DV M+ LR LG V E +
Sbjct: 12 LYGDVIRISGAKNAVLPLCATLLADAPVEISNVPLYHDVITMINLLRELGAGVTMNEGIE 71

Query: 72 AAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
A R++ V P + V L A L + A G A L G +
Sbjct: 72 AKGRSITVD-----PRWVRQRVVPYDLVKTMRASVLLLGPLLACYGAAEVALPGGCAIGS 126

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+ LGA++ G V G L GG+ +S LLMAA
Sbjct: 127 RPYDQHIRGLQSLGAEITVENGVIKASVSQ---GRLKGRFVFD-VVSVTGTENLLMAAA 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+A G +I+ P V + G + E + + R ++G ++ KS + A +
Sbjct: 183 VAQGT---SVIENAAEPEVVDLAECILITLGARVEGAGT-PRIVVEGVERLKSGQYAVLP 238

Query: 252 GDASSASYFLAGAAITGGTVTVE 274
D FL A+TGG ++++
Sbjct: 239 -DRIETGTFLVATAMTGGGRISMQ 260

>ref|ZP_02184329.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Carnobacterium sp. AT7]
gb|EDP68901.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Carnobacterium sp. AT7]
Length = 423

Score = 41.6 bits (96), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 99/404 (24%), Positives = 161/404 (39%), Gaps = 61/404 (15%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++++ K++SG V + G+K+ + ++ A L++ V++ + + +DVH ++ L +

Sbjct: 2 KKLIIINGGKKLSGEVTINGAKNSTVALIPAAILADSPVVLEGVPDIQDVHSLIDILNVMK 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ D G D V + + N I +SL A+ G G

Sbjct: 62 VETTFD-----GSTLTIDPTNMVSIPMPNGKI--KSLRASYYFMGALLTKFGQ 107

Query: 119 ATYVLDGVPVPRMRERPIGDLVVGLKQLGADVD-----CFLGTDCPPVRVNGIGGLPGGKVK 173
L G + RPI + G + LGA VD +L TD GL G ++

Sbjct: 108 GVVGLPGGCFLGPRPIDQHLKGFRALGATVDNEMGAMYLRTDEK-----GLVGTRLY 159

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
L +S +++AA A G II+ P + L+ G K + + D

Sbjct: 160 LD-VVSGIGATINVMLAAVKAAGKT---IENAAAREPEIIDVATLLNNMGAKVRGAGT-DI 214

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
I G + ++ + D A +L+ AA G V V+ L+G LE

Sbjct: 215 IRIDGVDELHGCRHTIIP-DRIEAGTYLSMAAAGSDVLVKNVIVEHLEG---LVAKLEE 270

Query: 294 MGAKVTWTETSVTVTGPPREPFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTA 349
MG + E S+ V +E HLKAI+V P D+ L + L A G +

Sbjct: 271 MGVPMEIGEDSIRV---KEA---THLKAINVKTLPPYGFATDLQQPLTPLLKATGTSL 323

Query: 350 IRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEK 392
I D + RVK EL ++GA D +I P K

Sbjct: 324 ITDTIYKRVKHIP-----ELVRMGAKARVESDMILIEGPIK 360

>ref|ZP_06750145.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 3_1_27]
gb|EFG33933.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 3_1_27]
Length = 423

Score = 41.6 bits (96), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 70/287 (24%), Positives = 121/287 (42%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I G +K+ GSK+ + I++ + +GT V+ N+ + D+ ++ L +LGL VE D

Sbjct: 11 KKIEGELKVDGSKNSTLPIMIATLVEKGTYVLRNVPDLRDIRTLVALLESGLGLEVEKLDA 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + G G D ++++ FL G+ V GG A +

Sbjct: 71 NSYKIINNGLSGAEASYDLVKMKMRASFLVMGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + G + LGA ++ G V GL GG + L S ++MAA

Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +++ P +E + + G K + R I G K + + + +

Sbjct: 177 VKAKGKT---VLENAAKEPEIEDLCNFLIKMGAKISGVGTG-RLEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK

Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAK 275

>ref|YP_315649.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thiobacillus
denitrificans ATCC 25259]
sp|Q3SHP2.1|MURA_THIDA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAZ97844.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thiobacillus
denitrificans ATCC 25259]
Length = 417

Score = 41.2 bits (95), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 72/315 (22%), Positives = 130/315 (41%), Gaps = 43/315 (13%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64

+ +++Q ++G V++ G+K+ + IL + L+ + N+ + +D+ ML L +G
Sbjct: 2 DALLIQGGNPLAGEVRISGAKNAALPILTASLLTAEPLRLGNVPHLKDISTMLALLGHMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ V D + V G P ++A E+ + + + AA+ G G
Sbjct: 62 VRVTLLDD---KNHVTLSGDSIPHKEAPYEM-----VKTMRRAILLVLGPTLARFGE 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLS 175
A L G + RP+ + GL+ +GAD+ ++ C L G ++ +
Sbjct: 109 ARVSLPGGCAIGSRPVDLHIKGLQAMGADISIEHGYIHARCKR-----LQGARIVMD 160

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
++ L+MAA LA G +++ P V R + G K E + + D
Sbjct: 161 -MVTVTGTENLMMAALAEGTT--VLENAAREPEVVDLARCLIAMGAKIEGAGT-DVIT 215

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMG 295
+ G + + + V D FL AA+TGG V +L+ + L G
Sbjct: 216 VHGVLEALHGAEYS-VMADRIETGTFLVAAAMTGGVRVATHTSPDTLEAVISK---LREAG 271

Query: 296 AKVT----WTETSVT 306
AKV+ W E T
Sbjct: 272 AKVSVGGDDWIEVEST 286

>ref|NP_298704.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella
fastidiosa 9a5c]
sp|Q9PDG4.1|MURA_XYLFA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAF84224.1|AE003972_9 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella
fastidiosa 9a5c]
Length = 425

Score = 41.2 bits (95), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 93/389 (23%), Positives = 153/389 (39%), Gaps = 40/389 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV---EADK 71
+ G V++ G+K+ IL L++ + N+ DV M+ LR LG V E +
Sbjct: 12 LCGDVRISGAKNAVLPILSATLLADAPVEISNVPLYHDVITMINLLRELGAQVTMNEGIE 71

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 131
A R++ V P + V L A L + A G A L G +
Sbjct: 72 AKGRSITVD-----PRWVRQHMPYDVLVKTMRASVLLLGPLLACYGAAEVALPGGCAIGS 126

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+ LGA++ G V G L GG+ +S LLMAA
Sbjct: 127 RPVDQHIRGLQSLGAEITVENGYIKASVSQ---GRLKGRFVFD-VVSVTGTENLLMAAA 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+A G +I+ P V + G + E + + R ++G ++ K + A +
Sbjct: 183 VAQGT---SVIENAAEMEPEVVDLAECIALGARIEGAGT-PRIVVEGVERLKGQYAVLP 238

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D FL A+TGG + + + + +L D ++ E GA + E S+ +
Sbjct: 239 -DRIETGTFLVATAMTGGRIQMQRVPTL--DAVLGKLTE-AGACIEIGEDSIRLDMQG 294

Query: 312 REPFGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
R P VN+ P D+ + A+G I++ + E M
Sbjct: 295 RRP-----CSVNLTAPYPGFPTDMQAQFMALNCVAEGVGVIKET----IFENRFMH 342

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLN 394
EL +LGA ++ I+ E+L+
Sbjct: 343 V--DELLRLGAKIQIEGHTAIVQGVERLS 369

>ref|ZP_03830667.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pectobacterium
carotovorum subsp. carotovorum WPP14]
Length = 420

Score = 41.2 bits (95), Expect = 0.29, Method: Compositional matrix adjust.

Identities = 100/431 (23%), Positives = 172/431 (39%), Gaps = 61/431 (14%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q ++G V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 6 VQGPTRLAGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTMMKLLGQLGARVE 65

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
+ G V+ + +V +F + +++++ A++ A G G
Sbjct: 66 RN-----GSVHVDAS--DVNVFCAPYDL-VKTMRASIWALGPLVARFGGQGV 110

Query: 123 LDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA + G V+ G L G + + +S
Sbjct: 111 LPGGCAIGARPVDLHIYGLEQLGAQIVLEEGY---VKATVDGRLKAHIVMD-KVSVGA 165

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK----- 237
++ AA LA G II+ P + T + G K + + D+ I+
Sbjct: 166 TVTIMSAATLAEGTT---IENAAREPEIVDTANFLNTLGAKISGAGT-DKITIEGVARL 221

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GG Y+ V D FL AA++ G + +L D A++ E GA+
Sbjct: 222 GGGVYR-----VVPDRIETGTFLVAAAVSRGQIMCRNTRPDTL--DAVLAKLRE-AGAE 272

Query: 298 VTWTETSVTVTGPPREFPGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA+ V + P D+ +++ L A+G I +
Sbjct: 273 IEIGEDWISLDMHGKRP-----KAVTVRTSPHPGFPTDMQAQFSLNLVAEGTGVITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADTYDDHRMAMAFSLA 413
+ E M EL ++GA E + I +KL+ + D R + + LA
Sbjct: 327 ----IFENRFMHV--PELIRMGAAEIESNTVICHGVDKLSGAQV-MATDLRASASLVLA 379

Query: 414 ACAEVPVTIRD 424
C VTI D
Sbjct: 380 GCIAEGVTIVD 390

>ref|ZP_00651089.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa Dixon]
ref|ZP_00683059.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa Ann-1]
gb|EA014247.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa Dixon]
gb|EA031421.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xylella fastidiosa Ann-1]
Length = 425

Score = 41.2 bits (95), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 68/263 (25%), Positives = 109/263 (41%), Gaps = 17/263 (6%)

Query: 15 ISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV---EADK 71
+ G V++ G+K+ IL L++ + N+ DV M+ LR LG V E +
Sbjct: 12 LYGDVIRISGAKNAVLPLCATLLADAPVEISNVPYLHDVITMINLLRELGAQVTMNEGIE 71

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
A R++ V P + V L A L + A G A L G +
Sbjct: 72 AKGRSITVD-----PRWVRQRVVPYDLVKTMRASVLLLGPLLACYGAAEVALPGGCAIGS 126

Query: 132 RPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+ LGA++ G V G L GG+ +S LLMAA
Sbjct: 127 RPVDQHIRGLQSLGAEITVENGVIKASVSQ---GRLKGRFVFD-VVSVTGTENLLMAAA 182

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+A G +I+ P V + G + E + + R ++G ++ KS + A +
Sbjct: 183 VAQGT---SVIENAAEPEVVDLAELITLGARVEGAGT-PRIVVEGVERLKSQYAVLP 238

Query: 252 GDASSASYFLAGAAITGGTVTVE 274
D FL A+TGG ++++
Sbjct: 239 -DRIETGTFLVATAMTGGRIISMQ 260

>ref|ZP_08035353.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Treponema phagedenis F0421]

gb|EFW39410.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Treponema
phagedenis F0421]
Length = 428

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 93/422 (22%), Positives = 167/422 (39%), Gaps = 65/422 (15%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTVK G+K+ + + A L++ + NL EDV ML + G SVE +
Sbjct: 12 VKGTVKASGNKNAALPCIAAAVLTDEPVRLLKNLPEIEDVGVM LDVFKAFGGSV EKKAPNE 71

Query: 75 RAVVVG--GGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+ + + P +A++ L + R+ A + GG+ + R
Sbjct: 72 YELRLETVRSSEIPANEARKIRASILFAGPLLARTKAILPPPGGDV-----IGRR 122

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNG-----IGGLPGGKVKLSGSISSQYLSALL 187
+ + L +LGA V +NG L G + L + + +A +
Sbjct: 123 RLDTHFLALTELGAQ-----VHINGRFVFSANKLIGKDIFLDEASVTATENA-V 170

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA +A G II+ S P+V+ RL+ G K S + I+G K +
Sbjct: 171 MAASMAEGTT---IINNAASEPHVQDLRLLTAMGAKISGIGS-NILTIEGVPKLHGAEF 226

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D F+ AA+T G++T+ + ++ +K A +G +TW+ T+
Sbjct: 227 T-IGPDFMEIGSFIGLAAVTRGSLTITDVKPSDMR-PIKLA--FNKLG--ITWSIEGSTL 280

Query: 308 TGPPREPFRGRHLKAIDVNMNMK-----PDVAMTLAVVALFADGPTAIRDVA 354
T P ++ ++ ++ M PD+ + V+A +G I +
Sbjct: 281 TVPAQQSL-----QVNCDLGGMIPKIDDSWPWPGFPDLTSMITVIATQVEGTVLIHE-- 332

Query: 355 SWRVKETERMVAIRTELTKLGASVEE-GPDYCIITPEKLNVTADTYDDHRMAMAFSLA 413
K E + +L +GA + P +++ P L+ + + D R MA +A
Sbjct: 333 ----KMFESRMFFVDKLI GMGARIILCDPHRAVVGSTLHGSEL-VSPDVRAGMALVIA 387

Query: 414 AC 415
AC
Sbjct: 388 AC 389

>ref|ZP_07899155.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
vortex V453]
gb|EFU42109.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
vortex V453]
Length = 427

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 90/409 (22%), Positives = 168/409 (41%), Gaps = 52/409 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
+++V++ + +SGT+++ G+K+ + IL + L+EGT + N+ + D+ ML L LG
Sbjct: 2 DKLVEIGGRPLSGTIRIHGAKNAALPILAAASLLAEGTVRLSNVPHLLDIEVMLSILGRLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
+ + V F V ED ++ MRS L + A G T
Sbjct: 62 SKCKHELETV-TVDTSSANSFHVPEDLMKQ-----MRSSIFLMGP LLARFGEVT 109

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADV-DCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 179
G + ER I + GL+ LGA++ + C R L G + L + S
Sbjct: 110 IYQPGGAIGERKIDLHLQLGLQALGAEIEESNDKIHCRASR-----LIGTDIHL DFA-S 162

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
++MAA ALG ++ P ++ + + G + + D I G
Sbjct: 163 VGATENIMMAAATALGTT---VLTNAAREPEIQDLQHFLNKMGANIIGAGT-DTITI HGV 218

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
++ +P + D A + AA+T G+VT+ + L VL+ G + +
Sbjct: 219 ERL-TPCEYEIIPDRIVAGTVMIAAAVTRGSVTLTKTNPSHL---TSLIHVLKRA GVQTS 274

Query: 300 WTETSVTVTGPPREPFRGRHLKAID-VNMNMKMP---DVAMTLAVVALFADGPTAIRD-V 353
+ ++ R KA++ + + P D+ + V+ ADG + +++ V

Sbjct: 275 VCNDIINISCSRP-----KAVERIVTSPYPSFPTDLQSQVMVLLSLADGFSVMKETV 327

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD 402

R K E EL+++GA + +Y I +++ ++ D

Sbjct: 328 FEGRFKHVE-----ELSRMGADISTDLNYAFIRGVQRIYGATVEATD 369

>ref|NP_457686.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]
ref|NP_462217.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]
ref|NP_806900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]
ref|YP_152311.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
ref|YP_218232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
ref|YP_001590281.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
ref|ZP_02345797.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]
ref|ZP_02575591.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]
ref|ZP_02656975.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]
ref|ZP_02668074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]
ref|ZP_02684654.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]
ref|ZP_02697385.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
ref|ZP_02831624.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
ref|YP_002042565.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
ref|YP_002047336.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]
ref|ZP_03077841.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
ref|YP_002148232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Agona str. SL483]
ref|ZP_03166099.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]
ref|YP_002143803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
ref|ZP_03215060.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
ref|ZP_03222015.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]
ref|ZP_03345909.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. E00-7866]
ref|ZP_03359400.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. E02-1180]
ref|ZP_03362594.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. E98-0664]
ref|ZP_03370733.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. E98-2068]
ref|YP_002638903.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594]
ref|ZP_04653938.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Tennessee str. CDC07-0191]
ref|ZP_06534162.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. AG3]

ref|ZP_06544985.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. E98-3139]
 sp|P65455.1|MURA_SALTI RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|P65454.1|MURA_SALTY RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|Q57JG1.1|MURA_SALCH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|Q5PLD1.1|MURA_SALPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|A9N756.1|MURA_SALPB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|B5F6V8.1|MURA_SALA4 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|B4TJ27.1|MURA_SALHS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|B4T720.1|MURA_SALNS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|B5BGL3.1|MURA_SALPK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 sp|C0PZK2.1|MURA_SALPC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT
 pir|AB0904 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
 gb|AAL22176.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]
 emb|CAD07824.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi]
 gb|AAO70760.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]
 gb|AAV78999.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
 gb|AAX67151.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
 gb|ABX69448.1| hypothetical protein SPAB_04124 [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
 gb|ACF65411.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
 gb|ACF66435.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]
 gb|EDX47060.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
 gb|EDX52020.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
 emb|CAR61211.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
 gb|ACH49951.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella

enterica subsp. enterica serovar Agona str. SL483]
gb|EDY26900.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Saintpaul str. SARA23]
gb|EDZ04091.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Virchow str. SL491]
gb|EDZ05194.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Javiana str.
GA_MM04042433]
gb|EDZ11011.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Saintpaul str. SARA29]
gb|EDZ14388.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar 4,[5],12:i:- str.
CVM23701]
gb|EDZ20607.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Kentucky str. CDC 191]
gb|EDZ24653.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Heidelberg str. SL486]
gb|EDZ30102.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Weltevreden str.
HI_N05-537]
gb|EDZ35019.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Hadar str. RI_05P066]
gb|ACN47462.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Paratyphi C strain
RKS4594]
emb|CBG26309.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Typhimurium str.
D23580]
gb|ACY90390.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Typhimurium str.
14028S]
emb|CBW19375.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Typhimurium str.
SL1344]
dbj|BAJ38308.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Typhimurium str.
T000240]
emb|CBY97516.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Weltevreden str.
2007-60-3289-1]
gb|EFX50328.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Typhimurium str.
TN061786]
gb|EFY12232.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
315996572]
gb|EFY15221.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
495297-1]
gb|EFY19709.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
495297-3]
gb|EFY23610.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
495297-4]
gb|EFY28142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
515920-1]
gb|EFY32065.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
515920-2]
gb|EFY39914.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str. 531954]
gb|EFY43579.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
NC_MB110209-0054]
gb|EFY45326.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.
OH_2009072675]
gb|EFY51384.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. enterica serovar Montevideo str.]

CASC_09SCPH15965]

gb|EFY53944.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 19N]

gb|EFY60370.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 81038-01]

gb|EFY63617.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MD_MDA09249507]

gb|EFY70795.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 414877]

gb|EFY71737.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 366867]

gb|EFY78323.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 413180]

gb|EFY80901.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 446600]

gb|EFZ07875.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Choleraesuis str. A50]

gb|ADX19097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. 4/74]

gb|EFZ81063.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 609458-1]

gb|EFZ84106.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 556150-1]

gb|EFZ89300.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 609460]

gb|EFZ92585.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 507440-20]

gb|EFZ96153.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 556152]

gb|EFZ99498.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB101509-0077]

gb|EGA05655.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB102109-0047]

gb|EGA08323.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB110209-0055]

gb|EGA14440.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB111609-0052]

gb|EGA17391.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 2009083312]

gb|EGA23384.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 2009085258]

gb|EGA26441.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 315731156]

gb|EGA30891.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2009159199]

gb|EGA37962.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008282]

gb|EGA39036.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008283]

gb|EGA46278.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008284]

gb|EGA47540.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008285]

gb|EGA52873.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella

enterica subsp. enterica serovar Montevideo str.
IA_2010008287]
Length = 419

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 100/421 (23%), Positives = 164/421 (38%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V +V +F + ++++ A++ A G G L G
Sbjct: 70 -----VHIDASQVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCT 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 117 IGARPVLDLHITGLEQLGATIKLEEGY---VKASVEGRKGAHIVMD-KVSVGATVTIMC 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVTLGAKIAGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+ G + +L D A+ L GA + E +++
Sbjct: 226 YRVLDPRIETGTFLVAAAISRGKILCRNAQPDTL--DAVLAK-LRDAGADIEVGEDWISL 282

Query: 308 TGPPREPFGKHLKADVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA++V P D+ ++ L A+G I + V E
Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFTITET---VFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
M EL+++GA E + I E L+ + D R + + LA C TI
Sbjct: 333 MHV--PELSRMGARAEIESNTVICHGVETLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|YP_001970990.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stenotrophomonas maltophilia K279a]
sp|B2FRX1.1|MURA_STRMK RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAQ44676.1| putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stenotrophomonas maltophilia K279a]
Length = 423

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 94/396 (23%), Positives = 159/396 (40%), Gaps = 56/396 (14%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+ G V + G+K+ IL L++ + N+ + DV + L LG V D+
Sbjct: 12 LHGEVVISGAKNAVLPLILCATLLADEPVEITNVPHLHDVVTTVKLLGELGAKVTIDQGTL 71

Query: 74 --KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDG 125
A+VV PV +L +++++ A++ G G A L G
Sbjct: 72 SRGSAIVVD---PRPVNQHVAPYEL-----VKTMRASILVLGPLLARFGAAEVSLPG 120

Query: 126 VPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+ RP+ + GL+ LGA++ + F+ R+ G G V ++G+
Sbjct: 121 GCAIGSRPVDQHIKGLQALGAEIVVENGFIKASAK--RLKG-GHFTFDMVSVTGT----- 172

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+LM A LA G ++D P V + G K E + R I+G ++
Sbjct: 173 -ENVLMGAVLAEGTT---VLDNCAMEPEVTDLAHCLIALGAKIEGLGTA-RLVIEGVERL 227

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
++ + D FL AA+TGG VTV ++ D ++++E GAK+ T+

Sbjct: 228 SGRHEVLP-DRIETGTFLVAAAMTGGKVTNRRPNTM--DAVLSKLVE-AGAKIETTD 283

Query: 303 TSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRV 358
S+T+ R P KA+++ P D+ + ADG I + +

Sbjct: 284 DSITLDMQGRRP-----KAVNLTTAPYPAFTDMQAQFMALNCVADGVGVINET----I 333

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
E M EL +LGA ++ I+ E L+

Sbjct: 334 FENRFMHV--NELLRLGADIQVEGHTAIVRGSEHLS 367

>ref|YP_002431941.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Desulfatibacillum alkenivorans AK-01]
sp|B8FKV1.1|MURA_DESAA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACL04473.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Desulfatibacillum alkenivorans AK-01]
Length = 416

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 94/403 (23%), Positives = 161/403 (39%), Gaps = 41/403 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++I+++ + +SG V++ G+K+ + IL + L +G N+ +D+ + L LG
Sbjct: 2 DKIIIEGGRTLSGEVQVSGAKNAALPILASLLVDGWNTFYNPVPELQDISTIGLLLEHLG 61

Query: 65 LSVEADKAAKRAVVVG-CGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
VE D + G C + P + + L + R A V+ GG A
Sbjct: 62 AKVEKDGHITIKIDASGLCETEAPYDLVRRMRASVLVLGPLTARLKKARVSLPGGCA---- 117

Query: 124 DGVRPMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
+ RPI + GL+ LGA V+ G V V L G + L + +
Sbjct: 118 -----IGARPIDQHLRGLEMLGATVELSHGY---VEVQA-EKLRGADIYLD-TPTVTGT 166

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
L+MAA LA G + I+ + P + L+ R G K E + S G +
Sbjct: 167 ENLMAACLAEG---VTILRNVAREPEIVALADLLNRMGGKVEGAGSP--VLTITGVEAL 221

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+P + D A F+ AA+T G V V+ LQ L + GA VT
Sbjct: 222 NPVEFTIIPDRIEAGTFMVAALTEGDVLVKDAVPAHLQA---LISKRLAGATVTEEGN 278

Query: 304 SVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVK 359
+ V G++ + ++DV P D+ V+ A G + I +
Sbjct: 279 GIRVQ-----GKRPICSVVDKTLPHPGFPTDMQAQFMVMTTAKGLSVIAETIF---- 327

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
R + +EL ++GA++ + +I + L+ + D
Sbjct: 328 -ENRFIHV-SELVRMGANISISQNSAVIRGVKHLAAPVMTD 368

>ref|ZP_02206262.1| hypothetical protein COPEUT_01025 [Coproccoccus eutactus ATCC 27759]
gb|EDP26808.1| hypothetical protein COPEUT_01025 [Coproccoccus eutactus ATCC 27759]
Length = 433

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 87/379 (22%), Positives = 154/379 (40%), Gaps = 37/379 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + + G V + G+K+ + IL A +++ ++N+ N D +L A++ +G
Sbjct: 2 EQYVIKGGRPLEGEVTIAGAKNAALGILAAAVMTDQEVTIENVPNVRDTRVLLQAIQGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+V + + V + G P D + + A L A+ ++ L
Sbjct: 62 ATV--NYVDEHTVRISGGTINPNSDLCDVDEFI--RKIRASYLLGALLGKYKHSQVALP 117

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA VD G + VN L G + + IS
Sbjct: 118 GGCDIGARPIDLHIKGFALGAKVDISNGM----ISVNA-DELVGSHIYMD-VISVGATI 171

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G IE K P++ L+ G + + + D I+G +
Sbjct: 172 NVMMAAVMAEGKTTIENAAKE---PHIVDVANLLNSMGANIKGAGT-DVIRIRGVKSLHG 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + D A F+ AA T G V ++ L+ L +GA VT + S
Sbjct: 228 TTYSIIP-DQIEAGTFMVAATAATRGVNLKINVIPKHLEA---ITSKLTDIGAHVTEYDDS 283

Query: 305 VVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRD-VASWRVK 359
V V R LKA ++ P D+ +AV ++G + + + + R K
Sbjct: 284 VRVMCDKR-----LKATNIKTLPYPGFPTDMQPQMAVTLALSNGTSIVTESIFENRFK 336

Query: 360 ETERMVAIRTELTKLGASV 378
EL+++GA +
Sbjct: 337 YV-----AELSRMGAHI 348

>ref|YP_226799.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
glutamicum ATCC 13032]
emb|CAF21220.1| UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE [Corynebacterium
glutamicum ATCC 13032]
Length = 421

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 161/431 (37%), Gaps = 39/431 (9%)

Query: 14 EISGTVKLPGSKSLSNRILLALLAALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK+ G+K+ +++ A L+EGTT + N DV M L LG V D +
Sbjct: 15 QLQGAVKVYGAKNSVLKLMMAALLAEGTTTTLTNCPEILDVPLMRDVLVGLGCDVTIDGST 74

Query: 74 KRAVV---VGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP LG +TA G A L G +
Sbjct: 75 VTITTPAELSSNADFPVAVTQFRASVCVLG-----PLTARCGRAVVSPLPGDAIG 123

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ GL++LGA G L G + L S +L A+
Sbjct: 124 SRPLDMHQSGLEKLGATTRISHGAVVAEAE-----KLVGANITLDFP-SVGATENILTAS 177

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+A G ++D P + R++ G E S I+G +K +P V
Sbjct: 178 VMAEGRT---VLDNAAREPEIVDLCLRLRSMGANIEGEGS-PTITIEGVEKL-TPTQHEV 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD A + AA+T G +TV G L + E L++ GAKV E V
Sbjct: 233 IGDRIVAGTWAYAAAMTRGDITVGGIAPRYLHLPL---EKLKIAGAKVETYENGFRVQ-- 287

Query: 311 PREPFGRKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETE-RMVAIRT 369
K +A D P L +A+ + + V + V E+ R V
Sbjct: 288 -----MDKQPEATDYQTLFPFGFPTDLQPMAGINAVSNGTSVITENVFESRFRFV---D 339

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E+ +LGA + +I E+L+ T++ + D A A CA+ + D
Sbjct: 340 EMLRLGADANVDGHHVIRGIEQLSSTSVWSSDIRAGAGLVLAALCADGVTEVHDFHID 399

Query: 430 KTFPDYFDVLS 440
+ +P++ + L
Sbjct: 400 RGYPNFVENLQ 410

>ref|YP_534260.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB18]
sp|Q20Y45.1|MURA_RHOPB RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABD89941.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodopseudomonas
palustris BisB18]
Length = 429

Score = 41.2 bits (95), Expect = 0.30, Method: Compositional matrix adjust.

Identities = 72/310 (23%), Positives = 130/310 (41%), Gaps = 41/310 (13%)

```
Query: 14  EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
          +++GT+ + G+K+ +   +++   L++ T ++DN+   DV +   L   G+ + A
Sbjct: 11  QLNGTIPISGAKNAALPLMIAGLLTDETLILDNVPRLADVAQLQRILGNHGVDIMA---- 66

Query: 74  KRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRS---LTAAVTAAGGNA 119
          GK P +   +   L +   I               MR+   + A + A   A
Sbjct: 67  -----AGKRPGDHEYQGQTLHISAKNIIDTTAPYELVSKMRASFVVIAPLLARMHEA 118

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG-SI 178
          L G   + RP+   L++ L++LGA   L D   V +   GGL G ++   ++
Sbjct: 119 KVSLPGGCAIGTRPVDLLIMALEKLGAT----LTIDGGYVIASAPGGLKGAAIEFPKVTV 174

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
          S   +++   LMAA LA G   +I   P +   + + G K   + + R   I+G
Sbjct: 175 SGTHVA--LMAATLARGTT---VIGNAAACEPEIVDVADCLNMGGKISGAGT-PRITIEG 228

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
          K   ++   +   + +Y +A   A+TGG V + G   LQ +   +VL   GA +
Sbjct: 229 VAKLHGARHTVLPDRIETGTYAMA-VAMTGGDVQLSGARPELLQSAL---DVLTTQAGATI 284

Query: 299 TWTETSVTVT 308
          T   + VT
Sbjct: 285 TVNNDGIRVT 294
```

```
>ref|ZP_05551474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
          sp. 3_1_36A2]
gb|EEU33130.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
          sp. 3_1_36A2]
Length = 423
```

Score = 41.2 bits (95), Expect = 0.31, Method: Compositional matrix adjust.
Identities = 70/287 (24%), Positives = 121/287 (42%), Gaps = 24/287 (8%)

```
Query: 13  KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
          K+I G +K+ GSK+ +   I++   + +GT V+ N+ +   D+   ++ L +LGL VE D
Sbjct: 11  KKIEGELKVDGSKNSTLPIMIATLVEKGTYVLRNVPDLRDIRTLVALLESGLVEVEKLDA 70

Query: 72  AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
          + + + G G   D   +++ FL   G+   V   GG A   +
Sbjct: 71  NSYKIINNGLSGAEASYDLVKKMRASFLVMGMLAIEKRKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
          RP+   + G + LGA ++   G   V   GL GG + L   S   ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
          A G   +++   P +E   + + G K   + R   I G K   + + + +
Sbjct: 177 VKAKGKT---VLENAAKEPEIEDLCNFLIKMGAKISGVGTG-RLEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
          + +Y +A + +   G++ V G   L   F   LE MGAK
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAK 275
```

```
>ref|YP_003241909.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
          sp. Y412MC10]
gb|ACX64102.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus
          sp. Y412MC10]
Length = 427
```

Score = 41.2 bits (95), Expect = 0.31, Method: Compositional matrix adjust.
Identities = 90/409 (22%), Positives = 168/409 (41%), Gaps = 52/409 (12%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
          +++V++ + +SGT+++ G+K+ +   IL + L+EGT + N+ +   D+   ML L LG
Sbjct: 2  DKLVIIEGGRPLSGTIRIHGAKNAALPILAAASLLAEGTVRLSNVPHLLDIEVMLSILGRLG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPV-EDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNAT 120
```

```

      + +      V      F V ED  ++      MRS  L  + A  G  T
Sbjct: 62  SKCKHELETV-TVDTSSANSFHPEDLMKQ-----MRSSIFLMGPILLARFGEVT 109

Query: 121  YVLDGVPVRMRERPIGDLVVGLKQLGADV-DCFLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
      G  + ER I  + GL+ LGA++ +      C  R      L  G  + L  + S
Sbjct: 110  IYQPGGCAIGERKIDLHLKGLQALGAEIEESNDKIHCASR-----LIGTDIHLDFAS 162

Query: 180  SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
      ++MAA  ALG      ++      P  ++      + + G      + + D  I  G
Sbjct: 163  VGATENIMMAAATAGTT---VLTNAAREPEIQDLQHFLNKMGANIIGAGT-DTITIIGHV 218

Query: 240  QKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT 299
      ++ + P      + D  A  +  AA+T G+VT+      + L      VL+  G  + +
Sbjct: 219  ERLE-PCEYEIIPDRIVAGTVMIAAAVTRGVSFTLTKTNPSHL---TSLIHLVKRAGVQTS 274

Query: 300  WTETSVTVTGPPREPFGGRKHLKAID-VNMNKM-----DVAMTLAVVALFADGPTAIRD-V 353
      + ++  R      KA++ + + P  D+  + V+  ADG  + +++ V
Sbjct: 275  ICNDIINISCMSRP-----KAVERIVTSPYPSFPTDLQSQVMVLLSLADGFSVMKETV 327

Query: 354  ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYD 402
      R  K  E      EL+++GA  +      +Y  I  +++      ++  D
Sbjct: 328  FEGRFKHVE-----ELSRMGADISTDLNYAFIRGVQRIYGATVEATD 369

```

```

>ref|YP_198570.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia
endosymbiont strain TRS of Brugia malayi]
sp|Q5GRP6.1|MURA_WOLTR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAW71328.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia
endosymbiont strain TRS of Brugia malayi]
Length = 425

```

Score = 41.2 bits (95), Expect = 0.32, Method: Compositional matrix adjust.
Identities = 99/432 (22%), Positives = 173/432 (40%), Gaps = 55/432 (12%)

```

Query: 7  IVLQPIKEISGTVKLPKSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLS 66
      +V  K  + G  +K+ GSK+  I+  + LS  + V+ N+ +  DVH M  L  LG
Sbjct: 5  LVRSNYKPLVGQIKINGSKNAILPIMAASLLSSSVLHNVPDLIDVHLMSELLEGLGAK 64

Query: 67  V----EADKAAKRAVVVGCGG---KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
      V      D  A  +  C      E  A  +  FL      +  + +  G
Sbjct: 65  VNFMHNKDHKANHTLETDCSNINNYAIQYETASKLRASFL-----MLGPMLSRFGK 115

Query: 119  ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
      A  G  + +RP+  +  L+++GA ++      D  +      G  L  G  K+  L  I
Sbjct: 116  ARTAFPGGCNIGKRPVDMHIKALEEMGAKIE----IDGYNIATVKGKLQGRKITLE-KI 170

Query: 179  SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
      S      ++MAA LA G  +  I+  + P  +  +  +++ G  + +++  +  I  G
Sbjct: 171  SVGATENIIMAATLAEG--VTTINNAATEPEILDLEFLKKIGADIKINNT--KVIITG 225

Query: 239  GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
      +K      +  +      + +Y LA A IT G  + +EG  + ++      A  LE  +GA V
Sbjct: 226  VKKLNGCIHKIISDRIEAGTYALA-AIITNGKLVLEGINLSDIRC---IANELEAIGAMV 281

Query: 299  TWTETSVTVTGPPREPFGGRKH--LKVIDNMNKM-----DVAMTLAVVALFADGPTAIRD 352
      + S+ ++      RK+  +K+ +V  +  P  D+  L      ADG  +  I  +
Sbjct: 282  ELYDGSIVIS-----RKNGSIKSTNVATDPYPNFPSPDMQPLMSAMCIADGISVIEE 333

Query: 353  VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKL--NVTADTYDDHRMAMA 409
      E  +  EL  KLGA++  +  I  + L  N+  A  D      + +A
Sbjct: 334  -----NIFENRFSHADELRLKLGANISIKKNKAAINGIKSLSGANLYATDLRSTAALVLA 387

Query: 410  FSLAACAEVPVT 421
      SL  A  E  +
Sbjct: 388  -SLVASGETTIN 398

```

```

>ref|YP_001538788.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salinispora

```

arenicola CNS-205]
gb|ABV99797.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salinispora
arenicola CNS-205]
Length = 445

Score = 41.2 bits (95), Expect = 0.32, Method: Compositional matrix adjust.
Identities = 107/457 (23%), Positives = 178/457 (38%), Gaps = 84/457 (18%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++GTV + G+K+ + +++ +A L+ G +V+ N+ D+ M LR L
Sbjct: 12 RMTGTVHVVGAKNSALKLMAVALLAPGRSVITNVPRITDIAIMGEVLRL----- 61

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAM-RSLTAAV-TAAGGNATYVLDGVPRMR- 130
GCG +F DA + V + + G+ RS+T V G A Y L V R+R
Sbjct: 62 -----CGGIRF---DADDPVDFPMVAHGGVPRSRSVTIDVPDVGAEADYEL--VRRLRA 110

Query: 131 -----ERPIGDL-----VVGLKQLGADV---CFLGTDCPPVRV 161
P GD V GL ++GA++ F+ P
Sbjct: 111 SICVLGPLLARRGSRVVAHPGGDAIGSRGLDMHVSGLARMGAEISGERGFVVASAPR--- 167

Query: 162 NGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERF 221
GL G ++ L S L+MAA LA G +ID P + ++ +
Sbjct: 168 ----GLRGAEIVLDFP-SVGATENLVMAAVLAG---TTVIDNAAREPEIVDICTMLNQM 219

Query: 222 GVKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTS 281
G + + + + G + ++A V GD A + GAA+T G VTV G L
Sbjct: 220 GALIDGAGT-STLTVVGVPLQPVRRHATV-GDRIVAGTWAFGAAMTRGDVTVTGASPAFL 277

Query: 282 QGDVKFAEVLEMMGAKVTWTETSVTVTGPPPREPFGRKHLKAIDVNMNMKMPDVAMTLAVVA 341
DV +++ GA V + + R +A+DV P A L +A
Sbjct: 278 --DVALDKLVS-AGALVETRRGAFRIRMADRP-----RAVDVVTLPYPGFATDLLPMA 327

Query: 342 LFADGPTAIRDVASW--RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAI 398
+ G A+ D AS + + M A E+ +LGA ++ + ++ E+L+ +
Sbjct: 328 I---GLAAVSDGASLITENIFDGRFMFA--NEMMLGADIQTDGHHAVVRGRERLSGAPV 382

Query: 399 DTYDDHRMAMAFSLAACAEVPVTIRDPGCTRKTFPDY 435
D A C + + + +PD+
Sbjct: 383 AATDIRAGAGLLIAGLCTDGVTEVSHAHHVDRGYPDF 419

>ref|YP_001408257.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
curvus 525.92]
gb|EAU00142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
curvus 525.92]
Length = 442

Score = 41.2 bits (95), Expect = 0.32, Method: Compositional matrix adjust.
Identities = 90/416 (21%), Positives = 166/416 (39%), Gaps = 58/416 (13%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++SG V++ G+K+ + ++ L L++ + N+ N D+ + LR LG S E +
Sbjct: 32 KLSGKVEISGAKNAALPLIALTLAKNEVKLSNIPNVADIKTLAQLRLNLGASCEFEN-- 89

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVP 127
+ + + GG V + N I +R + A++ G G+ L G
Sbjct: 90 ENLLKIDTGG-----VNSTMANYDI-VRKMRASILTLGPLLARFGHCEVSLPGGC 138

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGG-----KVKLSGSISSQY 182
+ +RPI + L+++GA ++ G + + GL K+ ++GS
Sbjct: 139 AIGQRPIDLHLHSALEKMGASIEIKQGY----IVASAPDGLKAASIVFDKITVTGS----- 189

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKY 242
++MAA LA G ++ + K P V ++ GVK E + + G K
Sbjct: 190 -ENIIMAAALAHGTTQLLNVAKE---PEVVQICEVLAASGVKIEGIGTSELSITGTGSKL 245

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
+ V D A +L AIT +++ + + LE MG +
Sbjct: 246 LDIGDVEVIPDRIEAGTYLCAGAITNSRISISKANANHM---LAMLAKLEEMGFGIKIDN 302

Query: 303 TSVTVTGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRV 358

+T+ K +K ++ + P D+ ++L A+G + I + R+
Sbjct: 303 DEITI-----LPAKKIKPCEIITTEYPGFPTDMQAQFMALSLIANGVSVIDE----RL 351

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAA 414
 E M +EL ++GA + + ++LN I D R + A LAA

Sbjct: 352 FENRFMHV--SELARMGADIRLNGHIASVYGKELNAADI-MATDLRASSALILAA 404

>ref|ZP_01969168.1| hypothetical protein RUMTOR_02753 [Ruminococcus torques ATCC 27756]
gb|EDK23076.1| hypothetical protein RUMTOR_02753 [Ruminococcus torques ATCC 27756]
Length = 440

Score = 41.2 bits (95), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 96/426 (22%), Positives = 172/426 (40%), Gaps = 43/426 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T +DNL + DV+ ML A+ +G
Sbjct: 12 EQYIIKGGNPLVGEVEIGGAKNAALAILAAAIMTDETVQIDNLPDVNDVNVMLEAIEGIG 71

Query: 65 LSVEADKAAKRAVVVGCGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ + G F +E D ++++ A L A+ A L
Sbjct: 72 AMVQRIDRHTVKINGSTIGDFNIEYDIKKIR-----ASYLLGALLGKYKRAEVAL 123

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV G L V + +I+
Sbjct: 124 PGGCNIIGSRPIDQHLKGFRALGADV DIEHGKIVAEAEKLRGTHLYFDVVTVGATIN---- 179

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA ++ G + I++ + P+V + G + + D I+G +
Sbjct: 180 --VMAAAMSEG---LTIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVRSLH 233

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + + D A F+ AA T G VTV L D +++++ +G +V +
Sbjct: 234 KTEYSIIP-DQIEAGTFMFAAAATKGDVTVLNVIPKHL--DATISKLV D-IGCEVEEFDD 289

Query: 304 SVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRV 358
+V V +K L+ V P D+ + V A G + I + + R
Sbjct: 290 AVRVV-----AKRLRCTQVKTLPGYPTDMQPPQIGVALALAKGTSTITESIFENRF 342

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
K EL ++GA V+ + I E+ + + + D R A +A A
Sbjct: 343 KYL-----GELARMGAQVKVEGNSATIEGVERFSAARV-SAPDLRAGAALCIAGLAAE 394

Query: 419 PVTIRD 424
+TI D
Sbjct: 395 GITIVD 400

>ref|NP_107611.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mesorhizobium
loti MAFF303099]
sp|Q986Q6.1|MURA2_RHILO RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2
dbj|BAB53397.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mesorhizobium
loti MAFF303099]
Length = 418

Score = 41.2 bits (95), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 98/409 (23%), Positives = 169/409 (41%), Gaps = 45/409 (11%)

Query: 13 KEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + G V + G+K+ + + A LS + NL + DV MLG +R G E ++
Sbjct: 10 RRLEGAVTISGAKNAALPQIAAALLSPYPLELTNLPDVTDVENMLGVVRLHG--AEVTRS 67

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
A A + E + + V+ MR+ + A + A G+A L G +
Sbjct: 68 AH-AATIDTSAAVSKETSYDTVR-----KMRATVLVLAPLLARFGHARVSLPGGCAI 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ V L LGA + G + + GL G ++ LS S S +MA

Sbjct: 119 GARPVDMHVAALAAALGAKIAIENGL----IVASAPNGLTGTRIVLS-SPSVGATETAMMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY 249
A A G+ EI + + + L M G + E + + R I G + + +

Sbjct: 174 ATTAKGETEILNAAREPEVADLAACLNAM---GARIEGAGT-HRILIAGDTGWHAARHDI 229

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
+ + +Y +A AAITGG + + L+ ++LE G V + + V+

Sbjct: 230 IPDRIEAGTYAIA-AAITGGQLELT---HARLEHMASVVQLLEATGVSVWPGDRGLIVS- 284

Query: 310 PPREFPGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
RE + LKA D+ P D+ + A+G + +R+ + E M

Sbjct: 285 --RE---RPLKAADLTTEPYPGFPTDLQAQFMALMCCAEGASLLRET----IFENRFMH 334

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAA 414
EL +LGA+++ ++ EKL+ + D R +++ LAA

Sbjct: 335 V--PELMRLGANIKLQGTMALVRGGEKLHGAQV-MATDLRASVSLVLAA 380

>ref|NP_623242.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Thermoanaerobacter
tengcongensis MB4]
ref|ZP_05092865.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
sp|Q8R9G7.1|MURA2_THETN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;
AltName: Full=Enoylpyruvate transferase 2; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase 2;
Short=EPT 2
gb|AAM24846.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Thermoanaerobacter
tengcongensis MB4]
gb|EEB75273.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Carboxydibrachium pacificum DSM 12653]
Length = 417

Score = 41.2 bits (95), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 70/265 (26%), Positives = 112/265 (42%), Gaps = 27/265 (10%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G V++ G+K+ IL L+EG +V+ N +DV M+ L +G V

Sbjct: 10 KRLYGEVEVHGAKNSILPILAAATILNEGVSVIHNCPRCLKDVDSMIEILEHIGCKVS---F 66

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+ R +VV V+D++ L MRS L A+ A A G +

Sbjct: 67 SGRDIVVDA---RDVKDSEIPDNLMR-----TMRSSIFLMGALIARNKKAFISFPGGCDI 118

Query: 130 RERPIGLDLVVLGKQLGADVDCFLG-TDCPPVRVNGIGGLPGKVKLSGSISSQYLSALLM 188
RPI + GLK+LG +++ G C VRV G ++ L S +++

Sbjct: 119 GHRPIDLHLKGLKGLGVEIEESYGYIRCKGVRVR-----GNEIHLDLDP-SVGATENIML 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G I +I P +E + G + + + + I+G +K +

Sbjct: 172 AATLADG---ITVIRNAAKEPEIEDLQNFLNSMGARITGAGT-NTIVIEGVKKLHDTEYT 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTV 273
+ D A +L AA+T G +TV

Sbjct: 228 IIP-DRIVAGTYLCAAAMTRGELTV 251

>ref|ZP_05060454.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [gamma
proteobacterium HTCC5015]
gb|EDY87404.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [gamma
proteobacterium HTCC5015]
Length = 421

Score = 41.2 bits (95), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 94/407 (23%), Positives = 164/407 (40%), Gaps = 63/407 (15%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ + + G ++ G+K+ IL LS+ V N+ + +DV M+ L ++G

Sbjct: 4 DKLIIEGGRRLDGELRASGAKNVLPILAATLLSDEPVSVSNVPHLQDVTTMVALLGSMG 63

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118

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          V V G + VE      ++ +      + +++++ A++      G      G
Sbjct: 64 -----VTVVIGDRLTVEIDPTTIEQCVAPYEL-VKTMRASIVVLGPLVARYGR 110

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGI-----GGLPGGKVK 173
          A L G + RP+ + GLK +GA+V      V NG      L G ++
Sbjct: 111 ARVSLPGGCAIGARPDQHIKGLKAMGAEV-----VVENGYIEARADRLKGARIV 160

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
          + +++      LLMAA LA G      I++      P V T + G K + +
Sbjct: 161 MD-TVTVGTENLLMAAALADGTT---ILENAACEPEVVDATDFLNAMGAKVSGAGT-ST 215

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
          ++G ++      N V D      FL AA+T G V V+      +L D A+ LE
Sbjct: 216 ITVEGVERLHG-TNYRVLPDRIETGTFLVAAAMTRGRVKVKTSPHAL--DAVLAK-LEE 271

Query: 294 MGAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTA 349
          GAKVT + + +      R P      KA+ + P      D+ + A+G +
Sbjct: 272 AGAKVTVGDDWIELDMEGRRP-----KAVSFRTDVYPGFPTDMQAQFMALNAVAEGAS- 324

Query: 350 IRDVASWRVKET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
          RV ET E      EL ++GA ++ + C+      E+L
Sbjct: 325 -----RVTETVFENRFMHVPELQRMGAKIDIEGNTCLCEGVEELT 364

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>ref|YP_003826360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
  [Thermosediminibacter oceani DSM 16646]
gb|ADL08737.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
  [Thermosediminibacter oceani DSM 16646]
Length = 416

```

Score = 41.2 bits (95), Expect = 0.34, Method: Compositional matrix adjust.
Identities = 92/402 (22%), Positives = 152/402 (37%), Gaps = 59/402 (14%)

```

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
          + GTV+ +K+ ++ + L+EG V++++ EDV M L LG E + +
Sbjct: 12 LKGTVRTSSAKNAVLPPVMAASLLAEGECVIEDVPELEDVRVMREVL SALGARCETKEGSL 71

Query: 75 RAV---VVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
          R + + C + P E ++      FL + + A ++ GG A      +
Sbjct: 72 RIIPDNIDTC--EAPYELVRKMRASFLVMGPPLLAKYGWAKISLPGGCA-----IGS 120

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQYLSA 185
          RPI + G LGA+++      G G +      KL GS+      S
Sbjct: 121 RPIDLHLKGFTALGAIEINL-----GHGSVEARCEKLGKSVIYLDFPSVGATEN 168

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
          ++MAA LA G +I+ P + + G + + D I+G + K
Sbjct: 169 IMMAAALAEGQT---VIENAAKEPEIVDLANFLNSMGAYIRGAGT-DVIKIEGVRNLKGI 224

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
          + D A FL AIT G V VE + L+ + A+++E GA+V E +
Sbjct: 225 SYTVIP-DRIEAGTFLIAGAITNGDVLVENNVSEHLKPLI--AKLIE-CGAEVIEGEDGI 280

Query: 306 TVTGPPREPFRGRKHLKAIDVNMNKMPDV-----AMTLAVVALFADGPTAIRDVASWRVKE 360
          V      GR +DV P      A +A ++L      V R
Sbjct: 281 RVV-----GRGRPNPVDVKTMPYPGFPTDMQAQMMAYLSLCTGTSMVTETVFENRFMH 333

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
          E      EL ++GA ++ I+ EKL+ + D
Sbjct: 334 VE-----ELKRMGAKIKIEGKSAIVEGVEKLSGAPVKATD 368

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>ref|NP_601757.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium
  glutamicum ATCC 13032]
sp|Q8NML5.1|MURA_CORGL RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
  AltName: Full=Enolpyruvate transferase; AltName:
  Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
  Short=EPT
dbj|BAB99951.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Corynebacterium
  glutamicum ATCC 13032]
Length = 418

```

Score = 41.2 bits (95), Expect = 0.34, Method: Compositional matrix adjust.
Identities = 103/431 (23%), Positives = 161/431 (37%), Gaps = 39/431 (9%)

Query: 14 EISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
++ G VK+ G+K+ +++ A L+EGTT + N DV M L LG V D +
Sbjct: 12 QLQGA VKVYGA KNSVLKLM AALLAEGTTTTLTNCPEILDVPLMRDVLVGLGCDVTIDGST 71

Query: 74 KRAVV---VCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ FP LG +TA G A L G +
Sbjct: 72 VTITTPAELSSNADFPVAVTQFRASVCVLG-----PLTARCGRAVVS L PGGDAIG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ GL++LGA G L G + L S +L A+
Sbjct: 121 SRPLDMHQSGLEKLGATTRISHGAVVAEAE-----KLVGANITLDFP-SVGATENILTAS 174

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
+A G ++D P + R++ G E S I+G +K +P V
Sbjct: 175 VMAEGRT---VLDNAAREPEIVDLRCMLRSMGANIEGEGS-PTITIEGVEKL-TPTQHEV 229

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTS LQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
GD A + AA+T G +TV G L + E L++ GAKV E V
Sbjct: 230 IGDRIVAGTWAYAAAMTRGDITVGGIAPRYLHLPL---EKLKIAGAKVETYENGFRVQ-- 284

Query: 311 PREPFGKRHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE-RMVAIRT 369
K +A D P L +A+ + + V + V E+ R V
Sbjct: 285 -----MDKQPEATDYQTLFPFGFPTDLQPMAGINAVSNGTSVITENVFESRFRFV---D 336

Query: 370 ELTKLGASVEEGPDYCIITPPEKLNVT AIDTYDDHRMAMAFSLAACAEVPTIRDPGCTR 429
E+ +LGA + +I E+L+ T++ + D A A CA+ + D
Sbjct: 337 EMLRLGADANVDGHVHVGIRGIEQLSSTSVWSSDIRAGAGLVLAALCADGVTEVHDFHID 396

Query: 430 KTFPDYFDVLS 440
+ +P++ + L
Sbjct: 397 RGYPNFVENLQ 407

>ref|YP_003796667.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Nitrospira defluviil]
emb|CBK40741.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Nitrospira defluviil]
Length = 418

Score = 41.2 bits (95), Expect = 0.35, Method: Compositional matrix adjust.
Identities = 70/280 (25%), Positives = 116/280 (41%), Gaps = 35/280 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
++I++Q + + G V+ G+K+ + IL L G V+ N+ DV M L LG
Sbjct: 2 DQIIIQGGRPLRGEVRTSGAKNAALPILASTILGGGECVLSNMPRVVDVLTMGKLLGMLG 61

Query: 65 LSV--EADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG----- 116
+SV EA+ A V A E L +R++ A+V G
Sbjct: 62 ISVAQEANHTIVEAQAV-----ASTEAPYDL-----VRTMRASVLVLGPLVARL 105

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSG 176
G A L G + RP+ + GL+++GA V+ G R L G ++
Sbjct: 106 GEAKVSLPGGCAIGSRPVNFHLAGLEKMGATVEIEHGYIKATARR-----LKGARIYFD- 159

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+ S L+MAA LA G +++ P + + + G + + D I
Sbjct: 160 TPSVTGTENLMMAAVLAEGTT---VLENAAKEPEISDLAAFLTKRGARITGAGT-DMITI 215

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC 276
+G +A + + +Y +AGA ITGG V ++ C
Sbjct: 216 EGVGTGLHGADHAVIPDRIEAGTYLVAGA-ITGGEVVIDDC 254

>ref|ZP_07378212.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pantoea sp. aB]
gb|EFM20206.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pantoea sp. aB]
Length = 419

Score = 41.2 bits (95), Expect = 0.35, Method: Compositional matrix adjust.
Identities = 98/422 (23%), Positives = 167/422 (39%), Gaps = 53/422 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLNRIILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +Q +SG V + G+K+ + IL A L+E + N+ D+ + L LG
Sbjct: 2 EKFRVQGPTRLSGEVTISGAKNAALPILFAALLAEEPVEIKNVPKLRDIDTTMKLLSQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE + G V+ + V +F + +++++ A++ A G G
Sbjct: 62 AKVERN-----GSVHVDASA--VDVFCAPYDL-VKTRASIWALGPLVARFQG 106

Query: 119 ATYVLDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + RP+ + GL+QLGA++ G V+ + G L G + + I
Sbjct: 107 GQVSLPGGCAIGARPVDLHITGLEQLGAEIKLEEGY---VKASVNGRLKGAIVMD-KI 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++ AA LA G +I+ P + T + G K + S D+ I+G
Sbjct: 162 SVGATVTIMSATLATGTT---VIENAAREPEIVDTANFLNTLGAKISGAGS-DKITIEG 217

Query: 239 GQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
++ Y V D FL AAI+GG V ++ D A+ L GA
Sbjct: 218 VERLGG--GVYRVLDPRIETGTFLVAAISGGKVMCHKTQPDIM--DAVLAK-LRDAGAD 272

Query: 298 VTWTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDV 353
+ E +++ + P KA++V P D+ ++ + A+G I +
Sbjct: 273 IETGEDWISLDMHGKRP-----KAVNVRTAPHPGFPTDMQAQFTLLNMVAEGTGLITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLA 413
R + I EL ++G E + I E L+ + D R + + LA
Sbjct: 327 IF-----ENRFMHI-PELIRMGGHAEIESNTAICHGVETLSGAQV-MATDLRASASLVLA 379

Query: 414 AC 415
C
Sbjct: 380 GC 381

>ref|ZP_04061074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
salivarius SK126]
gb|EEK11040.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
salivarius SK126]
Length = 423

Score = 41.2 bits (95), Expect = 0.35, Method: Compositional matrix adjust.
Identities = 76/267 (28%), Positives = 119/267 (44%), Gaps = 30/267 (11%)

Query: 15 ISGTVKLPKSKSLNRIILLALL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+SG V + G+K N +L LLAA SEG T + N+ DV+ M +R L ++V+ D
Sbjct: 13 LSGEVVIEGAK---NAVLPLLAATILASEGQTTLTNVPILSDVYTMNNVVRGLDIAVDFD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127
+ VVV G+ + E V MR+ + + A G+A + G
Sbjct: 70 E-ENNIVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNHAKVSMPPGCC 120

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + GL+ +GA + +G D N L G + + S L+
Sbjct: 121 TIGSRPIDLHLKGLEAMGAKI-TQVGGDITATAEN---LKGATIIYMDFP-SVGATQNL 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G IE + I V++ L L+ G + + + + IKG + K+
Sbjct: 175 MAATLADGVTTIENAAREPEI--VDLAL-LLNEMGADVKGAGT-ETLVIKGVKALHGTKH 230

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVE 274
A V+ D A F+ AA+T G V ++
Sbjct: 231 AVVQ-DRIEAGTFMVAAMTSGDVLIK 256

>ref|ZP_04667189.1| conserved hypothetical protein [Clostridiales bacterium 1_7_47_FAA]
gb|EEQ60410.1| conserved hypothetical protein [Clostridiales bacterium 1_7_47FAA]
Length = 430

Score = 41.2 bits (95), Expect = 0.36, Method: Compositional matrix adjust.

Identities = 87/422 (20%), Positives = 172/422 (40%), Gaps = 35/422 (8%)

```
Query: 5  EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + IL + +++ ++DNL + D++ +L A+ +G
Sbjct: 2  EQYIIKGGNPLVGDTVISGAKNAALGILAAASIMTDDDLIDNLPDVRDINVLEAIEEIG 61

Query: 65  LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
VE + + V + V E ++ A A+ +A L
Sbjct: 62  ARVE--RIDRHTVKINGSNIKEVSVDDEYIRKIR----ASYFIGALLGKYKSAQVPLP 114

Query: 125  GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGA+V G V + I L + L +S
Sbjct: 115  GGCNIGSRPIDQHIKGFALGAEVIERGA----VIAHAI-DLVASHIYLD-VVSVGATI 168

Query: 185  ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G I++ P++ + G + + + D IKG +
Sbjct: 169  NIMMAAALAEGQT--ILENAAKEPHIVDVANFLNSMGANIKGAGT-DTIRIKGVDRHLHG 224

Query: 245  PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + D A F+ AA T G + ++ L+ + L +G +V + +
Sbjct: 225  TEYSIIP-DQIEAGTFMCAAAATRGDIMIKNVIPKHLEA---ISAKLMEIGCEVAEFDDA 280

Query: 305  VTVTGPMPREPFGKHLKKAIDVNMNKMPP-DVAMTLAVVALFADGPTAIRD-VASWRVKETE 362
V V G P + +H + P D+ +AV + A+G + + + + R K +
Sbjct: 281  VRVVGKPSQ---RHTDIKTLPPGFTDMQPMQMAVALVLANGTSMVTESIFENRFKYVD 336

Query: 363  RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAEVPVTI 422
EL ++G++++ + +I ++L ++ D R A +A A T+
Sbjct: 337  -----ELARMGSNIKVEGNVAVIDGVKRLTGAQVNA-PDLRAGAALVIAGLAADGYTV 388

Query: 423  RD 424
D
Sbjct: 389  VD 390
```

```
>ref|YP_003518733.1| MurA [Pantoea ananatis LMG 20103]
gb|ADD75605.1| MurA [Pantoea ananatis LMG 20103]
Length = 424
```

Score = 41.2 bits (95), Expect = 0.37, Method: Compositional matrix adjust.
Identities = 103/427 (24%), Positives = 165/427 (38%), Gaps = 53/427 (12%)

```
Query: 9  LQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
+Q +SG V + G+K+ + IL A L+E + N+ D+ + L LG VE
Sbjct: 11  VQGPTRLSGEVTISGAKNAALPILFAALLAEPEVETNVPKLRDIDTTMKLLTQLGAKVE 70

Query: 69  ADKAAK---RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAA---VTAAGGNATYV 122
+ + V V C P E K MR+ A + A G
Sbjct: 71  RNSGVHVDASGVDFVCA---PYELVK-----TMRASIWALGPLVARFGQGEVS 115

Query: 123  LDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + RP+ + GL+QLGA++ G V+ + G L G + + +S
Sbjct: 116  LPGGCAIGARPVDLHITGLEQLGAEIKLEEGY----VKASVNGRLKGALIVMD-KVSVGA 170

Query: 183  LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
++ AA LA G +I+ P + T + G K + + D+ I+G ++
Sbjct: 171  TVTIMSAATLATGTT--VIENAREPEIVDTANFLNLTGAKISGAGT-DKITIEGVERL 226

Query: 243  KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
Y V D FL AAI+GG V +L D A+ L GA +
Sbjct: 227  GG--GVYRVLPDRIETGTFLVAAAISGGKVICRNAQPDTL--DAVLAK-LRDAGADIETG 281

Query: 302  ETSVTVTGPMPREPFGKHLKKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWR 357
E +++ + P KA++V P D+ ++ L A+G I +
Sbjct: 282  EDWISLDMHGKRP-----KAVNVRTAPHPGFTDMQAQFTLLNLVAEGTGLITETIF-- 333

Query: 358  VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAACAE 417
R + I EL ++GA E + I E L+ + D R + + LA C
Sbjct: 334  ---ENRFMHI-PELIRMGAAHAEIESNTAICHGVETLSGAQV-MATDLRASASLVLAGCIA 388

Query: 418  VPVTIRD 424
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T+ D
Sbjct: 389 EGTTLVD 395

>ref|ZP_04678375.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus warneri L37603]
gb|EEQ79508.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus warneri L37603]
Length = 421

Score = 41.2 bits (95), Expect = 0.37, Method: Compositional matrix adjust.
Identities = 91/371 (24%), Positives = 146/371 (39%), Gaps = 35/371 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAL-SEGTTVDNLLNSEDVHYMLGALRTL 63
++IV+ ++ G VK+ G+K+ +L + L S+GT+ + N+ DV + L TL
Sbjct: 2 DKIVINGGNQLKGEVKVEGAKNAVLVLTASLLASKGTSKLVNVPALSDVETINNVLSTL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V K + AVVV E E V + + M L A + G+A L
Sbjct: 62 NADVITY-KDENAVVVDATKTLNEEAPYEYVSKMRASI-LVMGPPLARL----GHAIVAL 115

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGA++ G + N GL G + L S
Sbjct: 116 PGGCAIGSRPIEQHIKGFALGAEIHLNGN----IYANAKDGLKGASIHLDFFP-SVGGT 170

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
L+MAA LA G +++ P + + G K + + D I G +
Sbjct: 171 QNLIMAASLASGKT---VLENAAKEPEIVDLANYINEMGGKITGAGT-DTITIHGVEYLT 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAKVTWTET 303
+++ + + +AG AIT G + V G + LE MG K+ + E
Sbjct: 227 GVEHSIIPDRIEAGTLLIAG-AITRGDIFVRGAIKEHMS---SLVYKLEEMGVKLDYQED 282

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVA----S 355
+ V+ LK +DV P D+ + + L A+G I +
Sbjct: 283 GIRVS-----AEGDLKPVDVKTLPHPGFPTDMQSQMIALLLTANGHKVITETVFNRF 335

Query: 356 WRVKETERMVA 366
V E RM A
Sbjct: 336 MHVAEFRMNA 346

>ref|YP_001564491.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Delftia acidovorans SPH-1]
gb|ABX36106.1| EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) [Delftia acidovorans SPH-1]
Length = 465

Score = 41.2 bits (95), Expect = 0.37, Method: Compositional matrix adjust.
Identities = 61/243 (25%), Positives = 94/243 (38%), Gaps = 26/243 (10%)

Query: 144 LGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIID 203
+GAD+D +GT VR GG P G + ++ L + GDVE+
Sbjct: 237 MGADIDG-IGTSRLTVR---GGAPLGGGDFTFEEDFHEITTFLALGAITGGDVEVRN-S 290

Query: 204 KLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP--KNAYVEGDASSASYFL 261
+ P ++ R +FGV+ EH + W R G K ++P N + +A+ YF
Sbjct: 291 TPDNFPLID---RTFAKFGVQVEHKNWSRALRSGPLKVQTPFTSNVLTKEAAPWPYFP 347

Query: 262 AGAAITGGTVTVEGCGTSL-----QGDVKFAEVLEMMGAKVTWTETSVTVTGPPREPFG 316
+ V G G + + L GA V ++ VT FG
Sbjct: 348 VDLLPIFIALGVHAQGNALFWNKIYDGLGWTGELSKFGAHVFSSDPHRVVT-----FG 401

Query: 317 RKHLKAIDVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGA 376
L V + VA+ L +VA +G + IR+ R + +R+ LGA
Sbjct: 402 GNPLTPAVVESPYIIRVAIALFMVASSIEGRSEIRNATPIIRAHPHFVENLRS----LGA 457

Query: 377 SVE 379
VE
Sbjct: 458 RVE 460

>ref|ZP_06371949.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 414]
gb|EFC32795.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 414]
Length = 418

Score = 40.8 bits (94), Expect = 0.37, Method: Compositional matrix adjust.
Identities = 87/404 (21%), Positives = 163/404 (40%), Gaps = 66/404 (16%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ I +SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L L
Sbjct: 6 IEGINHLSGNTISGAKNAALPLIVSSILAKNEVKINNIPNVADIKTLISLLENL----- 60

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GN 118
G K ++ + N IA +R + A++ G G+
Sbjct: 61 -----GAKVNFQNTALLNTSTLNQTIKDYDIVRKMRSILTLGPLLARFGH 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + +RPI ++ L+++GA++ G V G L G ++ L I
Sbjct: 108 CEVSLPGGCAIGQRPIDLHLLALEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKI 160

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFGVKAHSDSWDRFY 235
+ ++MAA LA G KL+++ P V +++ G+ + D
Sbjct: 161 TVTGENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEILKNAGLDIK-GIGTDELE 213

Query: 236 IKGGQK-YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMM 294
I G K K V D A +L AIT +T++ + L L M
Sbjct: 214 IYGTDKELLEIKEFSVIPDRIEAGTYLCAGAITNSKITLDKVNASHLSA---VLAKLHQ 270

Query: 295 GAKVTWTETSVTVTGPPREPFRGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAI 350
G + E S+T+ P +E +K I++ ++ P D+ +AL +G + I
Sbjct: 271 GFETLIKEDSITLL-PAKE-----IKPIEIMTSEYPGFPTDMQAQFMALALKTNGTSII 323

Query: 351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ R+ E M +EL ++GA ++ I ++LN
Sbjct: 324 DE----RLFENRFMHV--SELLRMGADIKLNGHIATIVGGKELN 361

>ref|YP_003809885.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [gamma proteobacterium HdN1]
emb|CBL44224.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [gamma proteobacterium HdN1]
Length = 424

Score = 40.8 bits (94), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 90/400 (22%), Positives = 153/400 (38%), Gaps = 52/400 (13%)

Query: 15 ISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-----LS 66
+SG V++ GSK+ S IL L +G V N+ + DV M+ L +G +
Sbjct: 12 LSGEVRISGSKNSSLPILAGTLLVDGKAKVSNIPHLHDVTTMIELLQMGVDVVDDHMV 71

Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 126
+E D + C + + L LG + A G A L G
Sbjct: 72 LEVDPRGLK----DCTAPYELVKTMRSILVLG-----PLVARFGEAIVSLPGG 116

Query: 127 PRMRERPIGDLVVLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+ +GA+++ G V+ G L G + L +++ L
Sbjct: 117 CAIGSRPVDLHLKGLEAMGANINVANGYIHATVK----GRLKGAHMLD-TVTVTG TENL 171

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+MAA LA G II+ P + + G + + S D I+G ++ +S +
Sbjct: 172 MMAASLANGRT---IIENAAREPEIVDLANFINAMGGNVQAGS-DTLVIEGVERLQSC 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ + + ++ +AG AIT G V L D + LE GA ++ +
Sbjct: 228 HTVIADRIETGTFLVAG-AITSGLVKCRNTDPRML--DTTLIK-LEEAGANISTGADWIE 283

Query: 307 VTGPPREPFRGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ R P VN+ MP + A F A+ +A TE +
Sbjct: 284 IDMRNRRPRA-----VNIRTMPHPGFPTDMQAQF----MALNTIAEGTSTITETIFE 331

Query: 367 IR----TELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
R +EL ++GA + + ++ E L + D
Sbjct: 332 NRFMHVSELARMGADIHVEGNTAVVRGVESLTAAPVMATD 371

>ref|ZP_08062751.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 903]
gb|EFX39512.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
parasanguinis ATCC 903]
Length = 427

Score = 40.8 bits (94), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 78/299 (26%), Positives = 124/299 (41%), Gaps = 35/299 (11%)

Query: 17 GTVKLPGSKSLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
GTVK+ G+K N +L LLAA SEG T + N+ DV M +R L V ++
Sbjct: 15 GTVKIEGAK---NAVLPLLAATVLA SEGVTTLKNVPVLSDFVTMNNVVRGLNAQVTFNEE 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRM 129
+ VVV K E + V MR+ + V A G+A + G +
Sbjct: 72 -ENTVVVDAQAKLSEEA PYKYVS-----KMRASIVVLGPVLARNGHAKVSMPPGGCTI 122

Query: 130 RERPIGLDVVGLKQLGADVDCFLG-TDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
RPI + GLK +GA++ G + R L G + + S ++M
Sbjct: 123 GSRPIDLHLKGLKAMGAEITQTAGYIEAKAER-----LKGAGHIYMDFP-SVGATQNIMM 175

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G + +I+ P + L+ + G + + + + I G + +
Sbjct: 176 AATLADG---VTVIENAAAREPEIVDLALLLNKMGANVKGAGT-ETLTIVGVESLHGANNH 231

Query: 249 YVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
V+ D A F+ GAA+TGG V +E + + ++ MG VT E + +
Sbjct: 232 VVQ-DRIEAGTFMIGAAMTGGDVLIEDA---IWEHNRPLLSKMQEMGVTVTEENGIRI 286

>ref|ZP_02074519.1| hypothetical protein CLOL250_01289 [Clostridium sp. L2-50]
gb|EDO58151.1| hypothetical protein CLOL250_01289 [Clostridium sp. L2-50]
Length = 433

Score = 40.8 bits (94), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 91/404 (22%), Positives = 157/404 (38%), Gaps = 42/404 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ V++ + + G V + G+K+ + IL A +++ +++N+ N D +L A+ +G
Sbjct: 2 EQYVIKGGQPLEGEVTIAGAKNAALGILAAVMTDQKVIIENVPNVRDTRVLLQAIEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V + V CG P D + + A L A+ + L
Sbjct: 62 AKV---RYIDEHTVSICGASINPNSDL CVDDEFIRKIR--ASYLLGALLGKYKRSQVAL 116

Query: 124 DGVPRMRERPIGLDVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LG A VD GT L G + + + +
Sbjct: 117 PGGCDIGARPINLHIKGFALGAQVDITNGTISTYAE-----ELIGSHIYMDVASVGATI 171

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
+ ++MAA LA G IE K P++ + G + + + D I+G ++
Sbjct: 172 N-IMMAAVLAEGKTTIENAAKE---PHIVDVANFLNSMGANIKGAGT-DVIRIRGVKELH 226

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AA T G V ++ L+ L +GA V +
Sbjct: 227 GTTYSIIP-DQIEAGTFMVAATAKGNVLKINVPKHLEA---ITSKLNEIGAHVIEYDD 282

Query: 304 SVTVTGPFPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRD-VASWRV 358
SV V R LK+ ++ P D+ +AV ++G + + + + R
Sbjct: 283 SVRVMSDKR-----LKSTNIKTLPYPGFPTMQPQMAVTLALSNGTSIVTESIFENRF 335

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKL---NVTATD 399
K ELT++GA + + II E NV A D
Sbjct: 336 KYV-----AELTRMGAHIRVEGNTAIDGVESFTGANVAAPD 372

>ref|ZP_01314861.1| hypothetical protein Wendoof_01000308 [Wolbachia endosymbiont of Drosophila willistoni TSC#14030-0811.24]
ref|ZP_03788214.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia endosymbiont of Muscidifurax uniraptor]
gb|EEH11979.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia endosymbiont of Muscidifurax uniraptor]
Length = 425

Score = 40.8 bits (94), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 83/381 (21%), Positives = 153/381 (40%), Gaps = 53/381 (13%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV----E 68
K + G +K+ GSK+ I+ + LS ++ N+ + DVH M L +LG V
Sbjct: 11 KPLVGKIKINGSKNAVLPIMAASLLSSSPVILHNVPDLIDVHLSKLLLESLGAEVNFMHN 70

Query: 69 ADKAAKRAVVVGCGG----KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ A + + C P + A + FL + + + G A
Sbjct: 71 KNYKANHTLKDSCNINNHVMPYKTASKLRTSFL-----ILGPMLSRFGKARTAFP 121

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L+++GA ++ D + G L G ++ IS
Sbjct: 122 GGCNIGKRPVDMHIKALEEMGAKIEI---DGYNIIATVKGLQGKEITFE-KISVGATE 176

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G + I+ + P V + +++ G E ++ + I G +
Sbjct: 177 NVIMAATFAEG---VTTINNAATEPEVLDLIDFLKKMGADIEIDNT--KVIITGVEALNG 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + +Y LA A ITGG + +EG + ++ LE +GA V +
Sbjct: 232 CVHKIIPDRIEAGTYALA-AIITGGKLELEGINLSDIRC---ITNELETIGAMVELYDGG 287

Query: 305 VTVTGPPEPFGGRKH--LKAIDVNMNKMPP---DVAMTLAVVALFADGPTAI-RDVASWR 357
+ ++ RK+ +K+ +V + P D+ L ADG + I ++ R
Sbjct: 288 IVIS-----RKNGSIKSANVATDPYPNFPSPDMQPLMSAMCIADGISVIEENIFENR 339

Query: 358 VKETERMVAIRTELTKLGASV 378
+ EL KLGA++
Sbjct: 340 FTHAD-----ELRKLGANI 353

>ref|ZP_00373787.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Wolbachia endosymbiont of Drosophila ananassae]
ref|YP_002727654.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia sp. wRi]
sp|C0R4M1.1|MURA_WOLWR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|EAL58698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Wolbachia endosymbiont of Drosophila ananassae]
gb|ACN95863.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Wolbachia sp. wRi]
Length = 425

Score = 40.8 bits (94), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 83/381 (21%), Positives = 153/381 (40%), Gaps = 53/381 (13%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV----E 68
K + G +K+ GSK+ I+ + LS ++ N+ + DVH M L +LG V
Sbjct: 11 KPLVGKIKINGSKNAVLPIMAASLLSSSPVILHNVPDLIDVHLSKLLLESLGAEVNFMHN 70

Query: 69 ADKAAKRAVVVGCGG----KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
+ A + + C P + A + FL + + + G A
Sbjct: 71 KNYKANHTLKDSCNINNHVMPYKTASKLRTSFL-----ILGPMLSRFGKARTAFP 121

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + +RP+ + L+++GA ++ D + G L G ++ IS
Sbjct: 122 GGCNIGKRPVDMHIKALEEMGAKIEI---DGYNIIATVKGLQGKEITFE-KISVGATE 176

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA A G + I+ + P V + +++ G E ++ + I G +
Sbjct: 177 NVIMAATFAEG---VTTINNAATEPEVLDLIDFLKKMGADIEIDNT--KVVITGVEALNG 231

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ + + +Y LA A ITGG + +EG + ++ LE +GA V +
Sbjct: 232 CVHKIIPDRIEAGTYALA-AIITGGKLELEGINLSDIRC---ITNELETIGAMVELYDGG 287

Query: 305 VTVTGPFPREPFGGRKH--LKAIDVNMNMKMP----DVAMTLAVVALFADGPTAI-RDVASWR 357
+ ++ RK+ +K+ +V + P D+ L ADG + I ++ R
Sbjct: 288 IVIS-----RKNCSIKSANVATDPYPNFPSPDMQQLMSAMCIADGISVIEENIFENR 339

Query: 358 VKETERMVAIRTELTKLGASV 378
+ EL KLGA++
Sbjct: 340 FTHAD-----ELRKLGANI 353

>gb|ABC00788.1| 5-enolpyruvylshikimate 3-phosphate synthase [Lolium rigidum]
Length = 24

Score = 40.8 bits (94), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 20/24 (83%), Positives = 21/24 (87%)

Query: 91 KEEVQLFLGNAGIAMRSLTAAVTA 114
KEEV+LFLGNAG AMR LTAAV A
Sbjct: 1 KEEVKLFLGNAGTAMRPLTAAVVA 24

>ref|YP_003615048.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cloacae subsp. cloacae ATCC 13047]
sp|P33038.1|MURA_ENTCC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
pdb|1NAW|A Chain A, Enolpyruvyl Transferase
pdb|1NAW|B Chain B, Enolpyruvyl Transferase
emb|CAA77856.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cloacae]
gb|ADF64099.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cloacae subsp. cloacae ATCC 13047]
Length = 419

Score = 40.8 bits (94), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 98/421 (23%), Positives = 166/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE +
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTMMKLLTQLGKTKVERN---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + V F + +++ A++ A G G L G
Sbjct: 68 -----GSWIDASN--VNNFSAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL++LGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHIFGLEKLGAIEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAEHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IENAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A++ E GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGKRP-----KAVTVRTAPHPAPFTDMQAQFTLLNLVAEGTGVTITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424

D
Sbjct: 390 D 390

>gb|EGC83932.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerococcus
hydrogenalis ACS-025-V-Sch4]
Length = 426

Score = 40.8 bits (94), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 67/278 (24%), Positives = 115/278 (41%), Gaps = 21/278 (7%)

Query: 1 MAGAEEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGAL 60
M E +V++ + G V + G+K+ + IL + L+ ++D + +D+ M+ L
Sbjct: 1 MNNEEILVVRKNGPLKGEVYISGAKNSALPILAASLASEEVILDEVPKLDIEVMVEIL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKF--PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGN 118
R+L V+ + KF P E + F+ G + AVT A G
Sbjct: 61 RSLNAKVDYLTETTLKIDSSNVNKFETPFELMDKMRASFI-VMGPLLSKFHGHAVTKAPGG 119

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
+ +RPI + G + LGA + + GL G + L
Sbjct: 120 CN-----IGKRPIDLHLKGFEALGAKTTM----NHEEISSKAKNGLKGEVIYLDFFP- 166

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S ++MAA LA G+ +I+ P + + + G K + + + IKG
Sbjct: 167 SVGATENIMMAATLAEGET---VIENAAKEPEIVDLASFLSKMGAKITGAGTSN-IIIKG 222

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVGEC 276
+K + ++ V +A+Y LA AAITGG +TV+
Sbjct: 223 VEKLRGTRHTIVPDRIEAATYMLA-AAITGGDITVKNV 259

>ref|ZP_07958830.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 8_1_57FAA]
gb|EFV19981.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lachnospiraceae
bacterium 8_1_57FAA]
Length = 430

Score = 40.8 bits (94), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 96/426 (22%), Positives = 172/426 (40%), Gaps = 43/426 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T +DNL + DV+ ML A+ +G
Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALAILAAAIMTDETVQIDNLPDVNDVNVMLEAIEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ + G F +E D ++++ A L A+ A L
Sbjct: 62 AMVQRIDRHTVKINGSTIGDFNIEYDIKKIR-----ASYLLGALLGKYKRAEVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV G L V + +I+
Sbjct: 114 PGGCNIGSRPIDQHLKGFRALGADVIEHKGKIVAEAEKLRGTHLYFDVVTGATIN---- 169

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA ++ G + I++ + P+V + G + + D I+G +
Sbjct: 170 --VMMAAMSEG---LTIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVRS 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVGECGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + + D A F+ AA T G VTV L D +++++ +G +V +
Sbjct: 224 KTEYSIIP-DQIEAGTFMFAAAATKGDVTVLNVIPKHL--DATISKLVLD-IGCEVEEFDD 279

Query: 304 SVTVTGPPREPFGFRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRD-VASWRV 358
+V V +K L+ V P D+ + V A G + I + + R
Sbjct: 280 AVRVV-----AKRLRCTQVKTLPPGYPTDMQPQIGVALALAKGTSTITESIFENRF 332

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEV 418
K EL ++GA V+ + I E+ + + + D R A +A A
Sbjct: 333 KYL-----GELARMGAQVKVEGNSATIEGVERFSAARV-SAPDLRAGAALCIAGLAAE 384

Query: 419 PVTIRD 424
+TI D

Sbjct: 385 GITIVD 390

```
>ref|YP_002217278.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
    enterica subsp. enterica serovar Dublin str.
    CT_02021853]
ref|YP_002245206.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
    enterica subsp. enterica serovar Enteritidis str.
    P125109]
sp|B5FIN7.1|MURA_SALDC RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
    AltName: Full=Enoylpyruvate transferase; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
    Short=EPT
sp|B5R0I0.1|MURA_SALEP RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
    AltName: Full=Enoylpyruvate transferase; AltName:
    Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
    Short=EPT
gb|ACH75047.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
    enterica subsp. enterica serovar Dublin str.
    CT_02021853]
emb|CAR34716.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
    enterica subsp. enterica serovar Enteritidis str.
    P125109]
Length = 419
```

Score = 40.8 bits (94), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 100/421 (23%), Positives = 164/421 (38%), Gaps = 53/421 (12%)

```
Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
Sbjct: 12  LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERNGS-- 69

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
      V +V +F + +++++ A++ A G G L G
Sbjct: 70  -----VHIDASQVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCT 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      + RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLEQLGATIKLEEGY---VKASVEGRLKGAHIVMD-KVSVGATVTIMC 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVTLGAKIAGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
      Y V D FL AAI+ G + +L D A+ L GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAAISRKILCRNAQPDTL--DAVLAK-LRDAGADIEVGEDWISL 282

Query: 308 TGPPPREPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
      + P KA++V P D+ ++ L A+G I + V E
Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFITET----VFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPVTIR 423
      M EL+++GA E + I E L+ + D R + + LA C TI
Sbjct: 333 MHV--PELSRMGARAEIESNTVICHGIETLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
      D
Sbjct: 390 D 390
```

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>ref|ZP_02234216.1| hypothetical protein DORFOR_01076 [Dorea formicigenerans ATCC
    27755]
gb|EDR47549.1| hypothetical protein DORFOR_01076 [Dorea formicigenerans ATCC
    27755]
Length = 430
```

Score = 40.8 bits (94), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 96/424 (22%), Positives = 174/424 (41%), Gaps = 39/424 (9%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
```

Sbjct: 2 E+ +++ + G V++ G+K+ + IL A +++ T ++NL + D++ +L A+ +G
EQYIIKGGHPLVGEVEIGGAKNAALAILAAAIMTDETVRIENLPDVNDINVLLDAIAGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
V+ + F +E D ++++ A L A+ +A L

Sbjct: 62 AMVQRTDRHTVKINAKAIHDFNIEYDYIKKIR-----ASYLLGAMLGKYKHAEVAL 113

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL 183
G + RPI + G + LGADV+ G ++ GK +S

Sbjct: 114 PGGCNIGSRPIDQHLKGFRALGADVEIEYG-----KILAEADRLVGKHIYFDVVSVGAT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243
++MAA +A G + I++ + P+V + G + + D I+G QK

Sbjct: 168 INVMMATMAEG---LTIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVQKLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTET 303
+ + D A F+ AA T G VTV L+ + A++LE +G +V +

Sbjct: 224 GTDYSVIP-DQIEAGTFMFAAAATKGDVTVLNVIPKHLEATI--AKLLE-IGCEVEEFDD 279

Query: 304 SVTVTGPPREPFGKRLKAI---DVMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKE 360
+V V + H+K + + P + +TL AL + R K

Sbjct: 280 AVRVV--SKGDLRSTHVKTLPYPGFPTDMQPMGVTL---ALCKGTSIVTESIFENRFKY 334

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPV 420
+ EL ++GA+V+ + I EKL+ + + D R A +A A +

Sbjct: 335 LD-----ELARMGANVKVEGNSATIEGVEKLSGARV-SAPDLRAGAALCIAGLATDGI 386

Query: 421 TIRD 424
TI D

Sbjct: 387 TIVD 390

>ref|ZP_01994898.1| hypothetical protein DORLON_00887 [Dorea longicatena DSM 13814]
gb|EDM63604.1| hypothetical protein DORLON_00887 [Dorea longicatena DSM 13814]
Length = 430

Score = 40.8 bits (94), Expect = 0.40, Method: Compositional matrix adjust.
Identities = 62/269 (23%), Positives = 115/269 (42%), Gaps = 18/269 (6%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V++ G+K+ + IL A +++ T ++DNL + D++ ++ A+ +G

Sbjct: 2 EQYIIKGGHPLVGEVEIGGAKNAALAILAAAIMTDETVLIDNLPDVNDINVLLDAIEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + + V + V+ + ++ A L A+ A L

Sbjct: 62 AQVH--RVDRTHTKINGASIKNVDIETYDYIKKIR-----ASYLLGALLGKYRRAEVALP 114

Query: 125 GVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RPI + G + LGADV G ++ GK +S

Sbjct: 115 GGCNIGSRPIDQHLKGFRALGADV DIEHG-----KIVAEADRLVGKHIYFDVVSVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA +A G + I++ + P+V + G + + D I+G Q+ S

Sbjct: 169 NVMAAAMAEG---LTILENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVQRLHS 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTTVT 273
+ + + D A F+ AA T G VTV

Sbjct: 225 TEYSVIP-DQIEAGTFMFAAAATRGDVT 252

>ref|ZP_04570031.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 2_1_31]
gb|EEO38205.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
sp. 2_1_31]
Length = 423

Score = 40.8 bits (94), Expect = 0.41, Method: Compositional matrix adjust.
Identities = 69/286 (24%), Positives = 121/286 (42%), Gaps = 24/286 (8%)

Query: 14 EISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKA 72
+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D

Sbjct: 12 KIAGELKVDGSKNSTLPIMIATLVEKGTYILRNVPDLRDIRTLVALLESGLGLEVEKLDAN 71

Query: 73 AKRAVVVGCGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + + G G D +++ FL G+ V GG A +

Sbjct: 72 SYKIINNGLSGAEASYDLVKKMRASFLVMGGMLAIEKRGKVALPGGCA-----IGA 122

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + G + LGA ++ G V GL GG + L S ++MAA

Sbjct: 123 RPVDLHLKGFEALGAKINIEHGY---VEATTENGLVGGNIVLDFP-SVGATENIIMAAV 177

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G I++ P +E + + G K + R I G +K + + +

Sbjct: 178 KAKGKT---ILENAAKEPEIEDLCNFLIKMGAKISGVGT-SRLEIDGVEKLTACEYTIIA 233

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK

Sbjct: 234 DRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGAK 275

>ref|YP_001139374.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Corynebacterium glutamicum R]
dbj|BAF55472.1| hypothetical protein [Corynebacterium glutamicum R]
Length = 418

Score = 40.8 bits (94), Expect = 0.41, Method: Compositional matrix adjust.
Identities = 103/430 (23%), Positives = 160/430 (37%), Gaps = 39/430 (9%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G VK+ G+K+ +++ A L+EGTT + N DV M L LG V D +

Sbjct: 13 LQGAVKVDGAKNSVLKLMMAALLAEGTTTTLTNCPEILDVPLMRDVLVGLGCDVTIDGSTV 72

Query: 75 RAVV---VGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ FP LG +TA G A L G +

Sbjct: 73 TITTPAELSSNADFPAVTQFRASVCVLG-----PLTARCGRAVVS LPGGDAIGS 121

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ GL++LGA G L G + L S +L A+

Sbjct: 122 RPLDMHQSGLEKLGATTRISHGAVVAEAE-----KLVGANITLDFP-SVGATENILTASV 175

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
+A G ++D P + R++ G E S I+G +K +P V

Sbjct: 176 MAEGRT---VLDNAAREPEIVDLCRMRLSMGANIEGEGS-PTITIEGVEKL-TPTQHEVI 230

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
GD A + AA+T G +TV G L + E L++ GAKV E V

Sbjct: 231 GDRIVAGTWAYAAAMTRGDITVGGIAPRYLHLPL---EKLKIAGAKVETYENGFRVQ--- 284

Query: 312 REPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETE-RMVAIRTE 370
K +A D P L +A+ + + V + V E+ R V E

Sbjct: 285 ----MDKQPEATDYQTLFPFGFPTDLQPMAGINAVSNGTSVITENVFESRFRFV---DE 337

Query: 371 LTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAACAEVPTIRDPGCTRK 430
+ +LGA + +I E+L+ T++ + D A A CA+ + D +

Sbjct: 338 MLRLGADANVDGHHVIRGIEQLSSTSVWSSDIRAGAGLVLAALCADGVTEVHDFHIDR 397

Query: 431 TFPDYFDVLS 440
+P++ + L

Sbjct: 398 GYPNFVENLQ 407

>ref|YP_001411799.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parvibaculum lavamentivorans DS-1]
sp|A7HQF9.1|MURA_PARL1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABS62142.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Parvibaculum lavamentivorans DS-1]
Length = 424

Score = 40.8 bits (94), Expect = 0.41, Method: Compositional matrix adjust.

Identities = 62/267 (23%), Positives = 110/267 (41%), Gaps = 29/267 (10%)

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+++GA++D G V GGL G ++ S +S L+MAA
Sbjct: 125 RPYDLIKGLQKMGAEIDLVEGY----VLAKAPGGKLGAVIR-SPIVSVGATHTLMMAAA 179

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G + +++ P + + G K E + I+G + + +
Sbjct: 180 LAEG---VTVLENAAREPEIGDVANCLVAMGAKIEGIGT-STLRIEGVDRHLGATHRVIA 235

Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWTETSVTVTGPP 311
+ +Y +A AA+TGG V +EG + + + VL GA V + +V +
Sbjct: 236 DRIEAGTYAVA-AAMTGGVEVLEGVEAETFEAALS---VLRAAGAGVESEQAVRIF--- 288

Query: 312 REPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ L+A DV P D+ + A+G + I + R + +
Sbjct: 289 ---RNGERLQATDVVTQVFPGFPTDLQAQFMALMTTAEGESEITETIF-----ENRFMHV 340

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLN 394
+ EL + GA++ D ++ EKL
Sbjct: 341 Q-ELARFGANISLHGDKALVHGVEKLN 366

>ref|YP_002352707.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dictyoglomus
turgidum DSM 6724]
gb|ACK42093.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dictyoglomus
turgidum DSM 6724]
Length = 433

Score = 40.8 bits (94), Expect = 0.41, Method: Compositional matrix adjust.
Identities = 67/281 (23%), Positives = 114/281 (40%), Gaps = 23/281 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++ V++ ++ G +++ GSK+ S I+ + L+ G ++DN+ +D M L+ LG
Sbjct: 10 DKFVIEGGHKLGELEIWSGSKNASLPMAASVLNSGDLILDNVPPVKDNITMAEILKVLG 69

Query: 65 LSV---EADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATY 121
+ V E DK + G + P E + F L + A G A
Sbjct: 70 MEVEFLEGDKVHIKGEKPY--RAPYELVSKMRASF-----ELMGPLLARFGEAEI 118

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
G R+ RP+ + G + LGA+V G C + GL G K+ L S
Sbjct: 119 PYPGGCRIGLRPVDLHIKGFESLGAETVEKGYVCARAK---KGLKGTKIHLDP-SVG 173

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
++MAA +A G+ +I+ P V ++ G + E + YIKG +
Sbjct: 174 ATRNIMMAAIAEGET---VIENAAACEPEVVDLGNFLKMMGAIEGLGT-STIYIKGKDD 229

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQ 282
K V D +A F+ + G + ++ LQ
Sbjct: 230 LKPVDDYKVIPDRIAAGTFIIAGVMLGKDLIKNVEPEHLQ 270

>ref|YP_002767348.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus
erythropolis PR4]
dbj|BAH34609.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus
erythropolis PR4]
Length = 419

Score = 40.8 bits (94), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 75/280 (26%), Positives = 118/280 (42%), Gaps = 23/280 (8%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E ++ + G V + G+K+ +++ A L+EGTTVV N + DV M LR L
Sbjct: 2 SEHFLVTGGNRLEGEVLVGGAKNSVLKMAAALLAEGTTVVNTCPDILDVPLMADVLRGL 61

Query: 64 GLSVEADKAAKRAVVVGCGKFPVE-DAKEEVQLFLGNAG-IAMRSLTAAVTAAGGNATY 121
G VE + + R + K+ + DA ++ + + G + R A V GG+A
Sbjct: 62 GCEVELEDSEVR-ITTPAEPKYHADFDVAVKQFRASVCVLGPLVARCRRRAVVALPGGDA-- 118

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181

```

      + RP+      GL+ LGA +   G C      +   L G ++L   S
Sbjct: 119 -----IGSRPLDMHQSGRLRLLGARSEIEHG--CVVAEAD---DLHGANIRLVFP-SVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
      +LMAA LA G+   +ID   P +   ++   G K   S   I+G +K
Sbjct: 166 ATENILMAAVLARGET---VIDNAAREPEIVDLNMLNEMGAKVSGGGS-STLTIQGVVK 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
      + P   V GD   A+ +   A++T G V V G   L
Sbjct: 222 LE-PTTHRVIGDRIVAATWGVAASMTRGDVRVRGVNHKHL 260

```

```

>sp|Q9Z3Z6.1|MURA_PSEPU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
      AltName: Full=Enoylpyruvate transferase; AltName:
      Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
      Short=EPT
gb|AAD17963.1| UDP-N-acetylglucosamine enolpyruvyl transferase homolog
      [Pseudomonas putida]
      Length = 419

```

Score = 40.8 bits (94), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 84/394 (21%), Positives = 156/394 (39%), Gaps = 53/394 (13%)

```

Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      + G +++ G+K+ +   IL   L++G   V NL +   D+   M+   +G+   D+
Sbjct: 12  LDGEIRISGAKNAALPILAAATLLADGPVTVGNLPHLHDITTMIELFGRMGIEPVIDE--- 68

Query: 75  RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
      K VE   ++ +   +   +++++ A++   G   G A   L G
Sbjct: 69  -----KLAVEIDPRTIKTLVAPYEL-VKTMRASILVLGPMVARFGEAEVALPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      + RP+   + GL+ +GA ++   ++   P   GGL G   ++S
Sbjct: 119 IGSRPVDLHIRGLEAMGAKIEVQGGYIKAKAPE-----GGLRGAHFFFD-TVSVTGTE 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
      ++MAA LA G   ++   P V   +   G K + + + D   I G ++   S
Sbjct: 172 IMMAAALAKGR---SVLQNAAREPEVVDLANFINAMGGKVQAGT-DTIVIDGVERLHS- 226

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
      N V D   +L AA+TGG V V+   T L+   E L+   GA +   E +
Sbjct: 227 ANYRVMPDRIETGTYLVAAAVTGGRVKVKDTPDPTILEA---VLEKLKEAGADINTGEDWI 283

Query: 306 TVTGPPPREPFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKET 361
      +   + P   KA+++   P   D+   +   A+G A+ +   + E
Sbjct: 284 ELDMHGKRP-----KAVNLRTPAPYPAFPTDMAQAFISLNAIAEGTGAVIET----IFEN 333

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPPEKLVN 395
      M   E+ ++GA ++   +   I+T   + L V
Sbjct: 334 RFMHVY--EMHRMGAQIQVEGNTAIVTGVKALKV 365

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>ref|ZP_04383823.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus
      erythropolis SK121]
gb|EEN88839.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodococcus
      erythropolis SK121]
      Length = 419

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Score = 40.8 bits (94), Expect = 0.43, Method: Compositional matrix adjust.
Identities = 75/280 (26%), Positives = 118/280 (42%), Gaps = 23/280 (8%)

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Query: 4  AEEIVLQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
      +E ++   + G V + G+K+   +++ A L+EGTTVV N +   DV M   LR L
Sbjct: 2  SEHFLVTGGRNLEGEVLVGGAKNSVLKLMMAALLAEGTTVVNTCPDILDVPLMADVLRGL 61

Query: 64  GLSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAG-IAMRSLTAAVTAAGGNATY 121
      G VE + + R +   K+ + DA ++ + +   G + R   A V   GG+A
Sbjct: 62 GCEVELEDSEVR-ITTPAEPKYHADFDVAVKQFRASVCVLGPLVARCRAVVALPGGDA-- 118

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQ 181
      + RP+      GL+ LGA +   G C      +   L G ++L   S

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Sbjct: 119 -----IGSRPLDMHQSLRLLGARSEIEHG--CVVAEAD---DLHGANIRLVFP-SVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
+LMAA LA G+ +ID P + ++ G K S I+G +K
Sbjct: 166 ATENILMAAVLARGET---VIDNAAREPEIVDLNMLNEMGAKVSGGGS-STLTIQGVK 221

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
+ P V GD A+ + A++T G V V G L
Sbjct: 222 LE-PTTHRVIGDRIVAATWGVAASMTGRGDVRVRGVNHKHL 260

>ref|ZP_01161681.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Photobacterium
sp. SKA34]
gb|EAR54503.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Photobacterium
sp. SKA34]
Length = 418

Score = 40.8 bits (94), Expect = 0.43, Method: Compositional matrix adjust.
Identities = 96/412 (23%), Positives = 162/412 (39%), Gaps = 53/412 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + G+K+ + IL A L+E + N+ D+ + L LG+ V + +
Sbjct: 12 LSGEVVISGAKNAALPILFAALLAEEPVEIANVPKLRDIDTTMELLSRLGVKVSRRNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V +V F + +++ A++ A G G L G
Sbjct: 70 -----VHIDASDVNEFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCA 116

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ +VGL+QLGA + D V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHIVGLEQLGATITL----DEGYVKASVDGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPKNA 248
AA LA G +I+ P +E T + G K + + I+G ++ +
Sbjct: 172 AATLAEGTT---VIENAAAREPEIEDTAAFLNALGAKISGAGTAT-ITIEGVERLGGGYHE 227

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
V D FL AA++GG + C T + LE GA V E +++
Sbjct: 228 VV-ADRIETGTFLVAAAVSGGKIM---CRNTKPELMEAVLAKLEEAGALVETGEDWISLD 283

Query: 309 GPPREPFGFRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
RE LKA+++ P D+ +++ L A G I + R
Sbjct: 284 MTERE-----LKAVNIRTAPHGPFPTDMQAQFSLNLMAGKTGIITETIF-----ENRF 332

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRMAMAFSLA 413
+ I EL ++GA E + I E L+ V A D + +A S+A
Sbjct: 333 MHI-PELIRMGAAHEVEGNTVICGDTGLSGAQVMATDLRASASLVIAGSIA 383

>ref|ZP_08117728.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium xylanolyticum LX-11]
gb|EGB24236.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermoanaerobacterium xylanolyticum LX-11]
Length = 416

Score = 40.8 bits (94), Expect = 0.44, Method: Compositional matrix adjust.
Identities = 93/408 (22%), Positives = 159/408 (38%), Gaps = 44/408 (10%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ GTV++ G+K+ + IL A L++ + +DNL + D+ + ++ LG +
Sbjct: 12 LKGTVEISGAKNSAVAILPAALLADTPSSIDNLPDINDIELLSKMIQYLGGKTIKKEHEI 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPI 134
G P + +++ A L A+ + A + G + RPI
Sbjct: 72 TIDPEGINSFCPPHELASQMR-----ASYYLIGALLSRFKEAAIAMPGGCNIGVRPI 123

Query: 135 GDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194
+ G + LGA G +RV L G + +S L++AA A
Sbjct: 124 DQHIKGFALGAKTTIEHGI----IRVKA-DKLVGNHIYFD-VVSVGATINLMLAACKAE 177

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYSKPKNAYVEGDA 254

G I++ P+V + G + + + D I G K ++ +
Sbjct: 178 GTT---ILENCAKEPHVVDVANFLNAMGANIKGAGT-DTIKIIGVDKLHGCRHTVIPDQI 233
Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGPPRE 313
+ +Y +A AA T G V V+G L+ + K +E MG K+ + + VT R
Sbjct: 234 EAGTYMVAAAA-THGDVIVKGIIPKHLESIIAKMSE----MGVKIEEYDEELRVTTDGR- 287
Query: 314 PFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI-RDVASWRVKETERMVAIR 368
LK +D+ P D+ +AV+ ADG + I +V R K +
Sbjct: 288 -----LKRVDIKTQPYPGFPTDMQQLMAVLLALADGVSVITENVYEGRFKYLD----- 335
Query: 369 TELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLAACA 416
EL K+G + + +I +KL + T D R A +A A
Sbjct: 336 -ELKKMGVNAKVEGRIAVIEGTQKLTGAPL-TATDLRAGAAMVIAGLA 381

>ref|ZP_06026389.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
periodonticum ATCC 33693]
gb|EFE87098.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
periodonticum ATCC 33693]
Length = 423

Score = 40.8 bits (94), Expect = 0.44, Method: Compositional matrix adjust.
Identities = 69/286 (24%), Positives = 121/286 (42%), Gaps = 24/286 (8%)

Query: 14 EISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DKA 72
+I+G +K+ GSK+ + I++ + +GT ++ N+ + D+ ++ L +LGL VE D
Sbjct: 12 KIAGELKVDGSKNSTLPIMIAITLVEKGTYIILRNVPDLRDIRTLVALESGLGLEVEKLDAN 71
Query: 73 AKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
+ + + G G D +++ FL G+ V GG A +
Sbjct: 72 SYKIIINGLSGAEASYDLVKKMRASFLVMGMLAIEKRGKVALPGGCA-----IGA 122
Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 123 RPVDLHLKGFEALGAKINIEHGY----VEATTENGLVGGNIVLDFP-SVGATENIIMAAV 177
Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
A G I++ P +E + + G K + R I G +K + + +
Sbjct: 178 KAKGKT---ILENAAKEPEIEDLCNFLIKMGAKITGVGT-SRLEIDGVEKLTACEYTIIP 233
Query: 252 GDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MGAK
Sbjct: 234 DRIVAGTYIIA-SILFDGSIKVSIVPEHLSS---FLLKLEEMGAK 275

>ref|YP_258058.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
fluorescens Pf-5]
sp|Q4KI75.1|MURA_PSEF5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AA90214.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
fluorescens Pf-5]
Length = 421

Score = 40.8 bits (94), Expect = 0.44, Method: Compositional matrix adjust.
Identities = 94/402 (23%), Positives = 155/402 (38%), Gaps = 71/402 (17%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLS-----LS 66
+ G +++ G+K+ + IL L +G V NL + D+ M+ +G LS
Sbjct: 12 LDGEIRISGAKNSALPILAAATLLCDGPVTVANLPHLHDITTMIELFGRMGIEPVIDEKLS 71
Query: 67 VEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVL 123
VE D + +V P E K MR+ + + A G A L
Sbjct: 72 VEIDPRTIKTLVA-----PYELVK-----TMRASILVLGPMVARFGEAEVAL 113
Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSISS 180
G + RP+ + GL+ +GA +D ++ P GGL G ++S
Sbjct: 114 PGGCAIGSRPVDLHIRGLEAMGAVIDVEGGYIKAKAPE-----GGLRGANFFFD-TVSV 166

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 ++MAA LA G ++ P V + G K + + D I G +
 Sbjct: 167 TGTENIMMAAALARGR---SVLQNAAREPEVVDLANFLIAMGAKISGAGT-DTITIDGVE 222

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVT- 299
 + S + + +Y +A AA+TGG V V+ T L+ E L+ GA+VT
 Sbjct: 223 RLHSAIYKVMPPDRIETGTYLVA-AAVTGGRVKVKDTPDPTILEA---VLEKLKEAGAEVTT 278

Query: 300 ---WTETSVTVTGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD 352
 W E ++ P KA++V P D+ + A+G A+ +
 Sbjct: 279 GSDWIELNMHGKRP-----KAVNVRTAPYPAPFTDMAQFISLNAIAEGTGAVIE 328

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
 + E M EL ++GA ++ + I+T E L
 Sbjct: 329 T---IFENRFMHVY--ELHRMGAKIQVEGNTAIVTGTEILK 364

>ref|ZP_02663066.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
 enterica subsp. enterica serovar Schwarzengrund str.
 SL480]
 ref|YP_002116257.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
 enterica subsp. enterica serovar Schwarzengrund str.
 CVM19633]
 sp|B4TWF9.1|MURA_SALSV RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
 gb|ACF91522.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
 enterica subsp. enterica serovar Schwarzengrund str.
 CVM19633]
 gb|EDY28442.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
 enterica subsp. enterica serovar Schwarzengrund str.
 SL480]
 Length = 419

Score = 40.8 bits (94), Expect = 0.45, Method: Compositional matrix adjust.
 Identities = 100/421 (23%), Positives = 163/421 (38%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPKSGKSLSNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
 + G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
 Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERNGS-- 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
 V +V +F + +++ A+ A G G L G
 Sbjct: 70 -----VHIDASQVNVFCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGGCT 116

Query: 129 MRERPIGDLVVGKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
 + RP+ + GL+QLGA + G V+ + G L G + + +S ++
 Sbjct: 117 IGARPVDLHITGLEQLGATIKLEEGY---VKASVEGRLKGAHIVMD-KVSVGATVTIMC 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
 AA LA G II+ P + T + G K + DR I+G ++
 Sbjct: 172 AATLAEGTT---IIENAAAREPEIVDTANFLVTLGAKIAGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
 Y V D FL AAI+ G + +L D A+ L GA + E +++
 Sbjct: 226 YRVLPDRIETGTFLVAAAISRKILCRNAQPDTL--DAVLAK-LRDAGADIEVGEDWISL 282

Query: 308 TGPPREPFGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
 + P KA++V P D+ ++ L A G I + V E
 Sbjct: 283 DMHGKRP-----KAVNVRTAPHPAPFTDMAQFLLNLVAQGTGFITET---VFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIR 423
 M EL+++GA E + I E L+ + D R + + LA C TI
 Sbjct: 333 MHV--PELSRMGARAEIESNTVICHGVETLSGAQV-MATDLRASASLVLAGCIAEGTTIV 389

Query: 424 D 424
 D
 Sbjct: 390 D 390

>ref|YP_692280.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alcanivorax
borkumensis SK2]
sp|Q0VS40.1|MURA_ALCBS RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAL16008.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Alcanivorax
borkumensis SK2]
Length = 420

Score = 40.8 bits (94), Expect = 0.45, Method: Compositional matrix adjust.
Identities = 96/434 (22%), Positives = 176/434 (40%), Gaps = 62/434 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
++++ + + G +++ G+K+ + IL L++ V NL + +DV ++ L +G
Sbjct: 2 DKLIITGGQRLDGDIDIRISGAKNAALPILAAATLLADEPVTGPNLPHLQDVTTLIELLGRMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+ V D + VE ++ + +++ A++ G G
Sbjct: 62 VHVVIDD-----RMNVEVNATTIKELTAPYEL-VKTMRASILVLGPMVAHFVK 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
A+ L G + RP+ + GL+ +GAD++ G V + G L G ++ + +
Sbjct: 109 ASVSLPGGCAIGSRPVDIHLRGLEAMGADIEVTNGY----VNASVDGRLKGARIVMD-VV 163

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
+ L+MAA LA G +E P V + G K + + D I+G
Sbjct: 164 TVTGTENLMMAAALAEGETTYLE---NAAREPEVVDLADFINAMGGKISGAGT-DTITIEG 219

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTV----TVEGCGTTSLQGDVKFAEVL 294
++ + + + +Y +A AAITGG + TV G LQ LE
Sbjct: 220 VERLTGCHHQVIADRIETGTYLIA-AAITGGRIKTKDTPVGTLDVAVLK-----LEE 271

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGP-TA 349
GAK+T + + + R P KA+ + P D+ + L A+G T
Sbjct: 272 GAKITTGDDWIELDMQGRRP-----KAVSLRTAPYPAMPPTDMQAQFMALNLVAEGTGTI 325

Query: 350 IRDVASVRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN---VTAIDTYDDHRM 406
+ + R + E+ ++GA +E + I E+L V A D +
Sbjct: 326 VETIFENRFMHVQ-----EMNRMGADIEVQGNTAICRGVEQLTGAPVMATDLRASASL 378

Query: 407 AMAFSLAACAEVPV 420
+A +LAA E V
Sbjct: 379 VIA-ALAAASGETTV 391

>ref|YP_374487.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
luteolum DSM 273]
sp|Q3B5D7.1|MURA_PELLD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABB23444.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Chlorobium
luteolum DSM 273]
Length = 424

Score = 40.8 bits (94), Expect = 0.45, Method: Compositional matrix adjust.
Identities = 71/295 (24%), Positives = 121/295 (41%), Gaps = 39/295 (13%)

Query: 117 GNATYVLGDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIG-GLPGGKV 172
G+A L G RPI ++ +++LGA + F+ R+ G P V
Sbjct: 107 GHARVSLPGGCAFGPRPIDLHLMAMEKLGARITITETGFIDAVAEGGRLKGATIDFPVSSV 166

Query: 173 KLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
+G+ LMAA LA G II + P +E ++ G + + +
Sbjct: 167 GATGNA-----LMAAVLAEGTT---IIRNAAAEPEIEALCHFLQAMGADIRGTGTE 215

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVTEGCGTTSLQGDV-KFAEVL 291
I G + + + + D A LA AAITGG+VT+ G + ++ + KF++
Sbjct: 216 -LIHGCDSLRHVEFSNIF-DRIEAGTILAAAAITGGSVTIRGVIPSHMESVLQKFSDA- 272

Query: 292 EMMGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGP 347
G ++ T+ +V + R LKA D+ P D+ + A+G
Sbjct: 273 ---GCRITETDDTVILKSTGR-----LKATDITAEFFPAFPTDMQAQWMALMTQAEGT 322

Query: 348 TAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
+ I D ER I EL +LGA ++ + ++ P+ L+ T + + D
Sbjct: 323 SEITDHVYH-----ERFNHI-PELNRLGAHIDIEGNRAVVGHPQALSGETKVMSTD 371

>ref|YP_003703632.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Syntrophothermus
lipocalidus DSM 12680]
gb|ADI03067.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Syntrophothermus
lipocalidus DSM 12680]
Length = 415

Score = 40.8 bits (94), Expect = 0.46, Method: Compositional matrix adjust.
Identities = 76/298 (25%), Positives = 117/298 (39%), Gaps = 25/298 (8%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV--EADKA 72
+ G V++ G+K+ S I+ + + +G TV++N+ DV + G L+ LG V + D +
Sbjct: 13 LRGRVRISGAKNASLVIMAASVMIKGETVLENVPRIRDVEVLGILQHLGARVAWQEDNS 72

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+V + P E AK+ L + R G A L G + R
Sbjct: 73 LCISVPENIDVETPYELAKKLRSNLLGSLGRK-----GQARICLPGGCNIGSR 123

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPL 192
P+ + GL LGA+V G G L G +V L S ++M A L
Sbjct: 124 PMDLHLKGLSALGAEVKLEHGFVEAYT-----GNLSGTRVYLDFF-SVGATENIMMLAAL 177

Query: 193 ALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEG 252
G +E K P + + G K + + D I+G ++ + + +
Sbjct: 178 TPGQTYVENAAKE---PEIVDLANFLNAAGAKVRGAGT-DLIRIEGVKELRGTRYTVIP- 232

Query: 253 DASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 310
D A F+A A TGG V VE T L L+ GA + V V GP
Sbjct: 233 DRIEAGTFMAAAVATGGDVLVENVIPHTL---YSIMAKLQETGAVIRQVNGGVRVIGP 287

>ref|YP_003239506.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ammonifex
degensii KC4]
gb|ACX52656.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Ammonifex
degensii KC4]
Length = 417

Score = 40.8 bits (94), Expect = 0.46, Method: Compositional matrix adjust.
Identities = 94/373 (25%), Positives = 146/373 (39%), Gaps = 52/373 (13%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL-----GLSV 67
+ G +++ G+K+ IL L +G +V+ + DV M LR L G ++
Sbjct: 11 LKGIKIRVSGAKNAILPILCACLLCDGESVIHGVPLQGDVAVMSAVLRHLKVLCCRREGETL 70

Query: 68 EADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGV 127
+ D ++ +E+ EE+ + + + M L A G G
Sbjct: 71 KVDTS-----LQLEIEPEELTRMRASCLVMGP LLARF----GRVKIAAPGGC 115

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
+ RPI + GLK +GA + T+ V L G ++ L S L+
Sbjct: 116 NIGARPIDLHLKGLKAMGAKI-----TERAGFIVAEERLRGAEIHLDP-SVGATENLM 169

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK-YKSPK 246
MAA LA G II P + + R G + + + I+G K ++PK
Sbjct: 170 MAAVLAEGTT---IIGNAAKEPEIVDLQNFLNRAGARIRGAGT-STIRIEGVSKPLQAPK 225

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D A L AA+TGG V VE L+ L GA+V E +
Sbjct: 226 GHQVIPDRIEAGTHLIAAALTGGEVEVENVIPEHLE---PLIAKLREAGAEVEVGEDKIW 282

Query: 307 VTGPPREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAI-RDVASWR---V 358
V + RK LKA+DV P D+ + + A+G + + ++ R V
Sbjct: 283 V-----WRRKPLKAVDVRTMPYPGFPTDLQAPMCALLSVAEGTSVVTENIFENRFRHV 335

Query: 359 KETERMVA-IRTE 370
E +RM A IR E
Sbjct: 336 PELQRMGADIRIE 348

>ref|YP_001307565.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
gb|ABR32609.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
beijerinckii NCIMB 8052]
Length = 420

Score = 40.8 bits (94), Expect = 0.46, Method: Compositional matrix adjust.
Identities = 70/285 (24%), Positives = 109/285 (38%), Gaps = 31/285 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+IV++ +KE+ G V + +K+ I+ L ++DN EDV + L L
Sbjct: 2 EKIVVKGVKELRGEVNISCAKNSILPIIAATILCPEPIIIDNAPRLEDVEVICKLLSELN 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
V R + K VE DA EE+ MR + A+ G G
Sbjct: 62 CDVNISNVNDRITI---NTKNIVEMDANEEL-----MRKMRASFLIMGPMRLARFG 108

Query: 118 NATYVLGDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
L G + RPI + G K LGA+V +G VR I G ++ L
Sbjct: 109 YCKLSLPGGCNIGSRPIDLHLKGFKLGAEV--VIGHGFVEVRAKKI---VGNRIYLDFFP 163

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S ++M + A G II+ P + + + G K E + + + I
Sbjct: 164 -SVGATENIMMVSFVFAEGTT---IENAAEEPEIWDLAQFLNKMGAKEGA-GFGKITIT 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQ 282
G + K + D A F+ AAIT + + G L+
Sbjct: 219 GVKNLKGISYTPYIY-DRIEAGTFMIAAAITNSKIKINGVNEEHLR 262

>ref|ZP_01308292.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanobacter sp.
RED65]
gb|EAT11082.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Oceanobacter sp.
RED65]
Length = 423

Score = 40.8 bits (94), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 91/418 (21%), Positives = 173/418 (41%), Gaps = 76/418 (18%)

Query: 1 MAGAEIIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGAL 60
M +++++Q ++G +++ G+K+ + I+ L++ + NL + DV M+ L
Sbjct: 1 MPSMDKLIQGGYPLNGEIRISGAKNSALPIIAATLLADTPITIGNLPHLHDVTTMINLL 60

Query: 61 RTLGLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---- 116
T+G+ V G ++ +E +++ ++ + +++++ A++ G
Sbjct: 61 GTMGVDVI-----MGEEYSIEVDSNKIETYVAPYEL-VKTMRASILVLGPLLA 107

Query: 117 --GNATYVLGDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKL 174
G A L G + RP+ + GL+ +GA++ G V+ G L G + +
Sbjct: 108 RFGEAEVSLPGGCAIGSRPVDIHLSGLEAMGANIKVEDGY---VKATVDGRLKGAHIFM 163

Query: 175 SGSISSQYLSALLMAAPLALGDV-----EIEIIDK---LISI--PYVEMTLRLMERFG 222
+++ LLMAA LA G E E++D LIS+ +++ G
Sbjct: 164 D-TVTVTGTENLLMAAVLADGTTYLENAAREPEVVDLAECCLISMGAKITGHGTDVIKVEG 222

Query: 223 VKAHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTSLQ 282
V++ H +D V D FL AA TGG V ++ L+
Sbjct: 223 VESLHGGRYD-----VMPDRIETGTFLVAAAATGGKVLLKDTRADILE 265

Query: 283 GDVKFAEVLEMMGAKVTWTE--TSVTVTGPPREPFRGRKHLKAIDVNMNKMP----DVAMT 336
+ LE GA V E S+ +TG + LKA+ + P D+
Sbjct: 266 SVI---HKLEEAGAAVEVGEDWISLDMTG-----RQLKAVSLKTAPYPAFPTDMAQ 314

Query: 337 LAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
V+ + A+G ++ + R + ++ EL ++GA +E + CI +KL

Sbjct: 315 FLVMNVVAEGTASVTETIF-----ENRFMHVQ-ELARMGAHIELQNTCITRGGDKLK 366

>ref|ZP_00963330.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfitobacter
sp. NAS-14.1]
gb|EAP80074.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sulfitobacter
sp. NAS-14.1]
Length = 423

Score = 40.8 bits (94), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 90/381 (23%), Positives = 150/381 (39%), Gaps = 38/381 (9%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+ IV++ +SG + + G+K+ ++ LSE + N D+ M LR+LG
Sbjct: 2 DSIVVKGGGALSGQIPIAGAKNACLTLMPATLLSEEPLTLTNAPRLSDIRMTTELLRSLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V + + + + C G+ + V+ A + + A G+A L
Sbjct: 62 AEVTSMDQGQ-VLAMSCHGEINTRAEDIVRKMR-----ASNVLGPLLAREGHAQVSLP 115

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLS 184
G + RP+ GL +GA++D G + GG G V S
Sbjct: 116 GGCAIGARPMDIHTDGLALMGAEIDLDRGY----LHAKAQGGALKGAVIDFPFASVGATE 171

Query: 185 ALLMAAPLALGDVEIEIIDLKISIPYEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G I + I + LR M G + E D R I+G +
Sbjct: 172 NIMMAATLAKGTTVINNAAREPEIVDLADCLRAM---GAQIE-GDGSRIEIQGVDRLHG 227

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
+ V +Y LA A+ GG V + G L F E L+ G VT T+
Sbjct: 228 ATRVVTDRIELGTMYLA-PAMCGGEVELLGGRIDLLSA---FCEKLDAAGIDVTETDKG 283

Query: 305 VTVTGPPEPFGGRKH--LKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWRV 358
+ V R++ + A++V P D+ + + ADG + + + ++
Sbjct: 284 LKVA-----RRNGVINAVNVTTTEPFGPFTDLQAQMALLCTADGTSVLEE---KI 331

Query: 359 KETERMVAIRTELTKLGASVE 379
E M A EL ++GA +E
Sbjct: 332 FENRFMHA--PELIRMGADIE 350

>ref|ZP_01786781.1| outer-membrane lipoprotein carrier protein precursor [Haemophilus
influenzae R3021]
gb|EDJ90948.1| outer-membrane lipoprotein carrier protein precursor [Haemophilus
influenzae R3021]
Length = 46

Score = 40.8 bits (94), Expect = 0.47, Method: Composition-based stats.
Identities = 25/37 (67%), Positives = 30/37 (81%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTT 41
E+I L PI + GT+ LPGSKLSNR LLLAAL++GT
Sbjct: 2 EKITLAPISAVEGTINLPGSKLSNRALLAALAKGT 38

>ref|YP_808563.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus
lactis subsp. cremoris SK11]
gb|ABJ72141.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus
lactis subsp. cremoris SK11]
Length = 426

Score = 40.8 bits (94), Expect = 0.47, Method: Compositional matrix adjust.
Identities = 99/446 (22%), Positives = 168/446 (37%), Gaps = 62/446 (13%)

Query: 14 EISGTVKLPKSGSKLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
++ G V++ G+K+ +L L SEG V+ N DV M + LG S+ D+
Sbjct: 12 KLQGEVEIEGAKNAVLPLLAATLLASEGEVVLTNAPILSDVFMNNLVDHLGTSISFDQE 71

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
AK+ ++ + E V MR+ + + A G A + G +
Sbjct: 72 AKK-IIAKANSEIKTTAPYEYVS-----KMRASIVVMGPILARNGQARVSMPGGCSI 122

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYL----- 183
RPI + G +Q+GA + G + KL G + YL
Sbjct: 123 GSRPIDLHLRGFEQMGATI-----TQNAGYIEAKADKLKG--AHYLDFPSVG 168

Query: 184 --SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
L++AA LA G + ++ P + L+ + G + + + D IKG +K
Sbjct: 169 ATQNLILAATLAEG---VTTLENAAREPEIVDLANLLNKMGANVKGAGT-DTIIIKGVEK 224

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
K++ V+ D A F+ AA+T G V ++ + + + L MG T
Sbjct: 225 MHGAKHSVVQ-DRIEAGTFMVAAAMTQGDVLIKDAIS---EHNRLISKLSEMGVNFQTQE 280

Query: 302 ETSVTVTGPPREPFGGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTA-IRDVASW 356
ET + V GP + LKA V P D+ +A A G + + V
Sbjct: 281 ETGLRVVGPVK-----LKATSVKTLPHPGFPTDMQSQMAAAQAIAAGESVMVETVFEN 333

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
R + E E+ ++G V+ + +I L A+ + D A L A
Sbjct: 334 RFQHLE-----EMRRMGLEVDITRNTALIQGNSNLQGAAVKSTDLRASAAILLGLVA 386

Query: 417 EVPVTIRDPGCTRKTFFDYFDVLSTF 442
+ T+R + + + + L
Sbjct: 387 KGQTTVRRLSHLDRGYKFKHEKLKAL 412

>ref|ZP_06306534.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase
[Cylindrospermopsis raciborskii CS-505]
gb|EFA71323.1| UDP-N-acetylglucosamine 1- carboxyvinyltransferase
[Cylindrospermopsis raciborskii CS-505]
Length = 443

Score = 40.8 bits (94), Expect = 0.48, Method: Compositional matrix adjust.
Identities = 91/373 (24%), Positives = 142/373 (38%), Gaps = 42/373 (11%)

Query: 15 ISGTVKLPKSKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+ G V++ G+K+ + I+ A L G + N+ DV M L LGLSVE K
Sbjct: 35 LEGNVRISGAKNSALVIMAGALLCSGDCRISNVPLADVESMGQVLTALGLSVERHKDTL 94

Query: 74 ---KRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
R + K P E + F I R A + GG A +
Sbjct: 95 NINARDITT---SKAPYELVTQLRASFFAIGPILARLGVAQMPLPGGCA-----IG 142

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ V GL+ +GAD++ G C G L G ++ L + S L+MAA
Sbjct: 143 ARPVDLHVRGLQAMGADMEIEHGI-CHAQVAGNNGRLQGARIYLD-TPSVGATETLMMAA 200

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G+ II+ P V G K + + + I G K S + + +
Sbjct: 201 TLADGET---IIENAAREPEVVDLANFCNSMGAKIQGAGTGT-ITIVGVDKLHSTEYSII 256

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D A FL AAIT + + + L + L+ +G + T P
Sbjct: 257 P-DRIEAGTFLIAAAITHSELLSPVKSEHL---IPVIAKLKDIGVSIFQEGTDCLRVKP 312

Query: 311 PREPFGGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
++ LKA +++ P D+ + ADG + I + E ++
Sbjct: 313 AQK-----LKATNIDTLPHPGFPTDMQAQFMALLSIADGDSIINESV-----FENRLS 360

Query: 367 IRTELTKLGASVE 379
+EL +LGA +
Sbjct: 361 HASELNRLGAEIR 373

>ref|ZP_05136197.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stenotrophomonas
sp. SKA14]
gb|EED40258.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Stenotrophomonas
sp. SKA14]
Length = 423

Score = 40.4 bits (93), Expect = 0.48, Method: Compositional matrix adjust.

Identities = 94/396 (23%), Positives = 159/396 (40%), Gaps = 56/396 (14%)

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Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
          + G V + G+K+   IL   L++   + N+ + DV   + L LG V D+
Sbjct: 12  LHGEVSI SGAKNAVLPI LCATLLADAPVEITNPHLHDVVTTVKLLGELGAKVTIDQGT L 71

Query: 74  --KRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDG 125
          A+VV      PV      +L      +++++ A++   G      G A   L G
Sbjct: 72  SRGSAIVVD---PRPVNQHVAPYEL-----VKTMRASILVLGPLLARFGAAEVSLPG 120

Query: 126 VPRMRERPIGDLVVGLKQLGADV---DCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQY 182
          + RP+   + GL+ LGA++   + F+           R+ G G       V ++G+
Sbjct: 121 GCAIGSRPVDQHIKGLQALGAEIVVENGFIKASAK--RLKG-GHFTFDMVSVTGT----- 172

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
          +LM A LA G   I+D   P V       + G K E   + R I+G ++
Sbjct: 173 -ENVLMGAVLAEGTT---ILDNCAMEPEVTDLAHCLIALGAKIEGLGTA-RLVIEGVERL 227

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
          ++   + D       FL AA+TGG VTV       ++ D   +++++E GAK+ T+
Sbjct: 228 SGGREHVL P-DRIETGTFLVAAAMTGGKVTVNRRPNM--DAVLSKLVE-AGAKIETTD 283

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRV 358
          S+T+   + P       KA+++   P   D+       + ADG I +   +
Sbjct: 284 DSITLDMQGR P-----KAVNLTTPAPFTDMQAQFMALNCVADGVGVINET----I 333

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
          E M       EL +LGA ++       I   E+L+
Sbjct: 334 FENRFMHV--NELLRLGADIQVEGHTAIARGHERLS 367

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>ref|ZP_01751008.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp.
  CCS2]
gb|EBA12682.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseobacter sp.
  CCS2]
Length = 421

```

Score = 40.4 bits (93), Expect = 0.48, Method: Compositional matrix adjust.
Identities = 95/377 (25%), Positives = 149/377 (39%), Gaps = 51/377 (13%)

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Query: 15  ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
          ++G + + G+K+ + ++   LSE   + N   D+ M   L++LG+ V + + K
Sbjct: 12  LNGQIAIAGAKNAALTLMPATLLSSEPLTLTNAPRLSDIATMTALLQSLGVEVTSMQDGK 71

Query: 75  RAVV-----VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
          V+           + +       L LG   + R   A V+ GG A       +
Sbjct: 72  VQVLSSHAMTSTTADYEIVRKMRASNLVLGP--LLARHHRVSVSLPGGCA-----I 120

Query: 130 RERPIGDLVVGLKQLGADV---DCFLGTD CPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
          RP+   V L+ +GA++   D+L   P       GGL G KV L + S       +
Sbjct: 121 GARPMDIHVTALEAMGAEIELKDGYLHAKAP-----GGLKGAKVPLRFA-SVGATENV 172

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
          LMAA LA G   IE   + I +   LR M   G + E +       I+G   +
Sbjct: 173 LMAATLAKGTTVIENAREPEIVDLAKCLRSM---GAQIE-GEGTATVTIQVDHLGAAT 228

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
          + V       +Y LA       GG V   G G   L G   F E L+ G VT T+ +
Sbjct: 229 HPVVTDRIELGTYMLA-PVFAGGEVECLG-GRLDLVG--SFVEKLDAAAGVDVTETKDGLK 284

Query: 307 VTGPPREPFGRKHLKAIDVNMNKM P---DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
          V   +   R   KA+DV   P   D+   + +   ADG + + +   ++ E
Sbjct: 285 V----KRRTDRA--KAVDVTTEVFPGFPTDLQAQMMAMLC TADGTSVLEE----KIFENR 334

Query: 363 RMVAIRTELTKLGASVE 379
          M A   EL ++GA +E
Sbjct: 335 FMHA--PELIRMGADIE 349

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>ref|YP_004129573.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Taylorella
  equigenitalis MCE9]

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gb|ADU91430.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Taylorella equigenitalis MCE9]
Length = 417

Score = 40.4 bits (93), Expect = 0.49, Method: Compositional matrix adjust.
Identities = 86/382 (22%), Positives = 154/382 (40%), Gaps = 62/382 (16%)

Query: 13 KEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K++ GT+K+ G+K+ + IL + L+ ++ N+ D+ + L+ LG+ V +
Sbjct: 10 KKLEGTIKVSAGAKNAALPILCASLLTSEPVLRLNPVELNDIKTSIRVLQQLGVKVRWIEP 69

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
+E +E++ F + ++++ A++ G G+A L G
Sbjct: 70 E-----VLELQADEIKSFEPYEL-VKTMRASILVLGPLLARFGHAKVSLPGG 116

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLG-----TDCPPVRVNGIGGLPGGKVKLSGSISSQ 181
+ +RP+ + GLK L AD+D G DC L G +K + ++
Sbjct: 117 CAIGQRPVDQHIKGLKLLSADIDVEHGFVVAKADC-----LKGASIK-TDMVTVG 165

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVK-AEHSDSWDRFYIKGGQ 240
LMA+ LA G I++ P V +++ G K + H S R I+G +
Sbjct: 166 GTEQFLMASVLSAGTT---ILENAAQEPEVYDLAQMLNSMGAKISGHGTS--RITIEGVE 220

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K + + D A FL TGG + + ++ V E L G +++
Sbjct: 221 KLHGTEYKIMP-DRIEAGTFLCCVGATGGYLELTDVLPHTM---VSIIEKLTEAGLEIST 276

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRDVASW 356
E + + R KA+ + + P D+ L + ADG + I +
Sbjct: 277 GEDWIKASMSCRP-----KAVSIITKEYPGFPTDMAQQLMALNSIADGESTIDE---- 325

Query: 357 RVKETERMVAIRTELTKLGASV 378
R+ E M EL +LGA +
Sbjct: 326 RIFENRFMHV--PELNRLGADI 345

>ref|YP_004111588.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Desulfurispirillum indicum S5]
gb|ADU65032.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Desulfurispirillum indicum S5]
Length = 418

Score = 40.4 bits (93), Expect = 0.50, Method: Compositional matrix adjust.
Identities = 64/268 (23%), Positives = 114/268 (42%), Gaps = 35/268 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + I+ + L+E ++N+ D++ + L+ +G + E D+A
Sbjct: 12 LQGHVNISGAKNAALPIAASVLTEQPMKINNVPRLRDIYTISKILQHMGATCELDEATN 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQ-----LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPR 128
V G +E E V+ LFLG + R A V+ GG A
Sbjct: 72 -CFHVHRNGMNRLEAPYELVKTMRASILFLGP--MVARYHEARVSLPGGCA----- 119

Query: 129 MRERPIGDLVVGLKQLGAD---VDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + L+++G + VD ++ C +R G + +++
Sbjct: 120 IGARPVNLHLDALRKMVGVELDIVDGYIIARCEELR-----GAAISFD-TVTVTGTEEN 170

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G ++ P V R + G E + + D I G ++ +
Sbjct: 171 IMMAATLAKGKT---VLKNAAKEPEVDLARCLTSMGAHIEGAGT-DTITIHGVEELRGT 226

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTV 273
+ + V D A F+A AAIT G VT+
Sbjct: 227 EYS-VMPDRIEAGTFMAAAAITAGHVTL 253

>gb|EGC82619.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Anaerococcus prevotii ACS-065-V-Coll3]
Length = 424

Score = 40.4 bits (93), Expect = 0.51, Method: Compositional matrix adjust.

Identities = 92/404 (22%), Positives = 161/404 (39%), Gaps = 55/404 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E +V+ + G V++ G+K+ + IL L ++D + +DV M+ L+ LG
Sbjct: 4 EILVINSNGPLKGEVEISGAKNSALPILAAACVLGTEEIIILDGVPELKDVEIMVEVLKHLG 63

Query: 65 LSVEADKAAKRAVVVGCGG----KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNAT 120
VE + ++ + G + P E + F+ + R A A GG
Sbjct: 64 SKVE--YIGRNSLSIDSSGINTCETPYELMDKMRASFVVMGPLLSRFSNAYTKAPGG--- 118

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
+ RPI + G LGA+ + + + GL G ++ L S
Sbjct: 119 -----CNIGSRPIDLHIKGFNALGAETRI----NDEEIAIEAKEGLKGNEIYLDFF-SV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA LA G+ II+ P + + + G K + + + I G +
Sbjct: 168 GATQNMMAATLADGET---IENAAKEPEIVDLASFLSKMGAKIKGAGT-STITINGVE 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVK--FAEVLEMMGAKV 298
K ++ + +A+Y LA AA+T G V + T + ++ A+++E +GA V
Sbjct: 224 KLTGTRHTIIPDRIEAAATYMLA-AAMTRGNVKI---TNVIGSHIRPVIKLE-IGADV 277

Query: 299 TWTETS--VTVTGPPREFPGRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRD 352
E + V P R LK+ ++ P DV + +DG +
Sbjct: 278 KEIEEEDIYVNAPNR-----LKSTNIQTLPPYGFPTDVQAQFMALLTSLDGE----- 326

Query: 353 VASWRVKET--ERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
R++ET E EL+K+GA + + I EKL+
Sbjct: 327 ----RIQETVFENRFMHVAELSKMGAVIATSGNRATIAGVEKLH 366

>ref|ZP_08139584.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas sp.
TJI-51]
gb|EGB99119.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas sp.
TJI-51]
Length = 421

Score = 40.4 bits (93), Expect = 0.51, Method: Compositional matrix adjust.
Identities = 67/301 (22%), Positives = 123/301 (40%), Gaps = 41/301 (13%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L++G V NL + D+ M+ +G+ D+
Sbjct: 12 LDGEIRISGAKNAALPILAAATLLADGPVTVGNLPHLDITTMIELFGRMGIEPVIDE--- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K VE ++ + + +++++ A++ G G A L G
Sbjct: 69 -----KLAVEIDPRTIKTLVAPYEL-VKTMRASILVLGPMVARFGEAEVALPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ +GA ++ ++ P GGL G ++S
Sbjct: 119 IGSRPVDLHIRGLEAMGAKIEVEAGYIKAKAPE-----GGLRGAHFFFD-TVSVTGTEN 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G ++ P V + G K + + + D I G ++ S
Sbjct: 172 IMMAAALAKGR---SVLQNAAREPEVVDLANFINAMGGKVQAGT-DTITIDGVERLASA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT----WT 301
+ + +Y +A AA+TGG V V+ T L+ E L+ GA++T W
Sbjct: 228 SYRVMPDRIETGYTLVA-AAVTGGRVKVKDTPITLEA---VLEKLKEAGAEITTGEDWI 283

Query: 302 E 302
E
Sbjct: 284 E 284

>ref|YP_003201498.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Nakamurella
multipartita DSM 44233]
gb|ACV78509.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Nakamurella
multipartita DSM 44233]
Length = 421

Score = 40.4 bits (93), Expect = 0.51, Method: Compositional matrix adjust.
Identities = 100/404 (24%), Positives = 149/404 (36%), Gaps = 75/404 (18%)

```
Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      +SGTV++ G+K+   +++ A L+EGTT + N   DV M   LR GL E   A
Sbjct: 10 SRLSGTVRVVAGAKNSVLKLMMAAALLAEGTTEISNCPEILDVPLMADVLR--GLGAEVALA 67

Query: 73 AKRAVV-----VCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP 127
      +       +       FP               LG + R   A V   GG+A
Sbjct: 68 GDTVTTITTPAELSFHADFPVAVGRLRASVCVLGP--LMGRCRAQVALPGGDA----- 117

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI-----SSQ 181
      + RP+       GL+ +GA +   G               + G   +L G++   S
Sbjct: 118 -IGSRPLDMHQSGLRAMGASMSIEHGK-----VVGSAELHGLIGLDFPSVG 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHS-----DSWDRF 234
      +LMAA LA G       +ID   P +   RL+++ G + E +       D DR
Sbjct: 165 ATENILMAAVLARGTT---VIDNAAREPEIIDLARLLQQMGAQIEGAGTATITIDGVDR 221

Query: 235 YIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTEGCGTTSLQGDVKFAEVLEMM 294
      +       P +       GD       +   AAIT G+V VEG   L   +   E L
Sbjct: 222 H-----PTSHRTVGDRVVGWTWAYAAAITQGSVRVEGVDPALFTAPL---ERLSSA 269

Query: 295 GAKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMMPDVAMTLAVVALFADGPTAIRDVA 354
      GA++       +V VT   R       KA+D       P       L   +AL       A+ VA
Sbjct: 270 GAQIETEPDAVRVTMAQRA-----KAVDFITMPYPGFPTDLQPMAL-----ALAAVA 316

Query: 355 SWRVKETERMVAIR----TELTKLGASVEEGPDYCIITPPEKLN 394
      TE +   R       EL ++GA       +   +   E+L+
Sbjct: 317 DGHSLITENVFEARFRFVDELIRMGADARTDGHASLRGREQLS 360
```

>ref|ZP_06596455.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
breve DSM 20213]
gb|EFE88418.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bifidobacterium
breve DSM 20213]
Length = 441

Score = 40.4 bits (93), Expect = 0.51, Method: Compositional matrix adjust.
Identities = 51/194 (26%), Positives = 84/194 (43%), Gaps = 22/194 (11%)

```
Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K ++GT+K+ G+K+   ++ ++ A L+ G +V+ N+   DVH +   LR G   V+ D
Sbjct: 15 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVVDLLRLHG--VDVDVN 72

Query: 73 AKRAVVVCGGKFPVEDAKEEVQL-----FLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
      ++ +V       + D +   L       L +   + R   A + A GG A
Sbjct: 73 GEKGIVTIDASHVQLADVADVDLTLGSSSRIPILFSGPLVHRLGEAFIPALGGCA----- 126

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
      + RPI   +   L++LGA VD       + +       GL G K+ L   S
Sbjct: 127 ---IGGRPIDFHLETLRKLGATVD---KEHKDGIHITAPNGLHGAKIHLPYP-SVGATEQ 179

Query: 186 LLMAAPLALGDVEI 199
      L+AA LA G   E+
Sbjct: 180 TLLAAVLAEGKTEL 193
```

>dbj|BAE61979.1| unnamed protein product [Aspergillus oryzae]
Length = 749

Score = 40.4 bits (93), Expect = 0.51, Method: Compositional matrix adjust.
Identities = 73/299 (24%), Positives = 118/299 (39%), Gaps = 28/299 (9%)

```
Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      ++++G V++ GSK+   ++   L+ G + +   L   D+ M   L+ LG V
Sbjct: 11 RDVTGNVRVSGSKNAGLPLMAATLLAPGPSTLHGLPPVSDIKNMGSIQLYLQYLGADVSQVSD 70

Query: 73 AKRAVVVCGGKGF---PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRM 129
      +F       + D+       LFLG               + A   G+A       G   +
Sbjct: 71 NFTIDTDTVTSRFVPAQLTDSLRSILFLG-----PLLARFGHACLSPFGGCSI 119
```

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RP+ + + GL++LGA C TD + + L G + + + ++ L+MA
Sbjct: 120 GNRPVEEHINGLRKLGA---CITVTDT-YIEAHA-SQLQGATIDMQTPSVTGTMN-LIMA 173

Query: 190 APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK-SPKNA 248
A LA G + I P V + + GV H D+ I G SP
Sbjct: 174 ACLARG---VTHIHNAAREPEVGDNLINFLVLMGVDI-HGAGTDQLVIHGCHSTPLSPCQY 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTTTETSSTV 307
V D FL AI G +TV C + V + L+ +GA+V ++ SVTV
Sbjct: 230 GVMEDRIEVGTFILILGAICGNPLTVYPCHP---EQHVMLIKNLKAVGARVDISDDSVTV 285

>ref|ZP_05736819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Granulicatella
adiacens ATCC 49175]
gb|EEW38218.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Granulicatella
adiacens ATCC 49175]
Length = 438

Score = 40.4 bits (93), Expect = 0.52, Method: Compositional matrix adjust.
Identities = 85/363 (23%), Positives = 144/363 (39%), Gaps = 47/363 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSE-GTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ GTVK+ G+K+ IL + L++ G T + N+ N DVH ML L +L + D+
Sbjct: 13 LQGTVKVEGAKNVLPILAASILADKGVTHLTNPVNLSDVHMMLNLVGLSLNVLSTFDEEE 72

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVPRMR 130
K A+ + A E V MR+ + + A G+A + G +
Sbjct: 73 K-AITLNATKDITTTAAFEYVS-----KMRASIVVMGPLLARFGHARVAMPGGCAIG 123

Query: 131 ERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALL 187
RPI + G + +GA + + ++ L G ++ L S ++
Sbjct: 124 SRPIDLHLKGFEAMGATIVQTEGYIEAHADE-----LHGARIYLDFF-SVGATQNM 174

Query: 188 MAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKN 247
MAA LA G +E + + P + ++ + G K + + + I+G ++ +
Sbjct: 175 MAATLAKGTTTHLENVARE---PEIVDLANILNKMGAIVGAGT-ENMRIEGVERLDGTIH 230

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTTTETSSTV 306
+ + D A F+ AA+T G V +E Q + K E MG + E +
Sbjct: 231 SIIP-DRIEAGTFMVAADVTKGNVFIEDAIAEHNQPLISKLGE---MGVQFIEEDGIR 285

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRD-VASWRVKET 361
V GP LK DV P D+ + + L A G + + + V R
Sbjct: 286 VIGPDS-----LKPTDVKTLPHPGFPTDMQAQMTIAQLLATGTSTMTETVFENRFNHL 338

Query: 362 ERM 364
E M
Sbjct: 339 EEM 341

>ref|YP_001697682.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
sphaericus C3-41]
gb|ACA39552.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Lysinibacillus
sphaericus C3-41]
Length = 187

Score = 40.4 bits (93), Expect = 0.52, Method: Compositional matrix adjust.
Identities = 47/205 (22%), Positives = 88/205 (42%), Gaps = 30/205 (14%)

Query: 33 LLAALSEGTTTVDNLLNSEDVHYMLGALRTLGLSVEADKAAKRAVVVGCGGKFPVEDAKE 92
+ +++ GTT V+ L ED + + LG+ +E + + + + P D+ +
Sbjct: 1 MFGSIATGTTTVEGFLLEDCLSTIDCFQKLGHVHIEVEGTSVKI-----ESPGMDSWQ 53

Query: 93 EVQ--LFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC 150
E L+ GN+G R + + AG + V+ G + +RP+ ++ L+Q+GA +
Sbjct: 54 EPTEVLYTGNSTTTTLMGLIL--AGSSVHSVMTGDASIGKRPMRVIDPLRQMGAHITG 111

Query: 151 FLGTDCPPVRVNGIGGLPGGKVKLSG-----SISSQYLSALLMAAPLALGDVEIEIIDK 204
P+ + G KL S+Q SA+L+A A G + +

Sbjct: 112 RADGQYTPLAIQG-----TKLQAEYNNMPVASAQVKSAILLAGLRAEGTTIVR--ET 161

Query: 205 LISIPYVEMTLRLMERFGVKAHSD 229

+S + E R++ +FG E D

Sbjct: 162 EVSRDHTE---RMLRQFGADVEVKD 183

>ref|NP_760986.1| EPSP synthase [Vibrio vulnificus CMCP6]
Length = 44

Score = 40.4 bits (93), Expect = 0.52, Method: Composition-based stats.
Identities = 17/26 (65%), Positives = 22/26 (84%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNR 30

E + LQPIK+++G V LPGSKS+SNR

Sbjct: 2 ESLTLQPIKKVNGEVNLPGSKSVSNR 27

>ref|ZP_04760892.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
delafieldii 2AN]
gb|EER62209.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Acidovorax
delafieldii 2AN]
Length = 426

Score = 40.4 bits (93), Expect = 0.53, Method: Compositional matrix adjust.
Identities = 70/282 (24%), Positives = 119/282 (42%), Gaps = 40/282 (14%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

+++++ + + G V + G+K+ + L A L+ + N+ +DV ML +R +G

Sbjct: 2 DKLLIRGGRALHGEVLVSGAKNAALPELCAALLTADPVTLLNVPRLQDVSTMLKLIRNMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118

V A++A V + E E V +++ A+V A G G

Sbjct: 62 --VAAERADDGTVRIDASALSTPEAPYELV-----KTMRASVLALGPLLARFGE 108

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS- 177

AT L G + RP+ + G+ +GA++ G I LP G +L G+

Sbjct: 109 ATVSLPGGCAIGSRPVDQHIKMAAMGAIEIVVEHYM-----IAKLPTGWTRLKGAR 160

Query: 178 ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAH-HSDSW 231

I++ ++ LMAA LA G+ +++ P + ++ G K E H S

Sbjct: 161 ITTDMVTVTGTENFLMAAALAEGET---VLENAAQEPEISDLAEMLIAMGAKIEGHGTS- 216

Query: 232 DRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTV 273

R I+G +K + V D A FL A TGG V +

Sbjct: 217 -RIRIQGVEKLHGCTHRVV-ADRIEAGTFLCAVAATGGDVVL 256

>ref|YP_001232776.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
uraniireducens Rf4]
sp|A5G8T5.1|MURA_GEOUR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABQ28203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacter
uraniireducens Rf4]
Length = 417

Score = 40.4 bits (93), Expect = 0.53, Method: Compositional matrix adjust.
Identities = 86/400 (21%), Positives = 159/400 (39%), Gaps = 51/400 (12%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

+++++ K+++G V + GSK+ S I + L+ + N+ D++ + L LG

Sbjct: 2 DKLIKGGKKLAGEVTVSGSKNASLPFISTILAPAEHEISNVFPLRDINTTIKVLQLG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118

V+ + + G V++ + +L ++++ A+V G G

Sbjct: 62 AKVDGNGNIVKIDTTG-----VDNFEATYEL-----VKTMRASVLVLGPLLARFGK 107

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178

A L G + RPI + GL +GAD++ G + L G ++ S

Sbjct: 108 ARVSLPGGCAIGARPINLHLKGLAAMGADINLTHGYVEAKAK-----QLKGARINFVST 162

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
L+MAA A G+ I++ P + ++ + G + + + D I G

Sbjct: 163 VGGT-EHLMMAAATAKGET---ILENAAREPEIVDLANVLTKMGARIDGAGT-DTIRISG 217

Query: 239 GQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKV 298
K P + V D A F+ AAITGG + V L V F L+ G ++

Sbjct: 218 -VKELGPVSHRVMPDRIEAGTFMIAAAITGGDIKVRNMQLHLDALV-FK--LQDAGVEI 273

Query: 299 TWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRDVA 354
+ V V GP + +K +++ P D+ + AD + I

Sbjct: 274 INKDNVVRVKGPP-----RKIKGVNIKTRPYPGFPTDMQAQFMALMCLADSASVI---- 322

Query: 355 SWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
S + E M +EL + GA + + + +KL+

Sbjct: 323 SENIFENRFMHV--SELMRFGADITTEGNTATVKGVKKLS 360

>ref|ZP_03244064.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Helicobacter pylori
HPKX_438_CA4C1]
Length = 146

Score = 40.4 bits (93), Expect = 0.54, Method: Composition-based stats.
Identities = 34/134 (25%), Positives = 61/134 (45%), Gaps = 5/134 (3%)

Query: 250 VEGDASSASYFLAGAAITGGT-VTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS--VT 306
+ D SSA +F AIT + + ++ + ++ E L+ MGA + + S +

Sbjct: 15 IANDPSSAFFFALACAITPKSRLLLLKNVLLNPTR--IEAFEALKMGASIEYAIQSKDLE 72

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ G +ID N+ + D L++ LFA G + +R+ R KE++R+ A

Sbjct: 73 IIGDIYIEHAPLKAISIDQNIASLIDEIPALSIAMLFAGKSMVRNAKDLRAKESDRIKA 132

Query: 367 IRTELTKLGASVEE 380
+ + LG EE

Sbjct: 133 VISNFKALGIECEE 146

>ref|ZP_05138598.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
gb|EEE40423.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Prochlorococcus
marinus str. MIT 9202]
Length = 437

Score = 40.4 bits (93), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 86/372 (23%), Positives = 150/372 (40%), Gaps = 37/372 (9%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++ G+K+ + ++ + LS+G + N+ DV M L T+G+ +++

Sbjct: 26 KFLKGNIEISGAKNSALVLMASILSKGEINLFNVPPQISDVSIMSKLLITMGIDIKSN-- 83

Query: 73 AKRAVVVGCGKFPVEDAKEEVQLF--LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A + P +D LF L NA + A G A L G +

Sbjct: 84 ANHLTINTKEITIPPQD-----LFFDLCNALRVSFFCIGPILARFGKAKIPLPGGCSIG 137

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + + LK+LG + +N L G + S LLMAA

Sbjct: 138 SRPIDEHIDSLKKGIVIFQ-YRNNYVIKVINPQKRLLGSSINFCKK-SVGATETLLMAA 195

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G I++ P + ++ G + + + S + I+G + K +

Sbjct: 196 SLAKGKT---ILNNAEEPEIVDLANMLNLMGARIKGAGS-ECITIEGESLKGCDYTVI 251

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D A FL AAIT T+++ C L+ + LE+ G K ++ + +

Sbjct: 252 P-DRIEAGTFLLAAAITRSTISLFPCEPNHLKALI---NKLELCGCKFEYSNFCLKII-- 305

Query: 311 PREPFGGRKHLKAIDVNMNKMPPDVAMTLA--VVALFA--DGPTAIRDVASWRVKETERMVA 366
P + LK++D+ PD L +AL A +G + I++ RM

Sbjct: 306 PNQI-----LKSVDMTTGPFPDFPTDLQAPFMALMATNGISKIKETVF-----ENRMHH 355

Query: 367 IRTELTKLGASV 378
++ EL +GA +
Sbjct: 356 VK-ELNHMGAKI 366

>ref|ZP_03461559.1| hypothetical protein BACPEC_00616 [Bacteroides pectinophilus ATCC 43243]
gb|EEC58484.1| hypothetical protein BACPEC_00616 [Bacteroides pectinophilus ATCC 43243]
Length = 430

Score = 40.4 bits (93), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 87/389 (22%), Positives = 159/389 (40%), Gaps = 58/389 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E+ +++ + G V + G+K+ + IL A +++ T ++N+ N D +L +G
Sbjct: 2 EQYIIKGGMPLCGDVSIGGAKNAALGILAAAIMADETVTIENVPNVRDTRALLQTFEGIG 61

Query: 65 L-----SVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG 116
SV+ + + V+V D+ ++++ A L A+
Sbjct: 62 AKVKYVYNSVQINGQSINDVIVD-----NDSIKKIR-----ASYLLGALLGKY 106

Query: 117 GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSG 176
A L G + RPI + G + LGA+V+ G + L G + L
Sbjct: 107 RRAEVALPGGCNIGSRPIDQHIKGFRLGANVEIKGMVIAEAK-----ELKGSHTYLD- 160

Query: 177 SISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+S +++AA +A G+ II+ P++ + G + + + D I
Sbjct: 161 VVSVGATINIMLAACMAEGNT---IIENSAKEPHIVDVANFLNSMGANIKGAGT-DVIRI 216

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMG 295
K G K+ S + D A F+ AA T G VT+ L+ K E+ G
Sbjct: 217 K-GVKHLSGTTYSIIPDQIEAGTFMFAAAATKGDVTIRNVIPKHLESISAKLIEI----G 271

Query: 296 AKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPATAIR 351
+VT + +V V G P +L++ +V P D+ +AVV A+G + +
Sbjct: 272 CEVTEYDDAVRVVGH-----NLRSTNVKTLPPYGFPTDMQPMQMAVVLALANGSSMVT 324

Query: 352 D-VASWRVKETERMVAIRTELTKLGASVE 379
+ + R K + ELT++GA ++
Sbjct: 325 ESIFENRFKYVD-----ELTRMGARIK 346

>ref|ZP_08016531.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sutterella wadsworthensis 3_1_45B]
gb|EFW01160.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sutterella wadsworthensis 3_1_45B]
Length = 417

Score = 40.4 bits (93), Expect = 0.56, Method: Compositional matrix adjust.
Identities = 77/312 (24%), Positives = 128/312 (41%), Gaps = 28/312 (8%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
E++ ++ + + G V++ G+K+ + IL + L+ G + N+ + DV ML L +G
Sbjct: 2 EKLKIRGARRLVGEVRVSGAKNAALPILASLLTAGDLELKNVPLADVRTMLKLLAGMG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRS--LT-AAVTAAGGNATY 121
+ VE + V + G E + V+ MR+ LT +TA G A
Sbjct: 62 VKVERSGSN---VTLNAGAITSTEAPYDLVK-----TMRASILTLCPLTARFGAARV 110

Query: 122 VLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQ 181
L G + RP+ + GL+ LGA V+ G + V ++G+
Sbjct: 111 SLPGGCAIGARPVDQHIKGLRALGAAVEIDHGYVVVESARLKAHAIATDMVTVTGT---- 166

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
L+MAA LA G +I+ P V + G K + + I+G ++
Sbjct: 167 --ENLMMAAVLAEGTT---VIENAAAREPEVVDLANCLNAMGAKISGAGT-PTLVIEGVER 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTW 300
K+A + D A FL AA T G V V C L+ + K E+ M+ W

Sbjct: 221 LHGAKHAVI-ADRIEAGSFLCAAATDGDVLVANCVPDLEAVILKLRMGAMVDVGSDW 279

Query: 301 TETSVTVTGPPR 312
+ + G P+

Sbjct: 280 VR--LKMAGRPK 289

>ref|ZP_04270550.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus BDRD-ST26]
gb|EEK97620.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Bacillus cereus BDRD-ST26]
Length = 419

Score = 40.4 bits (93), Expect = 0.57, Method: Compositional matrix adjust.
Identities = 69/276 (25%), Positives = 105/276 (38%), Gaps = 34/276 (12%)

Query: 105 MRSLTAAVTAAG-----GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPP 158
+R + A+V G G A L G + RPI + G + +GA V G
Sbjct: 74 VRKMRASVQVMGPELLARNGRARIALPGGCAIGSRPIDQHLKGFEAMGAKVQVGNGFVEAY 133

Query: 159 VRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM 218
V G L G K+ L S ++ AA LA G I++ P + +
Sbjct: 134 VE---GELKGAKIYLDFF-SVGATENIMSAATLAKGTT---ILENAAKEPEIVDLANFL 185

Query: 219 ERFVGKAEHSDSWDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGT 278
G K + + I+G K ++ + D A F+ AAITGG + +E
Sbjct: 186 NAMGAKVRGAGTGT-IRIEGVDKLYGANHSIIP-DRIEAGTFMVAAITGGDILIENAVP 243

Query: 279 TSLOGDVKFAEVLEMMGAKVWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVA 334
L+ +E MG K+ V V GP + LKA+D+ P D+
Sbjct: 244 EHLR---SITAKMEEMGVKIIENEGVRVIGPDK-----LKAVDIKTMHPHGFPTDMQ 293

Query: 335 MTLAVVALFADGPTAIRDVA----SWRVKETERMVA 366
+ + L A+G + I + V+E RM A
Sbjct: 294 SQMMALLLQAEGTSMITETVFENRFMHVEEFRMNA 329

>ref|YP_001532320.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dinoroseobacter shibae DFL 12]
sp|A8LS12.1|MURA_DINSH RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABV92719.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Dinoroseobacter shibae DFL 12]
Length = 422

Score = 40.4 bits (93), Expect = 0.58, Method: Compositional matrix adjust.
Identities = 101/426 (23%), Positives = 172/426 (40%), Gaps = 56/426 (13%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + G + + G+K+ ++ LS+ + N D+ M LR+LG
Sbjct: 2 DQIVIRGGVPLHGAIPAGAKNACLTLMPATLLSDEPLTLTNAPRLSDIATMTALLRSLG 61

Query: 65 LSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V + K V+ + A+ ++ +R + A++ G G+
Sbjct: 62 AEVSTLQDGK--VLALSSHRIDNHTAEYDI-----VRKMRASILVLGPMLARDGH 109

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADV---DCFLGTDCPPVRVNGIGGLPGGKVKLS 175
A L G + RP+ + GL+ LGAD+ D ++ P GGL G +
Sbjct: 110 AVVSLPGGCAIGARPVDLHLKGLEALGADLTLDGYVHAKAP-----GGLKGAVFEFP 162

Query: 176 GSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFY 235
+S +LMAA LA G ++ P + R + + G + E + R
Sbjct: 163 -FVSVGATENILMAATLAKGTT---VLKNAAREPEIVDLARCLRKMQAIE-GEGETSRIT 217

Query: 236 IKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOGDVKFAEVLEMMG 295
++G + + V +Y LA AITGG V + G L FAE L G
Sbjct: 218 VQGVDRLHGATHPVVTDRIELGTMYLA-PAITGGEVELIG---GRLDLVAFAERLAAAG 273

Query: 296 AKVTWTETSVTVTGPPREPFGGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIR 351

V+ T +TV + GR + A+DV P D+ + + ADG + +
Sbjct: 274 VDVSETAHGLTV----KRANGR--VGAVDVVTEPFPGFPTDLQAQMMALLCTADGVSVLE 327

Query: 352 DVASWRVKETERMVAIRTELTKLGASVE-EGPDYCIITPPEKLNVTATIDTYDDHRMAMAF 410
+ R+ E M A EL ++GA ++ G + P+ + T D R +++

Sbjct: 328 E----RIFENRFMHA--PELIRMGARIDVHGGTATVTGVPQLKGAPVMAT--DLRASVSL 379

Query: 411 SLAACA 416

LAA A

Sbjct: 380 ILAALA 385

>ref|ZP_00440255.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
GB8 horse 4]
ref|YP_994006.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei SAVP1]
ref|YP_001028330.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei NCTC 10229]
ref|YP_001081974.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei NCTC 10247]
ref|ZP_02269694.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
PRL-20]
ref|ZP_04883532.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei ATCC 10399]
ref|ZP_04910113.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
FMH]
ref|ZP_04915077.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
JHU]
ref|ZP_04976489.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|ABM51359.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei SAVP1]
gb|ABN00674.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei NCTC 10229]
gb|ABO05707.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei NCTC 10247]
gb|EDK52345.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
FMH]
gb|EDK57674.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
JHU]
gb|EDK87364.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
2002721280]
gb|EDP87886.1| putative 3-phosphoshikimate-1-carboxyvinyltransferase
[Burkholderia mallei ATCC 10399]
gb|EEP85862.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
GB8 horse 4]
gb|EES42829.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Burkholderia mallei
PRL-20]
Length = 435

Score = 40.4 bits (93), Expect = 0.58, Method: Compositional matrix adjust.
Identities = 22/59 (37%), Positives = 31/59 (52%)

Query: 9 LQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSV 67
+ P + GTV LP SK R LL+A L+ TT ++N+ + ALR GL+V

Sbjct: 6 VHPGALKGTVTLPASKPHVQRALLVALLNGATTRIENVSWCAETELQFAALRQFGLTV 64

>ref|YP_003553734.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Aminobacterium
colombiense DSM 12261]
gb|ADE57010.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Aminobacterium
colombiense DSM 12261]
Length = 435

Score = 40.4 bits (93), Expect = 0.58, Method: Compositional matrix adjust.
Identities = 97/394 (24%), Positives = 154/394 (39%), Gaps = 45/394 (11%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAAL-SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
+ G ++ G+K+ + I+ + L GT + + DV M LR LG ++ +K

Sbjct: 13 LRGKIEAQGAKNAALPIMAASLLLSGTLNIHKVPRLHDVLTMDLLRGLGAEIQYEKGE 72

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
+ ED E L A + + A G A L G + RP
Sbjct: 73 MSISIP-----EDLSWETPSNLVRKMRASSLVGLPLLARCGRAVLPLPGGCSIGSRP 124

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + GL ++GA +D G V GL G ++ L S LLMAA A
Sbjct: 125 IDLHLKGLSRMGASIDLHGA---VHATA-NGLKGCRYLDLDFP-SVGATENLLMAAVFA 178

Query: 194 LGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G+ +E + I + TL+ M G E + IKG + + +
Sbjct: 179 EGETVLENTAREPEITNLVQTLKSM---GASIE-EEGTGVIRIKGVDELHDAETIVIPDR 234

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
+ +Y LA + ++GG + +E + D A+ LE GA T SV V
Sbjct: 235 IETCTYILA-SIMSGGEIEIENVIPQHI--DSLIAK-LEEGGASFTVKNDVIV-----H 285

Query: 314 PFGRKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRD-VASWRVKETERMVAIR 368
P R LKA+ + P D+ + ADG + I++ V R
Sbjct: 286 PINR--LKAIVSLKTMYPGFPDLPQIMATLALADGASVIQEGVFQARFLHV----- 336

Query: 369 TELTKLGASVEEGPDYCIITPPEKL---NVT AID 399
+EL ++GA +E + ++T E L +V+A D
Sbjct: 337 SELNRMGARIELQGNTAVVTGVEHLVGADVSATD 370

>ref|YP_178947.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni RM1221]
sp|Q5HUT8.1|MURA_CAMJR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAW35282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni RM1221]
gb|ADT72637.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni S3]
Length = 418

Score = 40.4 bits (93), Expect = 0.59, Method: Compositional matrix adjust.
Identities = 88/409 (21%), Positives = 167/409 (40%), Gaps = 68/409 (16%)

Query: 13 KEISGTVKLPKSGKSLNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V
Sbjct: 10 NHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKV----- 64

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GNATYV 122
F A N IA +R + A++ G G+
Sbjct: 65 -----NFQNNALLNTNTL--NQTIAKYDIVRKMRASILTLGPLLARFGHCEVS 111

Query: 123 LDGVPRMRERPIGDLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
L G + +RPI ++ L+++GA++ G V G L G ++ L I+
Sbjct: 112 LPGGCAIGQRPIDLHLLEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKITVTG 164

Query: 183 LSALLMAAPLALGDVEIEIIDLKISI---PYVEMTLRLMERFG--VKAHSDSWDRFYIK 237
++MAA LA G KL+++ P V +++ G +K +D + Y
Sbjct: 165 SENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDGAGLEIKGIGTDELE-IYGS 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G+ + + + + + +Y AG AIT +T++ T L L MG +
Sbjct: 218 DGELLEFKFESVIPDRIEAGTYLCAG-AITNSKITLDKVNATHLSA---VLAKLHQMGFE 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDV 353
E S+T+ P +E +K +++ ++ P D+ +AL A+G + I +
Sbjct: 274 TLIAEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMALALKANGTSIIDE- 325

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTAIDTYD 402
R+ E M +EL ++GA ++ I ++LN + D
Sbjct: 326 ---RLFENRFMHV--SELLRMGADIKLNHGIATIVGGKELNAADVMTD 369

>ref|YP_002924690.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Hamiltonella defensa 5AT (Acyrtosiphon pisum)]

sp|C4K7J9.1|MURA_HAMD5 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACQ68542.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Candidatus
Hamiltonella defensa 5AT (Acyrtosiphon pisum)]
Length = 422

Score = 40.4 bits (93), Expect = 0.60, Method: Compositional matrix adjust.
Identities = 90/411 (21%), Positives = 166/411 (40%), Gaps = 49/411 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG V + GSK+ + IL LSE + N+ +D+ L L+ LG V+A
Sbjct: 12 LSGEVMTSGSKNAALPILFSTLLSEEPLELKNIPKIDITTLNLLKQLG--VKAKYQPP 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
++++ DAK V F + +++++ A++ A G G L G
Sbjct: 70 DSIIM-----DAK-AVNHFCAPIEL-VKTMRSIWLGLPLVARFGRGQVSLPGGCA 118

Query: 129 MRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GLKQLGA + G ++ + G L G + + +S ++
Sbjct: 119 IGARPVDLHIFGLKQLGAKIQIEEGY----IKASVEGRKLGAKHIVMD-KVSVGATLTVMs 173

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ + P + T + G + + + D+ ++G ++ + +
Sbjct: 174 AATLAEGT---SIIENVAREPEIVDTANFLNILGANIQGAGT-DKIVVEGVKRLRGGAYS 229

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVT 308
+ + ++ +AGA G V C T L GA++ + +++
Sbjct: 230 IMPDRIETGTFLVAGAVSRGKVV----CRHTQPATLEAVLAKLHEAGAQIEVGKDWISLD 285

Query: 309 GPPREPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERM 364
+ P KA++V P D+ ++ + A G I + + E M
Sbjct: 286 MKGKRP-----KAVNVRTTPYPGFPTDMAQFTLLNIVATGTGVITET---IFENRFM 335

Query: 365 VAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDYDDHRMAMAFSLAAC 415
EL ++GA V+ + I E+L+ + D R + + LA C
Sbjct: 336 HV--PELIRMGAVQKIESNTVICHGVERLSGAGV-MATDLRASASLVLAGC 383

>ref|YP_002561158.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Macroccoccus
caseolyticus JCSC5402]
dbj|BAH18462.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 [Macroccoccus
caseolyticus JCSC5402]
Length = 427

Score = 40.4 bits (93), Expect = 0.60, Method: Compositional matrix adjust.
Identities = 93/396 (23%), Positives = 157/396 (39%), Gaps = 55/396 (13%)

Query: 7 IVLQPIKEISGTVKLPGSKSLSNRILLALLAAL-SEGTTVVDNLLNSEDVHYMLGALRTLGL 65
I+++ +SG VK+ G+K+ I+ + L SEG + N+ DV + L L
Sbjct: 4 IIVKGGNRLSGRVKVEGAKNAVLPIMTASLLASEGVSEFTNVPALSDVDTISAVLEGLNA 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYV 122
VE + + VVV G+ + A E V MR+ + + A G A
Sbjct: 64 KVEKN-IEQNKVVDARGELSTQAAAYEFVS-----KMRASVLVLGPLLARFGYAEVA 114

Query: 123 LDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS----GSI 178
+ G + RPI + GL+ LGA ++ G V+ L G + L G+
Sbjct: 115 MPGGCAIGSRPIELHLKGLGALGAVIEQKNGYLVGTVKDR----LKGADIYLDFPSVGAT 170

Query: 179 SSQYLSALLMAAPLALGDV--EIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYI 236
+ ++A+L LG+V E EI+D + + G + + + D +
Sbjct: 171 QNILMAAVLAEGKTVLGNVAREPEIVD-----LANFLNQMGANIQQAGT-DTITV 219

Query: 237 KGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGA 296
G + K+ + D A FL AAIT G V VEG E + + A
Sbjct: 220 YGVETLTGAKHEIIP-DRIEAGTFLVAAAITRGDVYVEGA-----IYEHMHALIA 268

Query: 297 KVTWTETSVTVTGPPEPFGKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD 352
K+ + + ++LKAID+ P D+ + + L +G +++ +

Sbjct: 269 KLKEAGCHIEIDTRGIHLSAEQNLKAIDIKTMPHPGFPTDMQAQMMALMLSLEGNSSVNE 328

Query: 353 VASWRVKETERMVAIRTELTKLGASVEEGPDYCIIT 388

V E M A TE K+ A ++ + I+

Sbjct: 329 T---VFENRFMHA--TEFQKMNAQIKVDKRFAYIS 358

>ref|ZP_02042003.1| hypothetical protein RUMGNA_02779 [Ruminococcus gnavus ATCC 29149]
gb|EDN76883.1| hypothetical protein RUMGNA_02779 [Ruminococcus gnavus ATCC 29149]
Length = 430

Score = 40.4 bits (93), Expect = 0.61, Method: Compositional matrix adjust.
Identities = 95/426 (22%), Positives = 174/426 (40%), Gaps = 43/426 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64

E+ +++ + G V++ G+K+ + IL A +++ T ++DNL + D++ +L A++ +G

Sbjct: 2 EQYIIKGGNPLVGEVEIGGAKNAALAILAAIMTDETVLIDNLPDVNDINVLEAIQIGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123

V+ + F +E D ++++ A L A+ A L

Sbjct: 62 AMVQRFDRHTVKINGSAITDFNIEYDIKKIR-----ASYLLGAMLGKYKRAEVAL 113

Query: 124 DGVPFRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYL 183

G + RPI + G + LGADV G L G + +S

Sbjct: 114 PGGCNIGSRPIDQHLKGFRALGADVIEHGKIVAEAE-----HLRGTHLYFD-VVSVGAT 167

Query: 184 SALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYK 243

++MAA +A G + I++ + P+V + G + + D I+G +

Sbjct: 168 INVMMAAAMADG---LTIMENVAKEPHVVDVANFLNSMGANIRGAGT-DVIKIRGVKSLH 223

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLOQGDVKFAEVLEMMGAKVTWTET 303

+ + + D A F+ AA T G VTV L D +++++ +G +V +

Sbjct: 224 KTEYSIIP-DQIEAGTFMFAAATKGDVTVLNVIPKHL--DATISKLV-DIGCEVEEFDD 279

Query: 304 SVTVTGPPREPFRGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTAIRD-VASWRV 358

+V V R L++ V P D+ +VV A G + I + + R

Sbjct: 280 AVRVVAKNR-----LRSTQVKTLPPYGYPTDMQPQIGVVLALAQTSTITESIFENRF 332

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418

K + EL ++GA ++ + I EK + + + D R A +A A

Sbjct: 333 KYLD-----ELARMGAVIKVEGNSATIEGVEKFSGARV-SAPDLRAGAALCIAGLATD 384

Query: 419 PVTIRD 424

+TI D

Sbjct: 385 GITIVD 390

>ref|YP_002248837.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermodesulfovibrio yellowstonii DSM 11347]
sp|B5YKS2.1|MURA_THEYD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enolpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACI21379.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Thermodesulfovibrio yellowstonii DSM 11347]
Length = 416

Score = 40.4 bits (93), Expect = 0.62, Method: Compositional matrix adjust.
Identities = 82/360 (22%), Positives = 140/360 (38%), Gaps = 41/360 (11%)

Query: 15 ISGTVKLPKSGSKLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74

+ G V + G+K+ + I+ L++G + + DV M ++ +G VE ++ K

Sbjct: 12 LKGEVTISGAKNAALPIMASTLLAQGVHIFKRIPKLRDVFTMTelikRMGGIVEFNElCK 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPFRMRERPI 134

+ + K E L A + + A G A L G + RP+

Sbjct: 72 INTI-----KINKFEASYDLVKTMRASILVLGPLVARFGRKVSPLPGGCAIGARPV 122

Query: 135 GDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLAL 194

+ GL+++GA + G L G K+ + L+MAA LA

Sbjct: 123 NLHINGLQKMGAKISLQEGYIIAKA-----SRLMGTKIYFDIPTVTGT-ENLMMAATLAK 176

Query: 195 GDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGDA 254
G IE K I + L LM G K E + + ++G + K P+ + D
Sbjct: 177 GTTIIENAAKEPEIVDLANYLILM---GAKIEGAGT-SIIKVEGVDELKPPQEYEIIPDR 232

Query: 255 SSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW--TETSVTVTGPPR 312
F+A A GG +++GC + A +L+M A +++ E + V GP R
Sbjct: 233 IETGTFTAIAAGACGGDISLKGCRIDHID-----AIILKMKDAGISFKEIENGIRVIGPKR 287

Query: 313 EPFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVA----SWRVKETERM 364
L+A+D+ P D+ + A+G + I++ V E RM
Sbjct: 288 -----LQAVDIKTMPYPGFPTDMQAQFMAMMTVANGTSVIKETIFENRFMHVAELRRM 340

>ref|ZP_06926955.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Gardnerella vaginalis AMD]
gb|EFH27962.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Gardnerella vaginalis AMD]
Length = 477

Score = 40.4 bits (93), Expect = 0.63, Method: Compositional matrix adjust.
Identities = 86/374 (22%), Positives = 153/374 (40%), Gaps = 38/374 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ VE +
Sbjct: 51 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVSDLLRLHGV DVEVN-- 108

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+V K + D +V G++ I + + + G A G + R
Sbjct: 109 GPEGIVTIDATKVQLADVA-DVDTLSGSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 166

Query: 133 PIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS----GSISSQYLSALLM 188
PI + L++LGA+VD + + GL G K+ L G+ L+A+L
Sbjct: 167 PIDFHLETLRLKLGANVDK---DHEDGIHITAPNGLHGTKIHLPPYPSVGATEQTLLAAVLA 223

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247
L IE P + + +++ G A S DR F I+G ++ + +
Sbjct: 224 EGRTLSGAAIE-----PEIMDLVAVLQKMG--AIISVDVDRTFRIEGVKELQGYTH 273

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A+ + + A T G V ++G + + F V +G + T+ +
Sbjct: 274 TSLT-DRIEASWASALATHGDVFIKATQPEM---MTFLNVFRKVGQFDVTDKGIRF 329

Query: 308 TGPPREPFGKHLKAI--DVNMNMKMPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P G H AI DV+ M D L V A G + + + E
Sbjct: 330 W----HPGGDLHPVAIETDVHPPGFM TDWQQLVVALTQAKGLSIVHETVY-----ENRF 379

Query: 366 AIRTELTKLGASVE 379
L ++GA ++
Sbjct: 380 GFTKPLVQMGAMIQ 393

>ref|YP_003373468.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gardnerella vaginalis 409-05]
ref|ZP_06976911.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Gardnerella vaginalis 5-1]
gb|ADB13934.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Gardnerella vaginalis 409-05]
gb|EFH71400.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Gardnerella vaginalis 5-1]
Length = 453

Score = 40.4 bits (93), Expect = 0.63, Method: Compositional matrix adjust.
Identities = 86/374 (22%), Positives = 153/374 (40%), Gaps = 38/374 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++GT+K+ G+K+ ++ ++ A L+ G +V+ N+ DVH + LR G+ VE +
Sbjct: 27 KPLNGTIKVRGAKNFVSKAMVAALLAPGKSVLKNVPEIRDVHVSDLLRLHGV DVEVN-- 84

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 132
+V K + D +V G++ I + + + G A G + R

Sbjct: 85 GPEGIVTIDATKVQLADVA-DVDTLGSSSRIPIL-FSGPLLHRLGEAFIPALGGCNIGGR 142

Query: 133 PIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLS----GSISSQYLSALLM 188
PI + L++LGA+VD + + GL G K+ L G+ L+A+L

Sbjct: 143 PIDFHLETLRKLGANVDK---DHEDGIHITAPNGLHGTKIHLPPYVSGATEQTLLAAVLA 199

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR-FYIKGGQKYKSPKN 247
L IE P + + +++++ G A S DR F I+G ++ + +

Sbjct: 200 EGRTELSGAAIE-----PEIMDLVAVLQKMG--AIISVDVDRTFRIEGVKELQGYTH 249

Query: 248 AYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTV 307
+ D A+ + + A T G V ++G + + F V +G + T+ +

Sbjct: 250 TSLT-DRIEASWASALATHGDVFIKATQPEM---MTFLNVFRKVGQFDVTDKGIRF 305

Query: 308 TGPPREPFGRKHLKAI--DVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
P G H AI DV+ M D L V A G + + + E

Sbjct: 306 W----HPGGDLHPVAIETDVHPGFM TDWQQPLVVALTQAKGLSIVHETVY-----ENRF 355

Query: 366 AIRTELTKLGASVE 379
L ++GA ++

Sbjct: 356 GFTKPLVQMGAMIQ 369

>ref|YP_001482381.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni 81116]
sp|A8FLR7.1|MURA_CAMJ8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABV52404.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni 81116]
gb|ADN91036.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni M1]
gb|EFV10105.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni 327]
Length = 418

Score = 40.0 bits (92), Expect = 0.63, Method: Compositional matrix adjust.
Identities = 88/413 (21%), Positives = 169/413 (40%), Gaps = 68/413 (16%)

Query: 9 LQPIKEISGTVKLPKSGKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V

Sbjct: 6 IEGTNHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVNPNVADIKTLISLLENLGAKV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GN 118
F A N IA +R + A++ G G+

Sbjct: 65 -----NFQNNALLNTNTL--NQTIKYDIVRKMRASILTGLPLLARFGH 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + +RPI ++ L+++GA++ G V G L G ++ L I

Sbjct: 108 CEVSLPGGCAIGQRPIDLHLLALEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKI 160

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFG--VKAHSDSWDR 233
+ ++MAA LA G KL+++ P V +++ G +K +D +

Sbjct: 161 TVTGSENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDAGLEIKGIGTDELE- 213

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
Y G+ + + + + +Y AG AIT +T++ T L L

Sbjct: 214 IYGTGDELLEFKEFSVIPDRIEAGTYLCAG-AITNSKITLDKVNATHLSA---VLAKLHQ 269

Query: 294 MGAKVTWTETSVTVTGPPREPFGRKHLKAIDVNMNKMPP---DVAMTLAVVALFADGPTA 349
MG + E S+T+ P +E +K +++ ++ P D+ +AL A+G +

Sbjct: 270 MGFETLIAEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMALALKANGTSI 322

Query: 350 IRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
I + R+ E M +EL ++GA ++ I ++LN + D

Sbjct: 323 IDE----RLFENRFMHV--SELLRMGADIKLNHGIATIVGGKELNAADVMATD 369

>ref|YP_001983255.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cellvibrio
japonicus Ueda107]

sp|B3PBY5.1|MURA_CELJU RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ACE86115.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Cellvibrio
japonicus Ueda107]
Length = 420

Score = 40.0 bits (92), Expect = 0.64, Method: Compositional matrix adjust.
Identities = 93/397 (23%), Positives = 157/397 (39%), Gaps = 46/397 (11%)

Query: 15 ISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G +++ GSK+ + IL L++G + N+ + D+ M+ LRTLGL++E
Sbjct: 12 LTGELRISGSKNAALPILAAATILAQGKVRLANVPHLNDISTMIALRLTLGLTIEIQ--GD 69

Query: 75 RAVVVGCGG----KFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
V+V P E K L + R A V+ GG A +
Sbjct: 70 HVVIVDPNTINSYTAPYELVKTMRASILVLGPLLARYGEANVSFPGGCA-----IG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+ +GA ++ D +R G L G L +++ LLMAA
Sbjct: 121 SRPVDIHLRGLGAMGASIEI----DGGYIRARRQGRKLGCHF-LMDTVTVGGTENLLMAA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G I++ P + L+ G + + I+G + + +
Sbjct: 176 VLAEGKT---ILENAAREPEIVDLANLLVAMGARISGIGT-STLTIEGVESLTGCDYSVM 231

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQG-DVKFAEVLEMMGAKVTWTETSVTVTG 309
+ +Y +A AA + G V + + L+ VK E GA VT E + +
Sbjct: 232 PDRIETGTYLVA AAA-SRGKVRILTHTSASILEAVIVKLQEA----GADVTTGEDWIALDM 286

Query: 310 PPREFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMV 365
R P KA+ + P D+ + ADG + I + R+V
Sbjct: 287 NGRRP-----KAVSLKTAPYPAFPDMQSQFMALNAVADGISHITETIF-----ENRLV 335

Query: 366 AIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
+ EL ++GA +E + I+T E+L + D
Sbjct: 336 QV-AELKRMGAHIELEHNTAIVTGVERLKAAPVMASD 371

>ref|ZP_04922705.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp. Ex25]
ref|YP_003285042.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp. Ex25]
gb|EDN57051.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp. Ex25]
gb|ACY50577.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio sp. Ex25]
Length = 421

Score = 40.0 bits (92), Expect = 0.64, Method: Compositional matrix adjust.
Identities = 98/422 (23%), Positives = 164/422 (38%), Gaps = 51/422 (12%)

Query: 13 KEISGTVKLPKSGKSLNRIILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 11 KPLVGEVTISGAKNAALPILFASILAEEPVEVANVPHLRDIDTTMELLKRLGAKVSRN-- 68

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
G V+ ++ + + + + + A++ A G G L G
Sbjct: 69 -----GSVHVDPSR--ITEYCAPYDL-VKTMRSIALGPLVARFGQGQVSLPGG 115

Query: 127 PRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
+ RP+ + GL+QLGA + G V+ G L G + + +S +
Sbjct: 116 CAIGARPVDLHISGLEQLGATITLEDGY----VKAEDVGRKLGAHIVMD-KVSVGATITTI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
+ AA LA G +D P + T + + G K + + D I+G ++ K
Sbjct: 171 MCAAALAEGETT---TLDNAAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVERLGGCK 226

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ V D FL AA++GG V C T+ LE GA V E ++
Sbjct: 227 HNVV-ADRIETGTFLVAAAVSGGKV---CRNTNAHLLEAVLAKLEEAGALVETGEDWIS 282

Query: 307 VTGPPREFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
V RE LKA+ V P D+ ++ + A G I + + E

Sbjct: 283 VDMTARE-----LKAVSVRTAPHPGFPTDMQAQFTLLNMMAKGGGVITET----IFENR 332

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTALDITYDDHRMAMAFSLAACAEVPVTI 422
M EL ++GA E + I E L+ + D R + + +A C TI

Sbjct: 333 FMHV--PELMRMGAKAEIEGNTVICGDVESLSGAQV-MATDLRASASLVIAGCIAKGETI 389

Query: 423 RD 424
D

Sbjct: 390 VD 391

>ref|ZP_06425412.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Peptostreptococcus anaerobius 653-L]
gb|EFD04645.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Peptostreptococcus anaerobius 653-L]
Length = 417

Score = 40.0 bits (92), Expect = 0.65, Method: Compositional matrix adjust.
Identities = 73/298 (24%), Positives = 118/298 (39%), Gaps = 26/298 (8%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE-ADKAA 73
+ G VK+ G+K+ I+ L+ V+ ++ N DVH + LR LG V+ D

Sbjct: 12 LKGNVKIDGAKNAVLPIAATLLANDICVLKSVPNLRDVHVISDLLRHLGAKVDYRDGVL 71

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRER 133
+ P + K+ FL + R ++ GG A + RP

Sbjct: 72 TVDSTNIITYEAPYDLVKMRASFLVMGPELLARFNHTKISMPGGCA-----IGTRP 122

Query: 134 IGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
I + G K LGA+++ G V L G K+ L S ++M A LA

Sbjct: 123 IDLHLKGFKALGANINMDHGFVEAKTEV----LKGNKLYLDFP-SVGATQNIMMTAVLA 176

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G + II+ P + + G + + + IKG + ++ + D

Sbjct: 177 DG---VTIENAAEEPEIVDLANFLNEMGASVRGAGT-NTIKIKGVKSLHGAHTIIP-D 231

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDV-KFAEVLEMMGAKVTWTETSVTVTGP 310
AS ++ AA+T G VT+E L+ + K E GA+V E ++ V GP

Sbjct: 232 RIEASTYMVAAMTKGDVTIENVIIDHLKPVIAKLTEA---GAQVIEGENTIRVVGP 285

>ref|ZP_06124956.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Providencia
rettgeri DSM 1131]
gb|EFE53960.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Providencia
rettgeri DSM 1131]
Length = 420

Score = 40.0 bits (92), Expect = 0.65, Method: Compositional matrix adjust.
Identities = 95/413 (23%), Positives = 159/413 (38%), Gaps = 55/413 (13%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+ G V + G+K+ + IL A L+E + N+ + D+ + L LG V+ + +

Sbjct: 12 LEGEVTISGAKNAALPILFAALLAEEPVEIQNVPHLRDIDTTIKLLNQLGTQKVRNGSVY 71

Query: 74 --KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
V C V+ + + A + A G+ L G +

Sbjct: 72 VDASTVTITYCAPYDLVKTMRSIHAL-----APLVARFGHGEVSLPGGCAIGA 119

Query: 132 RPIGDVLVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+QLGA + G V+ G L G + + +S +++ AA

Sbjct: 120 RPVDLHISGLEQLGAKIALEDGY----VKATVDGRLKGACIVMD-KVSVGATVSIIMTAAT 174

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYKSPK 246
LA G II+ P +E T + G K + + DR I+ GG YK

Sbjct: 175 LAEGTT---IIENAAAREPEIEDTANLNTLGAKITGAGT-DRIVIEGVERLGGGVYK--- 227

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V D FL AA++ G V +L D A++ E GAK+ + ++

Sbjct: 228 ---VLPDRIETGTFLIAAAVSRGKVICRNARPDTL--DAVLAKLRE-AGAKIEIGDDWIS 281

Query: 307 VTGPPPREPFGRKHLKAIDVNMNKMMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362

+ + P KA+ + P D+ +++ L ADG I +
Sbjct: 282 LDMGKRP-----KAVTLRTAPHPGFPTDMQAQFSLNVLADGAGMITETIF-----EN 330

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAAC 415
R + I EL ++GA E + + EKL + D R + + +A C

Sbjct: 331 RFMHI--PELIRMGAAHEIESNTVLCHGVEKLTSAQV-MATDLRASASLVIAGC 381

>pdb|1DLG|A Chain A, Crystal Structure Of The C115s Enterobacter Cloacae Mura
In The Un- Liganded State
pdb|1DLG|B Chain B, Crystal Structure Of The C115s Enterobacter Cloacae Mura
In The Un- Liganded State
Length = 419

Score = 40.0 bits (92), Expect = 0.66, Method: Compositional matrix adjust.
Identities = 98/421 (23%), Positives = 165/421 (39%), Gaps = 53/421 (12%)

Query: 15 ISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKIDIDTMTKLLTQLGKTKVERX---- 67

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
G ++ + V F + +++ A++ A G G L G
Sbjct: 68 -----GSVWIDASN--VNNFSAPYDL-VKTMRASIWALGPLVARFVGQGVSLPGGSA 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL++LGA++ G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHIFGLEKLGAIEKLEEGY----VKASVNGRLKGAHIVMD-KVSVGATVTIMS 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
AA LA G II+ P + T + G K + DR I+G ++
Sbjct: 172 AATLAEGTT---IIENAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GV 225

Query: 249 Y-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLSQGDVVKFAEVLEMMGAKVTWTETSVTV 307
Y V D FL AAI+GG + +L D A++ E GA + E +++
Sbjct: 226 YRVLPDRIETGTFLVAAAISGKIVCRNAQPDTL--DAVLAKLRE-AGADIETGEDWISL 282

Query: 308 TGPPREPFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETER 363
+ P KA+ V P D+ ++ L A+G I + + E
Sbjct: 283 DMHGKRP-----KAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITET----IFENRF 332

Query: 364 MVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEVPTIR 423
M EL ++GA E + I EKL+ + D R + + LA C T+
Sbjct: 333 MHV--PELIRMGAAHEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVV 389

Query: 424 D 424
D
Sbjct: 390 D 390

>ref|YP_003697427.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Arcanobacterium
haemolyticum DSM 20595]
gb|ADH92808.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Arcanobacterium
haemolyticum DSM 20595]
Length = 440

Score = 40.0 bits (92), Expect = 0.67, Method: Compositional matrix adjust.
Identities = 75/306 (24%), Positives = 128/306 (41%), Gaps = 32/306 (10%)

Query: 13 KEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
+ + GT+ + G+K+ ++ ++ A L+E T+++ N+ DV + LR G V+ D+
Sbjct: 11 QPLHGTITVRGAKNFVSKAMVAALLTEETSILRNVPILRDVVDVSDLLRLHGADVVDYDQE 70

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD-GVPRMRE 131
A +V GK + + E+ G++ I + + A G ++ D G + +
Sbjct: 71 A--GIVTITPGKIHLPEDPAEMDRLAGSSRIPILFCGPLLHALG--EAFIPDLGGCHIGD 126

Query: 132 RPIGDLVVGLKQLGADVDCF-LGTDCCPPVRVNGIGGLPGGKVKL---SGSISSQYLSALL 187
RP+ + L+ GA D LG R GL KV L S + Q L A +
Sbjct: 127 RPVDFHLQVLEDFGAVRDVQELGLHLTAPR-----GLRARKVTLPPYPSVGATEQTLLAAV 181

Query: 188 MA---APLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
A L VE EI+D LIS+ +++ G A + S DR + G +
Sbjct: 182 RADGITELRGAAVEPEIMD-LISV-----LQKMG--ALITVSTDRTIVIEGVRELH 229

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETS 304
N + D A + A TGG + V+G + + F V +G + T+
Sbjct: 230 GYNHFALADRIEAGSWACAALATGGNIMVQGAQQEPM--MSFLNVFRKVGGEFVDVTDNG 286

Query: 305 VTVTGP 310
+ P
Sbjct: 287 IRFWHP 292

>ref|YP_524186.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodoferrax
ferrireducens T118]
sp|Q21U98.1|MURA_RHOFD RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABD70655.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodoferrax
ferrireducens T118]
Length = 421

Score = 40.0 bits (92), Expect = 0.67, Method: Compositional matrix adjust.
Identities = 90/406 (22%), Positives = 158/406 (38%), Gaps = 58/406 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
+++++ + + G V + G+K+ + L L+ + N+ +DV ML +R +G
Sbjct: 2 DKLLIRGGRSLKGEVLISGAKNATLPELCACLLTSAPVTLTNVRLQDVATMLKLIRNMG 61

Query: 65 LSVEADKAAKRAVVVCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
V A+++ V V E E V +++ A+V A G G
Sbjct: 62 --VAAERSDDGRVTVDASALSSPEAPYELV-----KTMRASVLALGPLLTRFGE 108

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS- 177
AT L G + RP+ + GL +GA++ G I LP G +L G+
Sbjct: 109 ATVSLPGGCAIGSRPVDQHIKGLTAMGAEIVVEHG-----YMIAKLPKGWTRLKGAR 160

Query: 178 ISSQYLSA-----LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWD 232
I++ ++ LMAA LA G + I++ P + ++ + G E S
Sbjct: 161 IATDMVTVTGTENFLMAATLAEG---VTILENAAQEPEITDLAEMLIKMGANIEGHGS-S 216

Query: 233 RFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLE 292
R I+G + + V D F+ A TGG V ++ L+ V E L
Sbjct: 217 RIRIQGVESLHGCTHQVV-ADRIETGTFCMAAATGGDVLLKHGRIDHLEAVV---EKL 272

Query: 293 MMGAKVTWTETSVTVTGPFPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPT 348
GA V E + V R LK+ + P D+ + + G
Sbjct: 273 DAGATVARVEGGIRVQSQGR-----LKSQSFRTTTEYPGFPPTDMQAQFMALNCISHGTA 325

Query: 349 AIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ + + E M E+ +LGA+++ ++ EKL+
Sbjct: 326 VVTET----IFENRFMHV--NEMVRLGANIQIDSKVAVVEGVEKLS 365

>ref|ZP_06871438.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 23726]
gb|EFG94729.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 23726]
Length = 423

Score = 40.0 bits (92), Expect = 0.68, Method: Compositional matrix adjust.
Identities = 69/287 (24%), Positives = 121/287 (42%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I+G +K+ GSK+ + I++ + +GT V+ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKIAGELKVDGSKNSTLPIMIATLVEKGTYYLNRNVPDLRDIRTLVALLESLEVEKLD 70

Query: 72 AAKRAVVVCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + G G D +++ FL G+ V GG A +
Sbjct: 71 NSYKIIINNGLSGAEASYDLVKMRASFLVMGGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
 RP+ + G + LGA ++ G V GL GG + L S ++MAA
 Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
 A G +++ P +E + + G K + R I G K + + + +
 Sbjct: 177 VKAKGKT---VLENAAKEPEIEDLCNFLIKMGAKISGVGT-SRLEIDGVDKLTACEYSII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
 + +Y +A + + G++ V G L F LE MG K
 Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIGVPEHLS---SFLKLEEMGTK 275

>ref|YP_932319.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Azoarcus sp.
 BH72]
 emb|CAL93432.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Azoarcus sp.
 BH72]
 Length = 416

Score = 40.0 bits (92), Expect = 0.68, Method: Compositional matrix adjust.
 Identities = 85/397 (21%), Positives = 163/397 (41%), Gaps = 45/397 (11%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
 +++++ + +SG V + G+K+ + IL A L+ N+ D+ +L L +G
 Sbjct: 2 DKLLIEGGRRLSGEVAISGAKNAALPILCAALLTREPVTFTNPRLNDIGTLLKLLGQMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
 + VE + R + PV A E+ + + + L A G+A L
 Sbjct: 62 VKVERED--DRVTLASALDNPV--APYEMVKTMRASILVLGPLVARC----GDARVSLP 113

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQ 181
 G + RP+ + GL+ +GA+V ++ P ++ G + ++
 Sbjct: 114 GGCAIGARPVDQHIGLQAMGAEVVRVEHGYVQAQVPRLK-----GARLFTDMVTVT 164

Query: 182 YLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQK 241
 L+MAA LA G+ +I+ P V + G + + + D I+G
 Sbjct: 165 GTENLMMAACLAQGET---VIENAAAREPEVVDLANCLVAMGAQISGAGT-DVIRIRGVDA 220

Query: 242 YKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWT 301
 + + + +Y A AA+TGG V + GT+S D +++++ G +V
 Sbjct: 221 LHGATHRIMPDIETGTYLCA-AAVTGGEVRLT--GTSSCYLDAVIDKLMD-AGCEVVSE 276

Query: 302 ETSVTVTGPPPREPFGRKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTAIRDVASWR 357
 ++ + PR P +A+++ P D+ + ADG IR+
 Sbjct: 277 RDAIRLAA-PRRP-----QAVNLRTPAPAFPTDMQAQFMALNCVADGAAMIRET---- 325

Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
 + E M A+ EL +LGA + + ++ E+L
 Sbjct: 326 IFENRFMHAV--ELQRLGADIRIDGNTAVVRGVERLQ 360

>ref|YP_003376608.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Xanthomonas
 albilineans GPE PC73]
 emb|CBA16616.1| probable udp-n-acetylglucosamine 1-carboxyvinyltransferase protein
 [Xanthomonas albilineans]
 Length = 424

Score = 40.0 bits (92), Expect = 0.69, Method: Compositional matrix adjust.
 Identities = 91/399 (22%), Positives = 157/399 (39%), Gaps = 43/399 (10%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
 +IV+ + G V + G+K+ IL L++ + N+ DV + L LG
 Sbjct: 3 KIVVTGGNALHGEVNIISGAKNAVLPILCATLLADAPVEITNVPQLHDTVITTVKLLGELGA 62

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNA 119
 V D+ + G V+ K + + +R++ A++ G G A
 Sbjct: 63 EVTIDEG-----TLARGSAITVDPRKVDQHIAPYEL---VRTMRASILVLGPLLAKFGEA 114

Query: 120 TYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSIS 179
 L G + RP+ + GL+ LGA++ G ++ + G L GG+ +S

Sbjct: 115 EVSLPGGCAIGSRPVDQHIKGLQALGAEISVENGY----IKASSNGRLKGGRYVFD-MVS 169

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
+LMAA LA G I +++ P V + G + E + + R ++G

Sbjct: 170 VTGTENVLMAATLAEG---ITVLENAAMEPEVGDLDCLIALGARIEGAGT-SRIVVQGV 225

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVT 299
++ ++A + D FL AA+TGG+VTV +L VL+ +

Sbjct: 226 ERLSGGRHAVLP-DRIETGTFLVAAAMTGGSVTVRRARADTLDA-----VLDKLTEAGA 278

Query: 300 WTETSVTVTGPPREPFGGRKHLKAIDVNMNKMPP----DVAMTLAVVALFADGPTAIRDVAS 355
ET V R K +A+++ P D+ + ADG I +

Sbjct: 279 SIETGVDFI---RLDMQGKRPRAVNLTAPYPAFPTDMQAQFMALNCVADGVGVINET-- 333

Query: 356 WRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLN 394
+ E M EL +LGA ++ I+ E+L+

Sbjct: 334 --IFENRFMHV--NELLRLGADIQIEGHTAIVRGSERLS 368

>ref|YP_001341265.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Marinomonas sp.
MWYL1]
gb|ABR71330.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Marinomonas sp.
MWYL1]
Length = 420

Score = 40.0 bits (92), Expect = 0.69, Method: Compositional matrix adjust.
Identities = 93/388 (23%), Positives = 147/388 (37%), Gaps = 46/388 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
++G V+ G+K+ + IL L++ + NL + D+ ML L ++G V D+

Sbjct: 12 LNGVVRASGAKNAALPILAAATLLTKELITIKNPLHLHDITTMLELLGSMGCGVVVDEKMS 71

Query: 75 RAVVV---GCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVP RMR 130
+ V C + + L LG + + G A L G +

Sbjct: 72 VQLDVLTLNCEAPYDLVKTMRASILVLG-----PLVSHFGKAVVSLPGGCAIG 120

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + GL+ +GA + G V G L G ++ ++ LLMAA

Sbjct: 121 SRPVDLHLRGLGELAMGATIAVEGGDIVASVD---GRLKGARIFFD-KVTVTGTENLLMAA 175

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY- 249
LA G I++ P V + G K + D I G + +Y

Sbjct: 176 TLADGQT---ILENAAREPEVVDLAELCIAMGAKIK-GHGTDTITIDGVEALHG--TSYP 229

Query: 250 VEGDASSASYFLAGAAITGGTIVTEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTG 309
V D FL AAITGG V V SL+ LE GAKVT + + V

Sbjct: 230 VMPDRIETGTFLVAAAITGGKVRVIDTNVKSLEA---VLSKLEEAGAKVTCGDDWIEVDM 286

Query: 310 PPREPFGGRKHLKAIDVNMNKMPPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIR- 368
R P VN++ P A + A F A+ +A+ + E + R

Sbjct: 287 EGRRPNA-----VNISTAPYPAFPTDMQAQF---VALNSIANGVGRVIENIFENRF 334

Query: 369 ---TELTKLGASVEEGPDYCIITPPEKL 393
E+ ++GA +E + I+ ++L

Sbjct: 335 MHVDEMLRMGADIEVNGNTAIVRGCDRL 362

>ref|YP_820512.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
thermophilus LMD-9]
gb|ABJ66316.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
thermophilus LMD-9]
Length = 423

Score = 40.0 bits (92), Expect = 0.69, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 121/274 (44%), Gaps = 44/274 (16%)

Query: 15 ISGTVKLPGSKSLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
+SG V + G+K N +L LLAA SEG T + N+ DV+ M +R L ++V+ D

Sbjct: 13 LSGEVVIEGAK---NSVLPPLAATILASEGQTTLTNVPILSDVYTMNNVVRGLDIAVD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127

+ VVV G+ + E V MR+ + + A G+A + G
 Sbjct: 70 E-ENNTVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNGHAKVSMPPGC 120
 Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSI-----SS 180
 + RPI + GL+ +GA ++ +GG + KL G+ S
 Sbjct: 121 TIGSRPIDLHLKLEAMGA-----KITQVGGDITATAEKLKGATIYMDFPSV 167
 Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
 L+MAA LA G IE + I V++ + L+ G + + + ++ IKG +
 Sbjct: 168 GATQNLMMMAATLADGVTTIENAAAREPEI--VDLAI-LLNEMGANVKGAGT-EKLVIKGVK 223
 Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
 ++A ++ D A F+ AA+T G V ++
 Sbjct: 224 SLHGTQHAVIQ-DRIEAGTFMVAAAMTSGNVLK 256

>ref|YP_002928087.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
 BW2952]
 sp|C4ZSS8.1|MURA_ECOBW RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
 AltName: Full=Enoylpyruvate transferase; AltName:
 Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
 Short=EPT
 gb|ACR65746.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Escherichia coli
 BW2952]
 Length = 419

Score = 40.0 bits (92), Expect = 0.70, Method: Compositional matrix adjust.
 Identities = 102/427 (23%), Positives = 170/427 (39%), Gaps = 53/427 (12%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
 +Q ++ G V + G+K+ + L A L+E + N+ +DV + L LG VE
 Sbjct: 6 VQGPTKLQGEVTISGAKNAALPNLFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVE 65
 Query: 69 ADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYV 122
 + G + DA+ +V +F + +++++ A++ A G G
 Sbjct: 66 RN-----GSVHI-DAR-DVNVFCAPYDL-VKTMRASIWALGPLVARFQGQVS 110
 Query: 123 LDGVPVRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
 L G + RP+ + GL+QLGA + G V+ + G L G + + +S
 Sbjct: 111 LPGGCTIGARPVDLHISGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGA 165
 Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
 ++ AA LA G II+ P + T + G K + DR I+G ++
 Sbjct: 166 TVTIMCAATLAEGTT---IIENAAAREPEIVDTANFLITLGAKISGQGT-DRIVIEGVERL 221
 Query: 243 KSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKAFAEVLEMMGAKVTWT 301
 Y V D FL AAI+ G + +L D A+ L GA +
 Sbjct: 222 GG--GVYRVLPDRIETGTFLVAAAISRKIIICRNAQPDTL--DAVLAK-LRDAGADIEVG 276
 Query: 302 ETSVTVTGPPREPFGFRKHLKAIDVNMNMKMP---DVAMTLAVVALFADGPTAIRDVASWR 357
 E +++ + P KA++V P D+ ++ L A+G I +
 Sbjct: 277 EDWISLDMHGKRP-----KAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFIETET---- 326
 Query: 358 VKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAE 417
 V E M EL+++GA E + I EKL+ + D R + + LA C
 Sbjct: 327 VFENRFMHV--PELSRMGAHAEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIA 383
 Query: 418 VPVTIRD 424
 T+ D
 Sbjct: 384 EGTTVVD 390

>ref|ZP_02871516.1| 3-phosphoshikimate 1-carboxyvinyltransferase [candidate division
 TM7 single-cell isolate TM7a]
 Length = 63

Score = 40.0 bits (92), Expect = 0.71, Method: Composition-based stats.
 Identities = 21/49 (42%), Positives = 33/49 (67%)

Query: 339 VVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCI 387
 ++A ++G T I + R+KE++R+ +I+TEL KLGA+V E D II

Sbjct: 1 MLAALSEGETRIINGERLRIKESDRITSIKTELNKLGANVAEEGDSLII 49

>ref|ZP_02959441.1| hypothetical protein PROSTU_01297 [Providencia stuartii ATCC 25827]
gb|EDU60760.1| hypothetical protein PROSTU_01297 [Providencia stuartii ATCC 25827]
Length = 420

Score = 40.0 bits (92), Expect = 0.72, Method: Compositional matrix adjust.
Identities = 94/408 (23%), Positives = 156/408 (38%), Gaps = 45/408 (11%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAA- 73
+ G V + G+K+ + IL A L+E + N+ D+ + L LG VE + +
Sbjct: 12 LEGETVISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTTIKLLNQLGKVERNGSIY 71

Query: 74 --KRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRE 131
R V C V+ + + A + A G+ L G +
Sbjct: 72 VDARNVTEYCAPYDLVKTMRASIWAL-----APLVARFGHGEVSLPGGCAIGA 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL+QLGA + G V+ G L G + + +S ++ AA
Sbjct: 120 RPVDLHISGLEQLGAHIILEDGY---VKATVDGRLKGACIVMD-KVSVGATVTIMTAAT 174

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVE 251
LA G IE P +E T + G K + + DR I+G ++ V
Sbjct: 175 LAEGTTTIE---NAAREPEIEDTANFLNTLGAKITGAGT-DRIVIEGVERLGG-GTYRVL 229

Query: 252 GDASSASYFLAGAAITGGTIVTEGCGTTSLSQGDVKFAEVLEMMGAKVTWTETSVTVTGPP 311
D FL AA++ G V +L D A++ E GAK+ E +++
Sbjct: 230 PDRIETGTFLIAAAVSKGKVVCRNARPDTL--DAVLAKLRE-AGAKIEVGEDWISLDMQG 286

Query: 312 REPFGKRHLKAIDVNMNKMP---DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAI 367
+ P KA+ + P D+ +++ L A+G I + R + I
Sbjct: 287 KRP-----KAVTLRTAPHPGFPTDMQAQFSLNLVAEGAGMITETIF-----ENRFMHI 335

Query: 368 RTELTKLGASVEEGPDYCIITPPEKLNVTIAIDTYDDHRMAMAFSLAAC 415
EL ++GA E + + EKL + D R + + +A C
Sbjct: 336 -PELIRMGAAHEIESNTVLCHGVEKLTGAQV-MATDLRASASLVIAGC 381

>ref|YP_001573242.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:-- str.
RSK2980]
sp|A9MP18.1|MURA_SALAR RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABX24100.1| hypothetical protein SARI_04318 [Salmonella enterica subsp.
arizonae serovar 62:z4,z23:--]
Length = 419

Score = 40.0 bits (92), Expect = 0.72, Method: Compositional matrix adjust.
Identities = 100/425 (23%), Positives = 164/425 (38%), Gaps = 61/425 (14%)

Query: 15 ISGTVKLPGSKSLSNRILLALLAALSEGTTVVNDLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +DV + L LG VE + +
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLRDIDTTIKLLNQLGKVERNGS-- 69

Query: 75 RAVVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
V +V +F + +++++ A++ A G G L G
Sbjct: 70 -----VHIDASQVNVFCAPYDL-VKTMRSI WALGPLVARFGQGQVSLPGGCT 116

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
+ RP+ + GL+QLGA + G V+ + G L G + + +S ++
Sbjct: 117 IGARPVDLHITGLEQLGATIKLEEGY---VKASVDGRLKGAHIVMD-KVSVGATVTIMC 171

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK-----GGQKYK 243
AA LA G II+ P + T + G K + DR I+ GG Y+
Sbjct: 172 AATLAEGTT---IENAAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVEHLGGGIYR 227

Query: 244 SPKNAYVEGDASSASYFLAGAAITGGTIVTEGCGTTSLSQGDVKFAEVLEMMGAKVTWTET 303
V D FL AAI+ G + +L D A+ L GA + E

Sbjct: 228 -----VLPDRIETGTFLVAAAIISRGKIICRNAQPDTL--DAVLAK-LRDAGADIEVGED 278

Query: 304 SVTVTGPPREPFGKHLKAIDVNMNKM-----DVMTLAVVALFADGPTAIRDVASWRVK 359
+++ + P KA++V P D+ ++ L A+G I + V

Sbjct: 279 WISLDMHGKRP-----KAVNVRTAPHPAFPTDMAQFTLLNLVAEGTGFTET----VF 328

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVP 419
E M EL+++GA E + I E L+ + D R + + LA C

Sbjct: 329 ENRFMHV--PELSRMGARAEIESNTVICHGVETLSGAQV-MATDLRASASLVLAGCIAEG 385

Query: 420 VTIRD 424
T+ D

Sbjct: 386 TTVVD 390

>gb|ADY11861.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Spirochaeta sp.
Buddy]
Length = 436

Score = 40.0 bits (92), Expect = 0.73, Method: Compositional matrix adjust.
Identities = 68/278 (24%), Positives = 114/278 (41%), Gaps = 38/278 (13%)

Query: 16 SGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAKR 75
SG V++ G+K+ + L L++ + N+ + EDV M+ L LG +V + A

Sbjct: 20 SGEVQISGNKNSALPCLAAATLLTDEPVHLLNVPDIEDVQVMIELLLDLGSTVVREDAHSY 79

Query: 76 AVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERPIG 135
+ G G+ R+L AV + +L +R P G

Sbjct: 80 TITSG-----SRNGLLKRNLVEAVRGSILLGLLATNDEVRLTPPG 121

Query: 136 DLVVGLKQLGADVDCF--LGTDCPPVRVNGIG-----GLPGGKVKLSGSISSQYLS 184
V+GL++L LG+DC +N +G L G + L + S

Sbjct: 122 GDVIGLRLDLTHFMGLTSLGSDCT---INEVEGIHIRCRHKSIGADIFLDEA-SVTATE 177

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
++MAA LA G+ II+ S P+V+ ++++ G E S +R IKG Q+

Sbjct: 178 NVIMAASLAKGE---SIINNAASEPHVQDVCAMLQKMGCPIEGIGS-NRLRIKQQRLGG 233

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSIQ 282
+ + D F+ A +GG + V+G L+

Sbjct: 234 CE-FRLGSDYMEIGSFIGLAGASGGQLLVKGVQHEHLR 270

>emb|CBZ54886.1| 3-dehydroquinate synthase, related [Neospora caninum Liverpool]
Length = 2867

Score = 40.0 bits (92), Expect = 0.74, Method: Compositional matrix adjust.
Identities = 32/109 (29%), Positives = 54/109 (49%), Gaps = 4/109 (3%)

Query: 320 LKAIDVNMNKMMPDVAMT--LAVVALFADGPTAIRDVA-SWRVKETERMVAIRTELTKL-G 375
LKA +++++PD + + + L + G TA A + K + I +L KL G

Sbjct: 1408 LKATGFHVDELDPDGLLIGDIRMSPLPSGGSTAAPQRALTKHEKNGDEREGIGEDLAKLSG 1467

Query: 376 ASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTIRD 424
P+ + E++ VTA+D+ DHR+AM+F++ V IRD

Sbjct: 1468 QGASTSPEMRDVEKSEQVEVTAVDSESDHRVAMSFALLGLVRTNVGIRD 1516

>ref|ZP_06374618.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni 1336]
gb|EFC30135.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter
jejuni subsp. jejuni 1336]
Length = 418

Score = 40.0 bits (92), Expect = 0.75, Method: Compositional matrix adjust.
Identities = 88/413 (21%), Positives = 169/413 (40%), Gaps = 68/413 (16%)

Query: 9 LQPIKEISGTVKLPGSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
++ +SG V + G+K+ + +++ + L++ ++N+ N D+ ++ L LG V

Sbjct: 6 IEGTNHLSGNVAISGAKNAALPLIVSSILAKNEAKINNVPNVADIKTLISLLENLGAKV- 64

Query: 69 ADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GN 118
F A N IA +R + A++ G G+
Sbjct: 65 -----NFQNNALLNTNTL--NQTIAKYDIVRKMRSILTLGPLLARFGH 107

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + +RPI ++ L+++GA++ G V G L G ++ L I
Sbjct: 108 CEVSLPGGCAIGQRPIDLHLLEALEKMGANIQIKQG-----YVVASGNLKGNEI-LFDKI 160

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISI---PYVEMTLRLMERFG--VKAHSDSWDR 233
+ ++MAA LA G KL+++ P V +++ G +K +D +
Sbjct: 161 TVTGSENIIMAAALAKGKT-----KLLNVAKEPEVVQLCEVLKDAGLEIKGIGTDELE- 213

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
Y G+ + + + + +Y AG AIT +T+ T L + L
Sbjct: 214 IYGSDGELLEFEKFSVIPDRIEAGTYLCAG-AITNSKITLNKVNATHLSAVLA---KLHQ 269

Query: 294 MGAKVTWTETSVTVTGPPEPFRGKHLKAIDVNMNKMMP---DVAMTLAVVALFADGPTA 349
MG + E S+T+ P +E +K +++ ++ P D+ +AL A+G +
Sbjct: 270 MGFETLIAEDSITLL-PAKE-----IKPVEIMTSEYPGFPTDMQAQFMTLALKANGTSI 322

Query: 350 IRDVASVRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYD 402
I + R+ E M +EL ++GA ++ I ++LN + D
Sbjct: 323 IDE---RLFENRFMHV--SELLRMGADIKLNHGIATIVGGKELNAADVMTAD 369

>ref|NP_602347.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
sp|Q8RIQ1.1|MURA_FUSNN RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|AAL93646.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Fusobacterium
nucleatum subsp. nucleatum ATCC 25586]
Length = 423

Score = 40.0 bits (92), Expect = 0.75, Method: Compositional matrix adjust.
Identities = 69/287 (24%), Positives = 120/287 (41%), Gaps = 24/287 (8%)

Query: 13 KEISGTVKLPKSGKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEA-DK 71
K+I+G +K+ GSK+ + I++ + +GT V+ N+ + D+ ++ L +LGL VE D
Sbjct: 11 KKIAGELKVDGSKNSTLPIMIATLVEKGTYVLRNVDPDLRDIRTLVALLESLEVEKLD 70

Query: 72 AAKRAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
+ + + G G D +++++ FL G+ V GG A +
Sbjct: 71 NSYKIINNGLSGAEASYDLVKKMRASFLVMGMLAIEKRGKVALPGGCA-----IG 121

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RP+ + G + LGA ++ G V GL GG + L S ++MAA
Sbjct: 122 ARPVDLHLKGFEALGAKINIEHGY---VEATTENGLIGGNIVLDFP-SVGATENIIMAA 176

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
A G +++ P +E + + G K + R I G K + + +
Sbjct: 177 VKAKGKT---VLENAAKEPEIEDLCNFIKMGAKISVGVT-SRLEIDGVDKLTACEYTII 232

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
+ +Y +A + + G++ V G L F LE MG K
Sbjct: 233 PDRIVAGTYIIA-SILFDGSIKVSIVPEHLS---SFLKLEEMGTK 275

>ref|ZP_05658949.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,230,933]
ref|ZP_05661541.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,502]
ref|ZP_05669775.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,410]
ref|ZP_05673103.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium 1,231,408]
ref|ZP_05713471.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium DO]
ref|ZP_05830927.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium C68]

ref|ZP_06676136.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1162]
ref|ZP_06678941.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1071]
ref|ZP_06701097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium U0317]
ref|ZP_07845259.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133a04]
ref|ZP_07848327.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133C]
ref|ZP_07851892.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0082]
ref|ZP_07854321.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133A]
ref|ZP_07859598.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133B]
ref|ZP_07862994.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133a01]
gb|EEV42282.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium 1,230,933]
gb|EEV44874.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium 1,231,502]
gb|EEV53108.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium 1,231,410]
gb|EEV56436.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium 1,231,408]
gb|EEW63510.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium C68]
gb|EFF21502.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1071]
gb|EFF29539.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium U0317]
gb|EFF35878.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1162]
gb|EFR66793.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133a01]
gb|EFR70137.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133B]
gb|EFR75329.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133A]
gb|EFR78700.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133C]
gb|EFS07381.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0133a04]
gb|EFS09589.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium TX0082]
Length = 423

Score = 40.0 bits (92), Expect = 0.76, Method: Compositional matrix adjust.
Identities = 89/414 (21%), Positives = 167/414 (40%), Gaps = 61/414 (14%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + ++G V + G+K+ + ++ A L++ +++ + + +DVH ++ L +G
Sbjct: 2 KKIVIKGNRPLAGEVTISGAKNSAVALIPAILADSPVILEGVPDIQDVHSLIEILEIMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+V D +E V + + + I SL A+ G G
Sbjct: 62 ATVHFSNNILEI-----DPREVVSIPMPHGKI--NSLRASYFFMGTLLGKFG 107

Query: 119 ATYVLDGVPRMRERPIGDLVVLGKQLGADVD-----CFLGTDCPPVRVNGIGGLPGGKVK 173
A L G + RPI V G + LGA+V +L T+ GL G ++
Sbjct: 108 AVVGLPGGCYLGPRLDLHVKGFEALGA EVTNEHGAMYLRTENK-----GLRGNRIF 159

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +S +++AA A G +I+ P + L+ G K + + D
Sbjct: 160 MD-VVSVGATINVMLAAVAKAKQT---VIENAAAREPEIIDVATLLNNMGAKVRGAGT-DV 214

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
I+G + ++ ++ D A +LA AA G + V+ L+ F L+
Sbjct: 215 IRIEGVETLHGCRH-FMIPDRIEAGTYLALAAAVGNGIKVKNVIFEHLE---SFIKQLQE 270

Query: 294 MGAKVTWTETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTA 349
+G + +E + V + K LK ++ P D+ L + L G +
Sbjct: 271 IGVHMKISEDEIEV-----YPSKELKPANIMTYPYPGFATDLQQPLTALLMTTGTSE 323

Query: 350 IRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
I D + + RV EL ++GA + + I+ P KL+ T + D
Sbjct: 324 IIDTIYAKRVNHV-----PELARMGADITVEGNMIIVGNPNKLHGTEVVASD 370

>ref|ZP_04742949.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseburia
intestinalis L1-82]
gb|EEV01881.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseburia
intestinalis L1-82]
emb|CBL08690.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseburia
intestinalis M50/1]
emb|CBL13930.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Roseburia
intestinalis XB6B4]
Length = 430

Score = 40.0 bits (92), Expect = 0.76, Method: Compositional matrix adjust.
Identities = 98/426 (23%), Positives = 172/426 (40%), Gaps = 43/426 (10%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEVDHYMLGALRTL 64
E+ V++ + G V++ +G+K+ + I+ A +++ T ++NL N D++ +L A+ +G
Sbjct: 2 EQYVIKGGNPLVGEVEIGGAKNAALAIISAAVMTDETVTIENLPNVRDINVLLNAISDIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGI-----AMRSLTAAVTAAGGNAT 120
V+ A V G F L + N I A L A+ +A
Sbjct: 62 AKVDRDLAH----TVKMNGSFI-----HNLVVDNEYIRKIRASYLLGALLGKYKHAE 110

Query: 121 YVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISS 180
L G + RP + G + LGA VD G + L G + L +S
Sbjct: 111 VALPGGCDIGSRPFDLHLKGFRALGATVDIRHGLVVADAK-----QLKGTHIYLD-KVSV 164

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
++MAA +A G +E K P+V + G ++ D I G +
Sbjct: 165 GATINIMMAAAMAEGKTTLENAAKE---PHVVDAAFLNSMGANIRGAGT-DVIRIVGVE 220

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
K + + + + ++ LA AA T G VTV+ L+ A++LE +G +V
Sbjct: 221 KLHKTEYSIIPDQIEAGTFMLAAAA-TKGDVTVKNVIPKHLEA--ISAKLLE-IGCEVEE 276

Query: 301 TETSVTVTGPPREPFGKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAIRD-VASWRV 358
+ +V V +P H + + P D+ +AVV ++G + + + + R
Sbjct: 277 FDDAVRVVSS--KPL--HHTQVTTLPYPGFPTDMQPQIAVVLGISEGTSTVTESIFENRF 332

Query: 359 KETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACAEV 418
K EL ++GA+ + + II E ++ D R A +A A
Sbjct: 333 KYV-----GELARMGANFKVESNIAIIGGIENYTGARVNA-PDLRAGAALVIAGLAAE 384

Query: 419 PVTIRD 424
+T+ D
Sbjct: 385 GITVVD 390

>ref|ZP_05922020.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium TC 6]
ref|ZP_06446956.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium D344SRF]
ref|ZP_06675801.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1039]
ref|ZP_06696332.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1636]
ref|ZP_06698740.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1679]
gb|EEW66097.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium TC 6]
gb|EFD09564.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium D344SRF]
gb|EFF22332.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus
faecium E1636]

gb|EFF25893.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1679]
gb|EFF30921.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterococcus faecium E1039]
Length = 423

Score = 40.0 bits (92), Expect = 0.80, Method: Compositional matrix adjust.
Identities = 89/414 (21%), Positives = 167/414 (40%), Gaps = 61/414 (14%)

Query: 5 EEIVLQPIKEISGTVKLPKSKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTL 64
++IV++ + ++G V + G+K+ + ++ A L++ +++ + + +DVH ++ L +G
Sbjct: 2 KKIVIKGNRPLAGEVTISGAKNSAVALIPAAILADSPVILEGVPDIQDVHSLIEILEIMG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
+V D +E V + + + I SL A+ G G
Sbjct: 62 ATVHFNSNILEI-----DPREIVSIPMPHGKI--NSLRASYFFMGTLGKFG 107

Query: 119 ATYVLDGVPFRMRERPIGDLVVGLKQLGADVD-----CFLGTDCCPVRVNGIGGLPGGKVK 173
A L G + RPI V G + LGA+V +L T+ GL G ++
Sbjct: 108 AVVGLPGGCYLGP RPIDLHVKGFEALGAEVNTNEHGAMYLR TENK-----GLRGNRIF 159

Query: 174 LSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDR 233
+ +S +++AA A G +I+ P + L+ G K + + D
Sbjct: 160 MD-VVSVGATINVMMLAAVKAKGQT---VIENAAREPEIIDVATLLNNMGAKVRGAGT-DV 214

Query: 234 FYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEM 293
I+G + ++ ++ D A +LA AA G + V+ L+ F L+
Sbjct: 215 IRIEGVETLHGCRH-FMIPDRIEAGTYLALAAVNGIKVKNVIFEHLE---SFIAKLQE 270

Query: 294 MGAKVTWTETSVTVTGPPREPFRGKHLKAIDVNMNKM P----DVAMTLAVVALFADGPTA 349
+G + +E + V + K LK ++ P D+ L + L G +
Sbjct: 271 IGVHMKISEDEIEV-----YPSKELKPANIMTYPYPGFATDLQQLTALLMTTGTSE 323

Query: 350 IRD-VASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDTYD 402
I D + + RV EL ++GA + + I+ P KL+ T + D
Sbjct: 324 IIDTIYAKRVNHV-----PELARMGADITVEGNMIIVNGPNKLHGTEVVASD 370

>ref|ZP_02963182.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium animalis subsp. lactis HN019]
ref|YP_002469111.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium animalis subsp. lactis AD011]
ref|YP_002967698.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis B1-04]
ref|YP_002969265.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis DSM 10140]
gb|EDT89340.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium animalis subsp. lactis HN019]
gb|ACL28535.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase
[Bifidobacterium animalis subsp. lactis AD011]
gb|ACS45636.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis B1-04]
gb|ACS47203.1| UDP-N-acetylglucosaminel-carboxyvinyltransferase [Bifidobacterium
animalis subsp. lactis DSM 10140]
gb|ADG32826.1| UDP-N-acetylglucosaminel- carboxyvinyltransferase
[Bifidobacterium animalis subsp. lactis V9]
Length = 442

Score = 40.0 bits (92), Expect = 0.82, Method: Compositional matrix adjust.
Identities = 19/58 (32%), Positives = 38/58 (65%)

Query: 13 KEISGTVKLPKSKSLSNRIILLALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
K ++GT+K+ G+K+ ++ ++ A L+ GT+V+ N+ DVH + LR G++V+ +
Sbjct: 16 KPLNGTIKVRGAKNFVSKAMVAALLAPGTSVLKNVPEIRDVHVSDLLRLHGVNVDVN 73

>ref|ZP_02188226.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [alpha
proteobacterium BAL199]
gb|EDP64943.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [alpha
proteobacterium BAL199]
Length = 439

Score = 39.7 bits (91), Expect = 0.83, Method: Compositional matrix adjust.
Identities = 72/286 (25%), Positives = 122/286 (42%), Gaps = 33/286 (11%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      ++I + + + G + + G+K+ + ++ L+ + N+ D+ M LR LG
Sbjct: 2  DQIRVHGGRPLHGRLPISGAKNAALPLMAAGLLTADPLRLTNVRLADIASMTSILRQLG 61

Query: 65  LSVEA----DKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG---- 116
      + +E D AA + G ED V + +R + A+V G
Sbjct: 62  VRIERMDGIDGAADALTLSG-----EDIISTVAPY-----DLVRKMRASVLVLGPLLA 109

Query: 117 --GNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCCPPVRVNGIGG-LPGG 170
      G AT L G + RP+ + GL +LGA V+ ++ P R +G G L GG
Sbjct: 110  RFGEATVSLPGGCAIGNRPVDLHLKGLSELGAVVEIESGYIKAVAPKGR-DGTGSRLRGG 168

Query: 171  KVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDS 230
      +V +S L+MAA AL D E +++ V++ RL+ G + E + +
Sbjct: 169  RVAFP-FVSVGATENLMAA--ALADGETVLVNSAREPEIVDLA-RLLTAMGAQIEGAGT 224

Query: 231  WDRFYIKGGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGC 276
      D +I+G + + + SY +A ITGG V +EG
Sbjct: 225  -DTIHQGCDTLSGAMHRVIPDRIETGSYAMA-VGITGGDVLLGA 268
```

>ref|YP_141530.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
thermophilus CNRZ1066]
gb|AAV62715.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus
thermophilus CNRZ1066]
Length = 428

Score = 39.7 bits (91), Expect = 0.84, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 121/274 (44%), Gaps = 44/274 (16%)

```
Query: 15  ISGTVKLPGSKSLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      +SG V + G+K N +L LLAA SEG T + N+ DV+ M +R L ++V+ D
Sbjct: 18  LSGEVVIEGAK---NAVLPLLAATILASEGQTTLTNVPILSDVYTMNNVVRGLDIAVD 74

Query: 71  KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127
      + VVV G+ + E V MR+ + + A G+A + G
Sbjct: 75  E-ENNTVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNGHAKVSMPPGC 125

Query: 128  RMRERPIGDLVVGLKQLGADVDCFLGTDCCPPVRVNGIGG-LPGGKVKLSGSI-----SS 180
      + RPI + GL+ +GA ++ +GG + KL G+ S
Sbjct: 126  TIGSRPIDLHLKGLEAMGA-----KITQVGGDITATAEKLKGATIMDFPSV 172

Query: 181  QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      L+MAA LA G IE + I V++ + L+ G + + + + IKG +
Sbjct: 173  GATQNLMAATLADGVTTIENAREPEI--VDLAI-LLNEMGANVKGAGT-EKLVIKGVK 228

Query: 241  KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
      ++A ++ D A F+ AA+T G V ++
Sbjct: 229  SLHGTQHAVIQ-DRIEAGTFMVAAAMTSGNVLK 261
```

>ref|YP_453891.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sodalis
glossinidius str. 'morsitans']
sp|Q2NWI9.1|MURA_SODGM RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
dbj|BAE73486.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Sodalis
glossinidius str. 'morsitans']
Length = 419

Score = 39.7 bits (91), Expect = 0.84, Method: Compositional matrix adjust.
Identities = 100/431 (23%), Positives = 172/431 (39%), Gaps = 53/431 (12%)

```
Query: 5  EEIVLQPIKEISGTVKLPGSKSLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTL 64
      ++ +Q +SG V + G+K+ + IL A L+E + N+ +D+ + L LG
Sbjct: 2  DKFCVQGPTRLSGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTMTKLLGQLG 61
```

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GN 118
VE + G V+ +V ++ + +++++ A++ A G G
Sbjct: 62 ARVERN-----GSVHVD--ASDVDVYCAPYEL-VKTMRASIWALGPLVARFGQ 106

Query: 119 ATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSI 178
L G + RP+ + GL+QLGA + G V+ + G L G + + +
Sbjct: 107 GQVSLPGGCAIGARPVDLHISGLEQLGATIKLEEGY----VKASVDGRLRGAHIVMD-KV 161

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKG 238
S ++ AA LA G II+ P + T + G K + + D+ I+G
Sbjct: 162 SVGATITIMSAAATLATGTT---IIENAAAREPEIVDTANFLITLGAKISGAGT-DKITIEG 217

Query: 239 GQKYKSPKNAY-VEGDASSASYFLAGAAITGGTVTVEGCGTSLQGDVKFAEVLEMMGAK 297
++ Y V D FL AAI+ G V +L D A++ E GA
Sbjct: 218 VERLGG--GVYRVLPDRIETGTFLVAAAISRGRVVCHATRPDTL--DAVLAKLRE-AGAD 272

Query: 298 VTWTETSVTVTGPFPREFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + +++ + P KA+ V P D+ +++ L ADG I +
Sbjct: 273 IAVGDDVSLDMHGQRP-----KAVTVRTAPHPGFPTDMQAQFSLNLVADGTGVITET 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYDDHRMAMAFSLA 413
+ E M EL ++GA E + I E L+ + D R + + LA
Sbjct: 327 ----IFENRFMHV--PELIRMGAAHAEIESNTVICHGVETLSGAQV-MATDLRASASLVLA 379

Query: 414 ACAEVPVTIRD 424
C VT+ D
Sbjct: 380 GCIAEGVTIVVD 390

>ref|YP_001127413.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
thermodenitrificans NG80-2]
ref|ZP_03148474.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
G11MC16]
gb|ABO68668.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus
thermodenitrificans NG80-2]
gb|EDY05417.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Geobacillus sp.
G11MC16]
Length = 428

Score = 39.7 bits (91), Expect = 0.87, Method: Compositional matrix adjust.
Identities = 93/401 (23%), Positives = 152/401 (37%), Gaps = 55/401 (13%)

Query: 14 EISGTVKLPGSKSLSNRILLALASEGTTVVNDNLNSEDVHYMLGALRTLGLSVEADKAA 73
+ GT+K+ G+K+ + ++ A L++ ++ L + DV + + +G S D
Sbjct: 11 RLQGTIKVSGAKNSAVALIPAAILADSPVTIEGLPDISDVRILGSLIEEIGGSFWFD--- 67

Query: 74 KRAVVVGCGGKFPVEDAKEEVQLFLGNAGI----AMRSLTAAVTAAGGNATYVLDGVPRM 129
GK + D V + L N + A L A+ A L G +
Sbjct: 68 -----GKKAIIIDPTNMVSMPLPNGKVKKLRSYYLMGAMLGRFKA VVGLPGGCHL 118

Query: 130 RERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMA 189
RPI + G + LGA V G +R L G ++ L +S +++A
Sbjct: 119 GPRPIDQHIKGFALGATVTNEQG--AIYLRAE---ELRGARIFLD-VVSVGATINIMLA 172

Query: 190 APLALGDVEIEIEIIDKLISIPYVEMTLRLMERFVGKAEHSDSWDRFYIKGGQKYKSPKNAY 249
A A G II+ P + L+ G K + + + D I G +K ++A
Sbjct: 173 AVRAKGR---IIENAAKEPEIIDVATLLSNMGAKIKGAGT-DVIRIDGVEKLSGCRHAI 228

Query: 250 VEGDASSASYFLAGAAITGGTVTVEGC---GTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
+ + +Y +A AA TG V ++ SL ++ V GA W
Sbjct: 229 IPDRIEAGTYMIAAAA-TGNEVVINDNVIPQHVESLTAKLREMGVHVETGADQIWI----- 282

Query: 307 VTGPPREFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRD-VASWRVKET 361
G LKA+DV P D+ L + ADG + + D + S R K
Sbjct: 283 -----CGSDVLKAVDVKTLVYPGFPTDLQQPLTALLTKADGTSVVTDTIYSARFKHI 334

Query: 362 ERMVAIRTELTKLGASVEEGPDYCIITPEKLNVTADITYD 402
+ EL ++ A+V+ IIT P L + D
Sbjct: 335 D-----ELRRMNANVKVEGRSAIITGPVNLQGA VKASD 368

```
>ref|YP_606819.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas
entomophila L48]
sp|Q1IEA0.1|MURA_PSEE4 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
emb|CAK14005.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Enoylpyruvate
transferase) (UDP-N-acetylglucosamine enolpyruvyl
transferase) (EPT) [Pseudomonas entomophila L48]
Length = 421
```

Score = 39.7 bits (91), Expect = 0.87, Method: Compositional matrix adjust.
Identities = 67/301 (22%), Positives = 122/301 (40%), Gaps = 41/301 (13%)

```
Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G +++ G+K+ + IL L++G V NL + D+ M+ +G+ D+
Sbjct: 12 LDGEIRISGAKNAALPILAATLLADGPVTVGNLPHLDITTMIELFGRMGIEPVIDE--- 68

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128
K VE ++ + + +++++ A++ G G A L G
Sbjct: 69 -----KLAVEIDPRTIKTLVAPYEL-VKTMRASILVLGPMVARFGEAEVALPGGCA 118

Query: 129 MRERPIGDLVVGLKQLGADVDC---FLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RP+ + GL+ +GA ++ ++ P GGL G ++S
Sbjct: 119 IGSRPVDLHIRGLEAMGAKIEVEGGYIKAKAPE-----GGLRGAHFFFD-TVSVTGTEN 171

Query: 186 LLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
++MAA LA G ++ P V + G K + + + D I G ++ S
Sbjct: 172 IMMAAALAKGR---SVLQNAAREPEVVDLANFINAMGGKVQGAGT-DTITIDGVERLASA 227

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT----WT 301
+ + +Y +A AA+TGG V V+ T L+ E L+ GA +T W
Sbjct: 228 TYRVMPDRIETGTYLVA-AAVTGGRVKVKDTDPITLEA---VLEKLEAGADITTEDWI 283

Query: 302 E 302
E
Sbjct: 284 E 284
```

```
>emb|CBK86766.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter
cloacae subsp. cloacae NCTC 9394]
Length = 419
```

Score = 39.7 bits (91), Expect = 0.91, Method: Compositional matrix adjust.
Identities = 99/418 (23%), Positives = 160/418 (38%), Gaps = 47/418 (11%)

```
Query: 15 ISGTVKLPGSKSLSNRILLALLSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+ G V + G+K+ + IL A L+E + N+ +D+ + L LG VE + +
Sbjct: 12 LQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLGQLGTVKVERNGSVW 71

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAV---TAAGGNATYVLDGVPRMRE 131
P E K MR+ A+ A G L G +
Sbjct: 72 IDASNVNNSAPYELVK-----TMRASIWALGPLVARFGQGQVSLPGGCAIGA 119

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAP 191
RP+ + GL++LGA++ G V+ + G L G + + +S ++ AA
Sbjct: 120 RPVDLHIFGLEKLGAEIKLEEGY---VKASVNGRLKGAHIVMD-KVSVGATVTIMSAT 174

Query: 192 LALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAY-V 250
LA G II+ P + T + G K + DR I+G ++ Y V
Sbjct: 175 LAEGTT---IIENAAREPEIVDTANFLVALGAKISGQGT-DRITIEGVERLGG--GVYRV 228

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D FL AAI+GG + +L D A+ L GA + E +++
Sbjct: 229 LPDRIETGTFLVAAAISGGKIVCRNAQPDTL--DAVLAK-LHDAGADIEIGEDWISLDMH 285

Query: 311 PREPFGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVA 366
+ P KA++V P D+ ++ L A+G I + + E M
Sbjct: 286 GQRP-----KAVNVRTAPHPAFPTDMAQQTLLNLVAEGTGFIETET----IFENRFMHV 335
```

Query: 367 IRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVPTIRD 424
EL ++GA E + I EKL+ + D R + + LA C T+ D
Sbjct: 336 --PELIRMGAAHEIESNTVICHGVEKLSGAQV-MATDLRASASLVLAGCIAEGTTVVD 390

>ref|ZP_06117045.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
hathewayi DSM 13479]
gb|EFC96364.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
hathewayi DSM 13479]
Length = 416

Score = 39.7 bits (91), Expect = 0.91, Method: Compositional matrix adjust.
Identities = 21/58 (36%), Positives = 36/58 (62%)

Query: 7 IVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 64
I +Q + + G +K+ GSK+ ++ A L +GTTV++N+ +DV MLG L ++G
Sbjct: 4 IEVQGLTPLEGEIKIQGSKNAVLPMMAAILHKGTTVIENVPRIQDVFCMLGILDSIG 61

>ref|YP_001679476.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase [Heliobacterium
modesticaldum Icel]
gb|ABZ83465.1| udp-n-acetylglucosamine 1-carboxyvinyltransferase [Heliobacterium
modesticaldum Icel]
Length = 420

Score = 39.7 bits (91), Expect = 0.91, Method: Compositional matrix adjust.
Identities = 72/303 (23%), Positives = 127/303 (41%), Gaps = 22/303 (7%)

Query: 6 EIVLQPIKEISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGL 65
+IV+ + G +++ +K+ IL+ + L+EG + + ++ + DV L+ +G
Sbjct: 4 KIVVHGGNPLIGHIRVSNNAKNAVLPIILIASILAEGESTIADVPHLADVDTTCALLQHMGC 63

Query: 66 SVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDG 125
V A ++ +V G E+A E + + + + L A + G A L G
Sbjct: 64 EV----ARQKGNIVIRAGSLSGEEAPYEFVRMMRASFLVLGPLLRL----GRAVISLPG 115

Query: 126 VPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA 185
+ RPI + GL+ +GA V G R L G ++ L S
Sbjct: 116 GCAIGSRPINLHLKGLEAMGAKVRLDHGHVEAHC-----RLQGAQIYLDFF-SVGATEN 169

Query: 186 LLMAAPLALGDVEIEIIDLKISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSP 245
L+MAA LA G +I+ P + + R G + + + + I+G ++ +
Sbjct: 170 LMMAASLAKGQT---VIENAAEEPEIVDLANYLNRMGARIKAGT-PVIKIEGVERLQGG 225

Query: 246 KNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSV 305
+ + SY +A AA GG +TV+ ++ L+ MGA V ETS+
Sbjct: 226 AYTPIDRIEAGSYMVAAAA-AGGDLTVDNIIIDHVK---PVIKAKLKMGTATVQEMETSL 281

Query: 306 TVT 308
VT
Sbjct: 282 RVT 284

>ref|YP_001279406.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Psychrobacter
sp. PRwf-1]
sp|A5WCR5.1|MURA_PSYWF RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
AltName: Full=Enoylpyruvate transferase; AltName:
Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
Short=EPT
gb|ABQ93456.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Psychrobacter
sp. PRwf-1]
Length = 432

Score = 39.7 bits (91), Expect = 0.91, Method: Compositional matrix adjust.
Identities = 95/416 (22%), Positives = 164/416 (39%), Gaps = 57/416 (13%)

Query: 15 ISGTVKLPKSGSKSLNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
I+G V + G+K+ + +L L+E T ++N+ + +DV ++ + LG+ +E K
Sbjct: 12 IAGEVTISGAKNAALPLLAAMILAETPTTLNNVPSLQDVRTLKLIAGLGIRIE-----K 66

Query: 75 RAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGVPR 128

```

      +   V C   +E+   +L   +++++ A++   G   G A   L G
Sbjct: 67 QGDTVTCDS-TIENYFAPYEL-----VKTMRASILVLGPLLARFGAEVSLPGGCA 117

Query: 129 MRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLM 188
      + RP+   +   K +GA++   G   R   G L G +   ++   +L+
Sbjct: 118 IGSRPVDQHLKAFKAMGAETVENVY--VKARAPEGGRLLIGCEFSFD-MVTVGGTENVLI 174

Query: 189 AAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNA 248
      AA LA G   +++   P V   ++   G K   +   I+G   +   + +
Sbjct: 175 AATLAKGTT---VLENCAREPEVVDLANMLVAMGAKVSGIGTA-TLTIEGVDSLQGCCEYS 230

Query: 249 YVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVT---WTETS 304
      V   + SY LAGA +T G VT +   LQ   +   E MGA +T   W
Sbjct: 231 VVPDRIETGSY-LAGALMTEGDVTTKNTDPALLQ---PVLQKFEEMGAIITGDDWIRAQ 286

Query: 305 VVTGTGPPREPFGGRKHLKAIDVNMNMKP----DVAMTLAVVALFADGPTAIRDVASWRVKE 360
      +TG P   K +D+   P   D+   L V   A+G + I   S + E
Sbjct: 287 --MTGRP-----KPVDIRTQPHGPFPTDMAQLMAVCCLAEGTSTI----SENIFE 331

Query: 361 TERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
      M   EL ++GA ++   II + N +   D R +M+ +AA A
Sbjct: 332 NRYMHV--PELKRMGADIQVDGHTAIIRGVDSFNAAPV-MATDLRASMSLVMAAAA 384

```

```

>sp|Q5LZI4.2|MURAI_STRT1 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;
  AltName: Full=Enoylpyruvate transferase 1; AltName:
  Full=UDP-N-acetylglucosamine enolpyruvyl transferase 1;
  Short=EPT 1
  Length = 423

```

Score = 39.7 bits (91), Expect = 0.92, Method: Compositional matrix adjust.
Identities = 73/274 (26%), Positives = 121/274 (44%), Gaps = 44/274 (16%)

```

Query: 15 ISGTVKLPKSKLSNRIL-LLAAL---SEGTTVVDNLLNSEDVHYMLGALRTLGLSVEAD 70
      +SG V + G+K   N +L LLAA   SEG T + N+   DV+ M   +R L ++V+ D
Sbjct: 13 LSGEVVIEGAK---NAVLPLLAATILASEGQTTLTNPILSDVYTMNNVVRGLDIAVDFD 69

Query: 71 KAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRS---LTAAVTAAGGNATYVLDGVP 127
      +   VVV   G+   +   E V   MR+   +   + A G+A   + G
Sbjct: 70 E-ENNTVVVDASGEILDQAPYEYVS-----KMRASIVVLGPILARNGHAKVSMPPGC 120

Query: 128 RMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGG-LPGGKVKLSGSI-----SS 180
      + RPI   + GL+ +GA   ++ +GG +   KL G+   S
Sbjct: 121 TIGSRPIDLHLKGLEAMGA-----KITQVGGDITATAEKLKGATIYMDFPSV 167

Query: 181 QYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQ 240
      L+MAA LA G   IE   +   I V++ + L+   G   + + + ++ IKG +
Sbjct: 168 GATQNLMAAATLADGVTTIENAAREPEI--VDLAI-LLNEMGANVKGAGT-EKLVKGVK 223

Query: 241 KYKSPKNAYVEGDASSASYFLAGAAITGGTVTVE 274
      ++A ++ D   A F+ AA+T G V ++
Sbjct: 224 SLHGTQHAVIQ-DRIEAGTFMVAAAMTSGNVLIK 256

```

```

>ref|YP_003578698.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
  capsulatus SB 1003]
gb|ADE86291.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rhodobacter
  capsulatus SB 1003]
  Length = 422

```

Score = 39.7 bits (91), Expect = 0.93, Method: Compositional matrix adjust.
Identities = 89/370 (24%), Positives = 146/370 (39%), Gaps = 37/370 (10%)

```

Query: 15 ISGTVKLPKSKLSNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
      +SG + + G+K+   ++   LSE   + N   D+ M   L +LG V A + K
Sbjct: 12 LSGQIPIAGAKNACLALMPATLLSEEPLTLTNAPRLSDIRTMTQLLASLGAEVTALQDGK 71

Query: 75 RAVVVGCGGKF-PVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMRERP 133
      +   C G   PV D   ++   N + + L A +   G+A   L G   + RP
Sbjct: 72 -VLATSCHGAINPVADYDIVRKMRSN--LVLGPLLARL---GHAVVSLPGGCAIGARP 124

```

Query: 134 IGD LVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLA 193
+ + L LGA+++ G + GGL G ++ + S LMAA LA
Sbjct: 125 MDIHIDALTALGAEIELKEGY----LHAQARGGLKAGVHEMRFA-SVGATENFLMAAVLA 179

Query: 194 LGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYVEGD 253
G ++ P + R + G + E + D I+G + + V
Sbjct: 180 KG---TSVLKNAAREPEIVDLARCLRAMGAEIEGEGTSD-ITIQGVDRHLHGATHPVVTD R 235

Query: 254 ASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGPPRE 313
+Y LA AI GG V G ++ F E L+ G V T + V +
Sbjct: 236 IELGTYMLA-PAICGGEVECLGGRIALVE---SFCEKLDAAGISVEETARGLKV---KR 287

Query: 314 PFGRKHLKAIDVNMNMKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRT 369
GR ++A+DV P D+ + + A+G + + + R+ E M A
Sbjct: 288 KNGR--IRAADVVTPEFPFGFPTDLQAQMMALLCTAEGTSVLEE----RIFENRFMHA--P 339

Query: 370 ELTKLGASVE 379
EL ++GA +E
Sbjct: 340 ELARMGARIE 349

>ref|YP_003317453.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermanaerovibrio
acidaminovorans DSM 6589]
gb|ACZ19171.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Thermanaerovibrio
acidaminovorans DSM 6589]
Length = 430

Score = 39.7 bits (91), Expect = 0.93, Method: Compositional matrix adjust.
Identities = 104/420 (24%), Positives = 169/420 (40%), Gaps = 47/420 (11%)

Query: 5 EEIVLQPIKEISGTVKLPGSKSLSNRILLALLAALSEGTTV-VDNLLNSEDVHYMLGALRTL 63
E +V++ + + G + G+K+ + I+ A L G + ++ + + +D+H M+ L L
Sbjct: 13 ERLVIRGGEPLKGVLTQAQAKNAALPIMASALLRGGRLTIERVPLQDIHTMMDLLDHL 72

Query: 64 GLSVEADKAAKRAVVVGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G+ VE K + + V E+ E L A + + A G A L
Sbjct: 73 GVKVEM-KDHRMTLDVP-----EESWETPASLVKMRASSLVGLPLVARCGRAVLPL 124

Query: 124 DGVPRMRERPIGD LVVGLKQLGADVDCFLGTDCPPVRVNG-IGGLPGGKVKLSGSISSQY 182
G + RPI V GL ++G + G +G GL ++ L S
Sbjct: 125 PGGCAIGSRPIDFHVKGAKMGTSFELVQGA-----FHGRTSGLKPARIYLDLP-SVGA 177

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
L+MAA L G+ +E + + + TLR M GV+ E S I+G ++
Sbjct: 178 TENLMMAASLVEGETILENAAREPEVNLAETLRAM---GVEIEGEGSGT-IKIRGAKEL 233

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTE 302
K + + +++Y LAG ITGG VTV ++ LE G V
Sbjct: 234 KDAHVSVIPDRIEASTYLLAGV-ITGGKVTVRQIVPEHIEA---LCSKLEEAGISVEIKG 289

Query: 303 TSVTVTGPPREPFGRKHLKAIDVNMNMKMP-----DVAMTLAVVALFADGPTAIRDVASW 356
VTV P GR V++ +P D+ + A+G + I +
Sbjct: 290 DDVTYV-----PSGRYR----GVSLKTLPPYGFPTDLQPQIMAAMCLAEGTSVIHE---- 336

Query: 357 RVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYDDHRMAMAFSLAACA 416
V E+ R + + +E ++GA V+ + I+T KL V A D R A L A
Sbjct: 337 SVFES-RFLHV-SEFKRMGAQVDLQGNIAIVTGVSKL-VGAEVHASDLRAGAALVLMGLA 393

>ref|ZP_08077826.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Succinatimonas
hippei YIT 12066]
gb|EFY07749.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Succinatimonas
hippei YIT 12066]
Length = 423

Score = 39.7 bits (91), Expect = 0.94, Method: Compositional matrix adjust.
Identities = 67/269 (24%), Positives = 112/269 (41%), Gaps = 41/269 (15%)

Query: 13 KEISGTVKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K ++G V + G+K+ + ILL L++ V+ N+ + DV+ L LG K
Sbjct: 10 KALNGEVTISGAKNAALPILLCTMLTDEKIVLKNVPDLRDVNTSFKLLEILG-----KKC 64

Query: 73 AKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIA----MRSLTAAVTAAG-----GNATYV 122
K G F V E A + +A ++++ A++ A G G ++
Sbjct: 65 TKIE-----DGVFAVEGAV-----TSNVAPYDLVKTMRASIMALGPLTAFLGESSVS 111

Query: 123 LDGVPRMRERPIGDLVVGLKQLGADVDC---FLGTDCPPVRVNGIGGLPGGKVKLSGSIS 179
L G + RP+ + GL+ +GA ++ ++ P GG G L +S
Sbjct: 112 LPGGCAIGARPVDLHIKGLQSMGAQIELNEGYIHAVAPA-----GGRLRGAEILMEKVS 165

Query: 180 SQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGG 239
L+MAA LA G I + I + LR+M G K D D+ I+G
Sbjct: 166 VTGTENLMMAALAEGTTVIANAAREPEIVDLADCLRMM---GAKVT-GDGS DKIVIEGV 221

Query: 240 QKYKSPKNAYVEGDASSASYFLAGAAITG 268
+K +++ V + +Y +AG A G
Sbjct: 222 KKLHGGEHSIVADRIEAGTYLIAGMATRG 250

>ref|YP_001922680.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
botulinum E3 str. Alaska E43]
ref|ZP_04821307.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
botulinum E1 str. 'BoNT E Beluga']
gb|ACD54205.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
botulinum E3 str. Alaska E43]
gb|EES48592.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Clostridium
botulinum E1 str. 'BoNT E Beluga']
Length = 420

Score = 39.7 bits (91), Expect = 0.95, Method: Compositional matrix adjust.
Identities = 90/409 (22%), Positives = 159/409 (38%), Gaps = 51/409 (12%)

Query: 5 EEIVLQPIKEISGTVKLPKSGSKSLNRIILLAL-SEGTTVVDNLLNSEDVHYMLGALRTL 63
E +++ + G+V++ G+K+ + IL A + SEG V+DN+ + EDVH + L +L
Sbjct: 2 ERLIINGGNILRGSVEINGAKNAAVAILPAAIMASEGKCVIDNIPDIEDVHCLERILESL 61

Query: 64 GLSVEADKAAKRAVVVCGCGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVL 123
G + K + + + + E+V+ A A+ A A VL
Sbjct: 62 GCNTV--KIDNNTLEIDSTNVSNFDASTEDVRRMR-----ASYFFIGALLARFKQAKVVL 114

Query: 124 DGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS----- 177
G + RPI + G + LGA+V G KL G+
Sbjct: 115 PGGCPIGVRPIDQHIKGFALGAEVKIEHGAVIVKAE-----KLQGTNIFFDV 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
+S +++AA LA G +E + K P+V + G + + + D I+
Sbjct: 163 VSVGATINVMIAATLADGVTTLENVAKE---PHVVDMANFLNSMGANIKGAGT-DVIRIQ 218

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVVEGCGTTSLQGDVKFAEVLEMMGAK 297
G +K K + + D A F+ A T G V V L+ + L+ MGA
Sbjct: 219 GVEKLKGCSSVIP-DQIEAGTFMIAAVATRGDVYVRNVIPKHLE---SISAKLKEMGAV 274

Query: 298 VTWTETSVTVTGPPREPFGKRHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDV 353
+ + + V LKA++V P D+ ++ + G + + +
Sbjct: 275 IEEDDDCIRVCAS-----DELKAVNVKTPYPGFPTDIQQPMSALLSVISGKSIVTE- 326

Query: 354 ASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADITYD 402
+ W + EL K+GA+++ II ++L + D
Sbjct: 327 SIWENRHKH-----IDELKKMGANIKVEGRVAIIIEGVKRLTGAVVKATD 370

>ref|NP_799037.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus RIMD 2210633]
ref|ZP_01991953.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ3810]
ref|ZP_05776251.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus K5030]
ref|ZP_05891689.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AN-5034]
ref|ZP_05904203.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus Peru-466]
ref|ZP_05908675.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio


```

parahaemolyticus AQ4037]
sp|Q87LF4.1|MURA_VIBPA RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase;
  AltName: Full=Enolpyruvate transferase; AltName:
  Full=UDP-N-acetylglucosamine enolpyruvyl transferase;
  Short=EPT
dbj|BAC60921.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus RIMD 2210633]
gb|EDM58175.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ3810]
gb|EFO37133.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus Peru-466]
gb|EFO42800.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AN-5034]
gb|EFO45070.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus AQ4037]
gb|EFO48716.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Vibrio
parahaemolyticus K5030]
Length = 418

```

Score = 39.7 bits (91), Expect = 0.96, Method: Compositional matrix adjust.
Identities = 97/422 (22%), Positives = 164/422 (38%), Gaps = 51/422 (12%)

```

Query: 13 KEISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
      K + G V + G+K+ + IL + L+E V N+ + D+ + L+ LG V +
Sbjct: 11 KPLVGEVTISGAKNAALPILFASILAEPEVEANVPHLRDIDTTMELLKRLGAKVSRN-- 68

```

```

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----GNATYVLDGV 126
      G V+ + + + + + + + + + + A++ A G G L G
Sbjct: 69 -----GSVHVPSS--INEYCAPYDL-VKTMRASIWALGPLVARFGQGQVSLPGG 115

```

```

Query: 127 PRMRERPIGDLVVLKQLGADVDCFLGTDCCPPVRVNGIGGLPGGKVKLSGSISSQYLSAL 186
      + RP+ + GL+QLGA + G V+ G L G + + +S +
Sbjct: 116 CAIGARPVDLHITGLEQLGATITLEDGY---VKAEDVGRCLKGAHIVMD-KVSVGATITI 170

```

```

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
      + AA LA G +D P + T + + G K + + D I+G ++ K
Sbjct: 171 MCAAALAEAGTT---TLDNAAREPEIVDTADFLNKLGAKISGAGT-DTITIEGVERLGGGK 226

```

```

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
      ++ V D FL AA++GG V C T+ LE GA V E ++
Sbjct: 227 HSVV-ADRIETGTFLVAAAVSGGKV---CRNTNGHLLLEAVLAKLEEAGALVETGEDWIS 282

```

```

Query: 307 VTGPPREPFPGRKHLKAIDVNMNKMP----DVAMTLAVVALFADGPTAIRDVASWRVKETE 362
      V RE LKA+ + P D+ ++ + A G I + + E
Sbjct: 283 VDMTDRE-----LKAVSIRTAPHPGFPPTDMQAQFTLLNMMAKGGGVITET---IFENR 332

```

```

Query: 363 RMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTADTYDDHRMAMAFSLAACAEVPVTI 422
      M EL ++GA E + I E L+ + D R + + +A C TI
Sbjct: 333 FMHV--PELMRMGAKAEIEGNTVICGDVESLSGAQV-MATDLRASASLVIAGCIAKGETI 389

```

```

Query: 423 RD 424
      D
Sbjct: 390 VD 391

```

```

>ref|YP_003273072.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Gordonia
bronchialis DSM 43247]
gb|ACY21179.1| UDP-N-acetylglucosamine1-carboxyvinyltransferase [Gordonia
bronchialis DSM 43247]
Length = 418

```

Score = 39.7 bits (91), Expect = 0.97, Method: Compositional matrix adjust.
Identities = 106/441 (24%), Positives = 173/441 (39%), Gaps = 61/441 (13%)

```

Query: 14 EISGTVKLPKSGKSLSNRILLALASEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAA 73
      ++G V + G+K+ +++ A L+EGTTV+ N DV M LR LG +V A +
Sbjct: 12 RLAGEVSVGGAKNSVLKLMMAALLAEGTTVLTAPEIADVPLMADVLRGLG-AVVATEGD 70

```

```

Query: 74 KRAVVVGCGGKFPVE-DAKEEVQLFLGNAGIAM-RSLTAAVTAAGGNATYVLDGVPRMRE 131
      + KF + DA + + + G M R A V GG+A +
Sbjct: 71 TVTITAPAEKPHADFDAVRQFRASVCVLGPLMARCRRAVVALPGGDA-----IGS 121

```

Query: 132 RPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSA-----L 186
RP+ GL+ LGA G C + + G P I+ ++ S +
Sbjct: 122 RPLDMHQSLRALGAHSSIEHG--CVVAEADALIGAP-----IALEFPSVGATENI 170

Query: 187 LMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPK 246
LMAA LA G+ ID P + ++++ G + + + + ++G ++ P
Sbjct: 171 LMAAVLAEGET---TIDNAAREPEIIVDLCEMLQQMGAQIDGAGT-STLTVRGVERLH-PT 225

Query: 247 NAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVT 306
V GD + + AA+T G VTV G LQ L GA+V
Sbjct: 226 THRVVGDRIVGATWGIAAAMTRGDVTVHGVREHLQ---LVLNKLVDTGARVDTFSDGFR 282

Query: 307 VTGPPREPFGGRKHLKAIDVNMNKM-----DVAMTLAVVALFADGPTAI-RDVASWRVK 359
V R + VN++ +P D+ +A A+G + I +V R +
Sbjct: 283 V-----RHDSRPTAVNVSTLPFGPPTDLQPMAGLAAIAEGMSVITENVFEARFR 333

Query: 360 ETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTATIDTYDDHRMAMAFSLAACAEVP 419
E MV +LGA + +I E+L+ + D R LA
Sbjct: 334 FVEEMV-----RLGADARTDGHHAIVIRGVERLSSAPV-WCSDIRAGAGLVLAGLVADG 385

Query: 420 VT-IRDPGCTRKTFPDYFDVL 439
VT + D + +P + ++L
Sbjct: 386 VTEVHDVEHIDRGYPHFVEIL 406

>ref|YP_001483244.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus str. MIT 9215]
gb|ABV49658.1| UDP-N-acetylglucosamine enolpyruvyl transferase [Prochlorococcus
marinus str. MIT 9215]
Length = 437

Score = 39.7 bits (91), Expect = 0.97, Method: Compositional matrix adjust.
Identities = 85/372 (22%), Positives = 151/372 (40%), Gaps = 37/372 (9%)

Query: 13 KEISGTVKLPKSGKSLNRILLAAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKA 72
K + G +++ G+K+ + ++ + LS+G + N+ DV M L T+G+++++
Sbjct: 26 KFLKGNIEISGAKNSALVLMASILSKGEINLFNVPQISDVSIMSKLLITMGINIKSN-- 83

Query: 73 AKRAVVVGCGGKFPVEDAKEEVQLF--LGNAGIAMRSLTAAVTAAGGNATYVLDGVPRMR 130
A + + P +D LF L NA + A G A L G +
Sbjct: 84 ANQLTINTKEIIIPPQD-----LFFDLNLRVSVFCCIGPILARFGKAKIPLPGGCSIG 137

Query: 131 ERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAA 190
RPI + + LK+LG + +N L G + S LLMAA
Sbjct: 138 SRPIDEHIDSLKKGIVIFQ-YRNNYVIKVINPQKRLGSSINFKCK-SVGATETLLMAA 195

Query: 191 PLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
LA G I++ P + ++ G + + + S + I+G + K +
Sbjct: 196 SLAKGKT---ILNNAEEPEIVDLANMLNLMGARIKAGS-ECITIEGVESLKGCDYTVI 251

Query: 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTWTETSVTVTGP 310
D A FL AAIT T+++ C L+ + LE+ G K ++ + +
Sbjct: 252 P-DRIEAGTFLAAAITRSTISLFPCEPNHLKALI---NKLELCGCKFEYSNFCLKII-- 305

Query: 311 PREPFGGRKHLKAIDVNMNKMPPDVAMTLA--VVALFA--DGPTAIRDVASWRVKETERMVA 366
P + L ++D+ PD L +AL A +G + I++ RM
Sbjct: 306 PNQI-----LNSVDITGPFDPFPTDLQAPFMALMATNGISKIKETVF-----ENRMHH 355

Query: 367 IRTELTKLGASV 378
++ EL +GA +
Sbjct: 356 VK-ELNHMGAKI 366

>gb|EGD33360.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Capnocytophaga
sp. oral taxon 338 str. F0234]
Length = 436

Score = 39.7 bits (91), Expect = 0.98, Method: Compositional matrix adjust.
Identities = 66/279 (23%), Positives = 124/279 (44%), Gaps = 35/279 (12%)

Query: 15 ISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVEADKAAK 74
+SG++ G+K+ + ++L L L++ + N+ + DV+ ++G L LG+ ++ K AK
Sbjct: 12 LSGSITPQGAKEALQVLCVLLTDEKVTIHNIPDILDVNKLIGLLENLGVKIQ--KLAK 69

Query: 75 RAVVVGCGGKFPVEDAKEEVQL-FLGNAGIAM--RSLTAAVTAAGG-NATYVLDGVPRMR 130
G + + +E+ + +L A A +SL ++ G A + G+P
Sbjct: 70 -----GSYSFQ--ADEINMDYLSTAFAQQSQSLRGSILILGPLLARFGYGGIP--- 116

Query: 131 ERPIGDLVVGLKQLGADVDCFL-----GTDCPPVRVNGIGGLPGGKVKLSGSISSQY 182
+P GD +G ++L D F+ + VN GL G + L + S
Sbjct: 117 -KPGGD-KIGRRRLDTHFDGFKLGATFTYSQEKHYTVAPEGLRGNIIILLDEA-SVTG 173

Query: 183 LSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKY 242
+ ++MAA LA G + PY++ R++ R G + E S + IKG +K
Sbjct: 174 TANIVMAASLAEGTTTLY--NAACEPYLQQVCRMLNRMGAIEGIGS-NLLTIKGVKKL 229

Query: 243 KSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSL 281
+ + + D ++ AA+T +T++ G L
Sbjct: 230 RGCTHRILP-DMIEIGSWIGMAAMTQSELTIKEVGWEHL 267

>ref|ZP_05069943.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Pelagibacter sp. HTCC7211]
gb|EDZ60942.1| 3-phosphoshikimate 1-carboxyvinyltransferase [Candidatus
Pelagibacter sp. HTCC7211]
Length = 439

Score = 39.7 bits (91), Expect = 0.99, Method: Compositional matrix adjust.
Identities = 20/46 (43%), Positives = 29/46 (63%)

Query: 23 GSKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTLGLSVE 68
G KS+S R +L A+L+ G + NLL SEDV + +R LG+ V+
Sbjct: 22 GDKSISIRWVLFASLANGNSKAKNLLISEDVKAIAKTKIRKLGIKVD 67

>ref|YP_001133588.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
gilvum PYR-GCK]
gb|ABP44800.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium
gilvum PYR-GCK]
Length = 417

Score = 39.7 bits (91), Expect = 0.99, Method: Compositional matrix adjust.
Identities = 96/373 (25%), Positives = 143/373 (38%), Gaps = 46/373 (12%)

Query: 4 AEEIVLQPIKEISGTVKLPKSGKSLSNRILLLAALSEGTTVVDNLLNSEDVHYMLGALRTL 63
+E V+ +SG V + G+K+ +++ A L+EGT+ + N + DV M LR L
Sbjct: 2 SERFVVTGGCRLSGEVAVGGAKNSVLKMAAALLAEGTSTITNCPDILDVPLMAEVLRLG 61

Query: 64 GLSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAG-----G 117
G +VE + R P DA A+R A+V G
Sbjct: 62 GATVELEGDVVRIT----SPDEPKYDADF-----AVRQFRASVCVLGPLVGRCK 107

Query: 118 NATYVLDGVPRMRERPIGDLVVGLKQLGADVDCFLGTDCPPVRVNGIGGLPGGKVKLSGS 177
A L G + RP+ GL+QLGA C + C + L G +++L
Sbjct: 108 KARVALPGGDAIGSRPLDMHQAGLRQLGA--RCNIEHGCVVAEAD---HLHGAEIQLEFP 162

Query: 178 ISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIK 237
S +LMAA LA G + I P V ++ + G + + S I
Sbjct: 163 -SVGATENILMAAVLADG---VTIHNAAAREPDVVDLCTMLNQMGAVTGAGSSTLTII- 217

Query: 238 GGQKYKSPKNAYVEGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
G P V GD A+ + AA+T G ++V G LQ L GA
Sbjct: 218 -GVDRHLPHTEHRVIGDRIVAATWGIAAAMTRGDISVTGVDPAHLQ---LVLHKLHDAGAT 273

Query: 298 VTWTETSVTVTGPPREPFGKHLKVIDNMNKMPPDVAMTLAVVAL----FADGPTAI-RD 352
VT ++ V R KA++V P L +A+ ADG + I +
Sbjct: 274 VTQSDDGFRVVQYERP-----KAVNVATLFPFGFPTDLQPMAGLAADGTSMTEN 326

Query: 353 VASWRVKETERMV 365
V R + E M+
Sbjct: 327 VFEARFRFVEEMI 339

>ref|YP_002929553.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium
eligenis ATCC 27750]
gb|ACR71106.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Eubacterium
eligenis ATCC 27750]
Length = 431

Score = 39.7 bits (91), Expect = 1.00, Method: Compositional matrix adjust.
Identities = 63/270 (23%), Positives = 109/270 (40%), Gaps = 18/270 (6%)

Query: 5 EEIVLQPIKEISGTVKLPKSGKSLSNRILLALLAALSEGTTVDNLLNSEDVHYMLGALRTL 64
E+ V++ + G V + G+K+ + IL A +++ T ++N+ N D +L A+ +G
Sbjct: 2 EQYVVKGGVPLRGKVSIGGAKNAALGILAAAIMTDDTVTIENVPNVRDTRVLLQAIEGIG 61

Query: 65 LSVEADKAAKRAVVVGCGGKFPVEDAKEEVQLFLGNAGIAMRSLTAAVTAAGGNATYVLD 124
V+ +V + G + ++ A L A+ A L
Sbjct: 62 AKVKY--VYNNVQINGGSICDTNVEYDYIRKIR-----ASYLLGALLGKYNEAHVALP 114

Query: 125 GVPRMRERPIGDLVVGLKQLGADVDCFLGTDCCPVRVNGIGLPGGKVKLSGSISSQYLS 184
G + RPI + G K LGADVD DC V L G V ++
Sbjct: 115 GGCNIGSRPIDQHIGFKALGADVD----IDCGVVHAKA-EKLTGAHVYFD-VVTVGATI 168

Query: 185 ALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKGGQKYKS 244
L+MA+ +A GD I++ P++ + G + + + D IKG ++
Sbjct: 169 NLMMAASMAEGDT---ILENAKEPHIVDVANFLNSMGANIKGAGT-DVIRIKGVKRLHG 224

Query: 245 PKNAYVEGDASSASYFLAGAAITGGTVTVE 274
+ + D A F+ AA T G V ++
Sbjct: 225 CTYSIIP-DQIEAGTFMMAAAATHGDEVVIQ 253

>gb|ABC84481.1| putative 5-enolpyruvylshikimate-3-phosphate synthase [Streptococcus
suis]
Length = 160

Score = 39.7 bits (91), Expect = 1.00, Method: Compositional matrix adjust.
Identities = 39/124 (31%), Positives = 68/124 (54%), Gaps = 11/124 (8%)

Query: 179 SSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLMERFGVKAHSDSWDRFYIKG 238
S+Q SAL+ AA A G E I++K ++ + E ++ +FG + E + R I+G
Sbjct: 11 SAQVKSALIFAALQAEG--ESVIVEKELTRNHTE---DMIVQFGGQLEVNGKEIR--IQG 63

Query: 239 GQKYKSPKNAYVEGDASSASYFL-AGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAK 297
GQ++ + + V GD SSA+++L AG I G + +E G + + +V++ MG K
Sbjct: 64 GQEFIA-QEITVPGDISAFAFLVAGLIIPGSKIVLENVGINETRTGI--LDVIKAMGGK 120

Query: 298 VTWT 301
+T +
Sbjct: 121 MTL 124

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Mar 24, 2011 1:21 AM
Number of letters in database: 4,577,707,244
Number of sequences in database: 13,366,630

Lambda	K	H
0.318	0.135	0.389

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 13366630
Number of Hits to DB: 3,935,045,207
Number of extensions: 162048026
Number of successful extensions: 443489

Number of sequences better than 1.0: 4088
Number of HSP's gapped: 431036
Number of HSP's successfully gapped: 4156
Length of query: 445
Length of database: 4,577,707,244
Length adjustment: 142
Effective length of query: 303
Effective length of database: 2,679,645,784
Effective search space: 811932672552
Effective search space used: 811932672552
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)